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Thesis Title: **Occurrence of *Staphylococcus aureus* in a commercial poultry plant and poultry farm**

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Occurrence of *Staphylococcus aureus* in a commercial poultry plant and poultry farm

A Thesis submitted in partial fulfilment of the requirement for the degree of Master of Food Technology

Massey University

Albany, New Zealand

Cheng QIAN

April, 2015

ABSTRACT

Poultry products are popular due to their healthier image compared to red meats. However, the products are susceptible to contamination by many spoilage microorganisms and pathogens, including *Staphylococcus aureus, Campylobacter* spp.*, Clostridium perfringens*, *Yesinia enterocolitica*, *Pseudomonas* spp. and *Escherichia coli.* In New Zealand (NZ), foodborne outbreaks caused by *S. aureus* infections may be uncommon but serious.

S. aureus can grow in a wide range of pH, temperature and salt concentrations. Some strains of *S. aureus* can produce heat-resistant enterotoxins, while others may be methicillin-resistant which can result in hospital-linked and community-linked infections. Raw (fresh) and frozen poultry products have been associated with *S. aureus* contamination in many countries. The common contamination sources of *S. aureus* in poultry products have been linked to poor hygiene of food handlers, processing equipment and skins of live chickens. The aim of this project was to identify potential contamination sources of products and processing equipment by *S. aureus* from a selected processing plant to the farm in Auckland, New Zealand.

Poultry meat samples were collected from Final Products, Frozen Mechanically Separated Meat (MSM), Frozen Skin, Frozen Skin-on Breast Fillet (SO BF) (further processing plant), Fresh MSM, Fresh Skin, Fresh SO BF (secondary processing plant). Swab samples were collected from the MSM conveyor, inside the Mechanically Deboning Machine (MDM), the Skinner Conveyor (secondary processing plant), Rubber Fingers in Pluckers (primary processing plant), skin and nostrils of live chicken at the farm. Viable cell counts of *S. aureus* were enumerated using Petrifilm™ Staph Express Count Plate to determine the contamination level of the samples. Isolates of *S. aureus* was confirmed by Gram-stain and coagulase-positive test. Six main sampling sites were selected for further investigation which comprised final products, Fresh MSM, Fresh Skin, Fresh SO BF, Rubber Fingers and live chickens. Ten representative *S. aureus* isolates grown on Petrifilms were randomly selected from samples of each of the six main sampling sites. Polymerase Chain Reaction (PCR) and Multilocus Sequence Typing (MLST) were then used to detect the presence of staphylococcal enterotoxins and identify sequence types of the sixty *S. aureus* isolates, respectively. eBURST was used to identify the relatedness of the sequence types. Also, the contamination sources of *S. aureus* in the samples were traced based on the sequence types of the sixty isolates.

In the further processing plant, all final product samples (n=36) were contaminated with *S. aureus*. Frozen MSM had the highest contamination level ranging from 2.00±1.02 to 2.50±0.48 Log_{10} CFU/g. Similarly, *S. aureus* in Fresh MSM from the secondary processing plant contained the highest *S. aureus* cell counts (1.79±0.25 to 2.85±0.51 Log_{10} CFU/g), followed by Fresh SO BF (1.85±0.56 to 2.33±0.50 Log_{10} CFU/g) and Fresh Skin (1.72±0.60 to 2.15 [1.67, 3.37] Log_{10} CFU/g). In primary processing, Rubber Fingers in Plucker 1 had the highest level of *S. aureus* (2.46±0.50 Log_{10} CFU/swab). *S. aureus* counts of chicken skin ranged from 1.00 [0.79, 1.48] to 1.36±0.45 Log_{10} CFU/swab, while nostrils contained 1.00 [0.85, 1.48] to 1.59±0.70 Log_{10} CFU/swab. Cell counts of live chicken increased with the age (first, third, sixth week) of the chicken. Eight different types of enterotoxin genes (*seg*, *sei*, *seh*, *sek*, *sel*, *sem*, *sen*, *seo*) were identified. Of the 60 *S. aureus* isolates, 59 were positive for at least two different staphylococcal enterotoxins. Six different sequence types were identified (ST5, ST2594, ST101, ST83, ST398, ST1). Sequence types of isolates that had at least five identical loci were assigned to a single clonal complex (CC). In this study, ST5, ST83 and ST2594 belonged to CC 5 with ST5 being the clonal ancestor.

MSM had the highest *S. aureus* contamination level due to cross-contamination inside the MDM, therefore, a proper hygiene and regular cleaning routine inside the MDM is recommended. The results suggested that the sources of *S. aureus* contamination in the final poultry products could be Fresh MSM, Fresh Skin, Fresh SO BF (secondary processing), Rubber Fingers in the Pluckers (primary processing) and live chickens at the farm. Chicken skin from live chickens at farm was most likely the origin of contamination of final products and equipment by *S. aureus*. Since not all the identified strains that colonised on the live chickens were traced back to the final products, further investigations on other potential contamination sources such as gloves and knifes used at the processing plant, feeders and drinkers at the farm are recommended.

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LIST OF ABBREVIATIONS

AOAC	=	Association of Official Analytical Chemists
ATCC	=	American Type Culture Collection
BFG	=	Bovine Fibrinogen Agar
BHI	=	Brain Heart Infusion
BLAST	=	Basic Local Alignment Search Tool
BPA	=	Baird-Parker Agar
CC	=	Clonal Complex
CCPs	=	Critical Control Points
ClO_2	=	Chlorine Dioxide
DNA	=	Deoxyribonucleic Acid
eBURST	=	Based Upon Repeat Sequence Types
EDTA	=	Ethylenediaminetetraacetic Acid
ELISA	=	Enzyme-linked Immuno-sorbent Assay
ELISA-M	=	Enzyme-linked Immuno-sorbent Assay Membrane
ELISA-T	=	Enzyme-linked Immuno-sorbent Assay Tube
ESR	=	Environmental Science and Research
FSMS	=	Food Safety Management System
HACCP	=	Hazard Analysis and Critical Control Points
HOCI	=	Hypochlorite
ISO	=	International Organization for Standardization
MAP	=	Modified Atmosphere Packaging
MAS	=	Microbial Assessment Scheme
MDCM	=	Mechanically Deboned Chicken Meat
MDM	=	Mechanically Deboning Machine
MRSA	=	Methicillin-resistant *Staphylococcus aureus*
MSA	=	Mannitol Salt Agar
MSM	=	Mechanically Separated Meat
NaCl	=	Sodium Chloride
PSE	=	Pale Soft Exudative
PSE	=	Petrifilm Rapid Staph Express Count

PCR	=	Polymerase Chain Reaction
MLST	=	Mutillocus Sequencing Typing
MPN	=	Most Probable Number
RPFA	=	Rabbit Plasma Fibrinogen Agar
RPLA	=	Reverse Phase latex agglutination
SEs	=	Staphylococcal Enterotoxins
SEA (*sea*)	=	Staphylococcal Enterotoxin A
SEB(*seb*)	=	Staphylococcal Enterotoxin B
SEC(*sec*)	=	Staphylococcal Enterotoxin C
SED(*sed*)	=	Staphylococcal Enterotoxin D
SEE(*see*)	=	Staphylococcal Enterotoxin E
SEG(*seg*)	=	Staphylococcal Enterotoxin G
SEH(*seh*)	=	Staphylococcal Enterotoxin H
SEI(*sei*)	=	Staphylococcal Enterotoxin I
SEJ(*sej*)	=	Staphylococcal Enterotoxin J
SEK(*sek*)	=	Staphylococcal Enterotoxin K
SEL(*sel*)	=	Staphylococcal Enterotoxin L
SEM(*sem*)	=	Staphylococcal Enterotoxin M
SEN(*sen*)	=	Staphylococcal Enterotoxin N
SEO(*seo*)	=	Staphylococcal Enterotoxin O
SEP(*seo*)	=	Staphylococcal Enterotoxin P
SEQ(*seq*)	=	Staphylococcal Enterotoxin Q
SER(*ser*)	=	Staphylococcal Enterotoxin R
SET-EIA	=	Staphylococcal Enterotoxin Enzyme-linked Immuno-sorbent Assay
SET-RPLA	=	Staphylococcal Enterotoxin Reverse Phase Latex Agglutination
SEU(*seu*)	=	Staphylococcal Enterotoxin U
SFP	=	Staphylococcal Food Poisoning
SLVs	=	Single-locus variants
ST	=	Sequencing Type
UK	=	United Kingdom
USA	=	United States
UV	=	Ultraviolet

1. Introduction

The origin of domesticated chickens dates back to thousands of years ago in Southeast Asia (Daghir, 2008; West & Zhou, 1988). Domestication of chickens is a process which humans raise chickens aimed to enhance desired traits, nowadays mostly for commercial trade due to huge demand of poultry meat products (Wiren et al., 2009). Poultry products, such as eggs, fresh chicken and roasted turkey, have become sources of daily meals worldwide (Davies & Board, 1998). In 2007, eggs and chickens processed products were produced by about 145,615 farms in America (EPA, 2013). In New Zealand, poultry production increased from 111,884 to 173,263 tonnes between 2000 and 2012. Chicken products remain the most favourite meat-based meals in New Zealand (PIANZ, 2010).

Chicken products are susceptible to contamination by many pathogens or spoilage microorganisms. Farmers raise chickens on litter floors which have higher risks of being contaminated with Enterobacteriaceae, such as *Salmonella, Escherichia coli* and *Yesinia enterocolitica* (Davies & Board, 1998). Waldroup (1996) reported the incidence of common pathogens on raw poultry products including *Campylobacter* spp*., Clostridium perfringens*, *Staphylococcus aureus*, *Yesinia enterocolitica* and *Pseudomonas*. *Campylobacter*, *Salmonella, Escherichia coli*, *Listeria monocytogenes* and *Staphylococcus aureus* are human pathogens which means that the contaminations are mainly attributed to poor food handling or cross-contamination during food processing (Davies & Board, 1998). The obsence of *S. aureus* is an indicator of good hygiene and correct handling practice (Jacxsens et al., 2011)

S. aureus strains are Gram-positive cocci and facultative anaerobes (Roberts & Greenwood, 2002). They however, grow better in the presence of adequate oxygen than anaerobic environment (Ministry of Primary Industry, 2001). *S. aureus* can grow in a wide range of pH (4.2 to 9.3), temperature (7°C to 48.5°C) and salt concentrations up to 15% (Bhatia & Zahoor, 2007; Kérouanton et al., 2007). The optimum temperature for their growth is 37°C. Low water activity is not an inhibiting factor for *S. aureus* to grow and produce staphylococcal

enterotoxins (SEs) (Ministry of Primary Industry, 2001). Raw (fresh) and frozen poultry have been associated with *S. aureus* in many countries. In Japan, about 66% of raw chicken meats were contaminated with *S. aureus* in 2004 (Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al., 2005). It grows well in processed meat as some normal organisms which may be competitive to *S. aureus* are killed or inhibited during processing (Ministry of Primary Industry, 2001).

Some strains of *S. aureus* have the ability to produce one or more staphylococcal enterotoxins (SEs), which are the main causes of foodborne illness (Lee, 2006; Matyi et al., 2013; Notermans et al., 1982). Many food poisoning issues caused by consuming contaminated raw poultry meat or poultry products are attributed to SEs (Kérouanton et al., 2007). *S. aureus* can synthesise SEs at temperature between 10 to 45°C, at pH of 4.8 to 9.0, under a water activity ranging from 0.86 to 0.99 (Ministry of Primary Industry, 2001). There are various SEs that have been reported most of which are stable even under a heat treatment of routine sterilisation in commercial processing (Balaban & Rasooly, 2000; Bhatia & Zahoor, 2007).

Also, there has been a great concern about methicillin-resistant *S. aureus* (MRSA) all over the world as it can cause not only hospital-linked infections but also community-acquired infections (De Boer et al., 2009; Kitai, Shimizu, Kawano, Sato, Nakano, Uji, et al., 2005). MRSA is regarded as the most prevalent nosocomial pathogen which is isolated from human (Lee, 2003; Melter et al., 1999). Animals can be carriers of this pathogen as well. The presence of MRSA strains in some food products has been detected recently, such as meat products including raw chicken meat, turkey, lamb, pig meat (De Boer et al., 2009; Kitai, Shimizu, Kawano, Sato, Nakano, Uji, et al., 2005; Kwon et al., 2006) and dairy products (Normanno et al., 2007). Some isolated MRSA from raw meat were reported to be resistant to some antibiotics (Pesavento et al., 2007), such as aminoglycosides, macrolides, chloramphenicol and tetracycline (Mandel et al., 2000). Therefore, MRSA is considered as a potential causative agent that is responsible for staphylococcal food safety problems. In New Zealand, about 7% of *S. aureus* isolates were methicillin-resistant (Ministry of Health, 2002).

Food safety issues can result in huge economic losses for the poultry manufacturer as well as issues of affecting their well-developed reputations (Matyi et al., 2013). According to Australia New Zealand Food Standards 1.6.1, the microbiological limit of coagulase-positive *Staphylococcus* is log 3 CFU/g (ComLaw, 2012). In Australia, 22 people were reported ill due to Staphylococcal food poisoning (SFP) at a buffet in June, 2012 and 20 of them had eaten chicken stir-fry (Pillsbury et al., 2013). New Zealand is one of the developed countries with high reports of the incidence rate for *S. aureus* infections (Williamson et al., 2014). Between 1989 to 1999, 24 outbreaks of staphylococcal foodborne illness were attributed to the consumption of contaminated yogurt, hot ham sandwiches, chicken salad, hot turkey sandwiches in NZ, causing totally 1762 food poisoning cases (Ministry of Primary Industry, 2001). From April to June, 2014, there was one SFP outbreak comprising 4 cases following the consumption of contaminated food in a restaurant in Taranaki area of Northland in New Zealand (ESR, 2014). It was believed that the sources of contamination by *S. aureus* were mainly from food workers by direct or indirect contact, live chicken and processing equipment (Davies & Board, 1998; Hayes, 1992; Montville & Matthews, 2008). Controlling cooling temperature and storage temperature can prevent the propagation of *S. aureus* in final products (Ministry of Primary Industry, 2001; Pillsbury et al., 2013). Therefore, food handlers must be adequately trained in food safety skills and good food handling hygiene. The processing equipment in poultry plants must be maintained and cleaned properly (ComLaw, 2010).

With the popularity of poultry products and the incidences of staphylococcal contaminations, it is critical to ensure microbial safety of the products, food processing environments and equipment (Lindblad et al., 2006). To investigate the contamination of *S. aureus* in poultry processing plants, it is essential to use reliable analytical methods to identify the enterotoxigenic and strains of *S. aureus* isolates to determine the potential contamination source (Gibbs, Patterson, & Thompson, 1978; Jacxsens et al., 2009; Jacxsens et al., 2011).

The aim of this project was to identify potential contamination sources of poultry products and processing equipment by *S. aureus* from a selected processing plant to the farm in Auckland, New Zealand. The specific objectives were to:

- determine the level of contamination of poultry meat and equipment by *S. aureus* at selected processing steps in a commercial poultry plant;
- determine the level of contamination of chicken skins and nostrils of live chickens by *S. aureus* at a supplying poultry farm;
- identify the main sampling sites;
- isolate *S. aureus* from samples of each of the main sampling sites;
- determine the presence of staphylococcal enterotoxins (SEs) from *S. aureus* isolated from main sampling sites using multiplex Polymerase Chain Reaction (PCR)
- determine the sequence type of the isolated *S. aureus* using the Multilocus Sequencing Typing (MLST) method
- identify the clonal complexes of the sequence types using eBURST

2. Literature Review

2.1 Poultry meat

Poultry meat had been increasingly welcomed by consumers in America from years ago as its unique properties, such as the consistent composition and a mild flavour. During the processing, the muscle of poultry meat is changed chemically, physically and structurally which determines the overall quality of final processed products (Sams, 2000).

Poultry meat quality attributes include colour, aroma, flavour, texture, and microbial levels, however, colour and texture are considered to be the most common indicator of quality attributes for poultry meat which are related to the selection for both raw poultry meat and processed poultry products by manufacturers and consumers (Boylston et al., 2012; Fletcher, 2002). Pre-slaughter of live chickens, processing conditions and microbiological controlling can affect the quality of processed poultry products (Hui et al., 2010; Sams, 2000). The dominant nutrient data of chicken breast with different cooking methods in many countries was analysed by Probst (2008) (Table 2.1).

Table 2.1 Dominant nutrient data of chicken breast under different cooking methods in some countries.

Country	Australia	Australia	Finland	Australia	USA	NZ	Australia
Cooking method	Baked	Casseroled	Raw	Raw	Raw	Raw	Stir-fried
Water (g)	67.600	66.700	-	75.000	74.760	75.500	68.600
Energy (KJ)	637.000	596.000	617.000	438.000	460.000	453.000	520.000
Total fat (g)	3.900	3.700	6.800	1.600	1.240	2.130	0.900
Total protein(g)	29.000	27.000	21.500	22.300	23.090	22.300	28.600
Ash (g)	1.200	1.000	-	1.100	1.020	-	1.200

Source: (Probst, 2008). (-) indicates that no data was available from the source.

2.2 Poultry processing procedures

From 1950 to 1960, manual operations poultry processing was changed into automatic and mechanical operations which lower the risk in cross-contamination of various microorganisms from human handling (Davies & Board, 1998; Tsola et al., 2008). Although the modernisation and standardisation of processing flow may lead to cross-contamination from the surface of equipment, the total loads of bacteria of end-products are less than that of old traditional manufacturing processing (Fuster-Valls et al., 2008; Tsola et al., 2008). Also, modern processing of poultry meat is much more efficient, slaughtering at least 5000 carcasses per hour (Notermans et al., 1982).

The main processing procedures of poultry meat consist of slaughtering, scalding, defeathering, evisceration, washing, chilling and packaging. (Tsola et al., 2008). After slaughtering and bleeding of chickens, they are scalded at temperature around 55°C for about 200s. Before eviscerated automatically, carcasses are defeathered by going through a series of defeathering machines. Spray washing normally with chlorinated water then is conducted before final chilling and packaging of chicken portions (Mead et al., 1993). More information about each stage is discussed below and Figure 2.1 illustrates a schematic processing of poultry.

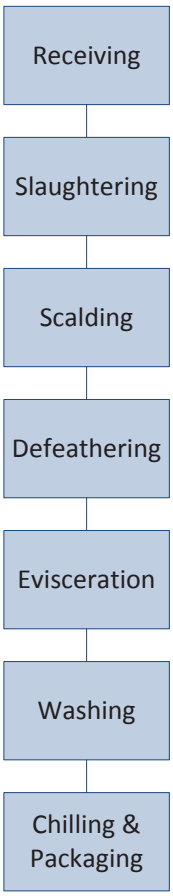


Figure 2.1 Schematic processing of poultry (Davies & Board, 1998; Tsola et al., 2008).

2.2.1 Slaughtering

Slaughtering of chickens includes hanging, stunning, killing and bleeding (Davies & Board, 1998). Before birds are slaughtered and bled out, stunning is usually applied to avoid the feeling of pain during bleeding, to minimise distress, to enable the bleeding of birds easily and accurately and also to prevent convulsions (Gregory, 1995). Raj (2006) used stunning methods, such as electrical water bath stunning and gas stunning to stun the birds. Chickens are hung upside down which involves their feet in shackles both during stunning and bleeding. They are bled out for at least 90s by cutting neck before going to next stage in the UK (Gregory & Wotton, 1986; Sparrey & Kettlewell, 1994).

2.2.2 Scalding

Temperature and time for chickens to be immersed in scalding liquid are the two important factors which manufacturers need to decide, because if the chicken is scalded at a high temperature for a long time, the skin would be overheated (Covell III, 1990). Mead et al. (1993) did a microbiological survey of five poultry processing plants in the UK, however, the temperature and time of scalding were all different from each other, ranging from 51.5°C to 56°C and 138s to 300s, respectively. The four plants investigated by Notermans et al. (1982) had different temperature and time at scalding stage as well. Generally, there are two kinds of scalding: soft scalding (50-53°C) and hard scalding (58-60°C) (Corry & Atabay, 2001). The viable counts of *Salmonella* on Chickens were less when using 52°C or 56°C scalding temperature while *Campylobacter* isolated from chickens showed a lower level when treated with 60°C scalding temperature (Slavik et al., 1995).

The purpose of scalding is to loose chicken feathers, making the feathers easily removable in the defeathering stage (Davies & Board, 1998). Traditional scalding of poultry processing only uses one single tank while modern industries usually scald chickens through a multi-stage process which consists of three or four scalder machines (Veerkamp, 1995; Veerkamp & Hofmans, 1973). This invention has been proved to reduce the loads of microorganisms on chicken carcasses after scalding, as scalding is a critical hazard point (Davies & Board, 1998; Veerkamp & Heemskerk, 1991). It is likely because of the warm temperature accelerates the growth of some bacteria and the cross-contamination from other carcasses through water (Tsola et al., 2008). The following figure (Figure 2.2.1) shows different effects of traditional scalding and multi-stage scalding methods on controlling of viable cells of microorganisms (Veerkamp, 1995). Dodd et al. (1988) examined the viable counts of

S. aureus during scalding and defeathering. The results showed that after scalding, the viable counts of *S. aureus* were reduced significantly while the defeathering stage showed the opposite situation.

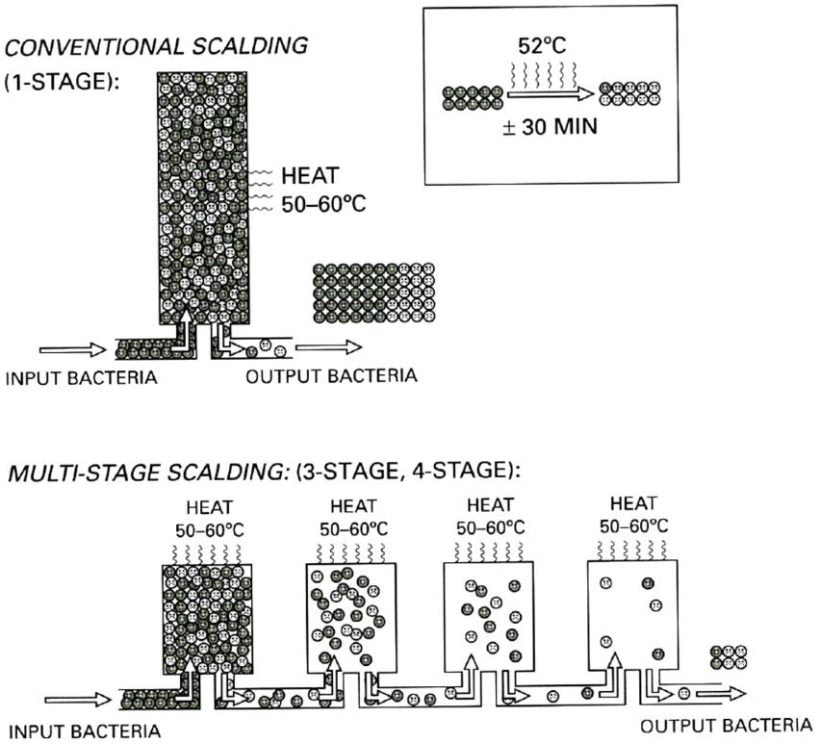


Figure 2.2.1 Different effects of traditional scalding and multi-stage scalding methods on controlling of viable cells of microorganisms (Davies & Board, 1998; Veerkamp, 1995).

2.2.3 Defeathering

During the defeathering stage, the feathers of chickens are removed in a plucker where rotation with rubber fingers and water spraying are also applied (Corry & Atabay, 2001). It is reported that chicken carcasses are contaminated with *S. aureus* at a high rate during defeathering stage when compared to other processing stages (Mead & Dodd, 1990; Notermans et al., 1982). For example, Mead et al. (1988) found that the viable counts of *S. aureus* after defeathering (10^7 CFU/swab) were 1000-fold

higher than that of *S. aureus* before defeathering (10^4 CFU/swab). They explained that the reason probably was because of the conditions during plucking, such as high temperature, humidity and available nutrients. Also, staphylococci can attach to the rubber fingers in a plucker at environmental temperature of 28°C for 6 hours (Mead et al., 1995).

The introduction of spray washing with water can reduce the viable counts of microorganisms (Mulder et al., 1978). Chlorinated water has been reported to prevent cross-contamination effectively during defeathering (Mead & Scott, 1994). A washing system was invented to lower the costs of water and improve the overall hygienic quality during defeathering. After spraying water onto the carcasses, the water is pasteurised and reused in scalding and next plucker ((Veerkamp, C. H & Pieterse, C cited by (Davies & Board, 1998)).

2.2.4 Evisceration

Evisceration of chicken carcasses is to remove the head, intestines, heart, liver and wings etc.. At the end of evisceration, chicken portions are sorted for edible parts and washed again (Davies & Board, 1998; Tsola et al., 2008). The entrails and other parts of chicken carcasses are detached and removed by using a vacuum scrubber if the evisceration stage is conducted automatically (Scheier & Haynes, 1974). Stals (1992) pointed out that the hygienic quality of carcasses were improved with automated transfer from slaughtering line to evisceration line due to less chances of cross-contamination by workers. Evisceration stage is considered as a critical control point in HACCP (Hazard Analysis and Critical Control Points) as a result of contamination from intestinal contents (physical) or microorganisms (microbiological) (Tsola et al.,

2008). Davies and Board (1998) described the process of opening chicken carcasses in details which is illustrated in Figure 2.2.2.

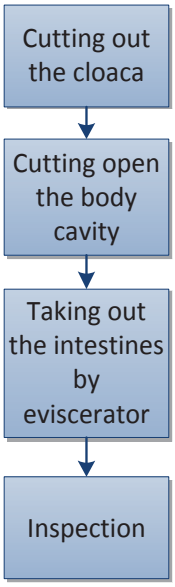


Figure 2.2.2 Generalised process of opening chicken carcasses (Davies & Board, 1998).

2.2.5 Chilling

Immersion chilling, air chilling and spin chilling are the three common chilling methods for poultry products. The chilling method is chosen depending on the types of final products. Immersion chilling with water is normally applied to freeze carcasses while water chilling and air chilling are both suitable for fresh poultry meat or non-frozen poultry meat (Davies & Board, 1998; James et al., 2006).

The original aim of chilling process of carcasses is to inhibit the propagation of various microorganism (James et al., 2006). However, it was reported that the viable

counts of microorganisms on broiler carcasses were not significantly different between water chilling and air chilling (Mulder & Veerkamp, 1974). In contrast, Blood and Jarvis (1974) found that water immersion chilling method could reduce contamination of carcasses more effectively than air chilling.

The usage of water volume and the chlorine concentration had an impact on the final viable counts of coliform and other bacteria. The combination of more water usage and high concentration of chlorine in water, the less loads of microorganisms are on the finished products (Blood & Jarvis, 1974). On the other hand, the taste, texture and appearance of final poultry products, to some extent, are influenced by the rate of chilling. Tough texture of poultry meat will be obtained if the meat is chilling rapidly while pale soft exudative (PSE) meat will be produced when chilling process is very slow (James et al., 2006).

2.2.6 Packaging

There are many packaging methods available commercially, such as vacuum packaging, traditional wrapping packaging, carbon dioxide flushing packaging and modified atmosphere packaging (MAP) (Sebranek et al., 1996; Thomas et al., 1984). The materials and methods used to pack poultry meat depend on the type of products and the slaughter process. For example, fresh or non-frozen poultry carcasses that are processed under high temperature of scalding and immersion chilling are normally packed with ice, avoiding the occurrence of discoloration of the carcasses (Thomas et al., 1984). Thomas et al. (1984) compared the microbiological quality and flavour of dry broilers that were packed using carbon dioxide flushing, vacuum packaging and stretch wrapping. They found that among these three packaging methods, vacuum packaging performed well with regards to the shelf-life. Narasimha Rao and

Sachindra (2002) pointed out that the colour of poultry meat that was packed by MAP remained longer than that of poultry meat under vacuum packaging. The growth of pathogens and spoilage microorganisms is the main concern during packaging. Only MAP can inhibit the growth of *Pseudomonads* on chicken breasts with skin. However, Lactobacilli, Enterobacteriaceae and *Brochothrix thermosphacta* can even propagate after chicken meat is MAP packed (Jiménez et al., 1997). Thus, it is important to keep the residence times short and keep the temperature low during both packaging and distribution stages (Davies & Board, 1998).

2.3 Contamination of raw chicken and chicken products

2.3.1 Microbiological contamination

Raw poultry meat can be contaminated with various pathogens and spoilage microorganisms. Microbiological contamination of poultry meat is more common than physical and chemical contaminations, as most Crital Control Points (CCPs) are decided according to the potential contamination with bacteria (Tsola et al., 2008). Figure 2.3 shows the occurrence of microbial counts in retail chicken parts and processed chicken products in Spain (Álvarez-Astorga et al., 2002).

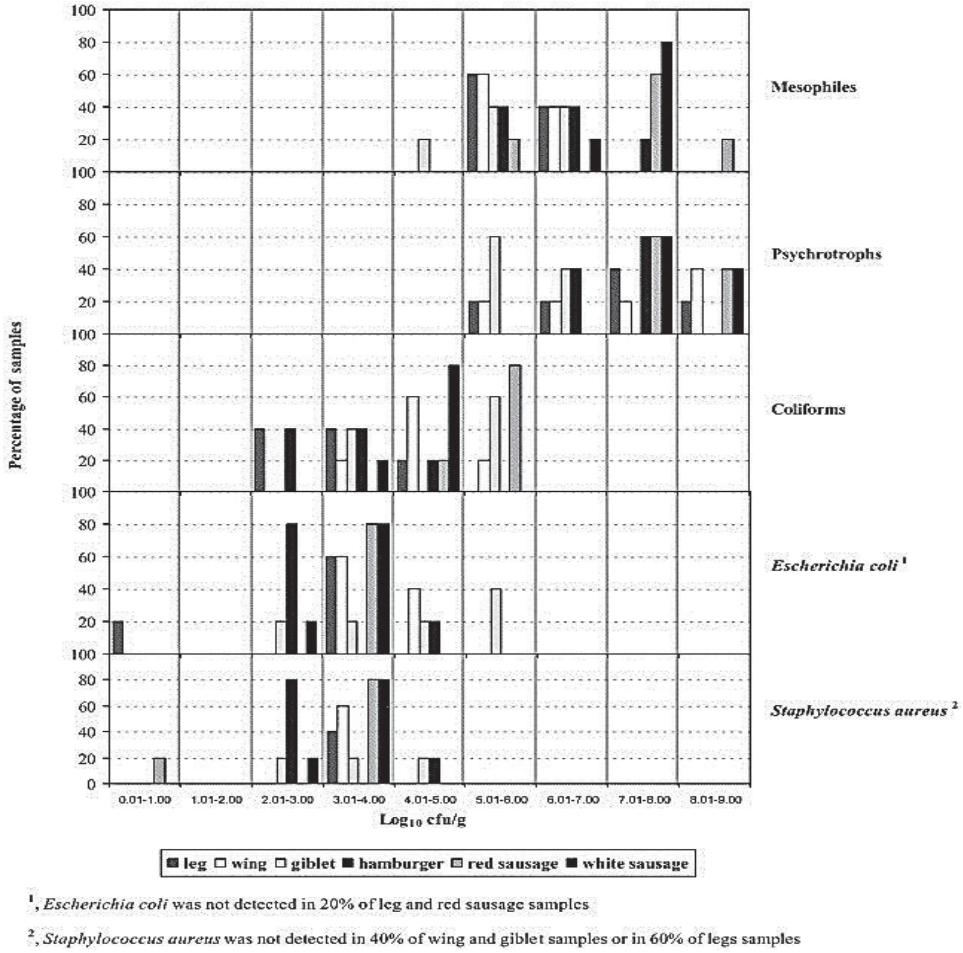


Figure 2.3 Occurrence of microbial counts in retail chicken parts and processed chicken products in Spain.

In different countries, some common pathogens have been isolated from poultry, including *Aeromonas* spp., *Campylobacter* spp., *Clostridium perfringens*, *Listeria* spp., *Salmonella* spp., *Shigella* and *Streptococcus* spp., *Staphylococcus aureus*, etc (Waldroup, 1996). Testing the occurrence of foodborne pathogens and spoilage microorganisms at poultry processing stages in a plant is a basic way to investigate the contamination of poultry products (Gibbs, Patterson, & Thompson, 1978; Mead et al., 1993; Notermans et al., 1982). For example, Lindblad et al. (2006) examined the prevalence and concentrations of microorganisms on 636 chilled broilers in Sweden. The results showed that, about 29%, 18%, 9% and 97% of all samples were

contaminated with *Listeria monocytogenes*, *Clostridium perfringens*, *Yersinia enterocolitica* and *Enterococcus*, respectively.

2.3.2 Contamination sources

Humans, live chickens and processing equipment are the three dominant sources that induce contamination or cross-contamination of foodborne microorganisms or pathogens on chicken meat (Chaffey et al., 1988; Jacxsens et al., 2009; Mead et al., 1988). Cross-contamination always occurs among live chickens during raising and transportation where chickens stay closely together with each other (Davies & Board, 1998). Gibbs, Patterson, and Thompson (1978) analysed the origin of *S. aureus* in a poultry processing plant and they found that the contamination source of this microorganism is live chickens rather than humans or processing equipment.

Hygienic working practices, such as wearing protective clothing and washing hands frequently, are usually developed to ensure that carcasses are free from being contaminated by workers (Aarnisalo et al., 2006). Chicken carcasses can be contaminated with micrococci, staphylococci, propionic bacteria through worker's skin and *E. coli* and *Salmonella* can contaminate products by workers' hands (Jacxsens et al., 2009). Good hygiene practices are also required to prevent cross-contamination during the cooking of raw chicken meat (Haysom & Sharp, 2004).

Through poultry processing, carcasses need to go through a series of equipment. The contact between carcasses and the surface of equipment is a high risk of cross-contamination, as some bacteria can attach to the surface (Kusumaningrum et al., 2003). Therefore, in order to avoid cross-contamination from equipment, it is

important to design and use a series of good hygienic equipment to produce poultry products (Aarnisalo et al., 2006). The level of contamination varies from different poultry products in a production line. For example, the chicken wings had a much higher viable counts of *Campylobacter* than other chicken portions (Habib et al., 2008).

To investigate the microorganisms contamination of poultry products throughout processing, sampling locations should be identified (Mead et al., 1988; Notermans et al., 1982). Microbial Assessment Scheme (MAS) is a systematic procedure to investigate the distribution of bacteria during processing in a plant, which includes the identification of critical sampling locations, the selection of microbiological parameters and sampling method of analysis, the assessment of sampling frequency, final data processing and interpretation (Jacxsens et al., 2009, 2011).

2.3.3 Decontamination of poultry products

Food Safety Management System (FSMS) is a comprehensive system to prevent microbiological contamination, to inhibit the growth of foodborne bacteria or pathogens in a food product and also to decontaminate food products (Jacxsens et al., 2011). There are many decontamination methods which are normally classified as chemical decontamination and physical decontamination. However, physical decontamination is more favourable than chemical decontamination, as the potential residues may be found in final products (Corry et al., 2007). Table 2.2 listed some examples of chemical and physical decontamination methods for poultry meat (Bolder, 1997). In European Union countries, it is not permitted to use chemical decontaminants (Corry et al., 2007; Whyte et al., 2003).

The effect of immersion in hot water of chicken carcasses was studied by Corry et al. (2007). The result showed that decreases in viable counts of *E. coli* K12 and Campylobacter jejuni AR6 were observed using 80°C for 20s immersion and 75°C for 30s immersion. However, on a smaller scale, hypochlorite was reported to reduce the contamination by *Salmonella* and *Campylobacter* spp. more significantly and effectively than detergent or hot water (Cogan et al., 1999). It was also proved that gamma radiation doses of 1.50 KGy was able to kill all *S. aureus* in deboned chicken meat samples before and after storage (Thayer & Boyd, 1992).

Table 2.2 Examples of chemical and physical decontamination methods for poultry meat.

	Method
Chemical:	Chlorine (hypochlorite, ClO_2)
	Organic acids (lactic acid, acetic acid, buffered lactic acid, gluconic acid, etc.)
	Inorganic phosphates (trisodium phosphate, polyphosphates)
	Organic preservatives (benzoates, propionates)
	Bacteriocins (nisin, magainin)
	Oxidizer (hydrogen peroxide, ozone)
Physical:	Water (rinse, spray, steam)
	Ultrahigh pressure
	Irradiation
	Pulsed-field electricity
	Ultrasonic energy
	UV light

Source: (Bolder, 1997)

2.4 Characterisation of *Staphylococcus aureus*

2.4.1 *Staphylococcus aureus*

Staphylococcus aureus is one of the micrococcaceae families which have spherical cells with grape like clusters (Bhatia & Zahoor, 2007; Fratamico et al., 2011). Figure 2.4.1 shows an electron micrograph of *S. aureus* (Montville & Matthews, 2008). *S. aureus* are Gram-positive coccus and facultative anaerobic bacteria (Bhatia & Zahoor, 2007). They are not motile and cannotform spores (Silva, 2012). During their

metabolism, mannitol is fermented to acid and, protein A, lipase, coagulase, thermonuclease and hemolysin are produced (Ray, 2001; Silva, 2012).

As mentioned in section 1, they can live in a wide range of temperatures from 7 to 48°C, low water activity (0.86), pH ranging from 4.2 to 9.3 and high sodium chloride concentrations of 15%, therefore, food matrix is a favourable environment for them to grow (Bhatia & Zahoor, 2007; Kérouanton et al., 2007; Ray, 2001). It is important to notice that *S. aureus* is not the causative agent of food poisoning because the cells can be killed at 66°C in 12 min or at 72°C in 15s (pasteurisation treatment), but instead, it is the enterotoxin produced by the bacteria which is heat-resistant that causes food poisoning (Fratamico et al., 2011).

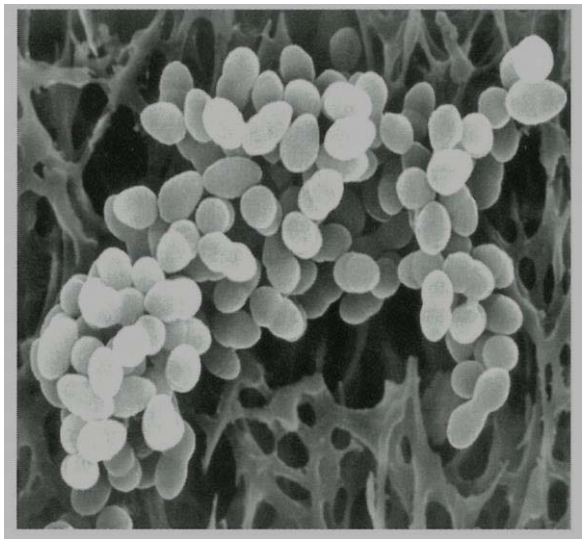


Figure 2.4.1 Electron micrograph of *S. aureus* (Montville & Matthews, 2008)

People are one of the carriers of *S. aureus* most of which is present in nose, skin and hair. Food contamination of *S. aureus* usually occurs during processing and preparation. People contaminate food and food products by poor hygiene hands or

dirty utensils (Montville & Matthews, 2008; Ray, 2001). Another source of *S. aureus* contamination is from animals such as cows, dogs and birds. For instance, cow mastitis is caused by *S. aureus* which influences the quality of the milk (Harvey et al., 1982; Montville & Matthews, 2008). Harvey et al. (1982) pointed out that strains of *S. aureus* which contaminate food from human were more common than that from animals.

2.4.1.1 Methicillin-resistantStaphylococcus aureus (MRSA)

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a typical type of *S. aureus* that is resistant to penicillinase-resistant penicillin (Lee, 2006). It was first discovered in the 1960s and after that hospitals and communities had shown the presence of MRSA (Gosbell, 2004). MRSA is one of the reasons for hospital-related infection as well as the cause of community diseases among people (Khanna et al., 2008). In Canada, MRSA causes nosocomial infections in humans and the infections have been increased since 1990s with MRSA possibly being a potential cause for foodborne illness (Crago et al., 2012).

It was reported that MRSA was first found in pigs as an animal carrier with a high prevalence (Crago et al., 2012; De Neeling et al., 2007). Recently, other animals, such as cows, dogs, cats, horses and chickens, have been reported to carry MRSA especially animals with scratches or wounds, causing a potential threat to meat products (De Boer et al., 2009; Kitai, Shimizu, Kawano, Sato, Nakano, Uji, et al., 2005). MRSA isolates have been found in not only meat products, but also other different kinds of food products, such as milk and cheese (Normanno et al., 2007; Pereira et al., 2009; Pu et al., 2009). Meat products are most likely to be contaminated by MRSA if carcasses are contaminated from MRSA-positive animals and the

environment during slaughtering (De Boer et al., 2009). Also, food workers infected with MRSA are another source of contamination during processing (Lozano et al., 2009).

The unique methicillin resistance characteristic of this organism is encoded by *mecA* gene which can be detected by PCR (De Boer et al., 2009; Khanna et al., 2008; Lee, 2006). MRSA Chromogenic agar, MRSA latex agglutination test and DNase assay are other alternative methods that have been used in relevant researches (Lozano et al., 2009).

2.4.2 Outbreaks of *Staphylococcus aureus*

Microbiological food poisoning is considered as the most serious food poisoning. Two reasons count for this: bacterial infection and food intoxication (Bhatia & Zahoor, 2007). *S. aureus* has the ability to produce enterotoxins in food leading to food intoxication. Outbreaks caused by enterotoxins of *S. aureus* have been widely reported all over the world, especially in the early 1900s (Ray, 2001). For example, 25%-35% of all microbial outbreaks in Japan were contributed to staphylococcus toxins before 1984 while in America, the percentage outbreaks of staphylococcus toxins was 14% (Bhatia & Zahoor, 2007). Raw poultry and poultry products are more vulnerable to be contaminated with *S. aureus* which has been proved by a study in UK, investigating the incidence among raw poultry and poultry products (75%), fish or shellfish (7%) and milk products (8%) (Waldroup, 1996). In NZ, from 1989 to 1999, 24 staphylococcal food poisoning (SFP) cases were reported. It was also reported that food products, such as yogurt, hot ham sandwiches, chicken salad, hot turkey sandwiches etc. were the SEs carriers which were responsible for totally 1762 cases in NZ (Ministry of Primary Industry, 2001).

2.4.3 Disease and symptoms

The symptoms of food poisoning produced by *S. aureus* includes nausea, vomiting diarrhoea, salivation, headache and sweating (Fratamico et al., 2011; Lee, 2006; Ray, 2001). The type of symptom depends on the amount of toxins and the type of that toxin (Bhatia & Zahoor, 2007). The disease caused by staphylococcal toxins not only occurs on humans but also on poultry, such as arthritic lesion of joints, foot abscesses, skin dermatitis (Mead & Dodd, 1990). It is reported that food with 100 to 200 ng toxins that are produced by *S. aureus* can infect a healthy man after consuming the food in 30 mins to 8 hours (Fratamico et al., 2011; Ray, 2001). However, there might be a little influence on human as our immune system will start to recover in 24 to 48 h with low intake of toxins (Montville & Matthews, 2008). With regard to the prevention of infections of staphylococcal toxin diseases, inspection of raw ingredients, sanitation of plant environment and good personal hygiene are essential (Ray, 2001).

2.4.4 Staphylococcal enterotoxins (SEs)

Some strains of *S. aureus* are able to produce one or more staphylococcal enterotoxins (SEs) which are the causative agents of staphylococcal food poisoning (SFP) (Lee, 2006; Matyi et al., 2013; Notermans et al., 1982). Food intoxication of *S. aureus* is caused by consuming food that has already been contaminated with *S. aureus* and most importantly the strains have produced enterotoxins into the food matrix (Bhatia & Zahoor, 2007; Ray, 2001). SEs are single chain proteins with a low molecular weight (Bergdoll, 1999). The 2D structures of some SEs were illustrated by Hennekinne et al. (2012) having a cysteine loop in the centre of each one (Figure 2.4.2) (Bergdoll, 1999).

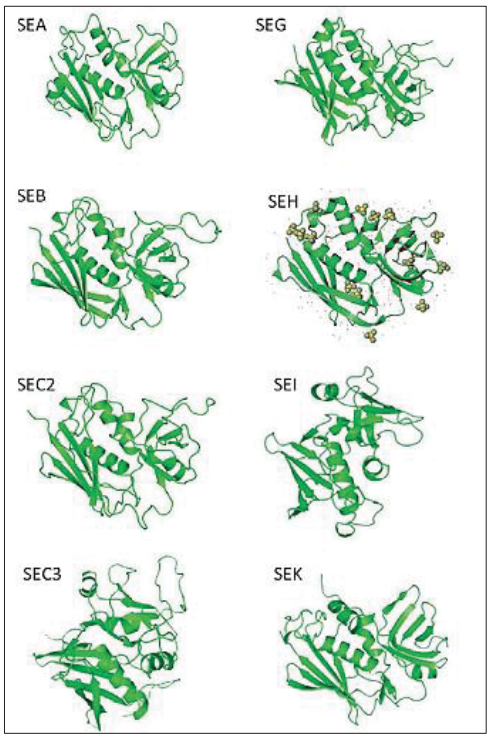


Figure 2.4.2 Structures of some staphylococcus enterotoxins (Hennekinne et al., 2012).

Raw poultry and poultry products are vulnerable to be contaminated with *S. aureus* because the pH, water activity of carcasses and temperature in some stages during manufacturing are suitable for *S. aureus* to grow and even synthesise SEs (Kérouanton et al., 2007; Pepe et al., 2006). SEs are named alphabetically according to the time that they have been discovered (Montville & Matthews, 2008; Roberts & Greenwood, 2002; Silva, 2012) Ten SEs (A to J) have been discovered before 2003 (Roberts & Greenwood, 2002). Until 2007, fourteen different SEs have been discovered from SEA to SEO without SEF while one year after Silva (2012) pointed that SER, SES, SET (new SEs) and enterotoxin-like proteins (SEls): SElU, SElV and SElW have been recognised. Poultry meat has been reported to carry enterotoxinic *S. aureus* isolates. Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al. (2005) detected SEB, SEA, SEC, SED, SEA+SEB and SEA+SEC from 360 *S. aureus*

isolates of 444 raw chicken meat samples in Japan. Strains that originate from birds usually produce SEC and SED while Pepe et al. (2006) found that 62% of *S. aureus* isolates from birds were SEA producer.

2.4.4.1 Inactivation of staphylococcal enterotoxin

There are three ways to inactivate SEs: irradiation inactivation, chemical inactivation, biological inactivation and thermal inactivation (Bhatia & Zahoor, 2007). SEs in food matrices are not suitable to be inactivated by irradiation as a relatively high dose is required to achieve the reduction of SEs level (Read & Bradshaw, 1967). It is reported that 16%-26% SEA could not be inactivated even under a dose of 23.7 KGy (Modi et al., 1990). Some researchers have used several chemical components to inactivate SEs. For example, Stelma Jr and Bergdoll (1982) used bromoacetic acid at pH 7.0 to induce the carboxmethylation of histidine residues in SEA which can inhibit activity of SEA's antibody. Suzuki et al. (2002) inactivated SEA successfully with electrolysed anodic NaCl solution [EW(+)]. For food with more organic compounds, high level of chlorine is also a solution with the combination of phosphate-buffered saline and hypochlorite (HOCI) (Suzuki et al., 2002; Warren et al., 1974). Biological inactivation needs to be further studied as SEs are tolerant to proteolytic enzymes. Lactic acid bacteria can slightly reduce the concentration of enterotoxin, but it is still unclear about the specific reason (Bhatia & Zahoor, 2007).

Thermal inactivation is the main study area to inactivate SEs, although SEs are stable to heat treatment. Z-values of SEs are 25-33°C, D-value at 121°C ranging from 8.3-34 min and F-value at 120°C is almost 30 mins (Bhatia & Zahoor, 2007). The time and temperature required to inactivated SEB were investigated by Read and Bradshaw (1966) using the double-gel-diffusion technique. The combination of thermal

inactivation and chemical inactivation probably is a more effective approach. Satterlee and Kraft (1969) pointed out that a heat treatment at 80°C of SEB of meat proteins in phosphate-saline buffer showed a more effective inactivation as 67.5% of the activity was lost at the beginning of 15 min and the SEB in ground-beef slurry showed a relatively faster loss of activity. Moreover, many factors play a role in inactivation of SEs, such as pH, initial concentration of SEs, ionic strength etc. (Bartlett et al., 1971; Denny et al., 1971; Schwabe et al., 1990).

2.5 Isolation of *Staphylococcus aureus*

There are several agars that can be used to isolate *S. aureus* such as colony counting with Baird-Parker agar, colony counting with rabbit plasma fibrinogen agar (RPFA), enrichment culture and Petrifilm (Roberts & Greenwood, 2002). The selection of isolation methods depends on the type of products being analysed (Roberts & Greenwood, 2002; Silva, 2012). For example, for dried food products, MPN technique is a proper one due to potential low numbers of coagulase-positive colonies and the injuries of bacteria cells (Roberts & Greenwood, 2002).

Apart from selective agar (Baird-Parker agar and RPFA), several agars are also available, such as Mannitol Salt agar (MSA), Egg Yolk Azide agar, Vogel-Johnson agar, Bovine Fibrinogen agar (BFG agar), Milk-Salt agar. Notermans et al. (1982) used BFG agar to investigate the contamination of chicken carcasses with *S. aureus* during processing in a plant. Tryptic Soy agar was used to study the effect on reduction of *S. aureus* on mechanically deboned chicken meat (MDCM) by different doses of gamma radiation (Thayer & Boyd, 1992). However, Silva (2012) pointed out that Baird-Parker agar is the most common and widely used agar to enumerate *S.*

aureus which have been proved by many researchers in their studies. The time and temperature required to incubate *S. aureus* are 24 to 48 h at 35 or 37°C (Gibbs, Patterson, & Thompson, 1978; Gundogan et al., 2005; Harvey et al., 1982; Lee, 2003, 2006; Mead et al., 1988; Tsola et al., 2008; Waters et al., 2011).

Petrifilms are convenient and flexible to use and it offers a good repeatability and reproducibility (Aarnisalo et al., 2006). It contains a cold-water-soluble gelling agent with modified Baird-Parker agar inside which is a selective and differential agar to identify *S. aureus* colonies. Basically it involves inoculation of sample onto the Petrifilm and then incubate the Petriflim for 24±2 hours (3M™, 2010b). 3M Petrifilm Rapid Staph Express Count (PSE) system was used to identify *S. aureus* isolated from chicken products (Pepe et al., 2006). The red-violet colonies on the plate are regarded as *S. aureus* (3M™, 2010b).

2.5.1 Confirmation tests of suspect *S. aureus* isolates

To confirm presumptive *S. aureus* colonies, Gram-staining, catalase test, coagulase test, carbohydrate fermentation, DNase, phosphatase tests etc. can be tested. The systematic confirmation biochemical tests of *S. aureus* have been outlined in Bergey's Manual (Bergey et al., 2001). Lancette and Bennett (2001) summarised the enumeration and confirmation methods including plate count method and Most Probable Number (MPN) technique of *S. aureus* (Figure 2.5.1 & Figure 2.5.2).

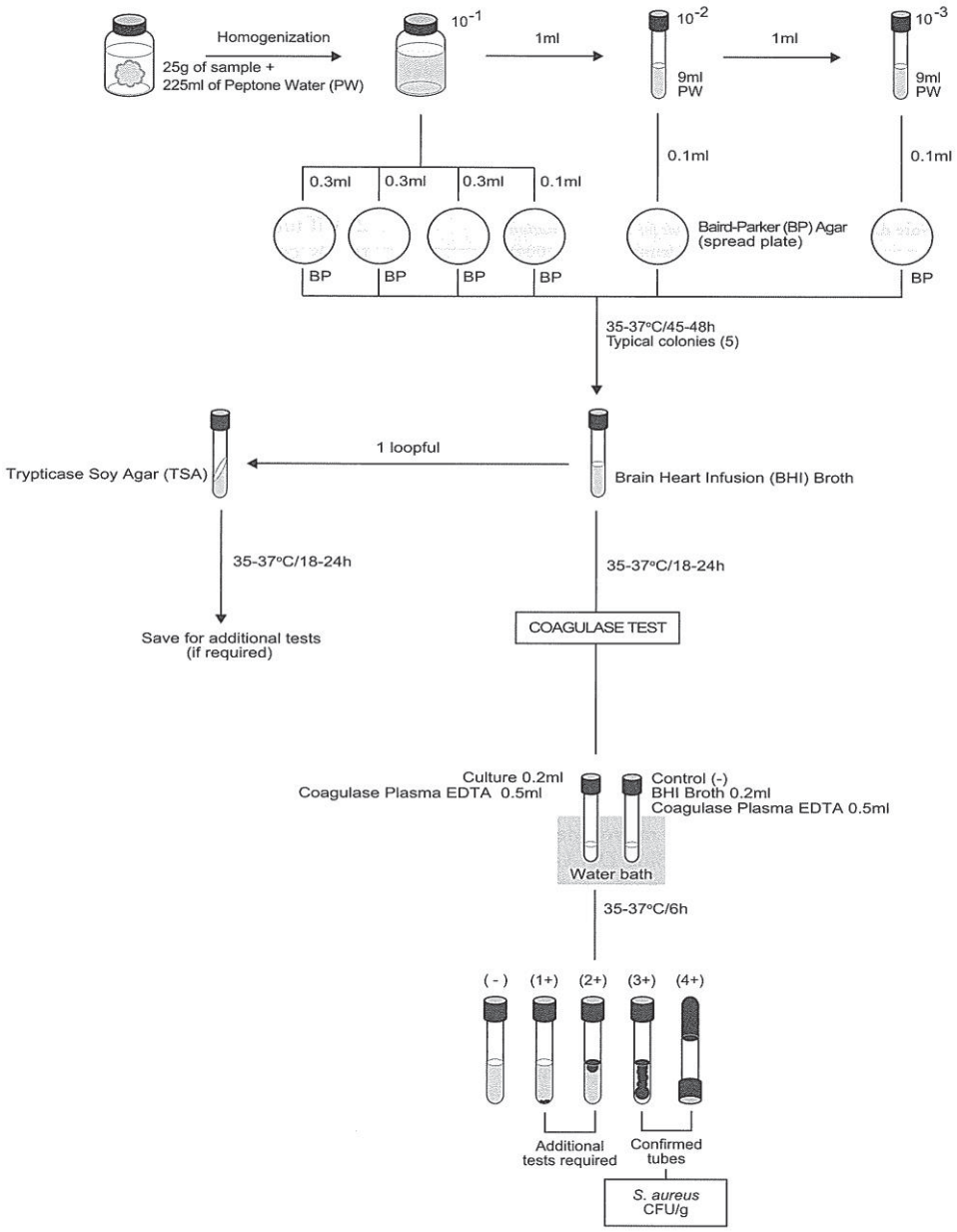


Figure 2.5.1 Schematic procedures of enumeration and confirmation (coagulase test) of *S. aureus* using plate count method APHA 2001(Lancette & Bennett, 2001; Silva, 2012).

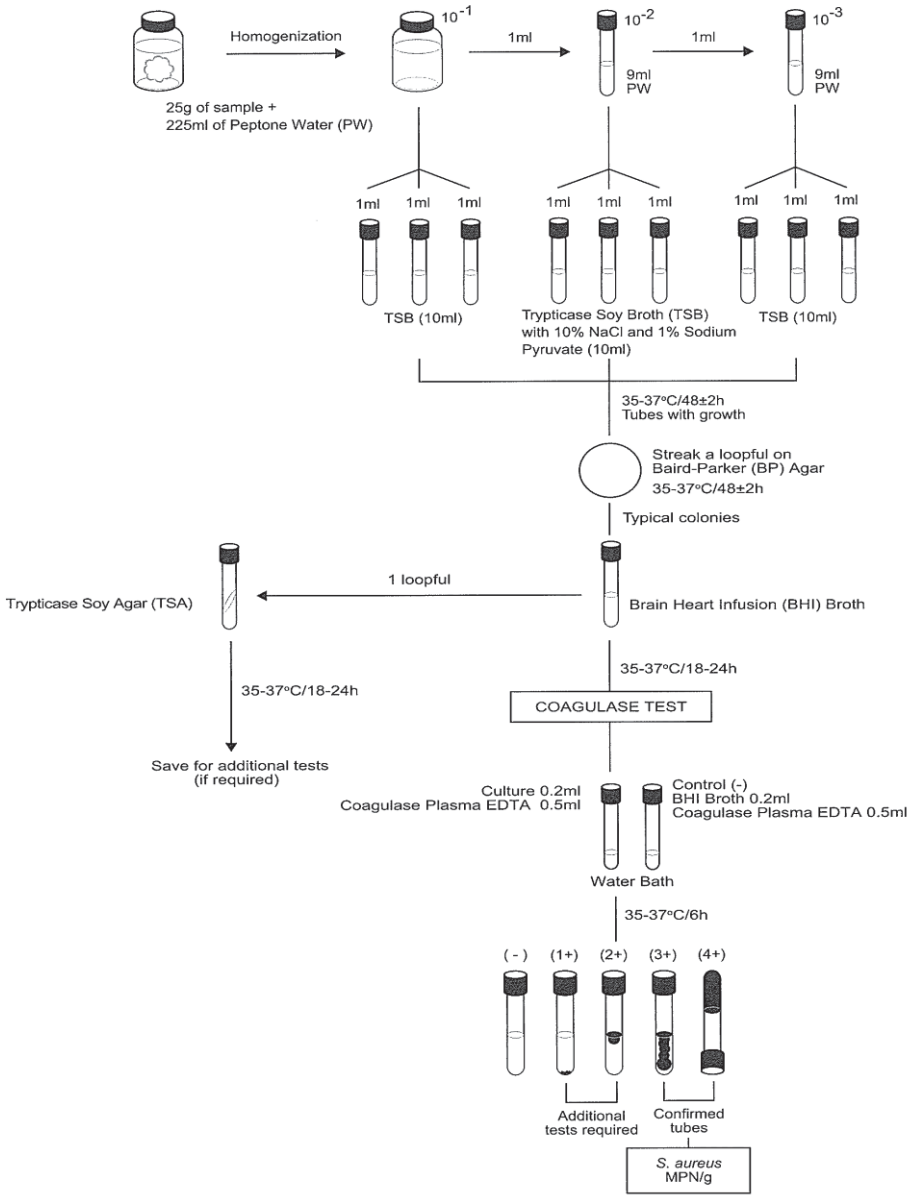


Figure 2.5.2 Schematic procedures of enumeration and confirmation (coagulase test) of *S. aureus* using plate count method APHA 2001 (Lancette & Bennett, 2001; Silva, 2012)

2.6 Detection of staphylococcal enterotoxins (SEs)

To identify SEs, many approaches, such as molecular biological methods, Reverse phase latex agglutination (RPLA), the enzyme-linked immuno-sorbent assay (ELISA), biosensors and polymerase chain reaction (PCR), are available nowadays. ELISA and

RPLA can detect SEs more sensitively and efficiently than other common microbiological methods (Rose et al., 1989). Hennekinne et al. (2012) classified them into bioassays, molecular biology (PCR) and immunological methods (ELISA).

2.6.1 Immunological methods

Immunological methods involve using monoclonal antibodies to detect SEs which are more difficult to conduct as pure toxins are required (Harvey et al., 1982; Hennekinne et al., 2012; Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al., 2005; Šimkovičová & Gilbert, 1971). ELISA is able to detect SEA to SEE at a very low level (1 ng/g food), but only SEA to SEE, SEG, SHE and SEIQ can be detected using this method (Bhatia & Zahoor, 2007; Chiang et al., 2008; Morandi et al., 2007; Schlievert & Case, 2007). Wieneke (1991) compared four immunological methods that were used to detect SEs: SET-EIA (staphylococcal enterotoxin ELISA), SET-RPLA, ELISA-M (ELISA-membrane) and ELISA-T (ELISA-tube) kits in terms of reagents used, time required, extraction procedure and cost (Table 2.6)

Table 2.6 Comparison of ELISA-B, SET-RPLA, ELISA-M and ELISA-T kits for the detection of staphylococcal enterotoxins.

	Kits			
	ELISA-B	SET-RPLA	ELISA-M	ELISA-T
Enterotoxins can be detected	SEA-SED	SEA-SED	SEA-SEE	SEA-SEE
Detection of individual enterotoxins	Yes	Yes	Yes	No
Cost (Pound/ number of tests per kit)	£66/10	£114/20-40	£230/25	£165/20
Time (h)	24	16	4	1.5
Sensitivity (ng/mL)	0.1-1	0.5	0.5	0.2
Extracts used (mL)	20	0.2	20	0.5

Source: (Wieneke, 1991)

2.6.2 Molecular biology methods

Molecular biology methods for detecting enterotoxins that are produced by *S. aureus* strains from contaminated food products are based on genes encoding. Polymerase Chain Reaction (PCR) has been widely used by researchers to detect SEs in chicken meat (Bhatia & Zahoor, 2007; Hwang et al., 2007; Kérouanton et al., 2007). Pepe et al. (2006) examined SEs from *S. aureus* stains of breaded chicken samples using PCR to detect SEs genes. Kérouanton et al. (2007) summarise the nucleotide sequences of primers which can be obtained from pervious relevant literatures for each staphylococcal enterotoxin. Specificity and rapidity are usually used to describe the advantages of PCR (Maurer, 2006). PCR can detect the presence of SEs according to the specific gene sequences of each enterotoxin even from heat-treated food products (Bhatia & Zahoor, 2007).

PCR is based on amplifications of the target genes in a PCR thermocycling machine which provides an optimum temperature for DNA to denature, anneal and synthesise (Maurer, 2006). The temperature of a standard PCR reaction first increase to 96°C separating the template DNA strands and then decrease to 55°C (annealing temperature) allowing primers to anneal to each DNA strand. Finally, the temperature increases to 72°C (extension temperature) which is the optimum temperature environment for *Taq* polymerase (Innis et al., 1999). Therefore, extracted DNA template, designed primers, deoxynucleotide triphosphates (dNTP) mixture, *Taq* polymerase, buffer and water are the essential reagents to run a PCR reaction. Experimental design and optimisation of a PCR protocol for an experiment of interest are usually required to amplify targeting genes successfully without non-specific amplifications, as PCR is so sensitive that reaction components and working conditions must provide an optimal environment for amplifications of a DNA

template. Such parameters as primer design, concentrations of each reagent and cycling conditions are required to optimise (Weissensteiner et al., 2010).

A single PCR uses only one pair of primers (forward and reverse) in each reaction while multiplex PCR application involves multiple primer pairs which can amplify several target genes in one single reaction (van Pelt-Verkuil et al., 2008). Compared to single PCR, multiplex PCR is more efficient if many DNA samples or target genes in a sample need to be tested (Innis et al., 1990). On the other hand, non-specific PCR products are a common problem of Multiplex PCR because the primer pairs in each reaction may anneal to each other if the annealing temperature or the design of each primer are not optimal (van Pelt-Verkuil et al., 2008).

Food samples need to be prepared before starting a PCR reaction. The preparation of food samples varies with the type of food which has been explained and summarised by Maurer (2006), including collection of from food sample, food sampling process, concentration or amplification of pathogens, template extraction and concentration (Figure 2.6).

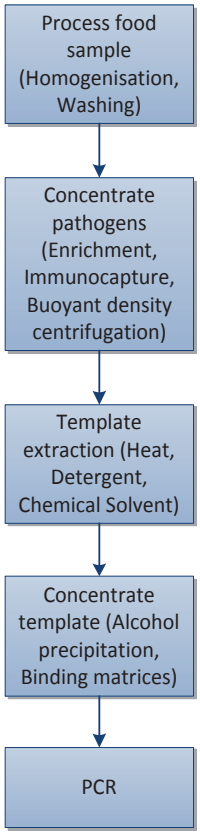


Figure 2.6 Preparation of food samples for PCR analysis (Maurer, 2006).

2.7 Identification the strain of *S. aureus*

Identifying the specific strains of *S. aureus* has been applied to investigate the source of contamination or an outbreak which can provide the relatedness within a range of isolates (Bannerman et al., 1995; McCullagh et al., 1998). To date, several methods are available to subtype *S. aureus* isolates, such as Phage Typing, Biotyping, Plasmid Typing, Pulsed-Field Gel Electrophoresis (PFGE), Amplied Fragment Length Polymorphism (AFLP) and Multilocus Sequence Typing (MLST) (Chaffey et al., 1988; Enright et al., 2000; Harbottle et al., 2006; McDougal et al., 2003; Murchan et al., 2003). Biotyping and Phase Typing were widely used around 1900s to distinguish the strains of *S. aureus* (Devriese, 1980; Gibbs, Patterson, & Thompson, 1978;

Harvey et al., 1982; Notermans et al., 1982). The occurrence of *S. aureus* and its contamination source in a poultry processing plant were investigated using Phase Typing, Plasmid Typing, PFGE and MLST (Chaffey et al., 1988; Gibbs, Patterson, & Thompson, 1978; Notermans et al., 1982). However, Phase Typing has several drawbacks such as poor reproducibility, low discriminatory power, high labour work and time-consuming (Bannerman et al., 1995; Harbottle et al., 2006). Plasmid typing is considered a better method for typing strains of *S. aureus*, but disadvantages such as average discriminatory and intense work still exist (Bannerman et al., 1995; Chaffey et al., 1988). PFGE and MLST both are molecular typing method with MLST possessing the highest reproducibility and discriminatory (Harbottle et al., 2006; Lv et al., 2014). MLST is a more rapid method which only needs 1-2 days to identify one strain while it takes at least 3 days using PFGE method (Bannerman et al., 1995). MLST method also makes it possible to transform and share the data between laboratories all over the world via Internet (Robinson & Enright, 2004).

The MLST method is based on sequencing the DNA fragment (~500bp) of seven house-keeping genes on both strands (Maiden et al., 1998). An allele number can be obtained from the MLST database which is available from the MLST website after submitting trimmed sequences (http://www.mlst.net/). The unique seven allele numbers of a specific strain are assigned a sequence type (ST) which is also called allelic profile (Urwin & Maiden, 2003). Figure 2.7 shows the overall steps on how to perform the MLST method (Spratt, 1999). The strains of pathogens, such as *Cryptococcus neoformans*, *Cryptococcus gattii*, *Pseudomonas aeruginosa*, *Escherichia coli* and *S. aureus*, have been successfully identified using MLST in some studies (Johnson et al., 2007; Lacher et al., 2007; Lv et al., 2014; Meyer et al., 2009). Moreover, Waters et al. (2011) used MLST to investigate the multidrug-resistant of *S. aureus* isolates in poultry meat in the United States.

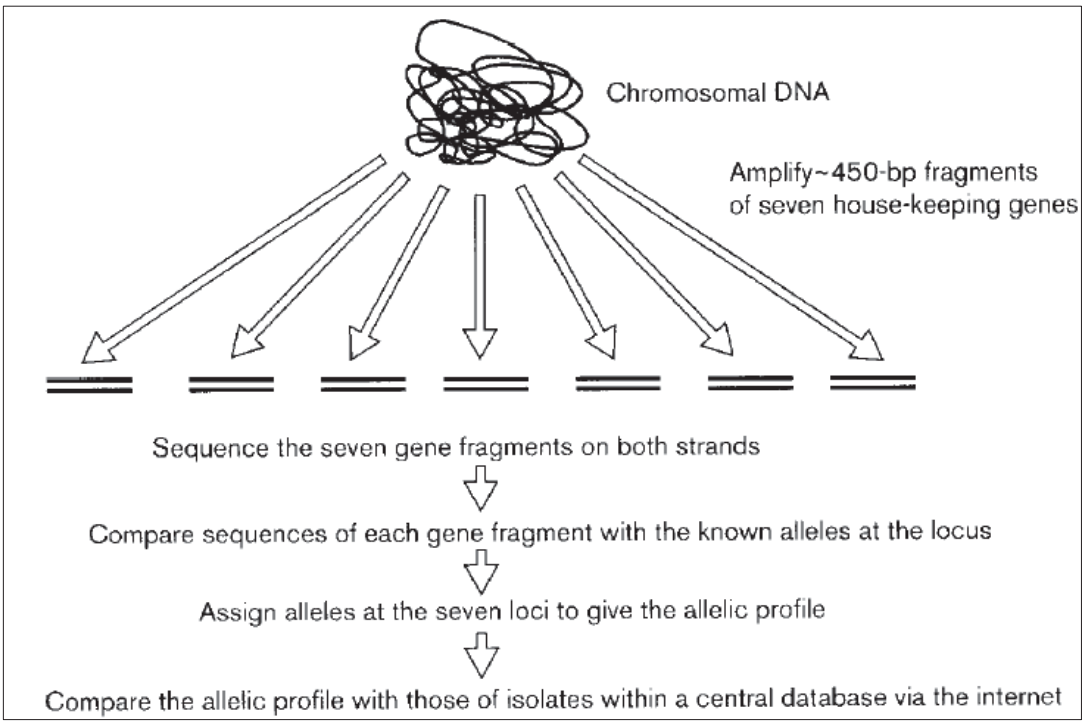


Figure 2.7 Overview of procedures for MLST method (Spratt, 1999).

The contamination sources in food products can be traced based on the sequence types (STs) of microorganisms isolates collected from processing line. The MLST data have been widely used to investigate the relatedness within some *S. aureus* isolates by Based Upon Repeat Sequence Types (eBURST) programme (Mellmann et al., 2008). Compared to using data of Pulsed-Field Gel Electrophoresis (PFGE), Randomly Amplified Polymorphic DNA Analysis (RAPD) and Phage Typing, MLST data can group isolates into a most unambiguous clonal complex (Grundmann et al., 2002). eBURST analyses the genetic relationships between each sequence type (ST) according to the similarity of the seven allele (de Sousa & De Lencastre, 2003; Feil et al., 2003; Grundmann et al., 2002; Schulte et al., 2013). Normally, STs that have identical allele at least five of the seven analysed genes are grouped into a clonal complex (CC). The stringent group definition can be modified if the research requires (MLST database, 2015). Single-locus variants (SLVs) were described as ST that differs from other STs in the group at only one allele number. Therefore, a clonal

ancestor in a group of STs is identifiable as the one with the largest number of SLVs (Grundmann et al., 2002; MLST database, 2015).

2.8 Critical sampling locations in poultry processing plants

2.8.1 Industrial environment

In section 2.2, the whole poultry processing procedures have been discussed, however, in order to understand the source of contamination of *S. aureus* during processing and also to eventually prevent the contamination of *S. aureus*, critical sampling locations should be identified. Many previous researchers have reported some critical sampling locations in terms of *S. aureus* contamination in poultry plants. For example, Notermans et al. (1982) collected their chicken samples before and after scalding, after defeathering, evisceration, washing and chilling. Mead et al. (1988) identified the critical sampling locations of broiler chickens as after bleeding, scalding, defeathering and chilling. Mead et al. (1993) regarded seven stages during poultry processing as sampling locations and they were after bleeding, scalding, defeathering, evisceration, washing, chilling and packaging. Similarly, Chaffey et al. (1988) examined chicken neck skin after bleeding, scalding, plucking and chilling to find the source of contamination of *S. aureus*. According to the distribution of *S. aureus* in a poultry plant that was reported by Gibbs, Patterson, and Thompson (1978), the viable counts of *S. aureus* were relatively high before scalding, defeathering, before and after evisceration.

2.8.2 Farm environment

Live poultry is considered as another potential contamination source of *S. aureus* causing skin lesion of live birds or poultry products contamination (Ministry of Primary Industry, 2001; Thompson et al., 1980). The symptom of infected chicken is dermatitis and depression will then occur (Kuramasu et al., 1967). Kibenge et al. (1982) collected their samples from chickens in an Australian poultry farm and the sampling sites were chickens with lesions, skin, nostril of normal chickens, air samples in the poultry sheds and inanimate hatcheries. Poultry skin is widely known as the source of *S. aureus* contamination especially in bruised skin. It is probably because that *S. aureus* grow better in bruised skin than normal skin (Kuramasu et al., 1967; Ministry of Primary Industry, 2001). Nostrils of live chicken are another potential sampling sites with high level of *S. aureus* as necrosis of skin was believed to originate from the inside surface of chicken wings after preening (Kuramasu et al., 1967).

2.9 Sampling methods of poultry meat

In poultry industries, it is essential to select a uniform sampling method to examine and control the microbiological quality of final products in order to simplify and standardise sampling procedures (Gill et al., 2005). Excision, swabbing, contact methods and rinse are the four available methods to sample poultry meat before microbiological analysis.

Each method has advantages and disadvantages. For example, excision and swabbing are the two popular sampling methods due to their convenience of conducting and

good reproducibility (Capita et al., 2004). However, excision needs more preparation steps of samples before plating than swabbing, such preparation steps are homogenisation and filtration (Pepperell et al., 2005). Also, excision method involves destruction of poultry samples normally by cutting or scrapping (Capita et al., 2004; Pepperell et al., 2005). Probably these factors can explain why swab technique is widely used in poultry plants (Capita et al., 2004). Cogan et al. (1999) and Gibbs, Patterson, and Thompson (1978) used swabbing method in their studies to investigate microbial contamination of chicken carcases in a poultry plant and in kitchen respectively.

Only excision method is preferred by EU to a standardised level of analysing microbiological performance of poultry carcasses (Pepperell et al., 2005). It is reported that swabbing method recovers less microorganisms than excision and rinse methods (Capita et al., 2004; Gill et al., 2005; Korsak et al., 1998; Pepperell et al., 2005). In general, using swabbing, the viable counts of bacteria of poultry carcasses were >0.5 log unit less than using excision and rinse, while there was no significant difference between excision and rinse (Gill et al., 2005). There are many factors that affect the variations of swabbing, such as the type of bacteria, the time of swabbing, the storage time before swabbing, swabbing area size, pressure used when swabbing etc. (Capita et al., 2004).

Contact methods requires few materials such as agar syringes and membrane filter blots, but this method can only be used when the counts of microorganisms is less than 100 CFU/cm^2 (Capita et al., 2004). In addition, there is no significant different on the counts of bacteria when samples are treated with contact method or swab technique (Salo et al., 2000).

3. Materials and Methods

Phase I

3.1 Identification of key processing steps in the plant

3.1.1 Industral level

Collection of samples was back-tracked from the final products at further processing to primary processing. The samples were collected as follows: (1) further processing plant: Final Products, Frozen Mechanically Separated Meat (MSM), Frozen Skin, Frozen Skin-On Breast; (2) secondary plant: Fresh MSM, MSM carcass, inside Mechanically Deboning Machine (MDM), MDM conveyor, Fresh Skin, Skinner conveyor and Fresh Skin-On Breast; 3) primary plant: Rubber Fingers in Plucker. Figure 3.1.1 shows the hierarchical relationships between the sampling sites.

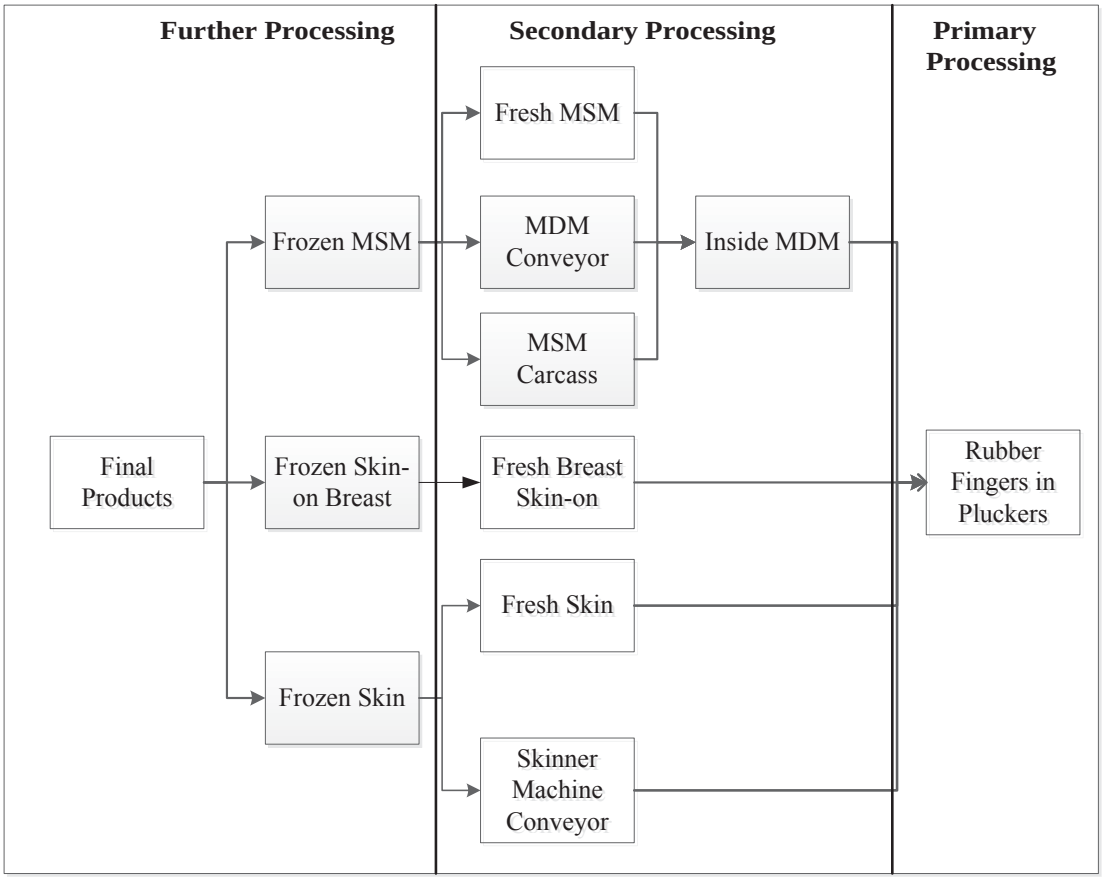


Figure 3.1.1 Hierarchical relationships of sampling sites in the poultry plant. Arrows indicate the route followed to collect Final Products. MSM=Mechanically Separated Meat; MDM=Mechanically Deboning Machine.

The results of the three frozen ingredients in the further processing plant discussed in section 5.1.2 showed high contamination by *S. aureus*. More samples were examined in the secondary processing plant focusing on Fresh MSM, Fresh Skin and Fresh Skin-on Breast (SO BF) to trace back the potential contamination sources. Eighteen samples (n=18) were collected in three batches (6 samples per batch) from fresh meat. Also, samples were collected during 6-h processing for three iterations (three batches) to investigate whether there was potential accumulation of *S. aureus* on the meat samples or surfaces of equipment.

3.1.2 Farm level

As mentioned in section 2.8.2, nostrils and skins of live chickens were regarded as the most likely sources of *S. aureus* (Ministry of Primary Industry, 2001; Thompson et al., 1980). Therefore, swabs from skins and nostrils of live chickens were randomly collected at a selected local poultry farm.

3.2 Collection of swab samples

3.2.1 Processing environment

Samples were collected from a commercial poultry processing plant located in Auckland, New Zealand for seven consecutive months from May (early winter) through to November (beginning of summer) 2014. From reception of live birds to final products, industrial poultry processing mainly uses mechanical equipment using standardised technology including one or more cooking steps. The entire factory consists of primary processing, secondary processing and the further processing plant. Chicken meat samples from processing stages and swab samples from equipment and surfaces were collected and transported to the Massey University Microbiological Research Laboratory at Albany, Auckland. The microbiological samples were kept chilled (~ 4°C) in a chilly bin with ice. Upon delivery, samples were stored at -20°C freezer until required for analysis.

3.2.2 Collection of samples at farm level

Samples from a local poultry farm which supplies live chicken to the commercial processor were collected from late November (early summer) to December (mid-

summer) 2014. Swabs from skins and nostrils of live chickens were collected and transported to the Massey University under chilled condition as described in section 3.2.1. Collected samples were stored in a -20°C freezer until required for further analysis.

3.3 Sampling

3.3.1 Fresh samples of chicken meat

Six final product samples were collected for six batches (n=36). Other fresh chicken meat samples were randomly collected from the processing line and placed into sterile stomacher bags (LABPLAS®, Canada). Six chicken meat samples (n=6) from each batch were collected during 6 h of processing at intervals of 1 h. A total of three batches of each fresh chicken meat samples were collected (n=18).

3.3.2 Frozen chicken meat

Small portions (about 100 grams) of frozen chicken meats were cut using a cutter that was aseptically cleaned using anti-bacterial general purpose wipes (Fabricell, New Zealand) from 15-kg cartons. The cut samples were placed into sterile stomacher bags (LABPLAS®, Canada). Six frozen meat samples were obtained from three different batches (n=18).

3.3.3 Collection of swab samples from processing plant equipment

Swab samples from the conveyors on Skinner machine and Mechanically Deboning Machine (MDM) were collected using the method of ISO 18593 (ISO, 2004) with some modifications. The sampling procedure used is shown in Figure 3.3.1. Swab samples were collected by wet and dry swabbing to maximise cell collection. To

collect samples, cotton swabs were immersed into peptone water to moisten the cotton and the tips were pressed against the wall of dilution bottle to remove excess water. Then the cotton swabs were placed on the conveyor surface of a random area to streak about 5 cm^2 horizontally and vertically. The swabs were simultaneously rotated between thumb and forefinger in two directions for approximately 30 s. Swab samples were then placed into dilution bottles containing 9 mL of sterile 0.1% peptone water. Cotton swab tips were then broken off aseptically and the bottles were closed. To maximise the collection of cells from the surface, wet swabbing was followed by dry swabbing of the same area and then the swabs (dry) were placed into the same diluent bottle. For each equipment, six independent swabs were collected again for three batches, giving a total of 18 samples (n=18).

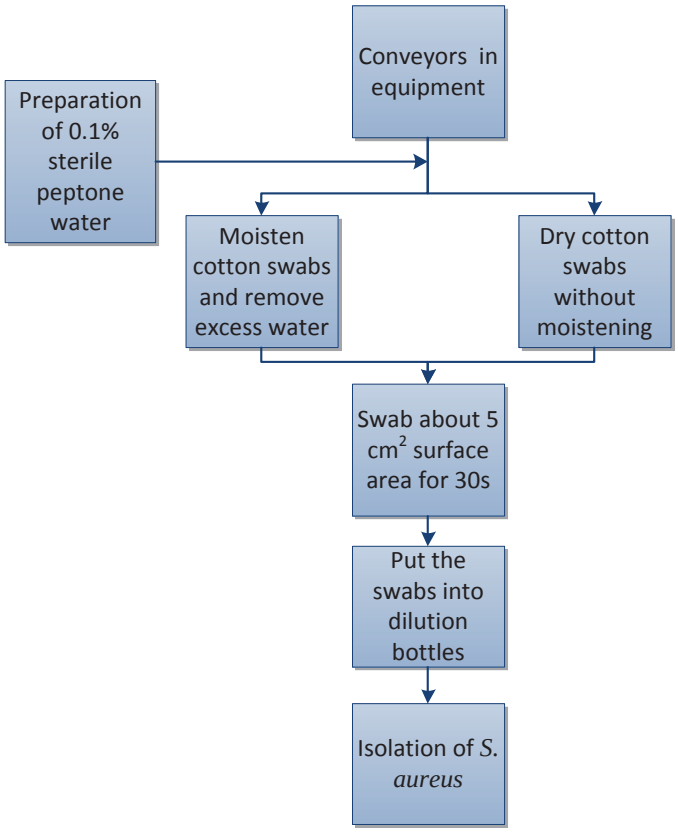


Figure 3.3.1 Procedure for collection of swab samples from conveyors on skinner machine, MDM conveyor, inside MDM equipment and Rubber Fingers in Pluckers. MSM=Mechanically Separated Meat; MDM=Mechanically Deboning Machine.

3.3.4 Collection of swab samples from live chicken at farm level

At the farm level, swab samples were collected from live chicken using sterile swabs as previously described in section 3.3.2. Six swab samples (n=6) were collected from the skin and nostrils of live chickens at the ages of one, three and six weeks old respectively, from November to December 2014 (n=18). All the swabs were placed directly into dilution bottles with 9 mL 0.1% sterile peptone water.

3.4 Enumeration of *S. aureus*

Enumeration of *S. aureus* was carried following the procedure of the AOAC Official Method 2003.11 (AOAC, 2005a) using 3M™ Petrifilm™ Staph Express Count Plate (3M™, USA). This method offers convenience and good reproducibility (Aarnisalo et al., 2006). The Petrifilm Staph Express Count Plate (3M™, USA) contains a cold-water-soluble gelling agent with modified Baird-Parker agar inside which is a selective and differential agar to identify *S. aureus* colonies. The red-violet colonies on the plate are regarded as *S. aureus* (3M™, 2010b). Figure 3.4.1 shows the overall isolation process.

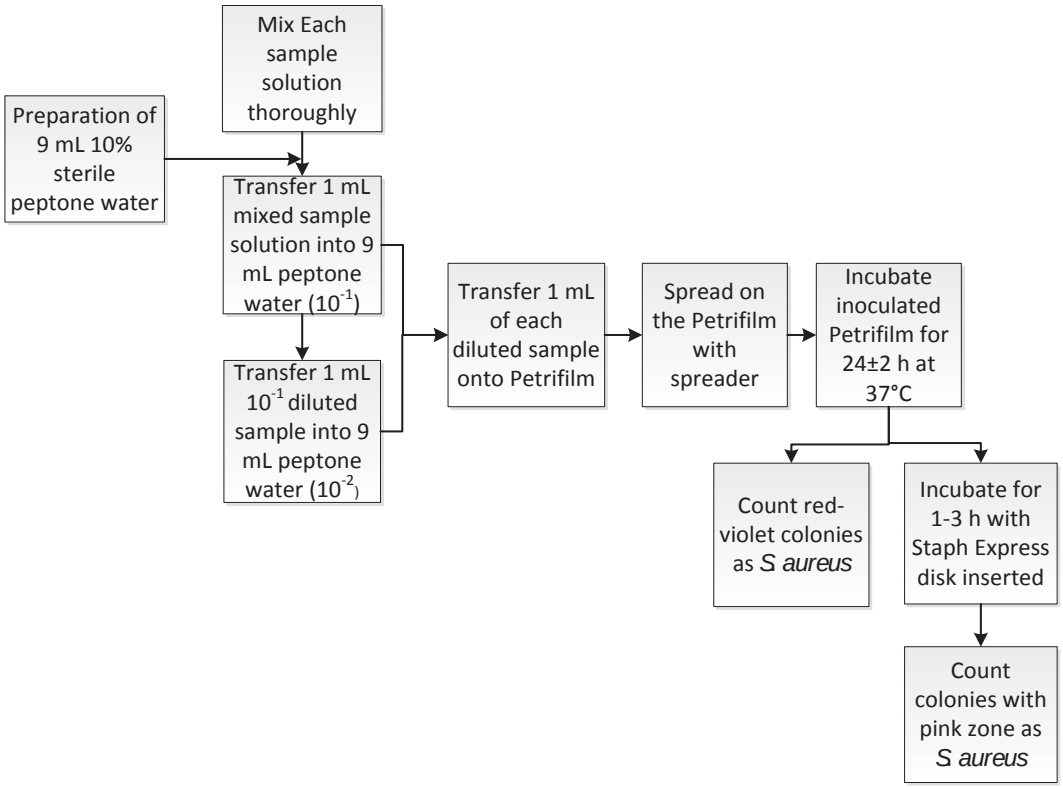


Figure 3.4.1 Isolation procedure of *S. aureus* from chicken meat and swab samples using 3M™ Petrifilm™ Staph Express Count Plate Method (3M™, 2010b).

3.4.1 Preparation of dilutions for meat and swab samples

The plating procedure was performed according to the Petrifilm™ Staph Express Count Plate Interpretation Guide (3M™, 2010b). A sterile stomacher bag was carefully placed into an empty 500 mL plastic beaker on a top-pan balance (PB3002 METTER TOLEDO, Switzerland) without touching the inside of the bag. About 25g of meat sample were weighed (exact weight of sample was recorded) and about 225 g of 0.1% peptone water was added giving a 10^{-1} dilution. Then the stomacher bag was placed into the stomacher (IUL Instrument, Spain) to blend the meat sample for approximately 90 s. In terms of swab samples, dilution bottles with 9 mL 0.1% peptone water with cotton swabs resulted in 10^{-1} dilutions. Bottles containing swabs

were mixed thoroughly for about 1 min using a vortex mixer (VM-96B JEIO TECH, Korea) (Waters et al., 2011).

For all samples, 10^{-2} dilutions were prepared by aseptically withdrawing 1 mL of mixed samples (10^{-1} diluted samples) to another dilution bottle with 9 mL sterile peptone water. Proper sample dilutions are essential to ensure the number of *S. aureus* grown colonies on the Petrifilm to fall within the countable range (15 to 150 cells/ Petrifilm). In this study, 10^{-1} and 10^{-2} dilutions were prepared.

3.4.2 Plating of samples on Petrifilms

After preparing a series of suitable dilutions (10^{-1} and 10^{-2}) for each sample, 1 mL of each dilution was plated onto the center of the bottom Petrifilm. Then the Petrifilm was covered carefully by rolling top film down. A plastic Staph spreader (3M™, USA) was pressed downward immediately to distribute sample inoculum over growth area evenly. The inoculated Petrifilms were incubated at 37°C for 24±2 h with clear side up after leaving them for about 1 min to allow the gel to solidify. The plating process was carried out in duplicate for each dilution of each sample (10^{-1} and 10^{-2}). After incubation, *S. aureus* colonies were counted when only red-violet colour isolates were present on the Petrifilm (Figure 3.4.2). Otherwise, a Petrifilm Staph Express disk was inserted into the well of the plate. In order to ensure the disk contact gelled uniformly, pressure was applied by sliding a finger firmly across the whole area of disk, especially the edges to eliminate air bubbles. Then the Petrifilms were incubated for 1 to 3 h more at 37°C. Finally, the colonies with pink zone on the Petrifilm (Figure 3.4.2) were counted as *S. aureus* using a plate counter (Ratek, Australia) and the results were expressed as $\log_{10}$ CFU/g or $\log_{10}$ CFU/swab.

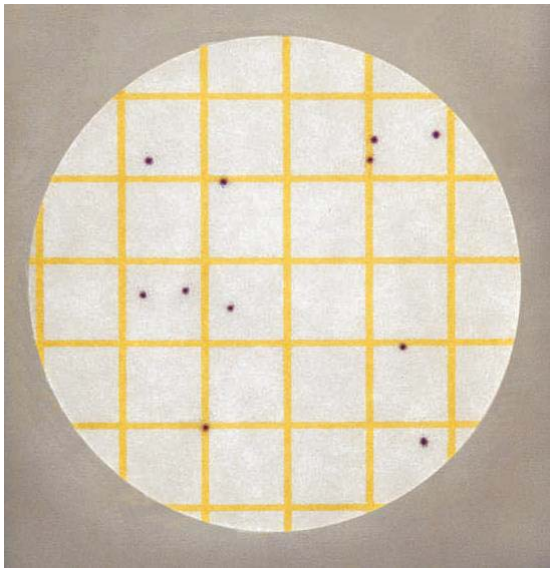


Figure 3.4.2 Petrifilm with typical red-violet colonies after 24±2 h incubation at 37°C (3M™, 2010b).

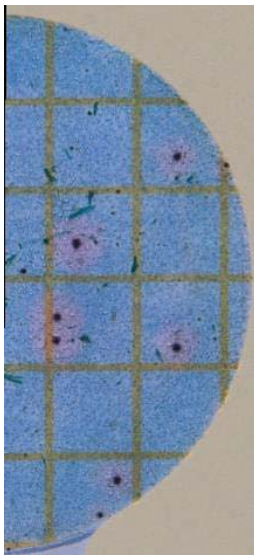


Figure 3.4.3 Incubated colonies with typical pink zones on the Petrifilm after inserting an Express disk (3M™, 2010a).

3.5 Confirmation tests for *S. aureus* isolates

S. aureus isolates are identified by red-violet coloured colonies (Pepe et al., 2006) or by colonies with pink zones after using the Petrifilm Staph Express disk (AOAC, 2005a). Confirmation tests, such as Gram-staining, catalase test, coagulase test,

carbohydrate fermentation, DNase and phosphatase tests are usually conducted as described in the Bergey's-Manual (Bergey et al., 2001). The confirmation tests have been widely used to confirm *S. aureus* isolates (Gibbs, Patterson, & Harvey, 1978; Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al., 2005; Lee, 2006; Matyi et al., 2013; Mead et al., 1988). In this study, the putative isolates of *S. aureus* were confirmed by conducting Gram-staining and coagulase test.

3.5.1 Gram-staining

Standard Gram stain of picked grown colonies was conducted as described by Harrigan (1998). A drop of water was added to a clear and dry slide (Interlab, New Zealand) before adding a well-isolated *S. aureus* colony picked from the Petrifilm. The colony was suspended in the water drop and spread evenly across the slide surface to obtain a thin film. Then the slide was passed through a Bunsen burner flame 3 times to heat-fix it before placing the slide on the rack over the sink. Crystal Violet and Gram's Iodine were added to the smear and washed off by running water after 1 min. Three to four drops of decolourising solution were then added onto the slide to rinse. Then the slide was washed under running water and excess water was gently shaken off. Then, Safranin was added onto the slide and washed off after 30 seconds by running water. Finally, the slide was examined on a DM 500 microscope (Leica, German) after the slide was dry. Purple cells were indicative of Gram-positive (*S. aureus*) and red cells indicated Gram-negative of the bacterium. As mentioned before, *S. aureus* is Gram-positive cocci (Figure 3.5.1).

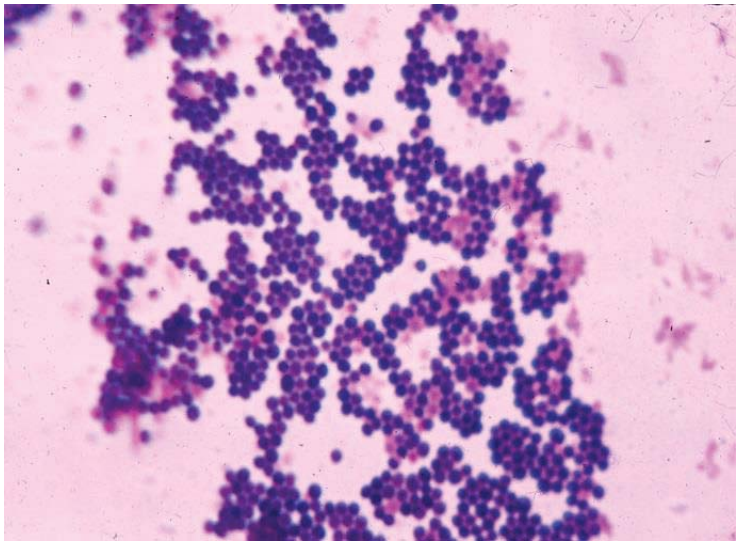


Figure 3.5.1 Typical appearance of Gram-stained *S. aureus* when examined under ×100 oil-immersion lens (nd, 2011)

3.5.2 Coagulate test

Coagulase test was performed based on the AOAC method (AOAC, 2005b). Brain Heart Infusion (BHI) broth (Oxoid, England) was prepared according to the manufacturer's instructions (Appendix A). Sterilised BHI broth was then distributed in 0.2 mL portions into small test tubes. Well-isolated colonies were picked using a sterilised inoculating loop after lifting the top film of the Petrifilm and transferred to the small test tubes containing sterile 0.2 mL BHI broth. Coagulase plasma with Ethylenediaminetetraacetic acid (EDTA) (BD BBL™, USA) were reconstituted following the manufacturer's instructions (Appendix A) and then 0.5 mL were added into the BHI cultures after incubation for 18 h at 37°C. All the tubes were incubated at 37°C and examined at 6-h interval. Presence of *S. aureus* was confirmed by coagulation of at least $^{3}/_{4}$ content of the tube (Figure 3.5.2).

Figure 3.5.2 Typical results of coagulate test for confirming suspect *S. aureus* colonies (Roberts & Greenwood, 2002), (a) negative, (b) weak positive, (c) positive.

Phase II

3.6 Characterisation of isolates of *S. aureus*

In order to investigate the potential contamination source linking the farm to the selected sampling location in the processing plant, ten representative *S. aureus* colonies from each location were selected for tracing back the contamination source from final products to live chickens which gives a total number of sixty *S. aureus* isolates.

As described in section 3.3.2, at each sampling location, individual samples were plated in duplicate for each dilution factor (10^{-1} and 10^{-2}). Depending on the growth of the cells on the Petrifilms, the sampling of *S. aureus* colonies of Phase II was carried out from one dilution factor (10^{-1} or 10^{-2}) in accordance with the enumeration of *S. aureus* in Phase I. Ten separated *S. aureus* isolates were selected from ten independent Petrifilms of each sampling location and coded. Figure 5.7 demonstrates the selection of *S. aureus* colonies from one sampling location and Table 3.6 shows the relationship between the number codes of *S. aureus* isolates and sampling sites.

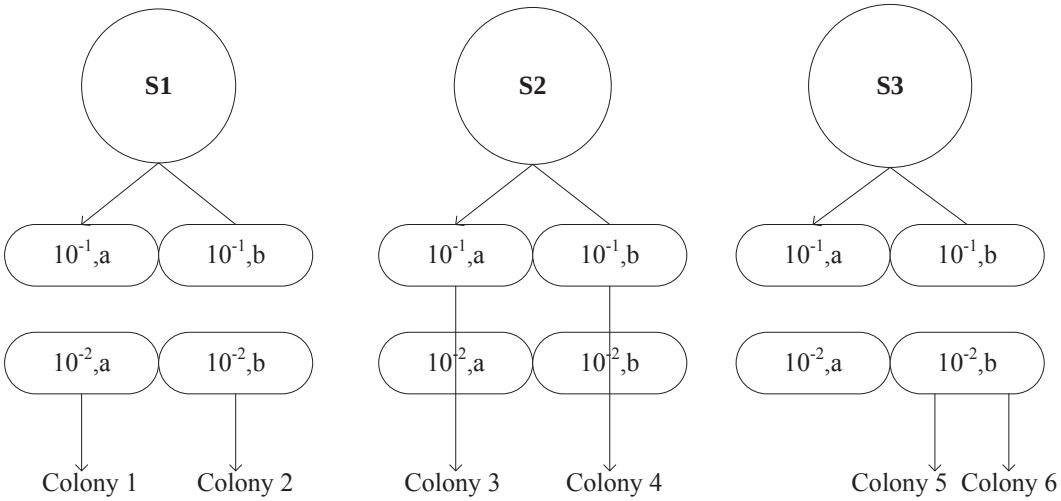


Figure 3.6 Typical selection *S. aureus* isolates from three samples at one sampling location. S1: sample 1, S2: sample 2, S3: sample 3; 10^{-1} and 10^{-2} are dilution factors; a and b are duplicates for each samples.

Table 3.6 The relationship between the codes of *S. aureus* isolates and source of samples.

Sampling sites	Colony code
Final Products	1-10
Fresh MSM	11-20
Fresh Skin	21-30
Fresh SO BF	31-40
Rubber Fingers	41-50
Live Chicken	51-60

Colony code 1-10 contains colonies 1 to 10; Colony code 11-20 contains colonies 11 to 20; Colony code 21-30 contains colonies 11 to 30; Colony code 31-40 contains colonies 31 to 40; Colony code 51-60 contains colonies 51 to 60. MSM=Mechanically Separated Meat. SO BF=Skin-On Breast Fillet.

3.7 DNA extraction

3.7.1 Recovery of *S. aureus* isolates

Ten *S. aureus* isolates from each main sampling site: Final Products, Fresh MSM, Fresh Skin, Fresh Skin-On Breast Fillet, Rubber Fingers in the Plucker and Live Chicken were selected. The sampling size was decided after consideration that: 1) the scope of this research focused on quality rather than quantity; 2) the aim of this study was to investigate as many sampling sites as possible to identify the potential contamination source of *S. aureus* within the

confines of the financial resources and time. Therefore, ten representative *S. aureus* isolates grown on Petrifilms were randomly selected from each of the six main sampling sites. In total, sixty representative *S. aureus* isolates were recovered from incubated Petrifilms using a sterile inoculation loop and streaked onto nutrient agar (OXOID, England)(Appendix A), followed by 24-h of incubation at 37°C to achieve maximum recovery of each isolate (EI-Jakee et al., 2013). After incubation, one isolated colony from the corresponding nutrient agar was inoculated into 10 mL of nutrient broth (OXOID, England)(Appendix A) in a 50 mL falcon tube (Greiner bio-one, USA) using a sterile loop and incubated overnight at 37°C.

3.7.2 DNA extraction from *S. aureus* isolates

DNA of each *S. aureus* isolate from nutrient broth was extracted using the QIAamp® DNA extraction kit (Qiagen, Germany). The extraction procedure was based on the manufacturer's instruction with some modifications (Figure 3.7.2). The falcon tube containing overnight incubated *S. aureus* isolate was centrifuged for 10 min at 5000×*g* (7500 rpm) using Heraeus Multifuge ×1R (Thermo Fisher, Germany). The supernatant was discarded with about 1 mL left in each tube and the remaining suspension was transferred into a clean 1.5 mL micro-centrifuge tube (LP Italian Spa, Italy) after mixing using a vortex mixer (VM-96B JEIO TECH, Korea) for about 15 s. The 1.5 mL mixture containing microbial cells was centrifuged for 10 min at 5000×*g* (7500 rpm) using an IEC MICROMAX micro-centrifuge (Thermo, China), after which, the supernatant was discarded and the cell pellet was suspended in 180 µL of enzyme solution which contained 20 mg/mL lysozyme in 20 mM Tris·HCl (pH 8.0), 2 mM EDTA and 1.2% Triton (Appendix A). Twenty (20) µL proteinase K and 200 µL Buffer AL (lysis buffer) were added into the samples after incubation at 37°C for 30 min in a heating block (CHB-350S, JEIO TECH, Korea). The samples were mixed by vortexing (VM-96B, JEIO TECH, Korea) and again incubated at 56°C for 30 min and then for a further 15 min at 95°C using a heating block (CHB-350S, JEIO TECH, Korea). The sample solution was centrifuged in an IEC MICROMAX micro-centrifuge (Thermo, China) at 6000×*g* (8000 rpm)

for 30 s before adding 200 µL 100% ethanol and mixed by pulse-vortexing (VM-96B JEIO TECH, Korea) for about 15 s. Sample solutions were again centrifuged (6000×*g*, 8000 rpm) for 30 s to remove the drops of liquid from the lid. The mixture was transferred to QIAamp Mini spin column (in a 2 ml collection tube) without wetting the rim and centrifuged at 6000×*g* (8000 rpm) for 1 min. The 2-ml collection tube containing the filtrate was discarded and the QIAamp Mini spin column was placed into a clean 2-ml collection tube (supplied with the QIAamp® DNA extraction kit). Then, 500 µL Buffer AW1 (wash buffer) was added into the QIAamp Mini spin column followed by centrifugation at 6000×*g* (8000 rpm) for 1 min. Two (2) ml collection tube containing the filtrate was discarded afterwards and the QIAamp Mini spin column was placed into a clean 2 ml collection tube. After that, 500 µL Buffer AW2 (wash buffer) was added into the QIAamp Mini spin column followed by centrifugation at 20,000×*g* (14000 rpm) for 3 min. The QIAamp Mini spin column was again placed in a new 2-ml collection tube with further centrifugation at 20,000×*g* (14000 rpm) for 1 min. The final step comprised adding 200 µL Buffer AE (elution buffer) after placing the QIAamp Mini spin column in a clean 1.5-mL micro-centrifuge tube. Further incubation at room temperature for 1 min and a centrifugation step at 6000×*g* (8000 rpm) for 1 min were required. The final step was repeated once.

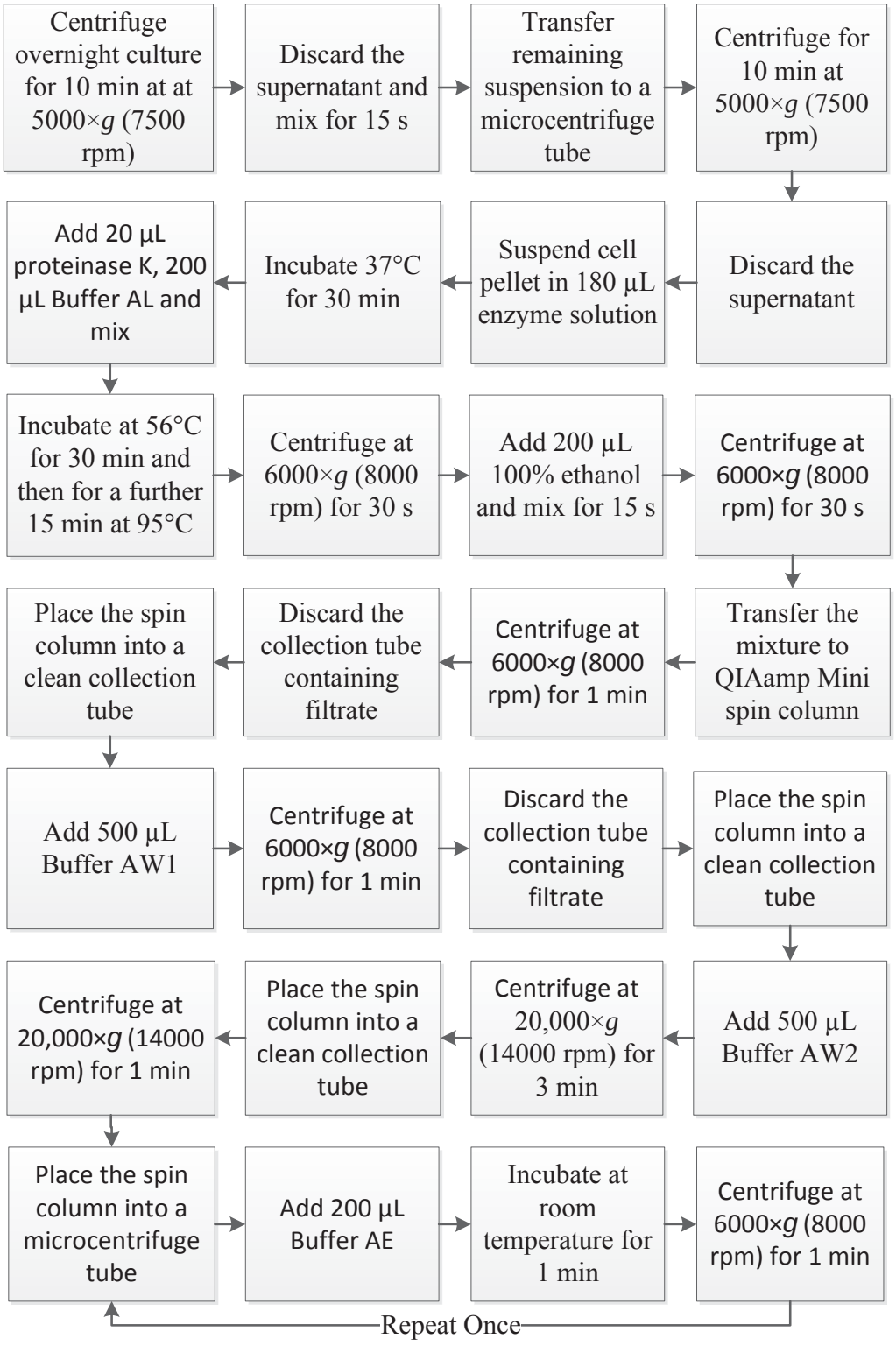


Figure 3.7.2 DNA extraction procedure (QIAGEN®, 2012).

3.7.3 Determination of the concentrations of extracted DNA

The concentration of the extracted DNA of each isolated *S. aureus* was determined using the GENOVA NANO spectrometer (JENWAY, UK) following the procedure described by QIAGEN® (2012). The equipment was set-up by first selecting the "DNA" button in the first panel and "ds DNA" button in the second panel. Before measuring the DNA concentration, about one µL of AE buffer (elution buffer in the QIAamp® DNA extraction kit (Qiagen, Germany)) was loaded onto the lower measurement pedestal for calibration. Then about one µL of DNA sample was loaded onto the lower measurement pedestal. Measurements of DNA concentration were taken by reading the absorbance of sample DNA at 260 nm. The reading was expressed in the unit of µg/mL. The pedestals (both upper and lower) were cleaned by Kimwipes (Kimtech Science, USA) between each measurement. Each extracted DNA sample was measured in duplicates. The data were recorded and DNA samples were stored at -20°C until for further analysis.

3.8 Identification of enterotoxigenic *S. aureus* isolates

3.8.1 Multiplex PCR protocol

3.8.1.1 Preparation of primers

The detection of enterotoxigenic *S. aureus* isolates were determined by Multiplex Polymerase Chain Reaction (PCR) according to Hwang et al. (2007). Eighteen (18) different types of enterotoxins were determined by amplifying their corresponding genes coding for enterotoxins: *sea* (enterotoxin A), *seb* (enterotoxin B), *sec* (enterotoxin C), *sed* (enterotoxin D), *see* (enterotoxin E), *seg* (enterotoxin G), *seh* (enterotoxin H), *sei* (enterotoxin I), *sej* (enterotoxin J), *sek* (enterotoxin K), *sel* (enterotoxin L), *sem* (enterotoxin M), *sen* (enterotoxin N), *seo* (enterotoxin O), *sep* (enterotoxin P), *seq* (enterotoxin Q) and *ser*

(enterotoxin R), *seu* (enterotoxin U). Also, *femA* gene was used to identify and confirm all sixty *S .aureus* isolates. All the primers pairs were divided into three reaction sets, detecting six to seven genes in one reaction. The primers in the three reactions are: 1) *seb, sed, sei, sej, sep, seq, ser, femA*; 2) *sea, sec, sek, sem, sen, femA*; 3) *see, seg, seh, sel, seo, seu, femA*. Information of the primers including the primer names, primer sequences, expected PCR product size and set of reactions are listed in Table 3.8.1.

Table 3.8.1 Primer information of enterotoxin genes and expected PCR product size.

Target gene	Primer	Oligonucleotide sequence (5′–3′)	Product size (bp)	PCR set
sea	SEA-f	ATGGTTATCAATGTGCGGGTGIIIIICCAAACAAAAC	344	2
	SEA-r	TGAATACTGTCCTTGAGCACCAIIIIIATCGTAATTAAC		
seb	SEB-f	TGGTATGACATGATGCCTGCACIIIIIGATAAATTTGAC	196	1
	SEB-r	AGGTACTCTATAAGTGCCTGCCTIIIIIACTAACTCTT		
sec	SEC-f	GATGAAGTAGTTGATGTGTATGGATCIIIIIACTATGTAAAC	399	2
	SEC-r	AGATTGGTCAAACTTATCGCCTGGIIIIIGCATCATATC		
sed	SED-f	CTGAATTAAGTAGTACCGCGCTIIIIIATATGAAAC	451	1
	SED-r	TCCTTTTGCAAATAGCGCCTTGIIIIIGCATCTAATTC		
see	SEE-f	CGGGGGTGTAACATTACATGATIIIIICCGATTGACC	286	3
	SEE-r	CCCTTGAGCATCAAACAAATCATAAIIIIICGTGGACCCTTC		
seg	SEG-f	ATAGACTGAATAAGTTAGAGGAGGTIIIIIGAAGAAATTATC	594	3
	SEG-r	TTAGTGAGCCAGTGTCTTGCIIIIIAATCTAGTTC		
seh	SEH-f	CATTCACATCATATGCGAAAGCAGIIIIITTACACG	218	3
	SEH-r	CTTCTGAGCTAAATCAGCAGTTGCIIIIITTACTCTC		
sei	SEI-f	AGGCGTCACAGATAAAAACCTACCIIIIICAAATCAACTC	154	1
	SEI-r	ACAAGGACCATTATAATCAATGCCIIIIITATCCAGTTTC		
sej	SEJ-f	TGTATGGTGGAGTAACACTGCATGIIIIIAATCAACTTTATG	102	1
	SEJ-r	CTAGCGGAACAACAGTTCTGATGCIIIIIATCCATAAAT		
sek	SEK-f	GTGTCTCTAATAATGCCAGCGCTIIIIICGATATAGG	282	2
	SEK-r	CGTTAGTAGCTGTGACTCCACCIIIIITGTATTTAG		
sel	SEL-f	ATTCACCAGAATCACACCGCTIIIIITACTCGTA	469	3
	SEL-r	GTGTAAAATAAATCATACGAGIIIIIAGAACCATCATTC		
sem	SEM-f	CGCAACCGCTGATGTCGGIIIIITGAATCTTAGG	572	2
	SEM-r	CAGCTTGTCCTGTTCCAGTATCIIIIIAGTCATAAG		
sen	SEN-f	TCATGCTTATACGGAGGAGTTACGIIIIITGATGGAAATC	103	2
	SEN-r	AACCTTCTTGTTGGACACCATCIIIIIATACATTAACGC		
seo	SEO-f	GTGGAATTTAGCTCATCAGCGATTTCIIIIIAATTTCTAGG	116	3
	SEO-r	GTACAGGCAGTATCCACTTGATGCIIIIIATGACAATGTGC		

Table 3.8.1 Primer information of 19 enterotoxin genes and expected PCR product size (continued).

sep	SEP-f	ATCATAACCAACCGAATCACCAGIIIIIGGGTGAAACTC	547	1
	SEP-r	GTCTGAATTGCAGGGAACTGCIIIIIGCAATCTTAG		
seq	SEQ-f	GGTGGAATTACGTTGGCGAATCAIIIIITAGATAAACC	330	1
	SEQ-r	CTCTGCTTGACCAGTTCCGGTGIIIIICAAATCGTATG		
ser	SER-f	TTCAGTAAGTGCTAAACCAGATCCIIIIICTGGAGAATTG	368	1
	SER-r	CTGTGGAGTGCATTGTAACGCCIIIIIATATGCAAACTCC		
seu	SEU-f	ATGGCTCTAAAATTGATGGTTCTAIIIIITTAAAAACAG	410	3
	SEU-r	GCCAGACTCATAAGGCGAACTAIIIIITTCATATAAA		
femA	Fem-f	ACAGCTAAAGAGTTTGGTGCCTIIIIIGATAGCATGC	723	1, 2, 3
	Fem-r	TTCATCAAAGTTGATATACGCTAAAGGTIIIIICACACGGTC		

IIIII: polydeoxyinosine

Source: Hwang et al. (2007)

All the primers were synthesised by Integrated DNA technologies (IDT®, New Zealand). A specification sheet of each primer was provided including the concentration of oligonucleotides, the weight of oligonucleotides in supplier tubes, and the absorbance at 260 nm. All the primers were diluted to a final concentration of 50 µM using sterile distilled water as stock solution from which working solution (2 µM) was prepared (Appendix B). Working solutions were dispensed in 1.5 mL aliquots into micro-centrifuge tubes and placed into a freezer (-20°C) for later use.

3.8.1. Multiplex PCR reactions

Multiplex PCR reaction was used to identify the enterotoxin types of *S. aureus* isolated from chicken meat, key processing equipment and from live chicken at the farm. The protocol described by Hwang et al. (2007) was used with all the isolates. The PCR reaction was carried out in a total volume of 50 µL including 25 µL of 2×Multiplex PCR Master Mix (Qiagen, Germany), 5 µL of 10• •primer mixture (0.2 µM of each primer), 0.5 µL of DNA template. The final volume was adjusted to 50 µL with RNase-free water (supplied with the kit).

Positive strains used in this study were ATCC 14458, ATCC 19095, FRI 913, FRI 472 and N315. Negative strain RN4220 and sterile distilled water were used as negative controls. These reference strains were selected based on the targeted genes coding for the types of enterotoxins. All ATCC strains were supplied by The Institute of Environmental Science and Research (ESR, NZ) while strain FRI 472 was supplied by Professor Luís Augusto Nero (Veterinary School, Universidade Federal de Viçosa, Brazil), strain FRI 913 was kindly supplied by Professor Iris Spiliopoulou (School of Medicine, University of Patras, Greece) and strain N315 were supplied by BEI Resources (http://www.beiresources.org/Catalog.aspx?q=N315). Figure 3.8.1 shows the multiplex PCR results of *S. aureus* reference strains for each reaction set. Negative controls (strain RN4220 & distilled water) were included in all PCR reactions. Basic information of these strains is listed in Table 3.8.2. ATCC strains were cultured according to ATCC' Bacterial Culture Guide (ATCC, 2014).

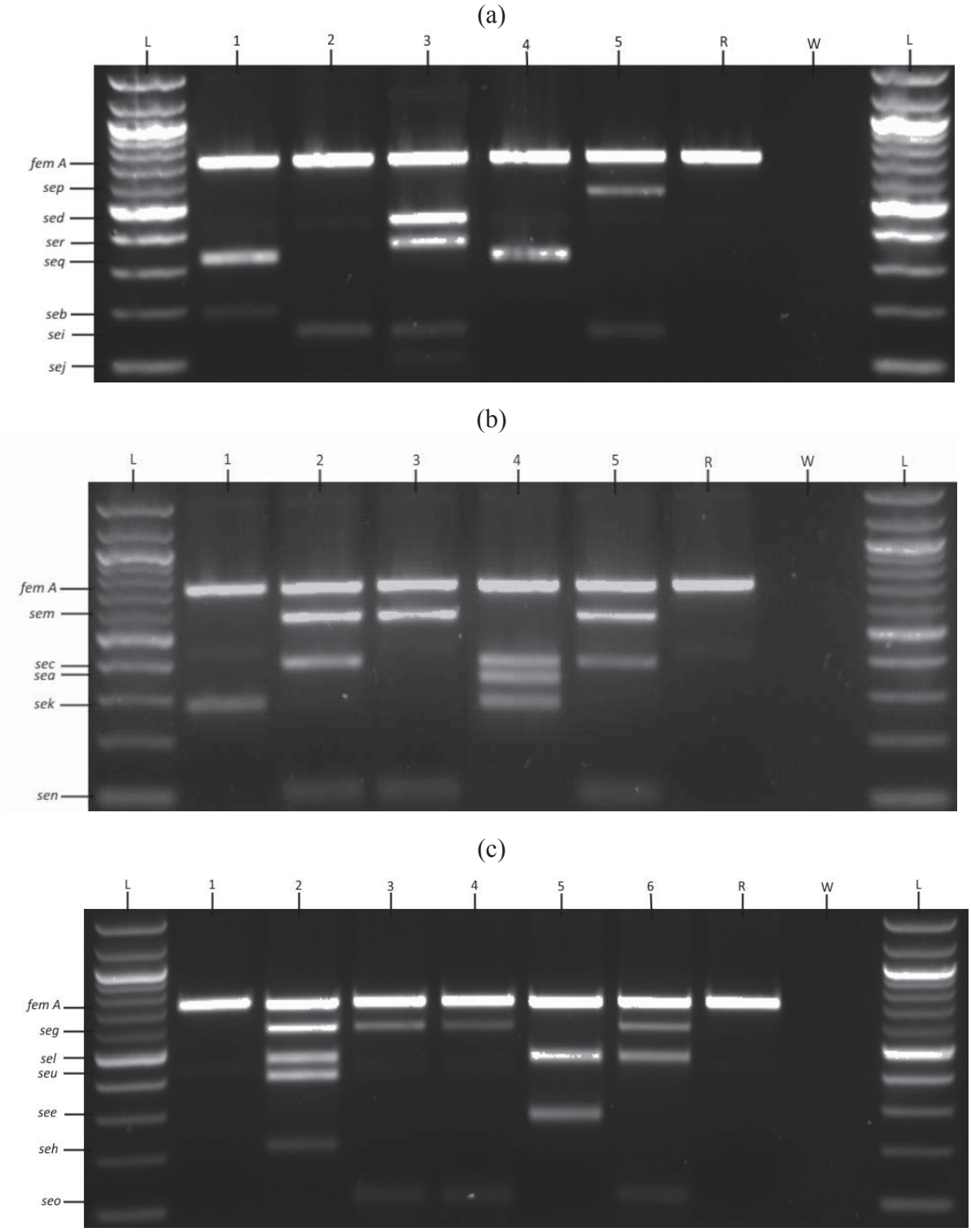


Figure 3.8.1 Multiplex PCR results of *S. aureus* reference strains for each PCR set. (a) Set 1: *sej* (102bp), *sei* (154bp), *seb* (196bp), *seq* (330bp), *ser* (368bp), *sed* (451bp), *sep* (547bp) and *femA* (732bp). (b) Set 2: *sen* (103bp), *sek* (282bp), *sea* (344bp), *sec* (399bp), *sem* (572bp) and *femA* (732bp). (c) Set 3: *seo* (116bp), *seh* (218bp), *see* (286bp), *seu* (410bp), *sel* (469bp), *seg* (594bp) and *femA* (732bp). L: 100bp DNA ladder, Lane 1: ATCC 14458 (*seb, seq, sek* and *femA*); Lane 2: ATCC 19095 (*sei, sem, sec, sen, seu, seh, sel, seg* and *femA*); Lane 3: FRI 472 (*sed, sei, sej, ser, sem, sen, seo, seg* and *femA*); Lane 4: FRI 913 (*seq, sec, sek, sea, sel, see* and *femA*); Lane 5: N315 (*sei, sep, sem, sen, sec, sel, seg, seo* and *femA*); Lane R: RN4220 (no toxin, *femA*); Lane W: distilled water (negative control).

Table 3.8.2 Basic information of the reference strains.

Strain Code	Enterotoxin gene (s)	Reference
ATCC 14458	*seb*	Johnson et al. (1991)
ATCC 19095	*sec, seg, seh, sei, sel, sem, sen, seu*	Bania et al. (2006)
FRI 472	*sej, seo, ser, sed, seg, sei, sem, sen*	Monday and Bohach (1999)
FRI 913	*sek, seq, sea, sec, see, sel, seq*	Bania et al. (2006)
N315	*sec, seg, sei, sel, sem, sen, seo, sep*	Kuroda et al. (2001)
RN4220	No toxin genes	Monday and Bohach (1999)

The amplification cycle steps were performed according to the cycling program described by Hwang et al. (2007) with the initial denaturation of 95°C for 15 min rather than 94°C for 15 min as which was suggested by the Multiplex PCR Master Mix manufacturer (QIAGEN®, 2010). PCR amplifications were carried out in a PTC1148 Thermal Cycler (BIO-RAD, Mexico) with an initial denaturation temperature of 95°C for 15 min to activate the HotStartTaq polymerase, followed by 30 cycles of 94°C for 30 s, 55°C for 90 s and 72°C for 2 min and a final extension at 72°C for 10 min.

3.8.1. Electrophoresis

Before resolving PCR products on 2% agarose gel by electrophoresis, 5 µL of 6× loading dye (Thermo Fisher, Lithuania) were added into 25 µL of the PCR reaction mixture as described by the manufacturer. A 2% agarose gel was prepared by dissolving 2 g agarose powder (AppliChem, GmbH, Germany) into 100 mL 1×TAE buffer (Thermo Fisher, Lathuania) or 0.6 g agarose powder into 30 mL 1×TAE buffer depending on the size of the electrophoresis apparatus. The solution was heated in a microwave for about 2 min to allow agarose powder to completely dissolve. Once the agarose gel solution was cooled (~40 °C), 1× SYBR® Safe DNA gel stain (Invitrogen, USA) was added. An electrophoresis apparatus (Owl, USA) was used to resolve the PCR products. The gel tray was placed in a buffer chamber before pouring cooled gel solution into the tray. Then a plastic comb was inserted into the gel immediately on the negative electrode side. The comb was gently pulled out of the gel after solidification of the gel solution. The 1×TAE buffer was then poured covering the gel completely. Ten (10) µL of amplified samples (25 µL amplified sample + 5 µL loading dye) were loaded into a sample well with 5 µL of 100 bp ladder (Biolabs®, Lithuania) loading into the first and the last sample well. The safety lid was replaced on top of the buffer chamber. Samples were

resolved at 60V for 60 min for small apparatus and at 100V for 60 min for large apparatus using a PowerPac™ Basic Power Supply (BIO-RAD, USA). Each gel was viewed under a Gel Doc™ EZ Imager (BIO-RAD, USA) and images were recorded.

3.9 Multilocus sequence typing (MLST) of *S. aureus* isolates

3.9.1 PCR protocol for MLST

All sixty *S. aureus* isolates were typed by the MLST method which involves the amplification and sequencing of the internal fragments of seven house-keeping genes of *S. aureus* (Enright et al., 2000). The seven loci are Carbamate Kinase (*arc*), Shikimate dehydrogenase (*aro*), Glycerol kinase (*glp*), Guanylate kinase (*gmk*), Phosphate acetyltransferase (*pta*), Triosephosphate isomerase (*tpi*) and Acetyle coenzyme A acetyltransferase (*yqi*) (http://saureus.mlst.net/misc/info.asp).

3.9.1.1 Preparation of primers

Information on the primer sequences of each locus were obtained from the MLST website (http://saureus.mlst.net/misc/info.asp). Table 3.7.1 shows the details of each primer including the expected product size (bp). The data on pimer sequences obtained from the website were in agreement with the information in the report by Enright et al. (2000) and the MLST method (http://saureus.mlst.net/misc/info.asp).

The primers were synthesised by Integrated DNA technologies (IDT®, New Zealand). As described in section 3.8.1.1, the concentration of oligonucleotides, the weight of oligonucleotides in supplied tube, absorbance at 260 nm of each primer were listed in the Certificate of Analysis. All the primers were diluted using sterile distilled water into a final concentration of 0.5 µg/µL as described by Enright et al. (2000)'s PCR protocol (calculations shown in Appendix B). All diluted primers were aliquoted into PCR tubes and stored in a freezer (~80 °C) for further analysis.

Table 3.9.1 Primer sequences and products size (bp).

Primer	Oligonucleotide sequence (5′–3′)	Product size (bp)
arc-f	5' TTG ATT CAC CAG CGC GTA TTG TC -3'	456
arc-r	5' AGG TAT CTG CTT CAA TCA GCG -3'	
aro-f	5' ATC GGA AAT CCT ATT TCA CAT TC -3'	456
aro-r	5' GGT GTT GTA TTA ATA ACG ATA TC -3'	
glp-f	5' CTA GGA ACT GCA ATC TTA ATC C -3'	465
glp-r	5' TGG TAA AAT CGC ATG TCC AAT TC -3'	
gmk-f	5' ATC GTT TTA TCG GGA CCA TC -3'	417
gmk-r	5' TCA TTA ACT ACA ACG TAA TCG TA -3'	
pta-f	5' GTT AAA ATC GTA TTA CCT GAA GG -3'	474
pta-r	5' GAC CCT TTT GTT GAA AAG CTT AA -3'	
tpi-f	5' TCG TTC ATT CTG AAC GTC GTG AA -3'	402
tpi-r	5' TTT GCA CCT TCT AAC AAT TGT AC -3'	
yqi-f	5' CAG CAT ACA GGA CAC CTA TTG GC -3'	516
yqi-r	5' CGT TGA GGA ATC GAT ACT GGA AC -3'	

3.9.1. PCR reactions

PCR amplification of the seven house-keeping genes of each *S. aureus* isolates was performed according to the protocol described by Enright et al. (2000) with some modifications. The PCR mixture had a total volume of 25 µL containing about 25 ng of DNA template, 0.5 µL of each primer, 0.1 U of *Taq* DNA polymerase (BioLabs®, Lithuania), 2.5 µL of 10 × buffer (supplied with *Taq* DNA polymerase), 0.2 mM of deoxynucleotide (dNTP) (BioLabs®, Lithuania) and the final volume was adjusted to 25 µL using sterile distilled water. The PCR reactions were carried out in a PTC1148 Thermal Cycler (BIO-RAD, Mexico) according to the following conditions: initial denaturation at 95 °C for 5 min, 30 cycles at 55 °C for 1 min, 72 °C for 1 min and 95 °C for 1 min, with a final extension at 72 °C for 5 min. Strain RN4220 was used as a positive control (Figure 3.9.1). Negative controls (sterile distilled water) were included in all PCR reactions.

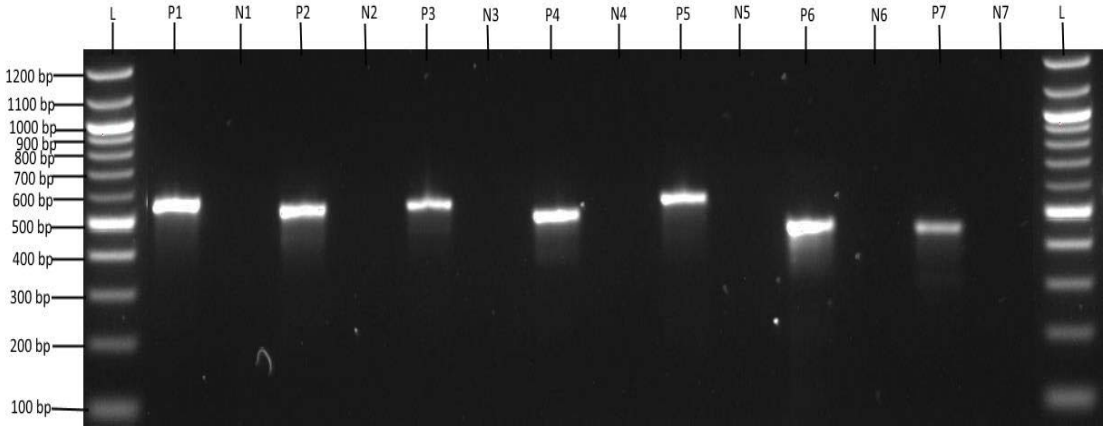


Figure 3.9.1 Amplification results of the seven house-keeping genes in RN4220 (positive control). L: 100bp DNA ladder; First letter P of each lane represents strain RN4220, N represents negative control (distill water); Last number of each lane represents the genes being amplified (1: *yqi* 516bp, 2: *arc* 456bp; 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp; 6: *gmk* 417bp, 7: *tpi* 402bp).

3 9.1 . E3l e c t r o p h o r e s i s

All amplified PCR products were analysed by electrophoresis. The procedure was similar to that described in section 3.8.1.3 with 5 µL of amplified products and 1 µL of loading dye being loaded onto the gel. Gels were examined under a Gel Doc™ EZ Imager (BIO-RAD, USA) and images were recorded.

3.9.2 Purification of amplified PCR products

Amplified PCR products were purified using QIAquick® PCR Purification Kit (Qiagen, Germany) according to the manufacturer's instructions (Figure 3.9.2). Twenty-four (24) mL of 100 % ethanol and 1:250 volume of pH indicator I were added into PE buffer (wash buffer) and PB buffer (binding buffer) respectively before conducting the purification procedure. The purification steps were performed as follows: 100 µL of PB buffer was added into PCR products and mixed by squirting up and down using a pipettor. The solution was transferred into a QIAquick column and centrifuged at 17,900 × *g* (13,000 rpm) for 1 min. The filtrate was discarded and the column was placed in the same tube. Then 750 µL PE buffer were added into the column and centrifuged at 17,900 × *g* (13,000 rpm) for 1 min, after which, the filtrate was discarded and the column was placed in the same tube. To remove residual wash buffer, the column was centrifuged again at 17,900 × *g* (13,000 rpm)

for 1 min. All the columns were placed in a clean 1.5 mL micro-centrifuge tubes before eluting the DNA. To elute the DNA, 30 µL EB (elution buffer) buffer were added onto the center of the QIAquick membrane with centrifugation at 17,900 × *g* (13,000 rpm) for 1 min. Finally, purified PCR products were analysed by resolving 5 µL of it on a 2% gel with 1 µL of 5× loading dye (supplied with the kit). The electrophoresis procedure was similar to that described in section 3.8.1.3.

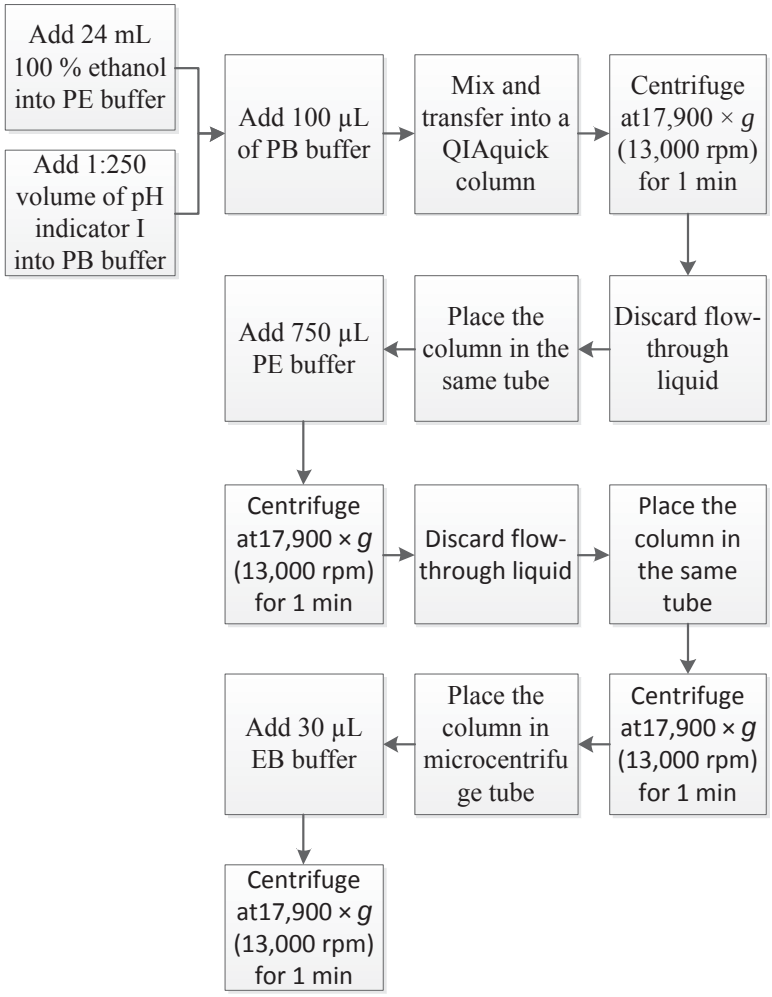


Figure 3.9.2 PCR products purification procedure.

3.9.3 Determination the concentrations of purified PCR products

After purification, the concentration of each PCR products was determined by GENOVA NANO spectrometer (JENWAY, UK). The procedure has been described in section 3.7.3. The concentration of each corresponding PCR product was recorded.

3.9.4 Sequencing of the seven house-keeping loci of each *S. aureus* isolate

Once the seven house-keeping genes of each *S. aureus* isolate were amplified and purified, all the samples were sent to Macrogen Inc. (Seoul, Korea) in a 96-well PCR plate for sequencing (Figure 3.9.3). Twenty (20) µL of each purified sample were transferred into a well using a pippetor with filter tips (Interlab, New Zealand). The prepared plate was sealed tightly with strip caps (Interlab, New Zealand) and shipped to Macrogen Inc. (Seoul, Korea) by air, together with all primers used for amplification initially in a FedEx pack. The sequencing of each purified PCR products was performed using 5 pmol/ µL of corresponding primer (Macrogen, 2014). An order sheet was completed with the information which included the sample name, corresponding primer name and sample concentration. The results were downloaded from Macrogen Inc. website (http://www.macrogen.com/eng/). Each amplified house-keeping gene was sequenced on both strands. For each *S. aureus* isolate, 100% correctly trimmed sequences of its seven loci were assigned a 7-digit allele number designating its sequencing type (ST).

The images of amplified PCR products were captured using Lab Image Software 4.1 (Bio-Rad, 2012) and were edited using Paint.NET 4.0.5 (dotPDN, LLC, Washington, USA). Sequences of seven loci of each *S. aureus* isolate were analysed using Bioedit 7.2 (Ibis Biosciences, California). As each locus was sequenced on both strands, the reverse sequence was reversed and aligned pairwise with the forward sequence to create a consensus sequence. The sequences of each amplified house-keeping genes were trimmed to the right region using Basic Local Alignment Search Tool (BLAST) against their corresponding reference sequence which can be obtained from the MLST database (http://saureus.mlst.net/misc/info.asp).

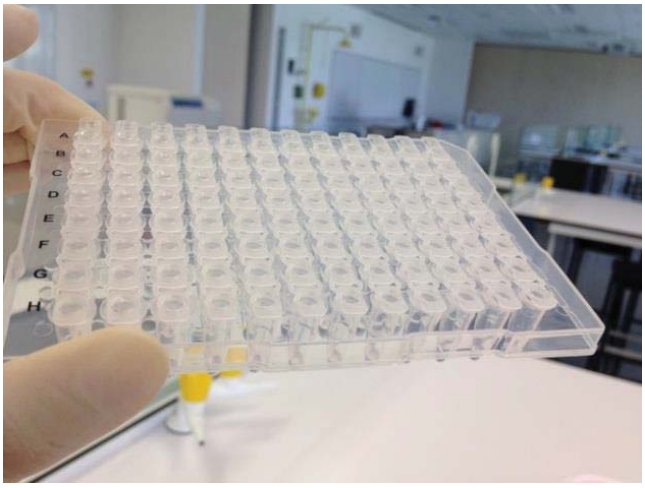


Figure 3.9.3 A prepared 96-well PCR plate for sequencing.

4.0 Identification of clonal complexes

Identified sequence types (STs) from MLST of all the sixty *S. aureus* isolates were grouped into clonal complexes using the eBURST (based upon related sequence types) programme which is available at: http://saureus.mlst.net/eburst/ (Feil et al., 2003; Grundmann et al., 2002). eBURST is a clustering analysis program that assigns isolates into a clonal complex (CC) if at least five out of seven allele numbers are identical (de Sousa & De Lencastre, 2003). The stringent group definition (5/7 shared alleles) was determined according to some relevant articles (Durand et al., 2006; Feil et al., 2003; Grundmann et al., 2002; Mellmann et al., 2008; Schulte et al., 2013). Single-locus variants (SLVs) were described as a sequence type (ST) that differs from other STs in the group at only one allele number (MLST database, 2015). Within a single CC, the ST that has the largest number of SLVs was identified as the clonal ancestor. Isolates that have no identical alleles with other isolates were considered as singletons (de Sousa & De Lencastre, 2003).

The BURST analysis was conducted according to the instructions given by the eBURST Readme instruction available at http://saureus.mlst.net/eburst/. The allelic profiles of all the isolates were entered into the programme for analysis. In the 'Analysis' panel, '5' was assigned to the minimum number of identical allele number for group definition. A diagram of clustered isolates can be obtained in the 'Diagram' panel of eBURST program (see section 5.9). Raw analysis data was shown in Appendix J.

4. Statistical analysis

Data of *S. aureus* counts at the key processing stages and from live chickens were analysed using SPSS software (Version 19.0, IBM corporation, New York, USA). Data were presented as means, SD, median [25^{th}, 75^{th} percentiles] or antilog mean [95% cl] according to the normality of each variable. The variables were tested for normality using the Kolmogorov-Smirnov and Shapiro-Wilk test. Normal distribution was confirmed when $P< 0.05$ (Field, 2009). Non-normally distributed data were Log transformed to obtain normality. Normally distributed data were further analysed by one-way ANOVA to investigate whether there is a significant difference of *S. aureus* level at each sampling location between batches. Turkey's test was used to determine any significant differences between the batches lies. In terms of non-normal distributed data, K Independent Samples (Kruskal-Wallis) was conducted. For the data of samples that were collected from fresh meat and two equipment (MDM conveyor and Skinner conveyor), one-way ANOVA (normal data) or Kruskal-Wallis (non-normal data) was performed with processing time (1-6 h) as a factor to examine any significant differences. The level of significance used in the statistical tests was $P<0.05$. The outputs are shown in Appendix H.

5. Results and Discussion

Phase I

5.1 Contamination of *S. aureus* in further processed poultry processing plant

5.1.1 Contamination of *S. aureus* in final processed products

Microbial data on contamination of final processed poultry products by *S. aureus* are shown in Figure 5.1.1. The results showed that all 36 samples (6 samples for each batch) were contaminated with *S. aureus* and the raw data are shown in Appendix F (Table E1). Other studies have reported similar results (Gibbs, Patterson, & Thompson, 1978). In their study, cell counts of *S. aureus* ranged from 1.3×10^3 to 1.1×10^5 CFU/16cm^2 in all chicken products. A study by Al-Ghamdi (2012) showed that all samples (n=20) collected from processed final chicken products (chicken fillet and chicken burger) in Saudi Arabia were contaminated by *S. aureus* with chicken burgers having the highest mean *S. aureus* counts of $1.2\bullet10^7$ CFU/mL. However, samples reported in the Saudi study were obtained from local markets rather than commercial further processing plants suggesting that the contamination was probably caused by improper handling or storage.

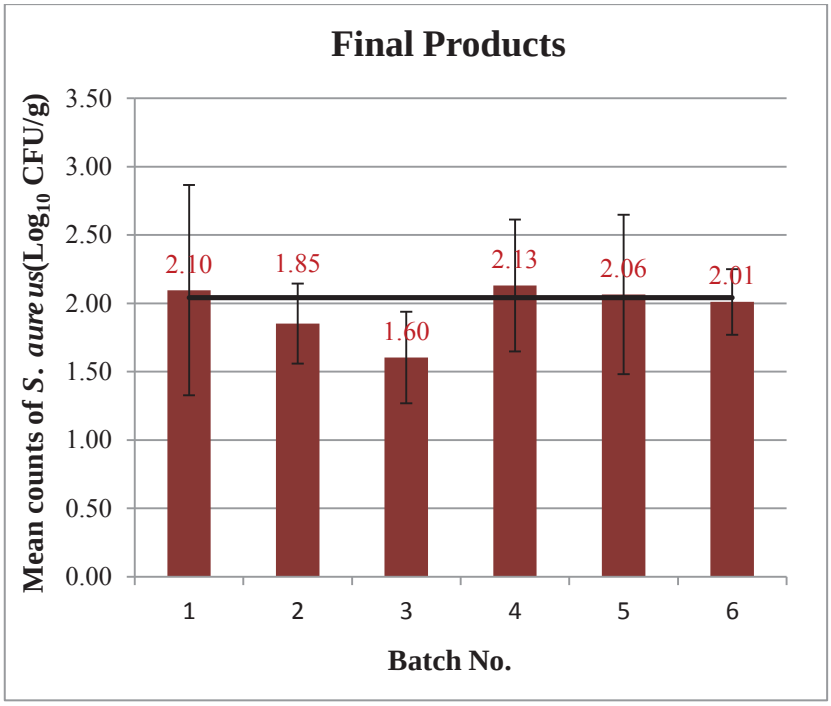


Figure 5.1.1 Mean *S. aureus* counts (Log_{10} CFU/g) in final products processed for six different batches and a standard level set by the processing plant. Each batch had six collected samples (n=6• 6). Error bars=Standard deviation from the mean.

The sample products had mean counts of *S. aureus* at approximate 2.0 Log_{10} CFU/g in all batches except that of Batch 3 had the least counts (Table 5.1.1). The viable cell counts were compared to the standard level (2.04 Log_{10} CFU/g) set by the commercial processing plant. Fifty per cent (50%) of samples (n=3) in Batches 1 and 4 were above the standard level, with Batch 4 having the highest *S. aureus* counts (2.16±0.46 Log_{10} CFU/g). Batches 2 and 3 had no sample that exceeded the standard level. However, all the final sample products were acceptable when compared to the Microbiological Reference Criteria of New Zealand (Ministry of Primary Industry, 2001). The regulation states that the acceptable level of *Staphylococcus* in partially processed raw poultry meat products is 3 Log_{10} CFU/g (Ministry of Health, 1995). According to the Adequate Processing Guidelines of Food Safety New Zealand, final minced poultry products should attain an internal temperature of at least 74 °C for 15 seconds to ensure consumer safety (Ministry of Primary Industry, 2001).

Table 5.1.1 Mean *S. aureus* counts (Log_{10} CFU/g) and samples (%) above the standard level (ASL) in each batch of final products.

Batch No.[a]	Sample ASL (%)	*S. aureus* (Log_{10} CFU/g)[b]
1	50	2.10±0.78
2	16.7	1.85±0.22
3	16.7	1.60±0.35
4	50.0	2.16±0.46
5	33.3	2.06±0.51
6	33.3	2.01±0.28

ASL=above standard level.
[a]Each batch has n=6
[b]Vaules are Mean±SD

5.1.2 Contamination of *S. aureus* in three frozen chicken meat ingredients

Figure 5.1.2 shows the contamination level of *S. aureus* in the three frozen ingredients that are used to produce the final chicken products (Table E2, Appendix E). Although fresh chicken skin has been widely regarded as the most potential source of contamination by *S. aureus* (Ministry of Primary Industry, 2001; Thompson et al., 1980), Frozen Skin samples analysed in this study had lower *S. aureus* cell counts than Frozen MSM which had the highest levels with Batch 1 recording the highest counts (2.50±0.48 Log_{10} CFU/g). Frozen SO BF had the lowest contamination level by *S. aureus* with Batch 2 showing the least cell counts of the cocci (1.07 [0.71, 2.29] Log_{10} CFU/g).

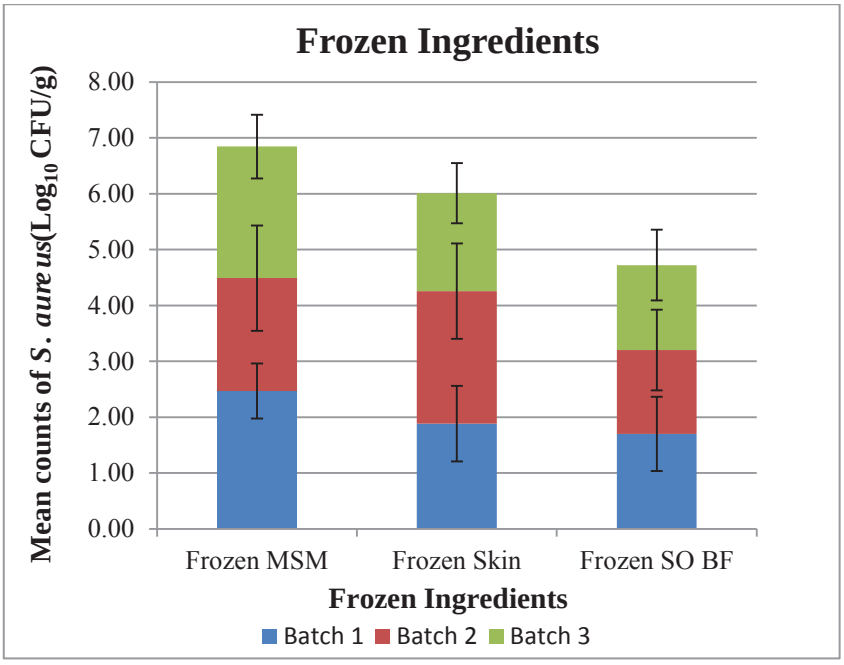


Figure 5.1.2 Stack-plot of *S. aureus* counts (Log_{10} CFU/g) of three different batches of frozen ingredients. Each stack has overall mean and SD bar, where n=6 in each stacked batch. MSM=Mechanically Separated Meat. SO BF=Skin-On Breast Fillet.

Samples of raw frozen chicken meat were frequently reported to be contaminated by *S. aureus* (Waldroup, 1996). In this study, the three raw frozen chicken meat ingredients had relatively high viable *S. aureus* counts. Comparing of the three frozen chicken meat samples to the standard level, at least 33% (n=2) of all the three frozen samples of ingredients were above the standard. Similarly, Frozen MSM had the highest number of samples that were above the standard level in Batches 1 and 3 (both with 83.3%) (Table 5.1.2). Of the Frozen Skin samples, 33.3%, 66.7% and 33.3 in Batches 1, 2 and 3 did not meet the standard level. With respect to Frozen SO BF samples, Batch 1 had the lowest number of samples above the standard level (16.7%), while Batch 2 had the least mean viable counts of *S. aureus* (1.07 [0.71, 2.29] Log_{10} CFU/g). As the three ingredients were frozen and stored in an industrial freezer (≤18•C) immediately after secondary processing where Fresh MSM, Fresh Skin and Fresh SO BF were produced, a proper freezing and storage regime is critical to inhibit the growth of *S. aureus* (Ministry of Primary Industry, 2001; Sams, 2000).

Table 5.1.2 Mean *S. aureus* counts (Log_{10} CFU/g) and samples (%) above the standard level (ASL) in each batch of three frozen ingredients.

Ingredient	Batch No.[a]	Samples ASL (%)	*S. aureus* (Log_{10} CFU/g)[b]
Frozen MSM	1	83.3	2.50±0.48
	2	33.3	2.00±1.02
	3	83.3	2.33±0.58
Frozen Skin	1	33.3	1.87±0.72
	2	66.7	2.34±0.93
	3	33.3	1.72±0.53
Frozen SO BF	1	16.7	1.70±0.70
	2	33.3	1.07 [0.71, 2.29][c]
	3	33.3	1.63±0.68

ASL=above standard level. MSM=Mechanically Separated Meat; SO BF=Skin-On Breast Fillet.
[a]Each batch has n=6
[b]Values are Mean±SD
[c][values] are median [25th, 75th percentiles] due to their non-normality.

5.2 Contamination of *S. aureus* in products in the secondary plant

5.2.1 Fresh MSM (Mechanically Separated Meat) processing

Fresh MSM processing includes using meat carcasses as ingredients, conveying the carcasses to MDM (Mechanically Deboning Machine) and producing Fresh MSM. Four MSM

processing steps were investigated, from Fresh MSM backtracked to Carcass and then Inside MDM. Figure 5.2.1 shows overall trends of viable counts of *S. aureus* for the samples obtained in the four MSM processing steps and raw data are shown in Appendix F.

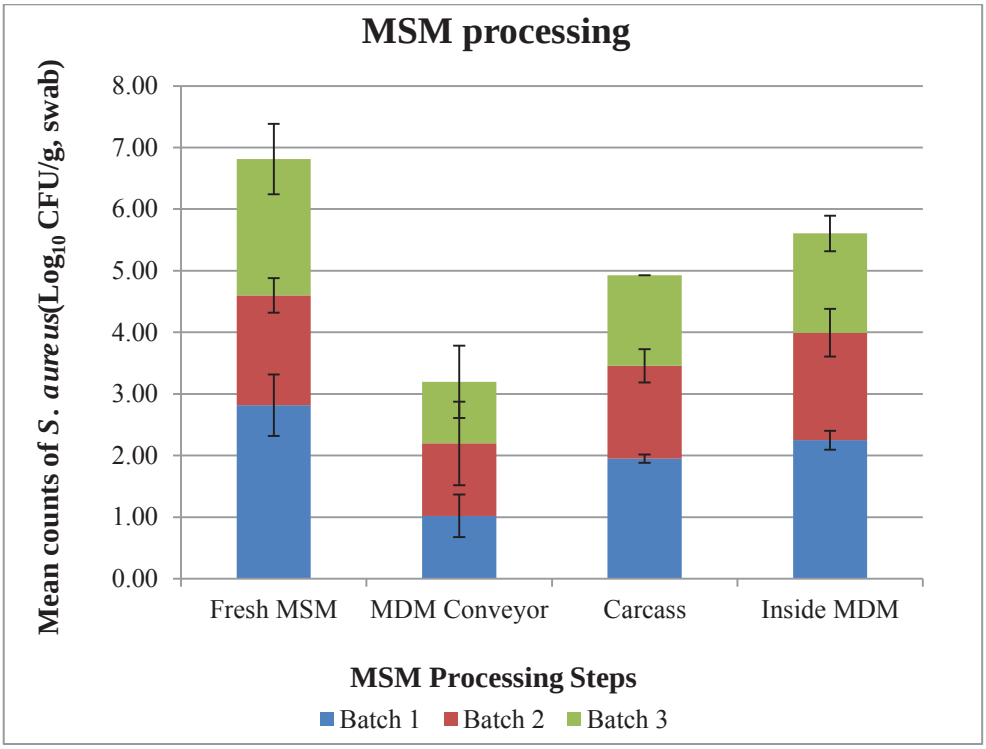


Figure 5.2.1 Stack-plot of *S. aureus* counts (Log_{10} CFU/g, swab) during MSM processing steps. Each stack has overall mean for 6-h processing, with n=6 in each stacked batch. Samples were collected and analysed in the following order: Fresh MSM (Log_{10} CFU/g), MDM conveyor (Log_{10} CFU/swab), carcass (Log_{10} CFU/g) and Inside MDM (Log_{10} CFU/swab). MSM=Mechanically Separated Meat, MDM=Mechanically Deboning Machine.

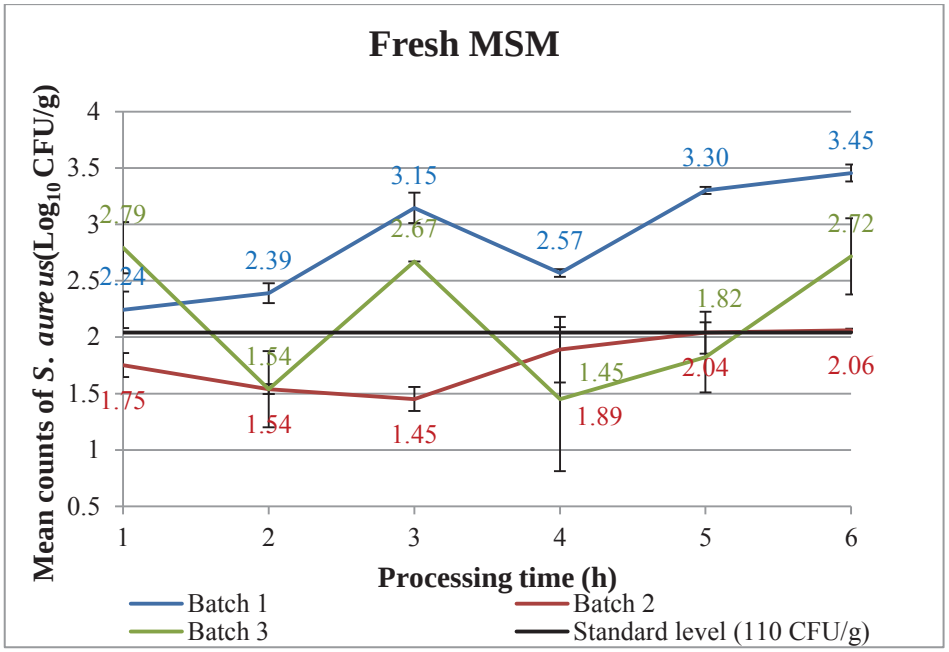


Figure 5.2.2 Mean *S. aureus* counts (Log_{10} CFU/g) of Fresh MSM samples during 6-h of processing n=3 batches and a standard level set by the processing plant.

The level of *S. aureus* in Fresh MSM samples was the highest among the other processing steps (Figure 5.2.1). There were 2.85±0.51, 1.79±0.25 and 2.17±0.63 (Log_{10} CFU/g) in Batches 1, 2 and 3 respectively (Table 5.2.1). Each batch contained Fresh MSM samples that did not meet the standard level with all the samples in Batch 1 being over the standard level (Table 5.2.1). Also, Batch 1 had a significantly higher level of *S. aureus* than Batch 2 (P<0.05). The trends of *S. aureus* counts in Fresh MSM samples throughout the 6-h processing time are shown in Figure 5.2.2. There was a slight decrease of *S. aureus* counts in Batch 3, from 2.79 to 2.72 (Log_{10} CFU/g). However, increase of *S. aureus* counts were observed in both Batches 1 and 2 with the former (Batch 1) increasing markedly from 2.24 to 3.45 (Log_{10} CFU/g), suggesting that there could be a build-up of contamination during the processing period. This observation agrees with the results of high counts of the *S. aureus* during 6-h processing (Table 5.2.1) in that by the end of processing, all the fresh MSM samples (n=6) were above the set limit.

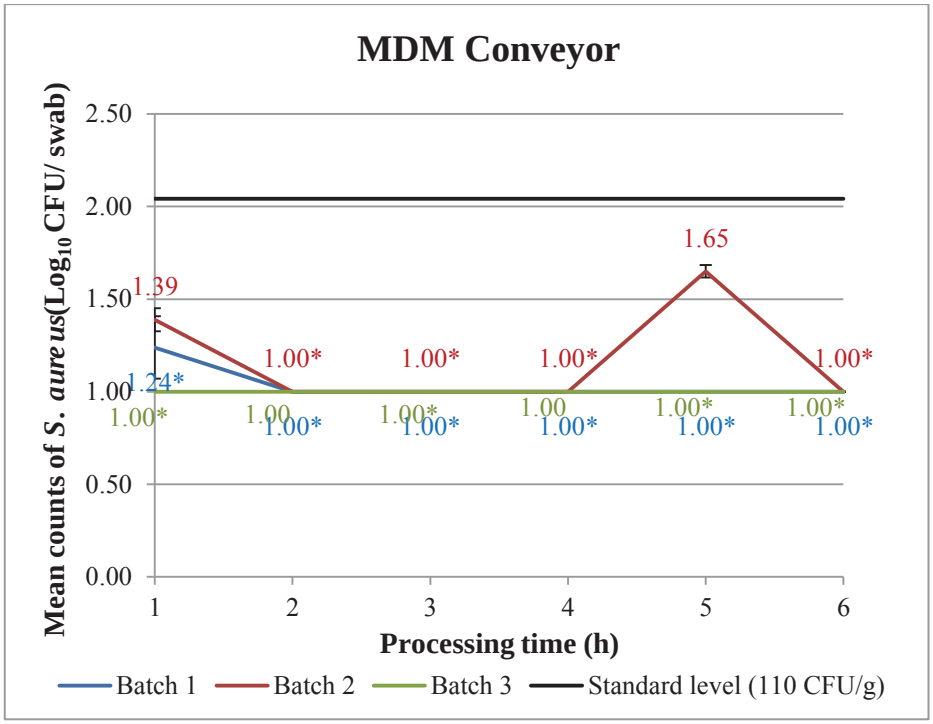


Figure 5.2.3 Mean *S. aureus* counts (Log_{10} CFU/swab) of MDM Conveyor during 6-h of processing for three batches and a standard level set by the processing plant. * Samples had less than 10 *S. aureus* counts.

Both samples from MDM Conveyor and Carcass recorded a considerately low level of *S. aureus*. The viable counts of *S. aureus* from MDM Conveyor, were 1.00 [0.94, 1.14], 1.00 [0.88, 1.47] and 1.00±0.00 Log_{10} CFU/swab in the first, second and third batch accordingly (Table 5.2.1), which were the lowest throughout the whole MSM processing procedure. Conveyors are the equipment surfaces where cross-contaminations are most likely to occur because they are frequently used to transfer poultry carcasses in a processing plant (Arnold & Silvers, 2000). In this study, *S. aureus* counts in all the samples from MDM Conveyor were under the critical limit and same results were found throughout the 6-h processing time. No build-up was observed during processing time as the viable *S. aureus* counts from MDM Conveyor in all batches were almost constant (Figure 5.2.3).

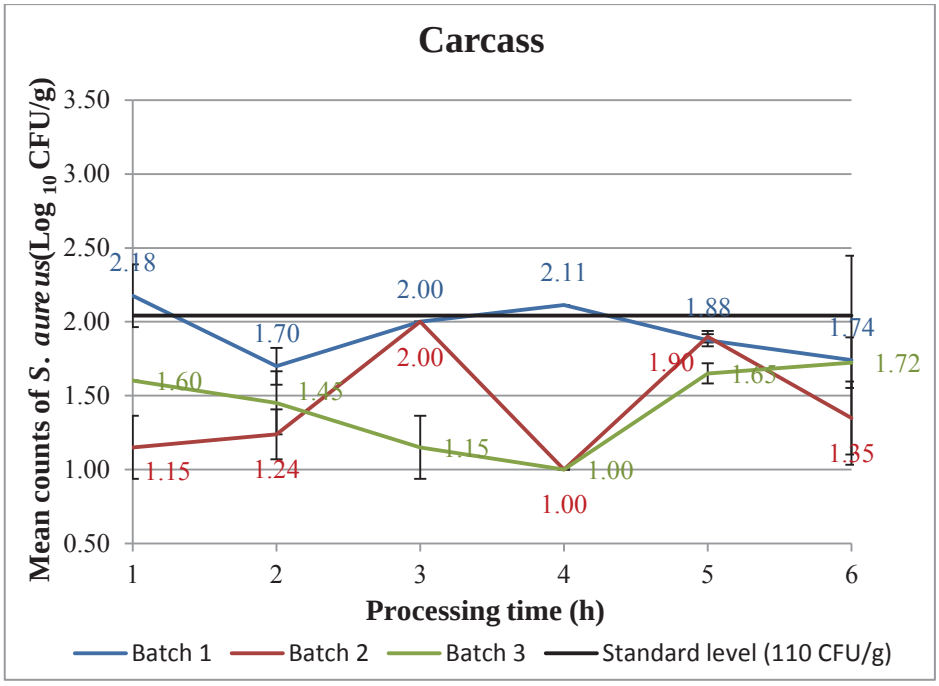


Figure 5.2.4 Mean *S. aureus* counts (Log_{10} CFU/swab) of Carcass during 6-h of processing for three batches and a standard level set by the processing plant.

The level of *S. aureus* contamination in Carcass was relatively low as well with the lowest counts observed in Batch 3 (1.43±0.29 CFU/g) and the contamination level in carcasses of Batch 2 was significantly (P<0.05) higher than that of other batches. Figure 5.2.4 shows the changes in *S. aureus* counts of carcasses during processing. Slight cell increases counts of the cocci were found in Batch 2 and Batch 3, from 1.60 to 1.72, 1.15 to 1.35 (Log_{10} CFU/swab) respectively. Only 33.3% carcasses in Batch 1 were higher than the standard level (Table 5.2.1). On the contrary, carcasses after evisceration with high contamination level of *S. aureus* have been reported in other studies (Devriese, 1980; Notermans et al., 1982). Factors such as evisceration residues of organs and cross-contamination by workers, were considered as the sources of contamination by *S. aureus* for carcasses after evisceration (Harvey et al., 1982), which indicates that the poultry plant in our study had a relatively good hygiene and sanitation system.

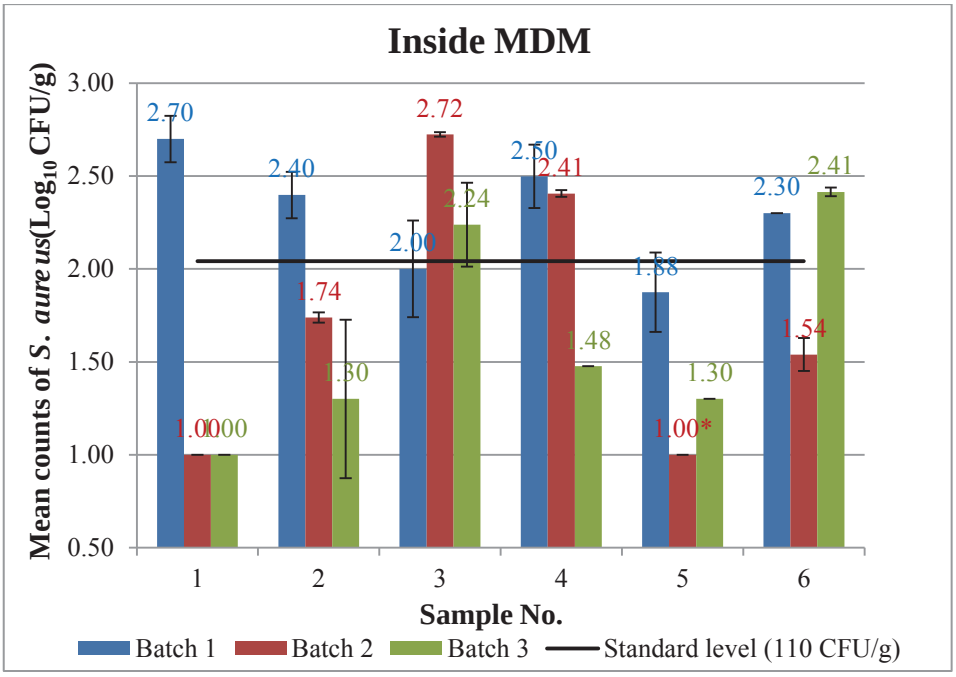


Figure 5.2.5 Mean *S. aureus* counts (Log_{10} CFU/swab) inside the MDM during 6-h of processing for three batches and a standard level set by the processing plant. * Samples had less than 10 *S. aureus* counts.

As the load of *S. aureus* in Fresh MSM increased markedly after relatively 'clean' carcasses being transferred to MDM by using the 'clean' MDM conveyor, six swabs were collected inside the MDM for three batches. The average amounts *S. aureus* counts in the three batches were 2.30±0.31, 1.73±0.71 and 1.62±0.57 (Log_{10} CFU/swab), with 66.7%, 33.3% and 33.3% swabs in Batches 1, 2 and 3 being above the standard level (Table 5.2.1), respectively. Compared to MDM Conveyor and Carcass, swabs taken inside MDM showed a much higher level of *S. aureus* counts (Figure 5.2.1), which explains the higher contamination level in Fresh MSM after processing less contaminated carcasses.

Table 5.2.1 Distribution of *S. aureus* (Log_{10} CFU/swab) enumerated from samples of MSM processing.

Source	Parameter	Sample	Sample ASL (%)	*S. aureus* (Log_{10} CFU/g, swab)[d]
Fresh MSM[b]	Batch No.[a]	1	100	2.85±0.51[f]
		2	16.7	1.79±0.25[f]
		3	50	2.17±0.63[f]
	Processing time (h)	1	66.7	2.24 [0.97, 3.56][e]
		2	33.3	1.54 [0.60, 3.04][e]
		3	66.7	2.67 [0.25, 4.60][e]
		4	33.3	1.89 [0.57, 3.37][e]
		5	33.3	2.04 [0.40, 4.37][e]
		6	100	2.72 [1.01, 4.48][e]
MDM Conveyor[c]	Batch No.[a]	1	0.0	1.00 [0.94, 1.14][e]
		2	0.0	1.00 [0.88, 1.47][e]
		3	0.0	1.00±0.00
	Processing time (h)	1	0.0	1.23 [0.72, 1.70][e]
		2	0.0	1.00±0.00
		3	0.0	1.00±0.00
		4	0.0	1.00±0.00
		5	0.0	1.00 [0.28, 2.15][e]
		6	0.0	1.00±0.00
Carcass[b]	Batch No.[a]	1	33.3	1.93±0.20[f]
		2	0.0	1.44±0.41[f]
		3	0.0	1.43±0.29[f]
	Processing time (h)	1	33.3	1.60 [0.37, 2.92][e]
		2	0.0	1.45 [0.89, 2.06][e]
		3	0.0	2.00 [0.50, 2.94][e]
		4	33.3	1.00 [-0.23, 2.97][e]
		5	0.0	1.87 [1.47, 2.15][e]
		6	0.0	1.72 [1.06, 2.15][e]
Inside MDM[c]	Batch No.[a].	1	66.7	2.30±0.31
		2	33.3	1.73±0.71
		3	33.3	1.62±0.57

ASL=above standard level; MSM=Mechanically Separated Meat. MDM=Mechanically Deboning Machine.
[a]Each batch has n=6.
[b]Meat samples (Log_{10} CFU/g)
[c]Swab samples (Log_{10} CFU/swab)
[d]Values are Mean±SD
[e][values] are median [25th, 75th percentiles] due to their non-normality.
[f]Significant differences among the three batches (P<0.05).

The results show that the high contamination level in Fresh MSM may be attributed to the colonisation of *S. aureus* inside the MDM. Mechanically deboned poultry meat was reported to be easily cross-contaminated by microorganisms, especially by *Salmonella*, *Staphylococcus* and coliforms, because the deboning process involves grinding the raw chicken carcasses with evisceration residues (Sadat & Volle, 2000). The temperature in the deboning machine is relatively high which may also accounts for the high level of *S. aureus* contamination (Froning, 1981). As MDM has a complicated inner structure consisting of several annular and rotating cutting parts (Logan, 1969), it is difficult to clean and sanitise the

inner parts of MDM thoroughly, resulting in some 'resident' *S. aureus* surviving and cross-contaminating the carcasses (Froning, 1981).

5.2.2 Detaching skin processing

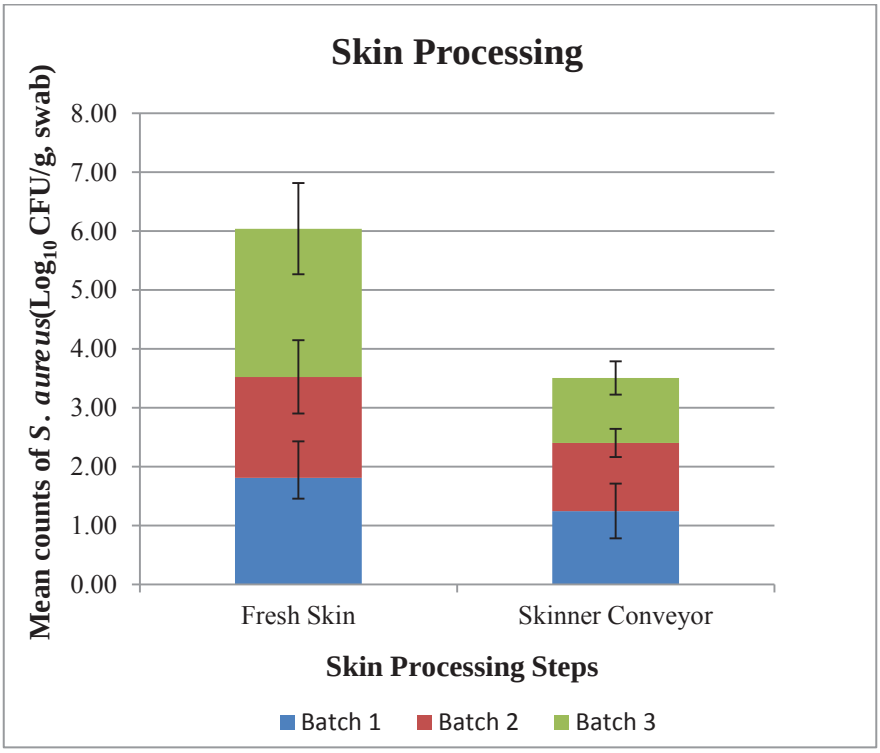


Figure 5.2.6 Stack-plot of *S. aureus* counts (Log_{10} CFU/g, swab) during Skin processing steps for three different batches. Each stack has overall mean for 6-h processing, where n=6 in each stacked batch. Samples were collected in the following order: Fresh Skin (Log_{10} CFU/g) to Skinner conveyor (Log_{10} CFU/swab).

Detaching skin was investigated by examining the distribution of *S. aureus* in Fresh Skin and Skinner Conveyor. Figure 5.2.6 shows a marked decrease of mean stack counts of *S. aureus* from Fresh Skin to Skinner Conveyor. *S. aureus* counts ranging from 10^2 to 10^7/16cm^2 on the chicken breast skin was reported by Harvey et al. (1982). In the present study, the mean counts in each batch were 1.82±0.37, 1.72±0.60 and 2.15 [1.67, 3.37] (Log_{10} CFU/g) for Fresh Skin which were much higher than that for Skinner Conveyor (Table 5.2.2). Also, 16.7%, 16.7% and 83.3% of fresh skin in Batches 1, 2 and 3 were above the limit while all the samples from Skinner Conveyor were under the limit in terms of contamination level of *S. aureus*.

Table 5.2.2 Distribution of *S. aureus* (Log_{10} CFU/g) enumerated from the detaching skin processing steps.

Source	Parameter	Sample	Samples ASL (%)	*S. aureus* (Log_{10} CFU/g)[a]
Fresh Skin	Batch No.[a]	1	16.7	1.82±0.37
		2	16.7	1.72±0.60
		3	83.3	2.15 [1.67, 3.37][b]
	Processing time (h)	1	0.0	1.50±0.51
		2	66.7	1.97±0.61
		3	33.3	1.84±0.80
		4	33.3	2.02±0.08
		5	66.7	2.82±1.13
		6	33.3	1.97±0.21
Skinner Conveyor	Batch No.[a]	1	0.0	1.00 [0.83, 1.66][b]
		2	0.0	1.15±0.20
		3	0.0	1.10±0.27
	Processing time (h)	1	0.0	1.00 [0.31, 2.11] [b]
		2	0.0	1.42±0.25
		3	0.0	1.00 [0.83, 1.27] [b]
		4	0.0	1.00±0.00
		5	0.0	1.00 [0.73, 1.17] [b]
		6	0.0	1.38±0.43

ASL=above standard level.
[a]Each batch has n=6
[b]Values are Mean±SD
[c][values] are median [25th, 75th percentiles] due to their non-normality.

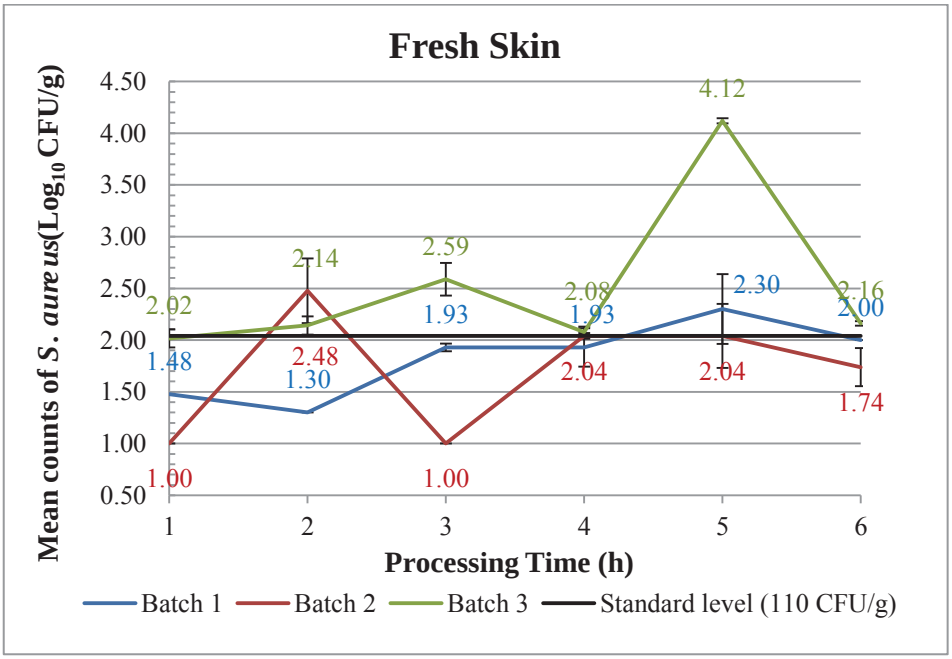


Figure 5.2.7 Mean *S. aureus* counts (Log_{10} CFU/g) of Fresh Skin during 6-h of processing for three batches and a standard level set by the processing plant.

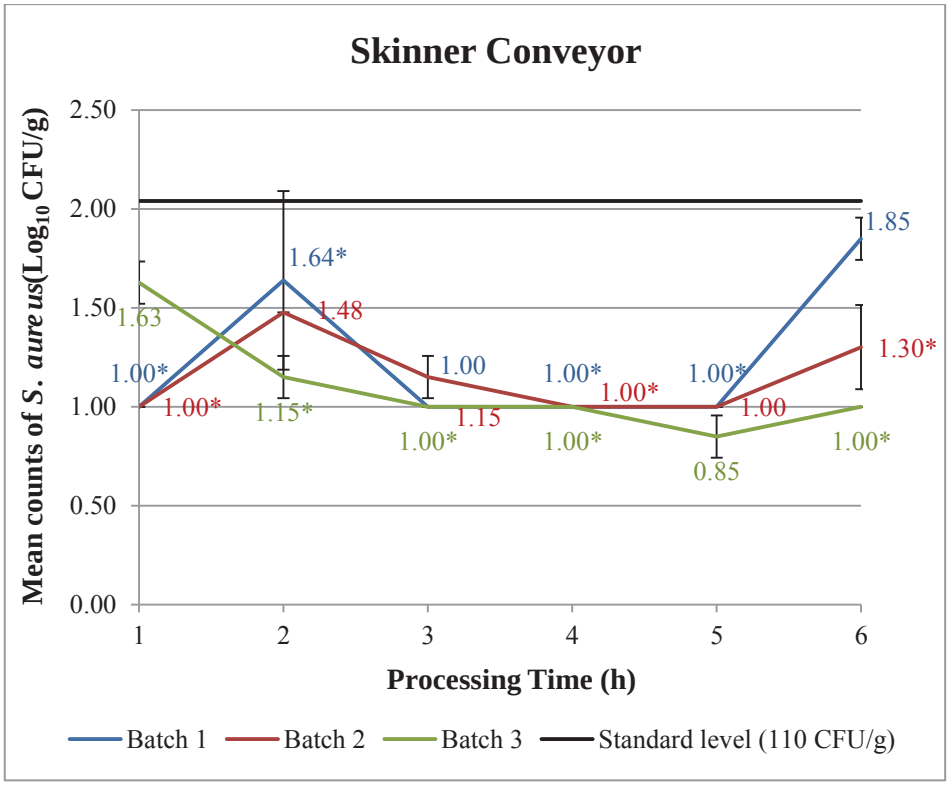


Figure 5.2.8 Mean *S. aureus* counts (Log_{10} CFU/swab) of Skinner Conveyor during 6-h of processing for three batches and a standard level set by the processing plant. *Samples with less than 10 *S. aureus* counts.

During 6-h of processing, *S. aureus* on fresh skin in all the batches gradually increased (Figure 5.2.7), suggesting that there might be a build-up in Skin Conveyor. However, the results of Skinner Conveyor shown in Figure 5.2.8 were contrary to the previous assumption, as the mean counts of *S. aureus* in Batch 3 decreased markedly from 1.63 to less than 1.00 (Log_{10} CFU/swab). Also, the mean *S. aureus* counts only showed a slight increase from the beginning to the end of processing (from 1.00 to 1.38 Log $_{10}$ CFU/swab). This suggested that the contamination of *S. aureus* in Fresh Skin was not only caused by cross-contamination in the Skin Conveyor. Instead, the fresh skin itself was also a potential contamination source of *S. aureus* (Ministry of Primary Industry, 2001; Thompson et al., 1980).

5.2.3 Fresh Skin-On Breast Fillet (SO BF)

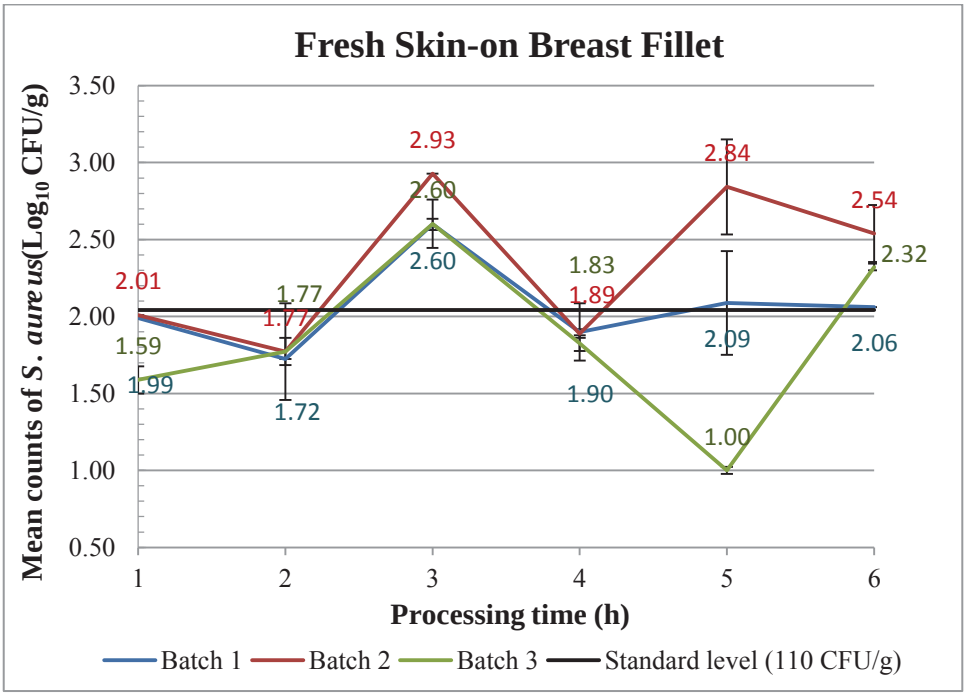


Figure 5.2.9 Mean *S. aureus* counts (Log_{10} CFU/g) of Fresh Skin-On Breast Fillet during 6-h processing of three different batches and a standard level set by the processing plant. Each point is a mean of each batches where n=6.

The trends of mean *S. aureus* counts in Fresh SO BF are shown in Figure 5.2.3. The mean counts in Batch 1, Batch 2 and Batch 3 were 2.06±0.29, 2.33±0.50 and 1.85±0.56 respectively. There were at least 16.7% of fresh Skin-On breast fillets in each batch above the standard level (Table 5.2.3). All the batches increased in *S. aureus* counts throughout the 6-h processing from 1.99 to 2.06 Log_{10} CFU/g in Batch 1, 2.01 to 2.54 Log_{10} CFU/g in Batch 2 and 1.59 to 2.32 Log_{10} CFU/g in Batch 3. Also, the unsatisfactory contamination level of Fresh SO BF during processing showed a considerable increase in cell counts for all the fillets at 3h and 6h, thus above the limit, suggesting an accumulation of the microbe during processing. The build-up was probably attributed to irregular change of gloves or sanitisation of knives as the breasts are filleted off the chicken carcasses manually using knives by workers wearing gloves. However, Fresh SO BF had a relatively low contamination rate compared to Fresh MSM and Fresh Skin. Low incidence of *S. aureus* contamination on chicken breast was also reported by Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al. (2005), but the study did not mention whether the type of chicken breasts examined were skinless or skin-on.

Table 5.2.3 Viable cell counts (Log_{10} CFU/g) and samples (%) above the standard level (ASL) of *S. aureus* enumerated from Fresh Skin-On Breast Fillet.

Source	Parameter	Sample	Samples ASL (%)	*S. aureus* counts (Log_{10} CFU/g)
Fresh Skin-On Breast Fillet	Batch No.[a]	1	16.7	2.06±0.29 [b]
		2	16.7	2.33±0.50 [b]
		3	83.3	1.85±0.56 [b]
	Processing time (h)	1	0.0	2.00 [1.27, 2.45][c]
		2	0.0	1.77 [1.69, 1.83][c]
		3	100	2.60 [2.24, 3.18][c]
		4	0.0	1.89 [1.77, 1.97][c]
		5	66.7	2.09 [0.32, 4.28][c]
		6	100	2.32 [1.71, 2.90][c]

ASL=above standard level.
[a]Each batch has n=6
[b]Values are Mean±SD
[c][values] are median [25th, 75th percentiles] due to their non-normality.

5.3 Contamination of *S. aureus* on Rubber Fingers in the Pluckers

To investigate the contamination of *S. aureus* in the three Pluckers, Rubber Fingers were swabbed on three different days and the results are shown in Figure 5.3.1. A steady decrease in the viable counts of *S. aureus* was observed from Plucker 1 to Plucker 2 during the three-day period with cell counts of Day one decreasing rapidly from 2.28 to 1.08 (Log_{10} CFU/swab). Rubber Fingers of Day two had the highest average counts of *S. aureus* (2.07±0.95 Log_{10} CFU/swab). Compared to the *S. aureus* counts in Plucker 2, the viable counts of all the Rubber Fingers in Plucker 3 increased significantly (P<0.05). However, the counts in Plucker 3 were still much less than that in Plucker 1 (P<0.05) which comfirms the exceeded standard level on Plucker 3 and Plucker 1 (50% and 83.3% respectively) (Table 5.3.1). Dodd et al. (1987) reported a similar trend of *S. aureus* counts in three Pluckers. Therefore, *S. aureus* on the Plucker may be introduced by chicken skin as Plucker 1 is the first contact equipment with chicken skin. This suggests that chicken skin probably is responsible for the contamination by *S. aureus* which supports the discussion in section 5.2.2.

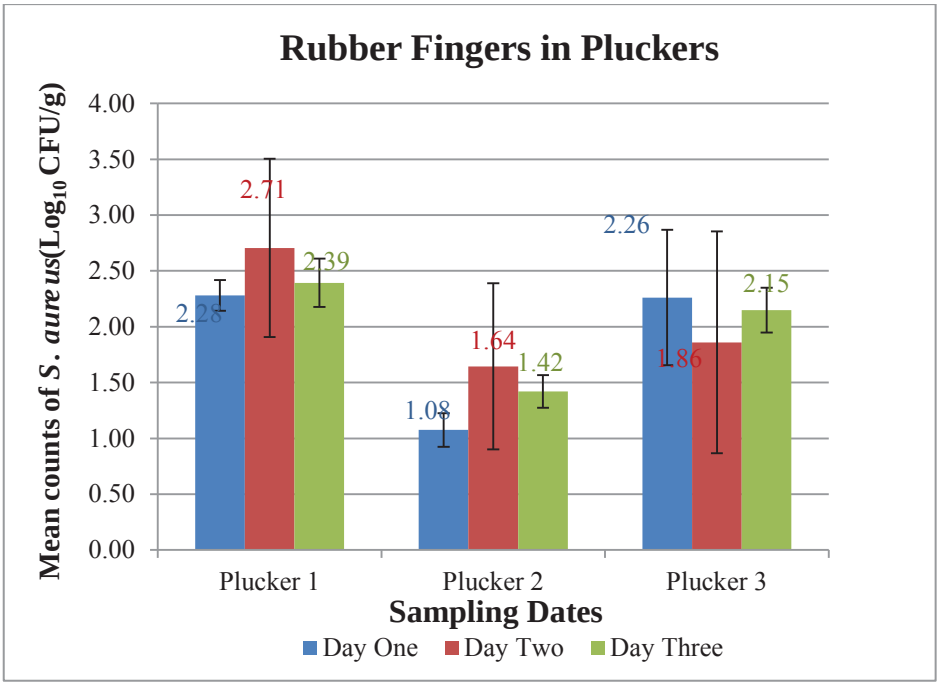


Figure 5.3.1 Stack-plot of *S. aureus* counts (Log_{10} CFU/swab) of Rubber Fingers on three Pluckers. Each stack has an overall mean, where n=2.

Table 5.3.1 Viable counts (Log_{10} CFU/swab) and samples (%) above the standard level (ASL) of *S. aureus* enumerated from Rubber Fingers on the three Pluckers.

Source	Parameter	Sample	Samples ASL (%)	*S. aureus* counts (Log_{10} CFU/swab)[a]
Rubber Fingers	Sampling Date	1	50	1.87±0.71
		2	50	2.07±0.95
		3	50	1.99±0.48
	Plucker No.	1	83.3	2.46±0.50[b]
		2	16.7	1.38±0.49[b]
		3	50	2.09±0.67[b]

ASL=above standard level.
[a]Values are Mean±SD.
[b]Significant differences among the three pluckers (P<0.05).

S. aureus has been reported to be easily colonised on Plukcers (Gibbs, Patterson, & Thompson, 1978; Mead & Dodd, 1990; Notermans et al., 1982). However, other materials, such as stainless steel, were more vulnerable to the colonisation of bacteria than rubber fingers (Arnold & Silvers, 2000). The colonisation is probably caused by some cracks that may occur after using the rubber fingers for a certain period of time where *S. aureus* could harbour and accumulate in the cracks and insufficient cleaning and sanitising agents are unable to reach the cracks (Mead & Dodd, 1990). Also, it seems that the plucker machines, with the warm temperature, humid and availability of rich nutrients, provides a favourable

growing environment for *S. aureus* (Mead & Dodd, 1990; Mead et al., 1988). It is therefore, recommended to replace the rubber fingers regularly as it is difficult to clean them thoroughly.

5.4 Contamination of *S. aureus* in Nostrils and Skin of live chickens at the farm

To investigate the potential contamination source of *S. aureus* from farm to final products, nostrils and skins of live chickens at a supplying broiler farm were swabbed for the enumeration of *S. aureus*. Figure 5.4.1 and Figure 5.4.2 show the trends of mean *S. aureus* counts colonised in nostrils and skins, respectively. All the swabs samples were positive for *S. aureus* while about 83% swab samples from live hens were contaminated with *S. aureus* in the report by Gibbs, Patterson, and Thompson (1978).

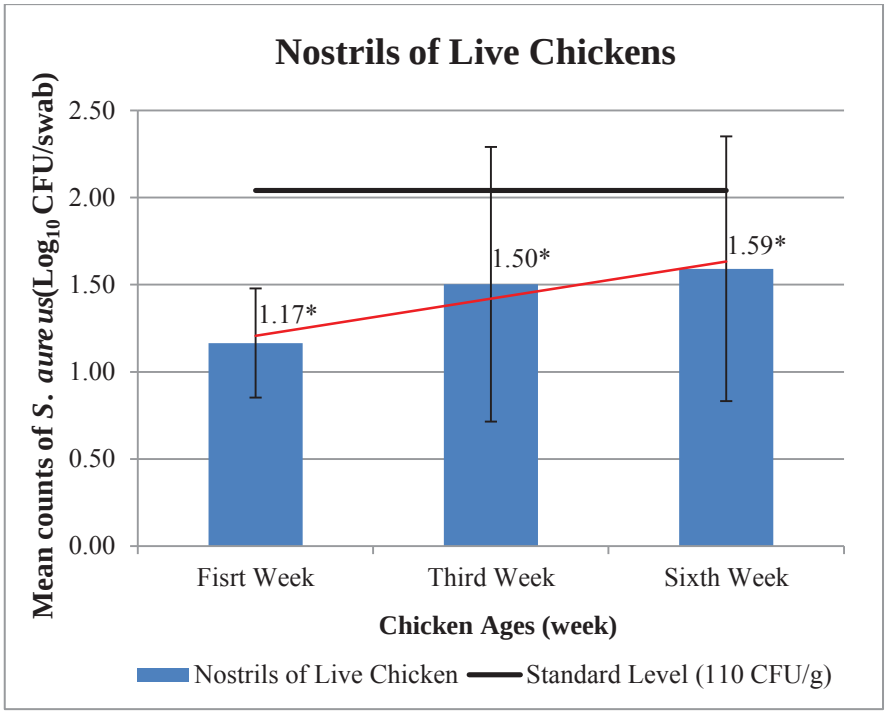


Figure 5.4.1 Viable log cell counts (Log $_{10}$ CFU/swab) of *S. aureus* isolated from the nostrils of live chickens at one week, three weeks and six weeks old and a standard level set by the processing plant. Each data point is mean of samples collected from chickens at the same age where n=6. *Samples with less than 10 *S. aureus* counts.

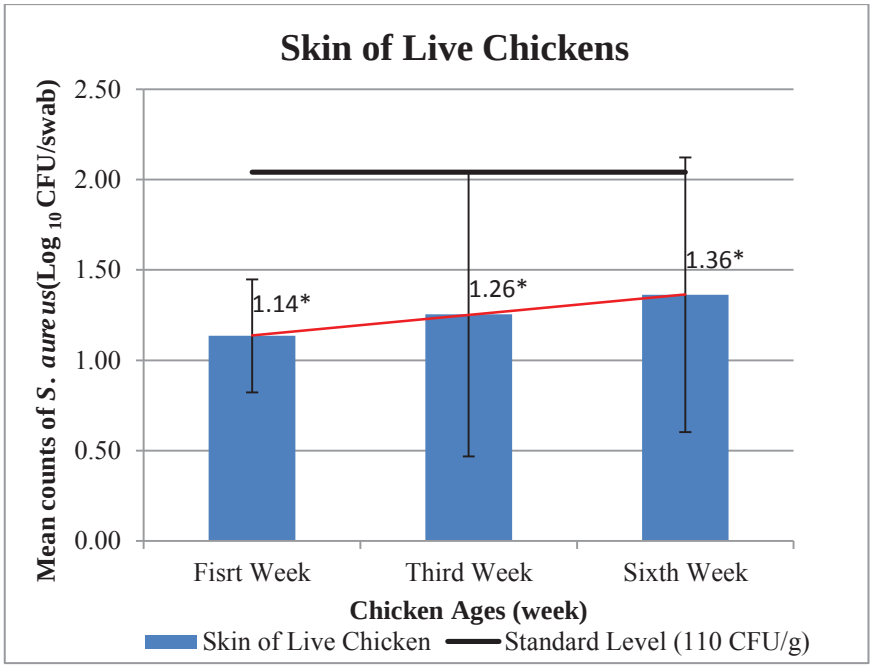


Figure 5.4.2 Viable log cell counts (Log_{10} CFU/swab) of *S. aureus* enumerated from the skin of live chickens at one week, three weeks and six weeks and a standard level set by the processing plant. Each data point is mean of samples collected from chickens at the same age where n=6. *Samples with less than 10 *S. aureus* counts.

With the growth of chicken ages from one week to six weeks, the amount of *S. aureus* in both nostrils and skins increased from 1.17 to 1.59 (Log_{10} CFU/swab), 1.14 to 1.36 (Log_{10} CFU/swab), respectively. However, 1.1×10^6 to 5.1×10^6 (CFU units) of *S. aureus* have been reported on chickens according to Devriese (1980). The increasing trend of *S. aureus* counts in the present study is in agreement with Thompson et al. (1980). Devriese and Devos (1975) indicated that after 7 to 10 weeks, *S. aureus* counts on live chickens remain stable.

Gibbs, Patterson, and Harvey (1978) reported the contamination of chicken nostrils by *S. aureus*, which agrees with results of the present study. The steady increase in cell counts in the nostrils suggested that the source of cross-contamination may be present at farm environment on equipment such as the feeder and drinker, which are frequently in contact with chicken nostrils. Cross-contamination may be also introduced by farmers when they are working in the sheds (Thompson et al., 1980). However, the poultry sheds become more crowded with the growth of chickens leading to more scratches occurring on chicken skins. The introduction of *S. aureus* may be through lesion skin due to scarification (Kuramasu et al., 1967). Also, lesion skin may occur as a result of preening and *S. aureus* present on the

skin can survive even after scalding, de-feathering and washing (Gibbs, Patterson, & Thompson, 1978). .

Table 5.4.1 Viable counts and samples (%) above the standard level (ASL) of *S. aureus* enumerated from the nostrils of live chickens at three different ages.

Swab sample	Age of Chicken (weeks)	Samples ASL (%)	*S. aureus* counts (Log $_{10}$ CFU/g)[b]
Nostril[a]	One week	0.0	1.00 [0.85, 1.48][c]
	Three weeks	16.7	1.50±0.83
	Six weeks	16.7	1.59±0.70
Skin[a]	One week	0.0	1.00 [0.79, 1.48] [c]
	Three weeks	0.0	1.15 [0.86, 1.65] [c]
	Six weeks	16.7	1.36±0.45

ASL=above standard level.
[a]Sampling size for each age of chicken is 6 (n=6).
[b]Values are Mean±SD
[c][values] are median [25th, 75th percentiles] due to their non-normality.

The average counts of *S. aureus* in nostrils and skins of chickens at all ages were under the standard contamination level, although 16.7% nostrils of three-weeks-old and six-weeks-old chicken and 16.7% chicken skins of six-weeks-old chickens exceeded the limit (Table 5.4.1). A reported high *S. aureus* counts in nostrils and skins of live chickens was indicated by Notermans et al. (1982). In our study, the relatively low counts indicated that the farm had proper handling, cleaning and chicken production procedures. Therefore, *S. aureus* in the processing plant are most likely introduced through the live chickens, but considering that the level of the pathogen on the live chickens is relatively low, there is possibly another contamination source or improper processing steps in the plant which lead to the accumulation and growth of *S. aureus* (Devriese, 1980).

Phase II

5.5 Identification of main sampling sites

The identification of main sampling sites in the plant was based on the results in section 5.2, 5.3 and 5.4. All the three ingredients for processing the final products recorded relatively high levels of *S. aureus* contaminations. Therefore, the final products in the further processing plant and the three fresh ingredients (Fresh MSM, Fresh Skin and Fresh SO BF) in the secondary processing plant were regarded as the main sampling sites for further analysis. Considering that Rubber Fingers in the Plucker have been widely reported as highly potential contamination sites by *S. aureus* (Gibbs, Patterson, & Thompson, 1978; Mead & Dodd, 1990; Notermans et al., 1982), they were therefore also included into the main sampling sites. The main sampling sites in the processing plant are shown in Figure 5.5. In order to identify the potential source of *S. aureus* contamination from farm to processing plant, live chickens at the farm were considered as a main sampling source (Waters et al., 2011).

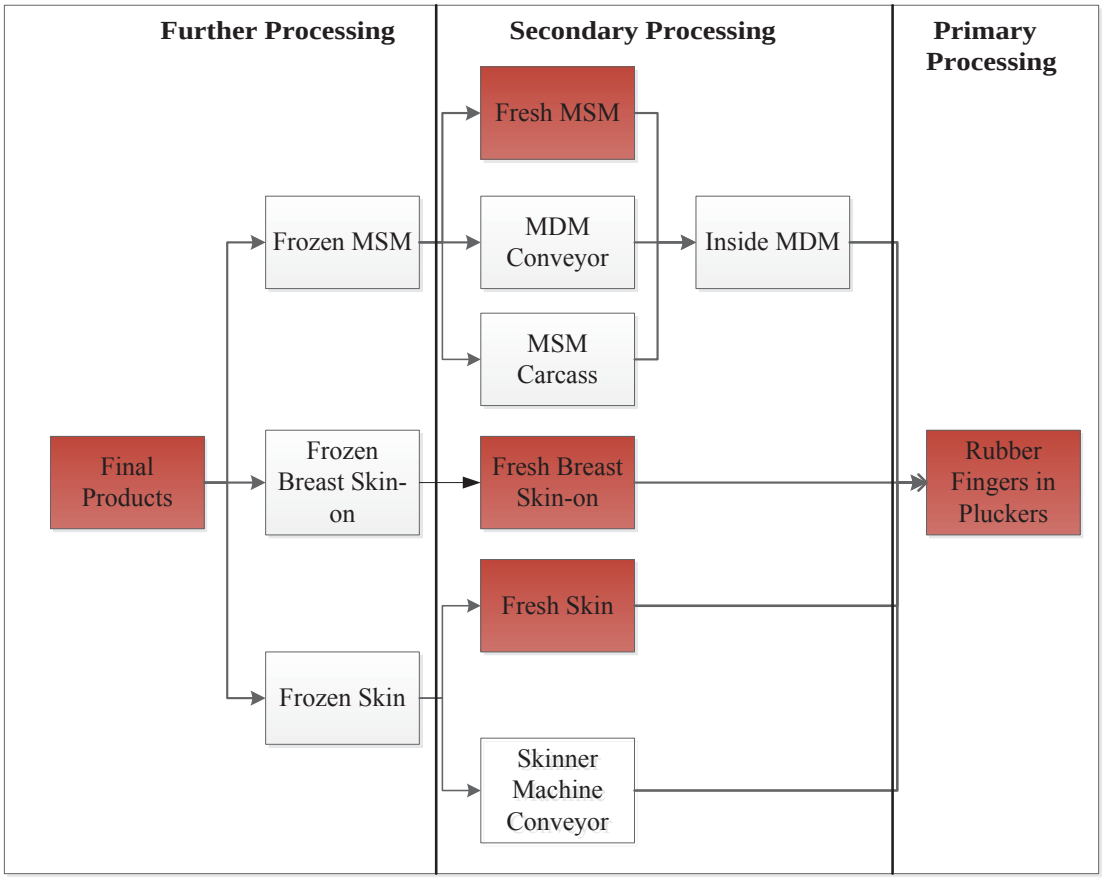


Figure 5.5 Main sampling sites in the processing plant (highlighted in red) from further processing to primary processing. Arrows indicate back-sampling commencing with Final Products.

5.6 Detection of enterotoxigenic *S. aureus* isolates

The enterotoxigenic properties of the sixty representative *S. aureus* isolates were detected using the Multiplex PCR method. The results of PCR products are shown in Appendix F. Several aspects were considered for undertaking this present study:

1. To conduct a pilot study on determining the potential source of contamination of chicken products by *S. aureus* in commercial poultry processing, to our knowledge, there is no such study that has been conducted in New Zealand, and yet, the prevalence of *S. aureus* food poisoning is high in the country (ESR, 2014).

2. To develop suitable methods (Multiplex PCR, MLST) for identification of toxigenic isolates of *S. aureus* in poultry meat.

All the sixty *S. aureus* isolates (n=60) were confirmed by detecting the characteristic *femA* gene. Fifty nine (59) isolates (98.33%) were able to produce at least two types of enterotoxins. Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al. (2005) reported only 21.7% of their *S. aureus* isolates (n=360) that were enterotoxigenic when they investigated the characterisation of *S. aureus* in raw chicken meat in Japan. However, in the present study, only one strain was not identified as an enterotoxin producer. Table 5.6 shows the distribution of enterotoxin genes encoded in each isolate from the main sampling sites and live chickens.

Eight (8) out of eighteen (18) enterotoxin genes were found and they were *seg*, *sei*, *seh*, *sek*, *sel*, *sem*, *sen* and *seo*. Fifty six isolates (93.33%) had the same enterotoxin genes: *sei, seg, sem, sen* and *seo*. Only one isolate was positive for the enterotoxin E encoding gene *see* in the present study. However, enterotoxins A to E are known as the classical enterotoxins of *S. aureus* in chicken products which are also responsible for most foodborne outbreaks (Kérouanton et al., 2007). In Japan, a similar study reported that the most common enterotoxin type was SEB in retail chicken meat (Kitai, Shimizu, Kawano, Sato, Nakano, Kitagawa, et al., 2005). In present study, no SEB producer was discovered among the sixty isolates. Instead, the most common enterotoxin type was SEI.

Table 5.6 Distribution of enterotoxigenic genotypes *S. aureus* isolates.

Source of samples	**Percentage of Enterotoxigenic Isolates**[a]	**Genotypes**																		
		s e a	***s e b***	***s e c***	***s e d***	***s e e***	***s e g***	***s e h***	***s e i***	***s e j***	***s e k***	***s e l***	***s e m***	***s e r***	***s e o***	***s e p***	***s e q***	***s e r***	***s e u***
Final products	10 (100%)						• •		• •				• •	• •	• •				
Fresh MSM	10 (100%)						• •		• •				• •	• •	• •				
Fresh Skin	10 (100%)						• •		• •				• •	• •	• •				
Fresh SO BF	9 (90%)						• •		• •				• •	• •	• •				
	1 (10%)																		
Rubber Fingers	9 (90%)						• •		• •				• •	• •	• •				
	1 (10%)						• •		• •					• •	• •				
Live chickens	1 (10%)					• •			• •				• •						
	1 (10%)						• •	• •	• •		• •	• •							• •
	8 (80%)						• •		• •				• •	• •	• •				

[a]The percentage was calculated based on ten *S. aureus* isolates from each sampling site.

Some new SEs: SEI (*sei*), SEG (*seg*), SEH (*seh*), SEM (*sem*), SEN (*sen*) and SEO (*seo*) were detected in the sixty isolates. The most frequently detected enterotoxin gene in the isolates was *sei* (n=59), followed by *seg* (n=58). This is not surprising because both genes belong to the enterotoxin gene cluster called *egc* region (Jarraud et al., 2001). All *S. aureus* isolates from the final products were positive for *sei*, *seg*, *sem*, *sen* and *seo* (Table 5.6). Kim et al. (2011) reported that enterotoxin G (*seg*), I (*sei*) and H (*seh*) have emetic toxicity causing foodborne outbreaks.

5.7 Multilocus Sequence Typing (MLST) of *S. aureus* isolates

The seven loci sequences of the sixty *S. aureus* isolates are shown in Appendix G. The seven loci sequences were designed to an allelic number giving a 7-digit allelic profile. All the sequence types (ST) of each isolate were obtained from the MLST database (http://saureus.mlst.net/) after submitting its allelic profile. More information of each ST can be obtained from the MLST database (http://saureus.mlst.net/) which is also shown in Table 5.8.

Out of the 60 *S. aureus* isolates, six different sequence types were found: ST5 (1, 4, 1, 4,12,1,10), ST2594 (1, 4, 320, 4, 12, 1, 10), ST101 (3, 1, 14, 15, 11, 19, 3), ST83 (1, 4, 1, 4,12,120,10), ST398 (3, 35, 19, 2, 20, 26, 39) and ST1 (1, 1, 1, 1, 1, 1, 1). The majority of the isolates were ST5 which comprised 55 colonies (91.67%). Similarly, Waters et al. (2011) reported ST5 as the most common sequence type in a study on chicken samples in USA, making up 74%. ST2594, ST101, ST83, ST398 and ST1 have one colony each which equates to 1.67% of the total isolates. ST398, ST101 and ST1 were also reported present in beef and chicken, pork retail meat in USA (Waters et al., 2011).

Table 5.7.1 MLST typing of the sixty *S. aureus* isolates[a].

ST	Allelic Profile	Country	Source	Year	MRSA[b]	No. of isolates (%)[c]
5	1, 4, 1, 4,12,1,10	Japan	Human	2006	R	55 (91.67)
2594	1, 4, 320, 4, 12, 1, 10	Brazil	Human	2012	R	1 (1.67)
101	3, 1, 14, 15, 11, 19, 3	Switzerland	Milk	2008	S	1 (1.67)
83	1, 4, 1, 4,12,120,10	Spain	Human milk	2007	S	1 (1.67)
398	3, 35, 19, 2, 20, 26, 39	Switzerland	Pig	2008	R	1 (1.67)
1	1, 1, 1, 1, 1, 1, 1	Australia	Human	1995	R	1 (1.67)

ST=sequence type.

[a]Source, year and country of isolate listed were one example of the information from MLST database. More information can be obtained from the MLST database (http://saureus.mlst.net/).

[b]R=methicillin resistant; S=not methicillin resistant.

[c]Based on total number of isolates (n=60) and values were expressed in two decimals.

Table 5.7.1 summarises the basic information of each sequence type. ST 5 has been reported to be a methicillin-resistant *S. aureus* (MRSA) isolate which agrees with the information from MSLT database (http://saureus.mlst.net/) (Enright, 2003; Enright et al., 2002; Ko et al., 2005; Urushibara et al., 2012). Five of the six different sequence types were MRSA resistant according to the information from the MLST database, however, additional confirmation tests are required.

The enterotoxigenic and MLST results of each *S. aureus* isolate are summarised in Table I (Appendix I). Fifty-four ST5 isolates were positive for *sei*, *seg*, *sem*, *sen* and *seo* while one ST5 isolate was encoded with *sei*, *sem* and *see* (Table 5.7.2). ST2594 had the same enterotoxigenic genes as the majority ST5 isolates (*sei*+*seg*+*sem*+*sen*+*seo*). In the study by Lv et al. (2014), three different groups of enterotoxin genes were encoded in ST5: 1) *sea, seb, seg, sek, seu;* 2) *sea, seb, seg, sek seu* and 3) *sea, seb, sec, seh, sek, sem, seu*, proving that the same sequence type *S. aureus* is possible to be encoded with different enterotoxin genes. Similar results were also found in Durand et al. (2006)'s study. On the contrary, *S. aureus* isolate that has different sequence types may be able to produce the same enterotoxins. This probably explains why 56 *S. aureus* isolates could produce the same enterotoxins while only 55 isolates shared the same sequence type based on the MLST assay.

Table 5.7.2 Sequence types and enterotoxin types of each *S. aureus* isolate.

Colony Code	Sequence Type	Enterotoxin Type
1-19	ST5	*sei+seg+sem+sen+seo*
20	ST2594	*sei+seg+sem+sen+seo*
21-39	ST5	*sei+seg+sem+sen+seo*
40	ST101	/
41-49	ST5	*sei+seg+sem+sen+seo*
50	ST83	*sei+seg+sen+seo*
51	ST5	*sei+sem+see*
52	ST5	*sei+seg+sem+sen+seo*
53	ST1	*sei+sek+seg+sel+seu+seh*
54-60	ST5	*sei+seg+sem+sen+seo*

Colony code 1-19 contains colonies 1 to 19; Colony code 21-39 contains colonies 21 to 39; Colony code 41-49 contains colonies 41 to 49; Colony code 54-60 contains colonies 54 to 60.

5.8 Clonal complexes of the six sequence types (STs)

According to the results above, six different STs were identified among the sixty isolates. In order to investigate the relateness of the *S. aureus* isolates, the eBURST programme was applied. eBURST is a clustering analysis program that assigns isolates into a clonal complex (CC) if at least five out of seven allele numbers are identical (de Sousa & De Lencastre, 2003; Mellmann et al., 2008). With this programme, the six different STs were divided into one major clonal complex and three singletons using eBURST (Figure 5.8).The major clonal complex comprised of three (3) different STs which were representedy by fifty-seven (57) isolates: ST5 (55), ST83 (1) and ST2594 (1) (Table 5.8). ST101, ST1 and ST398 were singletions as no ancenstral genotype could be assigned to them.

Table 5.8 eBURST analysis of clonal complex 5 (CC5).

ST	FREQ	SLV	Average Distance
5	55	2	1.0
83	1	1	1.5
2594	1	1	1.5
101	1	Singletions	
1	1		
398	1		

FREQ:the frequency of the ST
SLV:single locus variant

The ancestral genotype of the major clonal complex was ST5 which had the highest number of single locus variants (SLVs), therefore, this clonal complex was named CC5 (Feil et al.,

2003). ST83 and ST2594 belonged to CC5 with the same average distance to ST5 (1.5), which indicates that their relatedness is similar (Souza, 2014). The ancestral genotype of ST2594 and ST83 was ST5, suggesting that they are most likely to have similar microbiological properties as ST5 (de Sousa & De Lencastre, 2003). *S. aureus* ST5 is a MRSA and it has various antibiotic resistance abilities such as penicillin resistance, oxacillin resistance, kanamycin resistance and tobramycin resistance (Durand et al., 2006; Schulte et al., 2013). In agreement with this study, ST83 and ST2594 have been reported to belong to CC5 (de Sousa & De Lencastre, 2003; Souza, 2014).

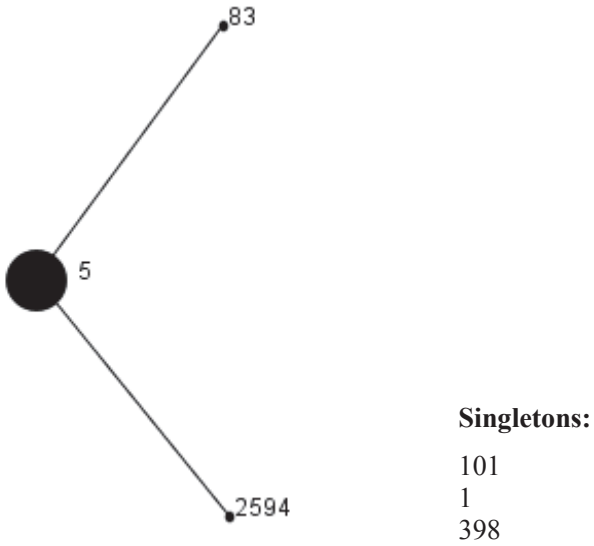


Figure 5.8 Identificatioan of clonal complexes of the *S. aureus* isolates. Each dot represents a sequence type. ST83, ST5 and ST2594 were clonal complex (CC) 5 with ST5 being the clonal ancestor. The relationships between the STs within CC5 are shown in solid line. ST101, ST1 and ST398 are singletons.

5.9 Potential contamination sources of *S a u r e u s*

The contamination source of poultry products by *S. aureus* was back-traced from final products in the processing plant to live chickens at one of the supplying farm by identifying the sequence types of the sixty isolates which consisted of ten representative isolates from each main sampling site. The sequence types and corresponding allelic profiles are listed in

Table 5.7.1 (section 5.7). The allelic profile, sequence types and source of each *S. aureus* isolate are shown in Table I (Appendix I).

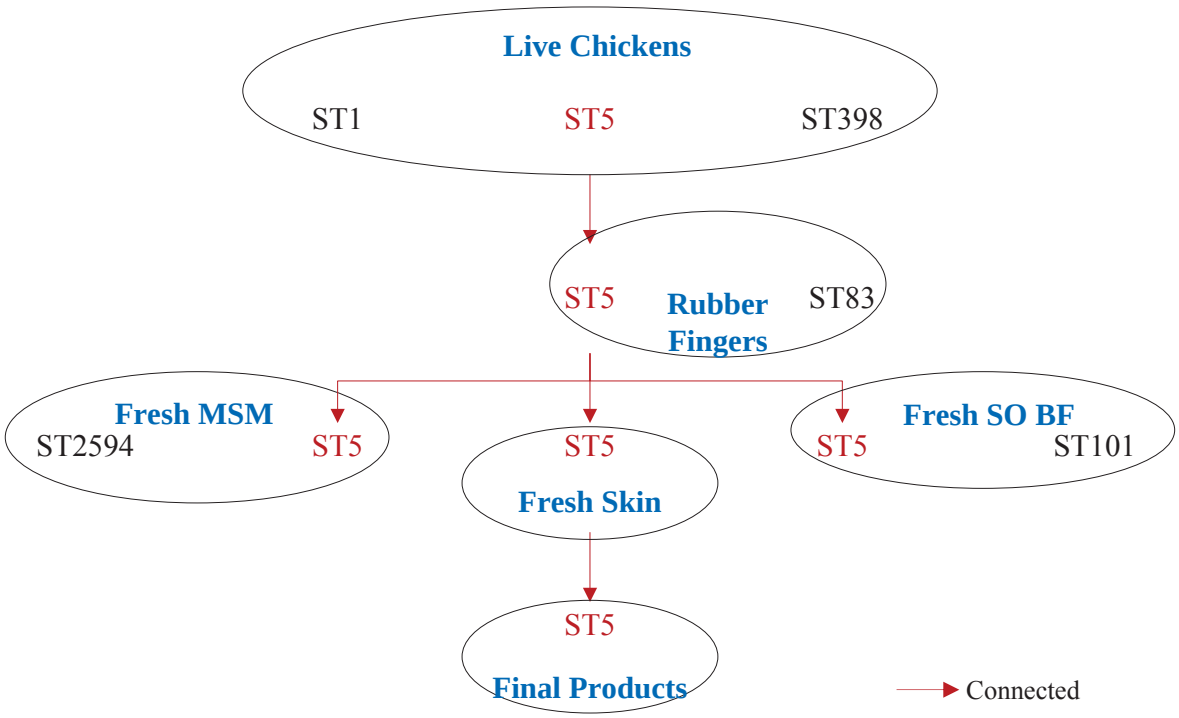


Figure 5.9 Sequence types of the sixty *S. aureus* isolates between each source of samples.

Figure 5.9 shows the strains of *S. aureus* from the main contamination sources. All the *S. aureus* isolates (n=5) in the final products appeared to originate from the same strain: ST5. In the secondary plant, three sequence types of *S. aureus* were present in the three fresh ingredients (Fresh MSM, Fresh Skin and Fresh SO BF). ST5 was detected in all the three samples of fresh ingredients, possibly leading to the *S. aureus* contamination in the final products. Fresh skin was most likely the main contamination source among the three samples of fresh ingredients since all the isolates (n=10) from Fresh Skin were identified as strain ST5. There were two different sequence types in Fresh MSM (ST5, n=9, ST2594, n=1) and Fresh SO BF (ST5, n=9, ST101, n=1) and no trace back samples were identified for ST2594 and ST101. The contamination source was traced back to rubber fingers in the primary processing as well with 9 out of 10 *S. aureus* isolates being ST5. Another isolate in the rubber fingers was ST83. Strain ST5 (n=8, 80%) was present in the live chickens swabs indicating

that live chickens could be the original carriers of *S. aureu*s to the final products. However, the original carrier of the pathogen is suspected to be farm workers who probably came into contact with the young chickens (Lv et al., 2014; Thompson et al., 1980). Swab samples were not collected from the hands of farm workers in this study.

S. aureus in the final products may be introduced through Fresh MSM, Fresh Skin, Fresh SO BF, Rubber Fingers in the Pluckers and live chickens at the farm. However, Fresh Skin was considered as the main contamination source based on the numbers of the same strain as that present in the final products, which also agreed with previous studies (Kibenge et al., 1982; Kuramasu et al., 1967). As shown in Figure 5.9, live chickens were considered as the original contamination source of *S. aureus*. However, *S. aureus* is able to colonise on both human and animals (Gao et al., 2012; Hasman et al., 2010; Lowder et al., 2009; Lv et al., 2014). According to the sequence type information in Table 5.8 (section 5.8), both human and live chickens seems to be associated with the sixty *S. aureus* isolates in this study. Considering that not all the strains present in the live chickens were traced back to the final products (ST398 and ST1), there might be other sources of contamination such as farm workers, breeder, hatchery, and transit vehicles (Lv et al., 2014; Thompson et al., 1980), but these sources were not investigated in this study.

6. Conclusion

All the samples collected from the processing plant and live chickens at the farm were contaminated by *S. aureus*. Of the 60 *S. aureus* isolates from the main sampling sites, 59 were enterotoxic. Six different strains of *S. aureus* were identified with strain ST5 being present at samples collected in the processing plant and live chickens at the farm. The source of *S. aureus* contamination in the final products was linked to the live chickens at the farm. A major clonal complex of the six different strains was identified as CC5. Chicken skin from the live chickens at the farm was most likely the origin of *S. aureus* contamination of the final products and the processing equipment.

Limitations and Recommendations

This study only focused on the contamination level and contamination source from processing steps and processing equipment in the plant, further investigations on hygiene status of workers are recommended as human is a common carrier of *S. aureus* (Ministry of Primary Industry, 2001). To minimise the contamination level of *S. aureus* in Fresh MSM, a proper hygiene and regular cleaning routine inside the MDM is required. Also, regular replacements of rubber fingers are recommended to reduce the cross-contamination rates. Although, the ST5 was identified as MRSA according to the information in the MLST database, it is recommended to confirm the information by amplifying the *mec* gene of the ST5 strains. Since not all the *S. aureus* strains colonised on the live chickens were traced back to the final products, further investigations on other potential contamination sources such as gloves and knifes used at the processing lines, feeders and drinkers at the farm are recommended.

References

3M™, Petrifilm™. (2010a). 3M™ Petrifilim™ staph express disk *3M™ Petrifilim™* (1st ed., pp. 3). USA: 3M™ Petrifilim™.

3M™, Petrifilm™. (2010b). 3M™ Petrifilm™ staph express count plate *3M™ Petrifilm™* (1st ed., pp. 1). USA: 3M™ Petrifilm™.

Aarnisalo, K, Tallavaara, K, Wirtanen, G, Maijala, R, & Raaska, L. (2006). The hygienic working practices of maintenance personnel and equipment hygiene in the Finnish food industry. *Food control, 17*(12), 1001-1011. doi: 10.1016/j.foodcont.2005.07.006.

Al-Ghamdi, A. Y. (2012). Incidence of *Staphylococcus aureus* contamination of marketed Processed Chicken products with special reference to its antibiotics sensitivity collected from Al Baha city markets, Saudi Arabia. *Pakistan Journal of Food Sciences, 22*(3), 168-170.

Álvarez-Astorga, M, Capita, R, Alonso-Calleja, C, Moreno, B, & García-Fernández, C. (2002). Microbiological quality of retail chicken by-products in Spain. *Meat Science, 62*(1), 45-50. doi: 10.1016/S0309-1740(01)00225-X.

AOAC. (2005a). *Official methods of analysis of AOAC International* (18th ed.). USA: AOAC International.

AOAC. (2005b). *Official methods of analysis of AOAC International* (18th ed.): AOAC International.

Arnold, J. W, & Silvers, S. (2000). Comparison of poultry processing equipment surfaces for susceptibility to bacterial attachment and biofilm formation. *Poultry Science, 79*(8), 1215-1221. doi: 10.1093/ps/79.8.1215.

ATCC. (2014). ATCC® Bacterial Culture Guide In ATCC (Ed.), (3rd ed.).

Balaban, N, & Rasooly, A. (2000). Staphylococcal enterotoxins. *International Journal of Food Microbiology, 61*(1), 1-10. doi: 10.1016/S0168-1605(00)00377-9.

Bania, J, Dabrowska, A, Bystron, J, Korzekwa, K, Chrzanowska, J, & Molenda, J. (2006). Distribution of newly described enterotoxin-like genes in *Staphylococcus aureus* from food. *International Journal of Food Microbiology, 108*(1), 36-41. doi: 10.1016/j.ijfoodmicro.2005.10.013.

Bannerman, T. L, Hancock, G. A, Tenover, F.C, & Miller, J. M. (1995). Pulsed-field gel electrophoresis as a replacement for bacteriophage typing of *Staphylococcus aureus*. *Journal of Clinical Microbiology, 33*(3), 551-555.

Bartlett, M. L, Jamlang, E. M, & Snyder, H. E. (1971). Effect of pH, protein concentration, and ionic strength on heat inactivation of staphylococcal enterotoxin B. *Applied Microbiology, 22*(6), 1034-1040.

Bergdoll, M. S. (1999). *Detection of staphylococcal enterotoxins* (1st ed.). USA: Academic Press.

Bergey, D. H, Boone, D. R, Castenholz, R .W, Brenner, D. J, Krieg, N. R, Staley, J. T, & Garrity, G. M. (2001). *Bergey's manual of systematic bacteriology* (2nd ed.). New York: Springer.

Bhatia, A, & Zahoor, S. (2007). *Staphylococcus aureus* enterotoxins: a review. *Journal of Clinical and Diagnostic Research, 3*, 188-197.

Blood, R. M, & Jarvis, B. (1974). Chilling of poultry: the effects of process parameters on the level of bacteria in spin• chiller waters. *International Journal of Food Science & Technology, 9*(2), 157-169. doi: 10.1111/j.1365-2621.1974.tb01759.x.

Bolder, N. M. (1997). Decontamination of meat and poultry carcasses. *Trends in Food Science & Technology, 8*(7), 221-227. doi: 10.1016/S0924-2244(97)01040-6.

Boylston, T, Chen, F, Coggins, P, Hydlig, G, McKee, L. H, Kerth, C, & Nollet, L. M. L. (2012). *Handbook of meat, poultry and seafood quality*: John Wiley & Sons.

Capita, R, Prieto, M, & Alonso-Calleja, C. (2004). Sampling methods for microbiological analysis of red meat and poultry carcasses. *Journal of Food Protection, 67*(6), 1303-1308.

Chaffey, B. J, Waites, W. M, & Dodd, C. E. (1988). Plasmid profiles as indicators of the source of contamination of *Staphylococcus aureus* endemic within poultry processing plants. *Applied and environmental microbiology, 54*(6), 1541-1549.

Chiang, Y. C, Liao, W. W, Fan, C. M, Pai, W. Y, Chiou, C. S, & Tsen, H. Y. (2008). PCR detection of Staphylococcal enterotoxins (SEs) N, O, P, Q, R, U, and survey of SE types in *Staphylococcus aureus* isolates from food-poisoning cases in Taiwan. *International journal of food microbiology, 121*(1), 66-73. doi: 10.1016/j.ijfoodmicro.2007.10.005.

Cogan, T. A, Bloomfield, S. F, & Humphrey, T. J. (1999). The effectiveness of hygiene procedures for prevention of cross• contamination from chicken carcases in the domestic kitchen. *Letters in Applied Microbiology, 29*(5), 354-358. doi: 10.1046/j.1472-765X.1999.00656.x.

ComLaw, Australian Government. (2010). Standard 4.2.2-Primary production and processing standard for poultry meat *Australia New Zealand Food Standards Code* (Vol. F2012L00292, pp. 1-2). Australia: ComLaw.

ComLaw, Australian Government. (2012). Standard 1.6.1-Microbiological limits for food *Australia New Zealand food standards code* (Vol. F2012C00862, pp. 1-2). Australia: ComLaw.

Corry, J. E. L, & Atabay, H. I. (2001). Poultry as a source of *Campylobacter* and related organisms. *Journal of Applied Microbiology, 90*(S6), 96S-114S. doi: 10.1046/j.1365-2672.2001.01358.x.

Corry, J. E. L, James, S. J, Purnell, G, Barbedo-Pinto, C. S, Chochois, Y, Howell, M, & James, C. (2007). Surface pasteurisation of chicken carcasses using hot water. *Journal of Food Engineering, 79*(3), 913-919. doi: 10.1016/j.jfoodeng.2006.03.018

Covell III, E. H. (1990). Poultry scalding system and process. Google Patents.

Crago, B, Ferrato, C, Drews, S. J, Svenson, L. W, Tyrrell, G, & Louie, M. (2012). Prevalence of *Staphylococcus aureus* and methicillin-resistant *S. aureus* (MRSA) in food samples associated with foodborne illness in Alberta, Canada from 2007 to 2010. *Food Microbiology, 32*(1), 202-205. doi: 10.1016/j.fm.2012.04.012.

Daghir, N. J. (2008). *Poultry production in hot climates* (2nd ed.). London, UK: CABI.

Davies, A. R, & Board, R. G. (1998). *The microbiology of meat and poultry* (1st ed.). UK: Thomson Science.

De Boer, E, Zwartkruis-Nahuis, J. T. M, Wit, B, Huijsdens, X. W, De Neeling, A. J, Bosch, T, Heuvelink, A. E. (2009). Prevalence of methicillin-resistant *Staphylococcus aureus* in meat. *International journal of food microbiology, 134*(1), 52-56. doi: 10.1016/j.ijfoodmicro.2008.12.007.

De Neeling, A. J, Van den Broek, M. J. M, Spalburg, E. C, van Santen-Verheuvel, M. G, Dam-Deisz, W. D. C, Boshuizen, H. C, Huijsdens, X. W. (2007). High prevalence of methicillin resistant *Staphylococcus aureus* in pigs. *Veterinary Microbiology, 122*(3), 366-372.

de Sousa, M. A, & De Lencastre, H. (2003). Evolution of sporadic isolates of methicillin-resistant *Staphylococcus aureus* (MRSA) in hospitals and their similarities to isolates of community-acquired MRSA. *Journal of Clinical Microbiology, 41*(8), 3806-3815. doi: 10.1128/JCM.41.8.3806-3815.2003.

Denny, C. B, Humber, J.Y, & Bohrer, C. W. (1971). Effect of toxin concentration on the heat inactivation of staphylococcal enterotoxin A in beef bouillon and in phosphate buffer. *Applied Microbiology, 21*(6), 1064-1066.

Devriese, L. A. (1980). Pathogenic staphylococci in poultry. *World's Poultry Science Journal, 36*(04), 227-236. doi: 0.1079/WPS19800012.

Devriese, L. A, & Devos, A. H. (1975). Suppressive effects of antibiotics on experimentally inoculated *Staphylococcus aureus* populations on the skin of poultry. *Avian Pathology, 4*(4), 295-302. doi: 10.1080/03079457509353878.

Dodd, C. E. R, Adams, B. W, Mead, G. C, & Waites, W. M. (1987). Use of plasmid profiles to detect changes in strains of *Staphylococcus aureus* during poultry processing. *Journal of Applied Bacteriology, 63*(5), 417-425. doi: 10.1111/j.1365-2672.1987.tb04863.x.

Dodd, C. E. R, Mead, G. C, & Waites, W. M. (1988). Detection of the site of contamination by Staphylococcus aureus within the defeathering machinery of a poultry processing plant. *Letters in applied microbiology, 7*(3), 63-66.

Durand, G, Bes, M, Meugnier, H, Enright, M. C, Forey, F, Liassine, N, Vandenesch, F. (2006). Detection of new methicillin-resistant *Staphylococcus aureus* clones containing the toxic shock syndrome toxin 1 gene responsible for hospital-and community-acquired infections in France. *Journal of Clinical Microbiology, 44*(3), 847-853. doi: 10.1128/JCM.44.3.847-853.2006.

EI-Jakee, J, Marouf, S. A, Ata, N. S, Abdel-Rahman, E. H, El-Moez, S. I. A, Samy, A.A, & El-Sayed, W. E. (2013). Rapid Method for Detection of *Staphylococcus aureus* Enterotoxins in Food. *Global Veterinaria, 11*(3), 335-341. doi: 10.5829/idosi.gv.2013.11.3.1140.

Enright, M. C. (2003). The evolution of a resistant pathogen–the case of MRSA. *Current Opinion in Pharmacology, 3*(5), 474-479. doi: 10.1016/S1471-4892(03)00109-7.

Enright, M. C, Day, N. P, Davies, C. E, Peacock, S. J, & Spratt, B. G. (2000). Multilocus sequence typing for characterization of methicillin-resistant and methicillin-susceptible clones of *Staphylococcus aureus*. *Journal of Clinical Microbiology, 38*(3), 1008-1015.

Enright, M. C, Robinson, D. A, Randle, G, Feil, E. J, Grundmann, H, & Spratt, B. G. (2002). The evolutionary history of methicillin-resistant *Staphylococcus aureus* (MRSA). *Proceedings of the National Academy of Sciences, 99*(11), 7687-7692.

EPA. (2013). Poultry production. Retrieved from http://www.epa.gov/oecaagct/ag101/poultry.html

ESR. (2014). *New Zealand public health surveillance report*. Wellington, New Zealand.

Feil, E. J, Cooper, J. E, Grundmann, H, Robinson, D. A, Enright, M. C, Berendt, T, Spratt, B. G. (2003). How clonal is *Staphylococcus aureus*? *Journal of Bacteriology, 185*(11), 3307-3316. doi: 10.1128/JB.185.11.3307-3316.2003.

Field, A. (2009). *Discovering statistics using SPSS* (3 rd ed). London: Sage publications Ltd.

Fletcher, D. L. (2002). Poultry meat quality. *World's Poultry Science Journal, 58*(02), 131-145. doi: 10.1079/WPS20020013.

Fratamico, P, Liu, Y, & Kathariou, S. (2011). *Genomes of foodborne and waterborne pathogens* (1st ed.). Washington, DC: ASM Press.

Froning, G. W. (1981). *Mechanical deboning of poultry and fish* (1st ed. Vol. 27). New York: Academic Press.

Fuster-Valls, N, Hernández-Herrero, M, Marín-de-Mateo, M, & Rodríguez-Jerez, J. J. (2008). Effect of different environmental conditions on the bacteria survival on stainless steel surfaces. *Food Control, 19*(3), 308-314. doi: 10.1016/j.foodcont.2007.04.013

Gao, J, Ferreri, M, Yu, F, Liu, X, Chen, L, Su, J, & Han, B. (2012). Molecular types and antibiotic resistance of *Staphylococcus aureus* isolates from bovine mastitis in a single herd in China. *The Veterinary Journal, 192*(3), 550-552. doi: 10.1016/j.tvjl.2011.08.030.

Gibbs, P. A, Patterson, J. T, & Harvey, J. (1978). Biochemical characteristics and enterotoxigenicity of *Staphylococcus aureus* strains isolated from poultry. *Journal of Applied Bacteriology, 44*(1), 57-74. doi: 10.1111/j.1365-2672.1978.tb00777.x.

Gibbs, P. A, Patterson, J. T, & Thompson, J. K. (1978). The distribution of *Staphylococcus aureus* in a poultry processing plant. *Journal of Applied Bacteriology, 44*(3), 401-410. doi: 10.1111/j.1365-2672.1978.tb00814.x.

Gill, C. O, Badoni, M, Moza, L. F, Barbut, S, & Griffiths, M. W. (2005). Microbiological sampling of poultry carcass portions by excision, rinsing, or swabbing. *Journal of Food Protection, 68*(12), 2718-2720.

Gosbell, I. B. (2004). Methicillin-resistant *Staphylococcus aureus*. *American Journal of Clinical Dermatology, 5*(4), 239-259. doi: 10.1086/646231.

Gregory, N. G. (1995). Stunning and Slaughter *Processing of Poultry* (1st ed., pp. 31-63): Springer US.

Gregory, N.G, & Wotton, S.B. (1986). Effect of slaughter on the spontaneous and evoked activity of the brain. *British poultry science, 27*(2), 195-205. doi: 10.1080/00071668608416872.

Grundmann, H, Hori, S, Enright, M. C, Webster, C, Tami, A, Feil, E. J, & Pitt, T. (2002). Determining the genetic structure of the natural population of *Staphylococcus aureus*: a comparison of multilocus sequence typing with pulsed-field gel electrophoresis, randomly amplified polymorphic DNA analysis, and phage typing. *Journal of Clinical Microbiology, 40*(12), 4544-4546. doi: 10.1128/JCM.40.12.4544-4546.2002.

Gundogan, N, Citak, S, Yucel, N, & Devren, A. (2005). A note on the incidence and antibiotic resistance of *Staphylococcus aureus* isolated from meat and chicken samples. *Meat science, 69*(4), 807-810. doi: 10.1016/j.meatsci.2004.10.011.

Habib, I, Sampers, I, Uyttendaele, M, Berkvens, D, & De Zutter, L. (2008). Baseline data from a Belgium-wide survey of *Campylobacter* species contamination in chicken meat preparations and considerations for a reliable monitoring program. *Applied and environmental microbiology, 74*(17), 5483-5489. doi: 10.1128/AEM.00161-08.

Harbottle, H, White, D. G, McDermott, P. F, Walker, R. D, & Zhao, S. (2006). Comparison of multilocus sequence typing, pulsed-field gel electrophoresis, and antimicrobial

susceptibility typing for characterization of Salmonella enterica serotype newport isolates. *Journal of Clinical Microbiology, 44*(7), 2449-2457. doi: 10.1128/JCM.00019-06.

Harrigan, W. F. (1998). *Laboratory methods in food microbiology* (3rd ed.). San Diego: Academic Press.

Harvey, J, Patterson, J. T, & Gibbs, P, A. (1982). Enterotoxigenicity of *Staphylococcus aureus* strains isolated from poultry: raw poultry carcases as a potential food• poisoning hazard. *Journal of Applied Microbiology, 52*(2), 251-258. doi: 10.1111/j.1365-2672.1982.tb04847.x.

Hasman, H, Moodley, A, Guardabassi, L, Stegger, M, Skov, R. L, & Aarestrup, F. M. (2010). *Spa* type distribution in *Staphylococcus aureus* originating from pigs, cattle and poultry. *Veterinary Microbiology, 141*(3), 326-331. doi: 10.1016/j.vetmic.2009.09.025

Hayes, R. (1992). *Food microbiology and hygiene*. London: Elsevier Science Publishers.

Haysom, I, & Sharp, K. (2004). Cross-contamination from raw chicken during meal preparation. *British food journal, 106*(1), 38-50. doi: 10.1108/00070700410515190.

Hennekinne, J. A, De Buyser, M. L, & Dragacci, S. (2012). *Staphylococcus aureus* and its food poisoning toxins: characterization and outbreak investigation. *FEMS Microbiology Reviews, 36*(4), 815-836. doi: 10.1111/j.1574-6976.2011.00311.x 815-836.

Hui, Y. H, Alarcón-Rojo, A. D, Alvarado, C, Bawa, A. S, Guerrero-Avendaño, F, Lundén, J, . . . Owens, C. M. (2010). *Handbook of Poultry Science and Technology, Secondary Processing* (Vol. 2). Hoboken: John Wiley and Sons.

Hwang, S. Y, Kim, S. H, Jang, E. J, Kwon, N. H, Park, Y. K, Koo, H. C, Park, Y. H. (2007). Novel multiplex PCR for the detection of the *Staphylococcus aureus* superantigen and its application to raw meat isolates in Korea. *International journal of food microbiology, 117*(1), 99-105. doi: 10.1016/j.ijfoodmicro.2007.02.013.

Innis, M. A, Gelfand, D. H, & Sninsky, J. J. (1999). *PCR applications: protocols for functional genomics* (1st ed.). San Diego: Academic Press.

Innis, M. A, Gelfand, D. H, Sninsky, J. J, & White, T. J. (1990). *PCR protocols: a guide to methods and applications* (1st ed.). San Diego: Academic Press.

ISO. (2004). Microbiology of food and animal feeding stuffs-horizontal methods for sampling techniques from surfaces using contact plates and swabs. Geneva: International Oraganisation of Standardisation.

Jacxsens, L, Kussaga, J, Luning, P. A, Van der Spiegel, M, Devlieghere, F, & Uyttendaele, M. (2009). A microbial assessment scheme to measure microbial performance of food

safety management systems. *International Journal of Food Microbiology, 134*(1), 113-125. doi: 10.1016/j.ijfoodmicro.2009.02.018.

Jacxsens, L, Luning, P. A, Marcelis, W. J, Van Boekel, T, Rovira, J, Oses, S, Uyttendaele, M. (2011). Tools for the performance assessment and improvement of food safety management systems. *Trends in Food Science & Technology, 22*, S80-S89. doi: 10.1016/j.tifs.2011.02.008.

James, C, Vincent, C, de Andrade Lima, T. I, & James, S. J. (2006). The primary chilling of poultry carcasses—a review. *International Journal of Refrigeration, 29*(6), 847-862. doi: 10.1016/j.ijrefrig.2005.08.003

Jarraud, S, Peyrat, M. A, Lim, A, Tristan, A, Bes, M, Mougel, C, Lina, G. (2001). egc, a highly prevalent operon of enterotoxin gene, forms a putative nursery of superantigens in *Staphylococcus aureus*. *The Journal of Immunology, 166*(1), 669-677. doi: 10.4049/jimmunol.166.1.669.

Jiménez, S. M, Salsi, M. S, Tiburzi, M. C, Rafaghelli, R. C, Tessi, M. A, & Coutaz, V. R. (1997). Spoilage microflora in fresh chicken breast stored at 4 C: influence of packaging methods. *Journal of Applied Microbiology, 83*(5), 613-618. doi: 10.1046/j.1365-2672.1997.00276.x.

Johnson, J. K, Arduino, S. M, Stine, O. C, Johnson, J. A, & Harris, A. D. (2007). Multilocus sequence typing compared to pulsed-field gel electrophoresis for molecular typing of *Pseudomonas aeruginosa*. *Journal of Clinical Microbiology, 45*(11), 3707-3712. doi: 10.1128/JCM.00560-07.

Johnson, W. M, Tyler, S. D, Ewan, E. P, Ashton, F. E, Pollard, D. R, & Rozee, K. R. (1991). Detection of genes for enterotoxins, exfoliative toxins, and toxic shock syndrome toxin 1 in *Staphylococcus aureus* by the polymerase chain reaction. *Journal of Clinical Microbiology, 29*(3), 426-430.

Kérouanton, A, Hennekinne, J. A, Letertre, C, Petit, L, Chesneau, O, Brisabois, A, & De Buyser, M.L. (2007). Characterization of *Staphylococcus aureus* strains associated with food poisoning outbreaks in France. *International journal of food microbiology, 115*(3), 369-375. doi: 10.1016/j.ijfoodmicro.2006.10.050.

Khanna, T, Friendship, R, Dewey, C, & Weese, J. S. (2008). Methicillin resistant *Staphylococcus aureus* colonization in pigs and pig farmers. *Veterinary Microbiology, 128*(3), 298-303. doi: 10.1016/j.vetmic.2007.10.006.

Kibenge, F. S, Wilcox, G. E, & Perret, D. (1982). *Staphylococcus aureus* isolated from poultry in Australia I. Phage typing and cultural characteristics. *Veterinary microbiology, 7*(5), 471-483. doi: 10.1016/0378-1135(82)90064-5.

Kim, N. H, Yun, A. R, & Rhee, M. S. (2011). Prevalence and classification of toxigenic *Staphylococcus aureus* isolated from refrigerated ready-to-eat foods (sushi,

kimbab and California rolls) in Korea. *Journal of Applied Microbiology, 111*(6), 1456-1464. doi: 10.1111/j.1365-2672.2011.05168.x.

Kitai, S, Shimizu, A, Kawano, J, Sato, E, Nakano, C, Kitagawa, H, Inamoto, T. (2005). Prevalence and characterization of Staphylococcus aureus and enterotoxigenic Staphylococcus aureus in retail raw chicken meat throughout Japan. *The Journal of veterinary medical science/the Japanese Society of Veterinary Science, 67*(3), 269-274. doi: 10.1292/jvms.67.269.

Kitai, S, Shimizu, A, Kawano, J, Sato, E, Nakano, C, Uji, T, & Kitagawa, H. (2005). Characterization of methicillin-resistant *Staphylococcus aureus* isolated from retail raw chicken meat in Japan. *The Journal of veterinary medical science/the Japanese Society of Veterinary Science, 67*(1), 107-110. doi: 10.1292/jvms.67.107.

Ko, K. S, Lee, J. Y, Suh, J. Y, Oh, W. S, Peck, K. R, Lee, N. Y, & Song, J. H. (2005). Distribution of major genotypes among methicillin-resistant *Staphylococcus aureus* clones in Asian countries. *Journal of Clinical Microbiology, 43*(1), 421-426.

Korsak, N, Daube, G, Ghafir, Y, Chahed, A, Jolly, S, & Vindevogel, H. (1998). An efficient sampling technique used to detect four foodborne pathogens on pork and beef carcasses in nine Belgian abattoirs. *Journal of Food Protection, 61*(5), 535-541.

Kuramasu, S, Imamura, Y, Takizawa, T, Oguchi, F, & Tajima, Y. (1967). Studies on Staphylococcosis in Chickens: I. Outbreaks of Staphylococcal Infection on Poultry Farms and Characteristics of *Staphylococcus aureus* Isolated from Chickens. *Zentralblatt für Veterinärmedizin Reihe B, 14*(7), 646-656. doi: 10.1111/j.1439-0450.1967.tb00267.x.

Kuroda, M, Ohta, T, Uchiyama, I, Baba, T, Yuzawa, H, Kobayashi, I, Nagai, Y. (2001). Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*. *The Lancet, 357*(9264), 1225-1240. doi: 10.1016/S0140-6736(00)04403-2.

Kusumaningrum, H. D, Riboldi, G, Hazeleger, W. C, & Beumer, R. R. (2003). Survival of foodborne pathogens on stainless steel surfaces and cross-contamination to foods. *International journal of food microbiology, 85*(3), 227-236. doi: 10.1016/S0168-1605(02)00540-8.

Kwon, N. H, Park, K. T, Jung, W. K, Youn, H. Y, Lee, Y, Kim, S. H, Kim, J. M. (2006). Characteristics of methicillin resistant *Staphylococcus aureus* isolated from chicken meat and hospitalized dogs in Korea and their epidemiological relatedness. *Veterinary Microbiology, 117*(2), 304-312. doi: 10.1016/j.vetmic.2006.05.006.

Lacher, D. W, Steinsland, H, Blank, T. E, Donnenberg, M. S, & Whittam, T. S. (2007). Molecular evolution of typical enteropathogenic *Escherichia coli:* clonal analysis by multilocus sequence typing and virulence gene allelic profiling. *Journal of Bacteriology, 189*(2), 342-350. doi: 10.1128/JB.01472-06.

Lancette, G. A, & Bennett, R. W. (2001). Staphylococcus aureus and staphylococcal enterotoxins. *Compendium of Methods for the Microbiological Examination of Foods, 4*, 387-403.

Lee, J. H. (2003). Methicillin (oxacillin)-resistant Staphylococcus aureus strains isolated from major food animals and their potential transmission to humans. *Applied and Environmental Microbiology, 69*(11), 6489-6494. doi: 10.1128/AEM.69.11.6489-6494.2003.

Lee, J. H. (2006). Occurrence of methicillin-resistant *Staphylococcus aureus* strains from cattle and chicken, and analyses of their *mecA*, *mecR1* and *mecI* genes. *Veterinary microbiology, 114*(1), 155-159. doi: 10.1016/j.vetmic.2005.10.024.

Lindblad, M, Lindmark, H, Thisted Lambertz, S, & Lindqvist, R. (2006). Microbiological baseline study of broiler chickens at Swedish slaughterhouses. *Journal of Food Protection, 69*(12), 2875-2882.

Logan, H. R. (1969). *Meat Deboner Machine*. Google Patents.

Lowder, B. V, Guinane, C. M, Zakour, N. L. B, Weinert, L. A, Conway-Morris, A, Cartwright, R. A, Fitzgerald, J. R. (2009). Recent human-to-poultry host jump, adaptation, and pandemic spread of *Staphylococcus aureus*. *Proceedings of the National Academy of Sciences, 106*(46), 19545-19550. doi: 10.1073/pnas.0909285106.

Lozano, Carmen, López, María, Gómez-Sanz, Elena, Ruiz-Larrea, Fernanda, Torres, Carmen, & Zarazaga, Myriam. (2009). Detection of methicillin-resistant *Staphylococcus aureus* ST398 in food samples of animal origin in Spain. *Journal of Antimicrobial Chemotherapy, 64*(6), 1325-1326. doi: 10.1093/jac/dkp378.

Lv, G. P, Xu, B. H, Wei, P. N, Song, J, Zhang, H. Y, Zhao, C, Zhao, B. H. (2014). Molecular characterization of foodborne-associated *Staphylococcus aureus* strains isolated in Shijiazhuang, China, from 2010 to 2012. *Diagnostic Microbiology and Infectious Disease, 78*(4), 462-468. doi: 10.1016/j.diagmicrobio.2013.12.006.

Macrogen, Inc. (2014). Sample submission guide. Retrieved from http://www.macrogen.com/eng/business/seq_support.html.

Maiden, M. C. J, Bygraves, J. A, Feil, E, Morelli, G, Russell, J. E, Urwin, R, Caugant, D. A. (1998). Multilocus sequence typing: a portable approach to the identification of clones within populations of pathogenic microorganisms. *Proceedings of the National Academy of Sciences, 95*(6), 3140-3145.

Mandel, G. L, Bennett, J. E, & Dolin, R. (2000). Principles and practices of infectious diseases. *New York: Livingstone*.

Matyi, S. A, Dupre, J. M, Johnson, W. L, Hoyt, P. R, White, D. G, Brody, T, Gustafson, J. E. (2013). Isolation and characterization of *Staphylococcus aureus* strains from a Paso

del Norte dairy. *Journal of dairy science, 96*(6), 3535-3542. doi: 10.3168/jds.2013-6590.

Maurer, J. (2006). *PCR methods in foods* (1st ed.). New York, United States: Springer.

McCullagh, J. J, McNamee, P. T, Smyth, J. A, & Ball, H. J. (1998). The use of pulsed field gel electrophoresis to investigate the epidemiology of *Staphylococcus aureus* infection in commercial broiler flocks. *Veterinary Microbiology, 63*(2), 275-281. doi: 10.1016/S0378-1135(98)00240-5.

McDougal, L. K, Steward, C. D, Killgore, G.E, Chaitram, J. M, McAllister, S. K, & Tenover, F. C. (2003). Pulsed-field gel electrophoresis typing of oxacillin-resistant *Staphylococcus aureus* isolates from the United States: establishing a national database. *Journal of Clinical Microbiology, 41*(11), 5113-5120. doi: 10.1128/JCM.41.11.5113-5120.2003.

Mead, G. C, & Dodd, C. E. R. (1990). Incidence, origin and significance of staphylococci on processed poultry. *Journal of Applied Bacteriology, 69*(S19), 81S-91S. doi: 10.1111/j.1365-2672.1990.tb01800.x.

Mead, G. C, Gibson, C, & Tinker, D. B. (1995). A model system for the study of microbial colonization in poultry defeathering machines. *Letters in Applied Microbiology, 20*(2), 134-136. doi: 10.1111/j.1472-765X.1995.tb01304.x.

Mead, G. C, Hudson, W. R, & Hinton, M. H. (1993). Microbiological survey of five poultry processing plants in the UK. *British Poultry Science, 34*(3), 497-503. doi: 10.1080/00071669308417605.

Mead, G. C, & Scott, M. J. (1994). Coagulase• negative staphylococci and coliform bacteria associated with mechanical defeathering of poultry carcasses. *Letters in Applied Microbiology, 18*(1), 62-64. doi: 10.1111/j.1472-765X.1994.tb00803.x.

Mead, G. C, Waites, W. M, & Dodd, C. E. R. (1988). Detection of the site of contamination by Staphylococcus aureus within the defeathering machinery of a poultry processing plant. *Letters in Applied Microbiology, 7*(3), 63-66. doi: 10.1111/j.1472-765X.1988.tb01253.x.

Mellmann, A, Weniger, T, Berssenbrügge, C, Keckevoet, U, Friedrich, A. W, Harmsen, D, & Grundmann, H. (2008). Characterization of clonal relatedness among the natural population of *Staphylococcus aureus* strains by using spa sequence typing and the BURP (based upon repeat patterns) algorithm. *Journal of Clinical Microbiology, 46*(8), 2805-2808. doi: 10.1128/JCM.00071-08.

Melter, O, Sanches, I. S, Schindler, J, de Sousa, M. A, Mato, R, Kovarova, V, De Lencastre, H. (1999). Methicillin-resistant *Staphylococcus aureus* clonal types in the Czech Republic. *Journal of Clinical Microbiology, 37*(9), 2798-2803.

Meyer, W, Aanensen, D. M, Boekhout, T, Cogliati, M, Diaz, M. R, Esposto, M. C, Kaocharoen, S. (2009). Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii*. *Medical Mycology, 47*(6), 561-570. doi: 10.1080/13693780902953886.

Ministry of Health. (1995). Microbiological reference : criteria for food. *Food Administration Manual, Version 2.0*, 23. http://ezproxy.massey.ac.nz/login?url=http://search.ebscohost.com/login.aspx?direct=true&db=cat00245a&AN=massey.b1619787&site=eds-live

Ministry of Health. (2002). Draft guidelines for the control of methicillin-resistant *Staphylococcus aureus* in New Zealand. Wellington: Ministry of Heath.

Ministry of Primary Industry, M. P. I. (2001). *Staphylococcus aureus* (pp. 1-4). Wellington: Ministry of Heath.

MLST database. (2015). eBURSTv3 readme instruction. from MLST Home http://eburst.mlst.net/

Modi, N. K, Rose, S. A, & Tranter, H.S. (1990). The effects of irradiation and temperature on the immunological activity of staphylococcal enterotoxin A. *International Journal of Food Microbiology, 11*(1), 85-92. doi: 10.1016/0168-1605(90)90041-3.

Monday, S. R, & Bohach, G. A. (1999). Use of multiplex PCR to detect classical and newly described pyrogenic toxin genes in staphylococcal isolates. *Journal of Clinical Microbiology, 37*(10), 3411-3414.

Montville, T, & Matthews, K. (2008). *Food microbiology : an introduction* (2nd ed.). Washington, DC: ASM Press.

Morandi, S, Brasca, M, Lodi, R, Cremonesi, P, & Castiglioni, B. (2007). Detection of classical enterotoxins and identification of enterotoxin genes in *Staphylococcus aureus* from milk and dairy products. *Veterinary Microbiology, 124*(1), 66-72. doi: 10.1016/j.vetmic.2007.03.014.

Mulder, R. W. A. W, Dorresteijn, L. W. J, & Van Der Broek, J. (1978). Cross• contamination during the scalding and plucking of broilers. *British Poultry Science, 19*(1), 61-70. doi: 10.1080/00071667808416443.

Mulder, R. W. A. W, & Veerkamp, C. H. (1974). Microbiological aspects of water-cooling on poultry carcasses. *LWT Lebensmitt Wissensch Technol, 1974*.

Murchan, S, Kaufmann, M. E, Deplano, A, de Ryck, R, Struelens, M, Zinn, C. E, El Solh, N. (2003). Harmonization of pulsed-field gel electrophoresis protocols for epidemiological typing of strains of methicillin-resistant Staphylococcus aureus: a single approach developed by consensus in 10 European laboratories and its

application for tracing the spread of related strains. *Journal of Clinical Microbiology, 41*(4), 1574-1585. doi: 10.1128/JCM.41.4.1574-1585.2003.

Narasimha Rao, D, & Sachindra, N. M. (2002). Modified atmosphere and vacuum packaging of meat and poultry products. *Food Reviews International, 18*(4), 263-293. doi: 10.1081/FRI-120016206.

nd. (2011). *Staphylococcus aureus* Retrieved 11 Oct., 2011, Retrieved from http://www.microbeworld.org/index.php?option=com_jlibrary&view=article&id=7611

Normanno, G, Corrente, M, La Salandra, G, Dambrosio, A, Quaglia, N. C, Parisi, A, Celano, G. V. (2007). Methicillin-resistant *Staphylococcus aureus* (MRSA) in foods of animal origin product in Italy. *International Journal of Food Microbiology, 117*(2), 219-222. doi: 10.1016/j.ijfoodmicro.2007.04.006.

Notermans, S, Dufrenne, J, & Leeuwen, W. V. (1982). Contamination of broiler chickens by *Staphylococcus aureus* during processing: incidence and origin. *Journal of Applied Microbiology, 52*(2), 275-280. doi: 10.1111/j.1365-2672.1982.tb04851.x.

Pepe, O, Blaiotta, G, Bucci, F, Anastasio, M, Aponte, M, & Villani, F. (2006). *Staphylococcus aureus* and staphylococcal enterotoxin A in breaded chicken products: detection and behavior during the cooking process. *Applied and environmental microbiology, 72*(11), 7057-7062. doi: 10.1128/AEM.00198-06.

Pepperell, R, Reid, C. A, Solano, S. N, Hutchison, M. L, Walters, L. D, Johnston, A. M, & Buncic, S. (2005). Experimental comparison of excision and swabbing microbiological sampling methods for carcasses. *Journal of Food Protection, 68*(10), 2163-2168.

Pereira, V, Lopes, C, Castro, A, Silva, J, Gibbs, P, & Teixeira, P. (2009). Characterization for enterotoxin production, virulence factors, and antibiotic susceptibility of *Staphylococcus aureus* isolates from various foods in Portugal. *Food Microbiology, 26*(3), 278-282. doi: 10.1016/j.fm.2008.12.008.

Pesavento, G, Ducci, B, Comodo, N, & Nostro, A. L. (2007). Antimicrobial resistance profile of *Staphylococcus aureus* isolated from raw meat: A research for methicillin resistant *Staphylococcus aureus* (MRSA). *Food Control, 18*(3), 196-200. doi: 10.1016/j.foodcont.2005.09.013.

PIANZ. (2010). *Industry information.* Retrieved from http://www.pianz.org.nz/industry-information/industry-statistics/meat-consumption/chicken-remains-new-zealands-favourite-meat

Pillsbury, A, Chiew, M, Bates, J, & Sheppeard, V. (2013). An outbreak of staphylococcal food poisoning in a commercially catered buffet. *Communicable Diseases Intelligence Quarterly Report, 37*(2), E144.

Probst, Y. (2008). *Nutrient composition of chicken meat*. Austraila: RIRDC.

Pu, S, Han, F, & Ge, B. (2009). Isolation and characterization of methicillin-resistant *Staphylococcus aureus* strains from Louisiana retail meats. *Applied and Environmental Microbiology, 75*(1), 265-267. doi: 10.1128/AEM.01110-08.

QIAGEN®. (2010). QIAGEN® Multiplex PCR Handbook (pp. 48). nd: QIAGEN® .

QIAGEN®. (2012). QIAamp® DNA Mini and Blood Mini Handbook. nd: QIAGEN®.

Raj, A. B. M. (2006). Recent developments in stunning and slaughter of poultry. *World's Poultry Science Journal, 62*(03), 467-484. doi: 10.1017/S0043933906001097.

Ray, B. (2001). *Fundamental food microbiology* (2nd ed.). Florida: CRC Press.

Read, R. B, & Bradshaw, J. G. (1966). Thermal inactivation of staphylococcal enterotoxin B in veronal buffer. *Applied Microbiology, 14*(1), 130-132.

Read, R. B, & Bradshaw, J. G. (1967). γ Irradiation of staphylococcal enterotoxin B. *Applied Microbiology, 15*(3), 603-605.

Roberts, D, & Greenwood, M. (2002). *Practical food microbiology* (3rd ed.). Oxford: Blackwell Science.

Robinson, D. A, & Enright, M. C. (2004). Multilocus sequence typing and the evolution of methicillin• resistant *Staphylococcus aureus*. *Clinical Microbiology and Infection, 10*(2), 92-97.

Rose, S. A, Bankes, P, & Stringer, M. F. (1989). Detection of staphylococcal enterotoxins in dairy products by the reversed passive latex agglutination (SET-RPLA) kit. *International Journal of Food Microbiology, 8*(1), 65-72. doi: 0.1016/0168-1605(89)90081-0

Sadat, T, & Volle, C. (2000). Integration of a linear accelerator into a production line of mechanically deboned separated poultry meat. *Radiation Physics and Chemistry, 57*(3), 613-617. doi: 10.1016/S0969-806X(99)00506-X.

Salo, S, Laine, A, Alanko, T, Sjoberg, A. M, & Writanen, G. (2000). Validation of the microbiological methods Hygicult dipslide, contact plate, and swabbing in surface hygiene control: a Nordic collaborative study. *Journal of AOAC International, 83*(6), 1357-1365.

Sams, A. R, Owens, C. M, & Alvarado, C. Z. (2000). *Poultry meat processing* (2nd ed). Florida: CRC Press.

Satterlee, L. D, & Kraft, A. A. (1969). Effect of meat and isolated meat proteins on the thermal inactivation of staphylococcal enterotoxin B. *Applied Microbiology, 17*(6), 906-909.

Scheier, D. J, & Haynes, H. A. (1974). Method and apparatus for use in evisceration of poultry: US Patent.

Schlievert, P. M, & Case, L. C. (2007). Molecular analysis of staphylococcal superantigens. *Methicillin-Resistant Staphylococcus aureus (MRSA) Protocols* (pp. 113-126). doi:10.1007/978-1-59745-468-1_9.

Schulte, B, Bierbaum, G, Pohl, K, Goerke, C, & Wolz, C. (2013). Diversification of clonal complex 5 methicillin-resistant *Staphylococcus aureus* strains (Rhine-Hesse clone) within Germany. *Journal of Clinical Microbiology, 51*(1), 212-216. doi: 10.1128/JCM.01967-12

Schwabe, M, Notermans, S, Boot, R, Tatini, S. R, & Krämer, J. (1990). Inactivation of staphylococcal enterotoxins by heat and reactivation by high pH treatment. *International Journal of Food Microbiology, 10*(1), 33-42. doi: 10.1016/0168-1605(90)90005-P.

Sebranek, J. G, Olson, D.G, Dickson, J. S, & Lee, M. (1996). Irradiation and packaging of fresh meat and poultry. *Journal of Food Protection, 59*(1), 62-72.

Silva, N. (2012). *Microbiological examination methods of food and water : a laboratory manual* (1st ed.). London: CRC Press.

Šimkovičová, M, & Gilbert, R. J. (1971). Serological detection of enterotoxin from food-poisoning strains of *Staphylococcus aureus*. *Journal of Medical Microbiology, 4*(1), 19-30. doi: 10.1099/00222615-4-1-19.

Slavik, M. F, Kim, J. W, & Walker, J. T. (1995). Reduction of Salmonella and Campylobacter on chicken carcasses by changing scalding temperature. *Journal of Food Protection, 58*(6), 689-691.

Souza, C. S. M. D. (2014). *Staphylococcus aureus: resistência de virulência e tipagem de MRSA pelas técnicas de MLST e spa typing* (Master dissertation, Universidade Estadual Paulista, Araraquara - SP, Brazil). Retrieved from http://acervodigital.unesp.br/handle/unesp/159214?mode=full

Sparrey, J. M, & Kettlewell, P. J. (1994). Shackling of poultry: is it a welfare problem? *World's Poultry Science Journal, 50*(02), 167-176. doi: 10.1079/WPS19940014

Spratt, B. G. (1999). Multilocus sequence typing: molecular typing of bacterial pathogens in an era of rapid DNA sequencing and the Internet. *Current Opinion in Microbiology, 2*(3), 312-316. doi: 10.1016/S1369-5274(99)80054-X.

Stals, P. (1992). From manual labour to automation. *Poultry International*(31), 9-82.

Stelma Jr, G. N, & Bergdoll, M. S. (1982). Inactivation of staphylococcal enterotoxin A by chemical modification. *Biochemical and Biophysical Research Communications, 105*(1), 121-126. doi: 10.1016/S0006-291X(82)80019-3.

Suzuki, T, Itakura, J, Watanabe, M, Ohta, M, Sato, Y, & Yamaya, Y. (2002). Inactivation of Staphylococcal enterotoxin-A with an electrolyzed anodic solution. *Journal of Agricultural and Food Chemistry, 50*(1), 230-234. doi: 10.1021/jf010828k.

Thayer, D. W, & Boyd, G. (1992). Gamma ray processing to destroy *Staphylococcus aureus* in mechanically deboned chicken meat. *Journal of Food Science, 57*(4), 848-851. doi: 10.1111/j.1365-2621.1992.tb14308.x.

Thomas, Y. O, Kraft, A. A, Rust, R. E, & Hotchkiss, D. K. (1984). Effect of carbon dioxide flushing and packaging methods on the microbiology of packaged chicken. *Journal of Food Science, 49*(5), 1367-1371. doi: 10.1111/j.1365-2621.1984.tb14992.x.

Thompson, J. K, Gibbs, P. A, & Patterson, J. T. (1980). *Staphylococcus aureus* in commercial laying flocks: incidence and characteristics of strains isolated from chicks, pullets and hens in an integrated commercial enterprise. *British Poultry science, 21*(4), 315-330. doi: 10.1080/00071668008416675.

Tsola, E, Drosinos, E.H, & Zoiopoulos, P. (2008). Impact of poultry slaughter house modernisation and updating of food safety management systems on the microbiological quality and safety of products. *Food control, 19*(4), 423-431. doi: 10.1016/j.foodcont.2007.05.003.

Urushibara, N, Kawaguchiya, M, & Kobayashi, N. (2012). Two novel arginine catabolic mobile elements and staphylococcal chromosome cassette mec composite islands in community-acquired methicillin-resistant *Staphylococcus aureus* genotypes ST5-MRSA-V and ST5-MRSA-II. *Journal of Antimicrobial Chemotherapy, 67*(8), 1828-1834. doi: 10.1093/jac/dks157.

Urwin, R, & Maiden, M. C. J. (2003). Multi-locus sequence typing: a tool for global epidemiology. *Trends in Microbiology, 11*(10), 479-487. doi: 10.1016/j.tim.2003.08.006.

van Pelt-Verkuil, E, Van Belkum, A, & Hays, J P. (2008). *Principles and technical aspects of PCR amplification*. New York: Springer.

Veerkamp, C. H. (1995). Developments in primary processing technology. *Poultry International*(34), 6-30.

Veerkamp, C. H, & Heemskerk, W. (1991). Multi-stage scalding. *Poultry International, 30*(12), 62-67.

Veerkamp, C. H, & Hofmans, G. J. P. (1973). New development in poultry processing: simultaneous scalding and plucking. *Poultry international*.

Waldroup, A. L. (1996). Contamination of raw poultry with pathogens. *World's Poultry Science Journal, 52*(01), 7-25. doi: 10.1079/WPS19960002.

Warren, J. R, Spero, L, & Metzger, J. F. (1974). Isothermal denaturation of aqueous staphylococcal enterotoxin B by guanidine hydrochloride, urea, and acid pH. *Biochemistry, 13*(8), 1678-1683. doi: 10.1021/bi00705a019.

Waters, A. E, Contente-Cuomo, T, Buchhagen, J, Liu, Cindy M, Watson, L, Pearce, K, Engelthaler, D. M. (2011). Multidrug-resistant *Staphylococcus aureus* in US meat and poultry. *Clinical Infectious Diseases, 52*(10), 1227-1230. doi: 10.1093/cid/cir181.

Weissensteiner, T, Nolan, T, Bustin, S. A, Griffin, H. G, & Griffin, A. (2010). *PCR technology: current innovations* (2nd ed.). Florida: CRC Press.

West, B, & Zhou, B. X. (1988). Did chickens go north? New evidence for domestication. *Journal of Archaeological Science, 15*(5), 515-533. doi: 10.1079/WPS19890012.

Whyte, P, McGill, K, & Collins, J. D. (2003). An assessment of steam pasteurization and hot water immersion treatments for the microbiological decontamination of broiler carcasses. *Food Microbiology, 20*(1), 111-117. doi: 10.1016/S0740-0020(02)00084-9.

Wieneke, A. A. (1991). Comparison of four kits for the detection of staphylococcal enterotoxin in foods from outbreaks of food poisoning. *International Journal of Food Microbiology, 14*(3), 305-312. doi: 10.1016/0168-1605(91)90122-6.

Williamson, D. A, Zhang, J, Ritchie, S. R, Roberts, S. A, Fraser, J. D, & Baker, M. G. (2014). *Staphylococcus aureus* infections in New Zealand, 2000–2011. *Emerging infectious diseases, 20*(7), 1157. doi: 10.3201/eid2007.131923.

Wiren, A, Gunnarsson, U, Andersson, L, & Jensen, P. (2009). Domestication-related genetic effects on social behavior in chickens–Effects of genotype at a major growth quantitative trait locus. *Poultry Science, 88*(6), 1162-1166. doi: 10.3382/ps.2008-00492.

Appendix

Appendix A. Preparation of reagents and media

Table A1 Instruction of rehydrating BBL Coagulase Plasma.

Product size	Sterile purified water	Approximate number of tests can be rehydrated
3 mL	3 mL	6 tests

The BBL Coagulase Plasma was prepared according to supplier's instructions.

Table A2 Instruction of preparing BHI broth.

Product Name and Number	Brand	Instructions
CM1135 Brain Heart Infusion	Oxoid, UK	Add 37 g to 1 litre of distilled water. Mix well and distribute into final containers. Sterilise by autoclaving at 121°C for 15 minutes.

Table A3 Instructions for preparing 0.1% peptone water.

Product Name and Number	Brand	Instructions
Universal peptone M66	Merck KGaA	Add 0.1% g (powder) of final volume to distilled water. Mix well and distribute into final containers. Sterilise by autoclaving at 121°C for 15 minutes.

Table A4 Preparation of Nutrient agar plate.

Product Name and Number	Brand	Instructions
CM0003 Nutrient agar	OXOID, UK	Suspend 28 g in 1 litre of distilled water. Bring to the boil to dissolve completely. Sterilize by autoclaving at 121°C for 15 minutes.

Table A5 Preparation of Nutrient broth.

Product Name and Number	Brand	Instructions
CM0001 Nutrient agar	OXOID, UK	Add 13 g to 1 litre of distilled water. Mix well and distribute into final containers. Sterilize by autoclaving at 121°C for 15 minutes.

Table A6 Preparation of 40 mL lysozyme solution.

Description	20 mg/mL lysozyme in 20 mM Tris·HCl, pH 8.0, 2 mM EDTA, 1.2% Triton
Lysozyme	0.8 g
Tris	800 μL
EDTA	160 μL
Triton	480 μL

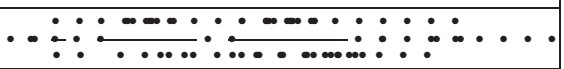
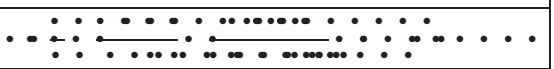
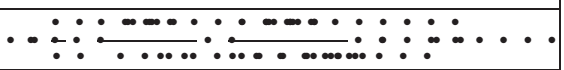
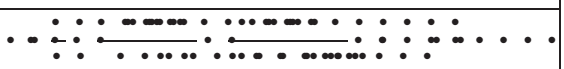
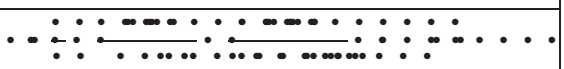
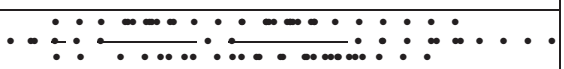
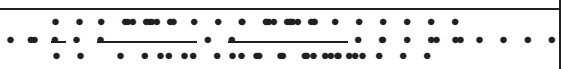
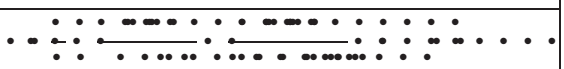
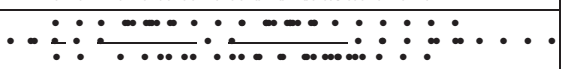
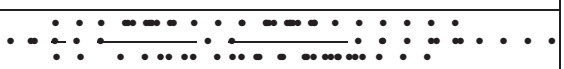
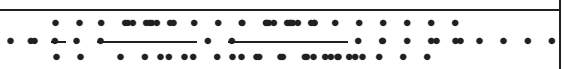
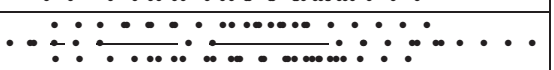
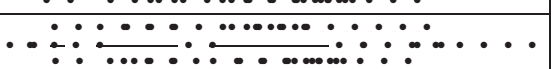
Table A7 Preparation of 900 mL TAE buffer.

Description	Dilution of 900 mL TAE buffer from 50× to 1×

50×Tris base, acetic acid and EDTA (TAE) buffer	18 mL
Distilled water	882 mL

Appendix B. Calculations of primers for enterotoxin detection and MLST

Table B1 Calculations of primer stock solution for enterotoxin detection

Primer name	Concentration on COA (nmol)	Calculation steps
SEA-f	14.3	
SEA-r	21	
SEB-f	20.8	
SEB-r	24.4	
SEC-f	23.8	
SEC-r	21.8	
SED-f	20.2	
SED-r	23.1	
SEE-f	18.8	
SEE-r	21.1	
SEG-f	23.8	
SEG-r	25.8	
SEH-f	19.1	
SEH-r	19	
SEI-f	20.7	
SEI-r	24.2	
SEJ-f	21.8	
SEJ-r	22.1	
SEK-f	20.2	
SEK-r	21.1	
SEL-f	23.4	
SEL-r	25.7	
SEM-f	19	
SEM-r	20.6	

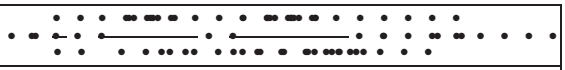
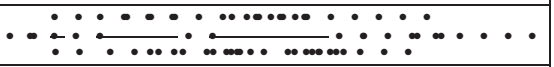
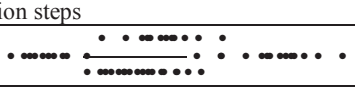
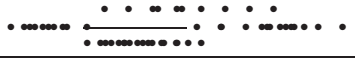
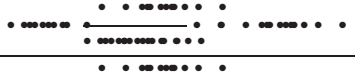
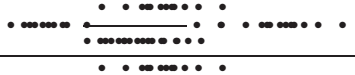
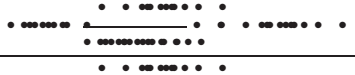
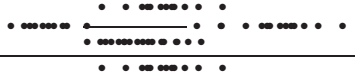
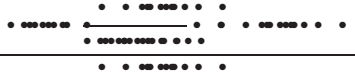
SEN-f	19.1	
SEN-r	16	
SEU-f	18.5	
SEU-r	21	

Table B2 Calculations of primers for MLST

Primer name	Weight of the primer (mg)	Calculation steps
arc-up	0.22	
arc-dn	0.17	
aro-up	0.19	
aro-dn	0.20	
glp-up	0.16	
glp-dn	0.21	
pta-up	0.13	
pta-dn	0.21	
tpi-up	0.24	
tpi-dn	0.18	
gmk-up	0.15	
gmk-dn	0.15	
yqi-up	0.20	
yqi-dn	0.18	

Appendix C. Concentrations of extracted DNA and purified PCR products

Table C1 Extracted DNA concentration of each *S. aureus* isolates.

Colony No.	DNA concentration (μg/mL)	
	Duplicate 1	Duplicate 2
1	74.182	66.670
2	12.834	15.599
3	12.624	14.486
4	65.985	37.659
5	13.807	21.577
6	26.354	40.799
7	20.663	15.669
8	10.911	8.976
9	3.188	7.137
10	18.484	24.565
11	22.660	21.937
12	5.861	16.830
13	11.873	10.160
14	56.961	16.300
15	8.471	5.381
16	30.14	20.507
17	21.715	15.697
18	20.178	23.248
19	17.571	34.211
20	32.742	26.428
21	12.757	39.036
22	54.152	22.219
23	33.902	33.511
24	36.047	12.400
25	39.454	10.822
26	88.835	108.42
27	7.688	5.758
28	57.794	22.329
29	13.941	13.923
30	7.447	3.860
31	13.771	10.759
32	14.837	16.776
33	6.139	17.688
34	5.484	3.705
35	13.518	5.995
36	38.509	42.027
37	98.819	16.007
38	20.080	20.466
39	23.521	12.546
40	14.654	14.544
41	12.274	6.039
42	16.927	22.420
43	26.568	56.017
44	26.859	32.651
45	31.291	13.492
46	13.568	11.057
47	46.706	32.503
48	15.189	10.713
49	35.865	42.410
50	40.048	69.770
51	26.109	26.506
52	9.845	9.375
53	18.709	24.864

54	19.151	38.159
55	47.045	47.217
56	13.066	12.629
57	33.502	22.509
58	15.955	18.618
59	19.085	28.549
60	17.504	20.270

Table C2 DNA concentration of purified PCR products in MLST

Colony No.	DNA concentration (μg/mL)	Colony No.	DNA concentration (μg/mL)
11	42.153	12	6.593
13	15.199	14	69.908
15	7.733	16	12.376
17	10.421	21	9.479
22	24.868	23	9.971
24	7.045	25	95.524
26	18.637	27	10.685
31	22.085	32	2.417
33	13.370	34	6.878
35	9.385	36	15.553
37	16.881	41	8.994
42	6.375	43	19.715
44	8.219	45	12.552
46	5.994	47	17.721
51	9.531	52	8.243
53	10.375	54	90460
55	46.612	56	10.203
57	7.115	61	27.722
62	9.453	63	10.455
64	11.211	65	5.045
66	28.542	67	28.133
71	22.824	72	29.137
73	13.948	74	3.353
75	14.360	76	33.496
77	8.501	81	16.529
82	16.069	83	15.254
84	14.359	86	11.082
87	8.967	91	20.786
92	25.979	93	20.526
94	3.767	95	8.944
96	11.804	97	5.411
101	9.898	102	7.047
103	4.889	104	7.847
105	19.536	106	18.945
107	30.348	111	26.490
112	43.076	113	8.204
114	23.941	115	9.344
116	26.165	117	15.264
121	21.484	122	34.865
123	22.849	124	19.920
125	12.287	126	10.729
127	6.583	131	12.948
132	16.674	133	14.662
134	16.676	135	4.645
136	7.686	137	9.466
141	2.701	142	11.068
143	7.522	144	4.815
145	7.250	146	6.970

147	11.443	151	13.542
152	8.654	153	5.546
154	10.514	155	12.554
156	11.564	157	6.554
161	20.525	162	14.638
163	8.459	164	7.868
165	25.563	166	18.674
167	35.166	171	49.569
172	32.900	173	31.052
174	16.230	175	16.477
177	28.878	181	25.485
182	20.141	183	23.441
184	8.654	185	9.214
186	4.225	187	6.248
191	17.548	192	15.947
193	18.247	194	7.245
195	11.254	196	14.978
197	16.757	201	12.667
202	17.396	203	10.967
204	12.221	205	6.764
206	9.338	207	13.804
211	7.784	212	8.014
213	9.669	214	20.890
215	21.964	216	5.204
217	8.333	221	9.642
222	9.778	223	10.969
224	15.630	225	18.665
226	16.302	227	10.551
231	9.546	232	11.641
233	9.669	234	5.677
235	14.354	236	12.363
237	10.715	241	8.702
242	12.215	243	15.324
244	16.012	245	13.336
246	4.687	247	8.299
251	3.282	252	2.419
253	10.148	254	7.425
255	10.164	256	13.842
257	9.589	261	4.887
262	2.704	263	2.032
264	6.787	265	2.135
266	6.519	267	12.708
271	9.654	272	10.857
273	7.666	274	8.301
275	8.014	276	15.554
277	13.001	281	25.586
282	14.849	283	27.493
284	11.989	285	11.292
286	6.929	291	4.805
292	6.496	293	10.360
294	35.500	295	4.579
296	6.706	297	16.497
301	24.644	302	23.019
303	20.198	304	17.262
305	16.354	306	10.781
307	12.604	311	52.260
312	8.969	313	7.688
314	1.426	315	11.917
316	3.102	317	2.943
321	9.444	322	2.235
323	5.698	324	14.688

325	16.703	326	3.473
327	5.511	331	8.135
332	10.647	333	11.247
334	9.914	335	5.146
336	8.074	337	8.284
341	8.639	342	10.687
343	12.551	344	18.214
345	11.318	346	11.973
347	13.640	351	9.005
352	18.363	353	12.360
354	10.475	355	12.024
356	9.125	357	11.713
361	15.816	362	8.610
363	15.674	364	9.912
365	5.591	366	4.516
367	3.069	371	14.657
372	16.206	373	6.705
374	12.709	375	5.061
376	10.445	377	8.873
381	14.330	382	11.974
383	9.248	384	8.694
385	12.725	386	14.248
387	10.853	391	9.210
392	15.647	393	14.214
394	11.336	395	19.364
396	12.356	397	15.668
401	17.395	402	13.644
403	10.621	404	12.354
405	11.235	406	22.549
407	15.218	411	18.277
412	19.217	413	19.368
414	27.228	415	10.854
416	25.219	417	18.705
421	20.671	422	16.107
423	14.484	424	10.810
425	15.232	426	19.017
427	13.718	431	19.227
432	14.328	433	17.879
434	21.564	435	18.212
436	20.725	437	24.390
441	25.339	442	20.143
443	12.543	444	27.301
445	19.667	446	20.908
447	28.961	451	24.820
452	24.305	453	25.241
454	21.325	455	19.764
456	18.218	457	29.821
461	21.545	462	20.962
463	22.012	464	25.648
465	20.112	466	25.629
467	18.374	471	19.889
472	25.248	473	23.028
474	20.814	475	25.024
476	21.302	477	20.118
481	29.019	482	22.821
483	20.549	484	21.851
485	27.692	486	22.367
487	23.202	491	24.255
492	26.921	493	20.807
494	24.878	495	21.713
496	20.541	497	23.085

501	22.220	502	21.536
503	20.842	504	25.223
505	20.105	506	19.857
507	17.804	511	20.394
512	21.083	513	20.147
514	19.781	515	24.020
516	21.317	517	22.224
521	19.259	522	19.603
523	26.468	524	25.818
525	24.606	526	26.262
527	28.588	531	26.960
532	22.635	533	24.911
534	23.576	535	20.708
536	21.557	537	21.737
541	19.995	542	26.517
543	20.658	544	22.002
545	22.561	546	20.323
547	19.817	551	24.085
552	15.028	553	21.176
554	22.308	555	23.128
556	22.111	557	25.810
561	24.621	562	22.974
563	22.259	564	20.894
565	27.010	566	19.909
567	23.819	571	20.196
572	25.044	573	22.451
574	23.732	575	20.021
576	14.520	577	20.484
581	28.259	582	24.535
583	23.267	584	21.554
585	21.521	586	25.642
587	20.924	591	21.285
592	23.318	593	25.045
594	20.833	595	19.247
596	12.921	597	20.457
601	22.225	602	25.568
603	22.304	604	19.874
605	21.726	606	23.514
607	21.776		

Appendix D. Gram-staining and coagulation results of isolated *S. aureus* colonies

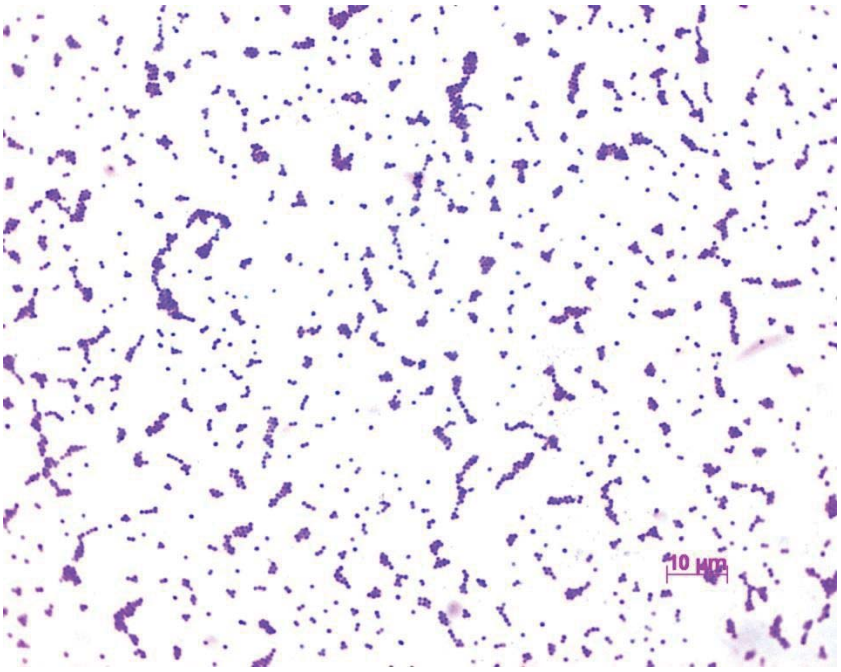


Figure D1 Gram-staining of one counted *S. aureus* isolate.

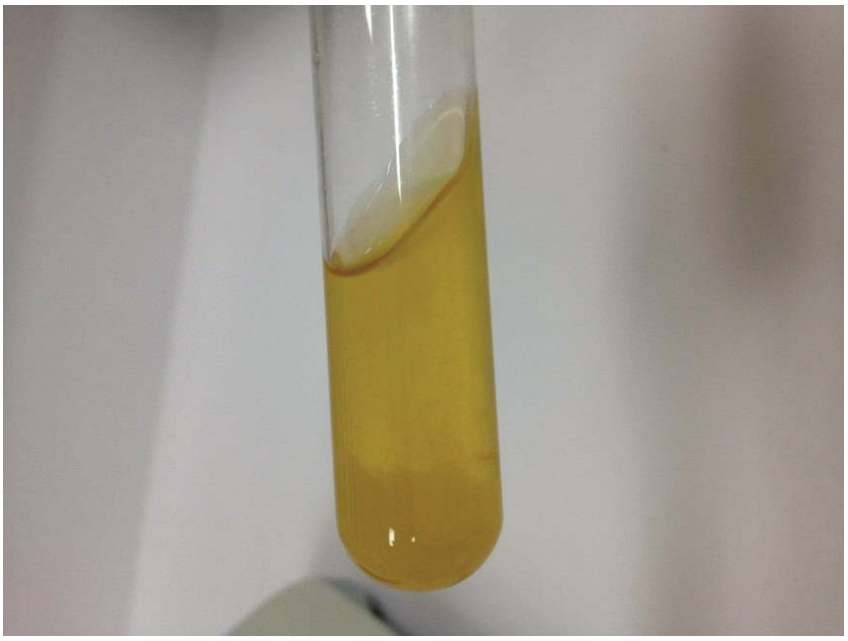


Figure D2 An example of coagulate-positive result of one counted colony from a Petriflim.

Appendix E. Raw data of *S. aureus* isolations

Table E1 Raw data of viable counts of *S. aureus* (CFU/g) enumerated from final products.

Product Name	Batch no.	*S. aureus* counts (CFU/g)			S. aureus counts (Log 10 CFU/g)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Final Products	1	1000	700	850	3.00	2.85	2.93	0.11
Final Products	1	10	40	25	1.00	1.60	1.40	0.43
Final Products	1	1200	1500	1350	3.08	3.18	3.13	0.07
Final Products	1	40	10	25	1.60	1.00	1.40	0.43
Final Products	1	30	40	35	1.48	1.60	1.54	0.09
Final Products	1	100	200	150	2.00	2.30	2.18	0.21
Final Products	2	60	40	50	1.78	1.60	1.70	0.12
Final Products	2	110	200	155	2.04	2.30	2.17	0.18
Final Products	2	40	30	35	1.60	1.48	1.54	0.09
Final Products	2	200	20	110	2.30	1.30	2.04	0.71
Final Products	2	100	40	70	2.00	1.60	1.85	0.28
Final Products	2	80	50	65	1.90	1.70	1.81	0.14
Final Products	3	90	50	70	1.95	1.70	1.85	0.18
Final Products	3	50	30	40	1.70	1.48	1.60	0.16
Final Products	3	20	20	20	1.30	1.30	1.30	0.00
Final Products	3	20	30	25	1.30	1.48	1.40	0.12
Final Products	3	200	100	150	2.30	2.00	2.18	0.21
Final Products	3	30	10	20	1.48	1.00	1.30	0.34
Final Products	4	300	100	200	2.48	2.00	2.30	0.34
Final Products	4	60	60	60	1.78	1.78	1.78	0.00
Final Products	4	600	1000	800	2.78	3.00	2.90	0.16
Final Products	4	80	400	240	1.90	2.60	2.38	0.49
Final Products	4	100	50	75	2.00	1.70	1.88	0.21
Final Products	4	50	50	50	1.70	1.70	1.70	0.00
Final Products	5	40	30	35	1.60	1.48	1.54	0.09

Final Products	5	800	600	700	2.90	2.78	2.85	0.09
Final Products	5	300	400	350	2.48	2.60	2.54	0.09
Final Products	5	120	40	80	2.08	1.60	1.90	0.34
Final Products	5	100	10	55	2.00	1.00	1.74	0.71
Final Products	5	50	80	65	1.70	1.90	1.81	0.14
Final Products	6	90	80	85	1.95	1.90	1.93	0.04
Final Products	6	40	60	50	1.60	1.78	1.70	0.12
Final Products	6	80	100	90	1.90	2.00	1.95	0.07
Final Products	6	300	200	250	2.48	2.30	2.40	0.12
Final Products	6	30	90	60	1.48	1.95	1.78	0.34
Final Products	6	200	200	200	2.30	2.30	2.30	0.00

Table E2 Raw data of viable counts of *S. aureus* (CFU/g) enumerated from Frozen MSM, Frozen skin and Frozen Skin-on Breast Fillet

Product Name	Batch no.	*S. aureus* counts (CFU/g)			*S. aureus* counts (Log 10 CFU/g)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Frozen MSM	1	70	30	50	1.85	1.48	1.70	0.26
Frozen MSM	1	400	460	430	2.60	2.66	2.63	0.04
Frozen MSM	1	500	400	450	2.70	2.60	2.65	0.07
Frozen MSM	1	160	190	175	2.20	2.28	2.24	0.05
Frozen MSM	1	500	300	400	2.70	2.48	2.60	0.16
Frozen MSM	1	1500	1300	1400	3.18	3.11	3.15	0.04
Frozen MSM	2	10	20	15	1.00	1.30	1.15	0.21
Frozen MSM	2	30	70	50	1.48	1.85	1.66	0.26
Frozen MSM	2	5500	5800	5650	3.74	3.76	3.75	0.02
Frozen MSM	2	400	400	400	2.60	2.60	2.60	0.00
Frozen MSM	2	10	20	15	1.00	1.30	1.15	0.21
Frozen MSM	2	30	40	35	1.48	1.60	1.54	0.09
Frozen MSM	3	110	140	125	2.04	2.15	2.09	0.07
Frozen MSM	3	700	800	750	2.85	2.90	2.87	0.04
Frozen MSM	3	340	480	410	2.53	2.68	2.61	0.11
Frozen MSM	3	210	220	215	2.32	2.34	2.33	0.01
Frozen MSM	3	500	800	650	2.70	2.90	2.80	0.14
Frozen MSM	3	20	20	20	1.30	1.30	1.30	0.00
Frozen Skin	1	100	100	100	2.00	2.00	2.00	0.00

Frozen Skin	1	100	80	90	2.00	1.90	1.95	0.07
Frozen Skin	1	1000	1000	1000	3.00	3.00	3.00	0.00
Frozen Skin	1	10	20	15	1.00	1.30	1.18	0.21
Frozen Skin	1	10	10	10	1.00	1.00	1.00	0.00
Frozen Skin	1	110	140	125	2.04	2.15	2.10	0.07
Frozen Skin	2	550	560	555	2.74	2.75	2.74	0.00
Frozen Skin	2	150	220	185	2.18	2.34	2.26	0.06
Frozen Skin	2	30	50	40	1.48	1.70	1.59	0.08
Frozen skin	2	10	40	25	1.00	1.60	1.30	0.21
Frozen Skin	2	8000	8700	8350	3.90	3.94	3.92	0.01
Frozen Skin	2	190	140	165	2.28	2.15	2.21	0.05
Frozen Skin	3	10	40	25	1.00	1.60	1.30	0.43
Frozen Skin	3	90	100	95	1.95	2.00	1.98	0.02
Frozen Skin	3	20	10	15	1.30	1.00	1.15	0.21
Frozen Skin	3	220	330	275	2.34	2.52	2.43	0.12
Frozen Skin	3	100	200	150	2.00	2.30	2.15	0.21
Frozen Skin	3	20	20	20	1.30	1.30	1.30	0.00
Frozen breast skin on	1	50	50	50	1.70	1.70	1.70	0.00
Frozen SO BF	1	80	120	100	1.90	2.08	1.99	0.12
Frozen SO BF	1	870	620	745	2.94	2.79	2.87	0.10
Frozen SO BF	1	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	1	40	50	45	1.60	1.70	1.65	0.07
Frozen SO BF	1	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	2	590	610	600	2.77	2.79	2.78	0.01
Frozen SO BF	2	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	2	10	20	15	1.00	1.30	1.15	0.21
Frozen SO BF	2	100	140	120	2.00	2.15	2.07	0.10
Frozen SO BF	2	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	2	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	3	10	10	10	1.00	1.00	1.00	0.00
Frozen SO BF	3	20	20	20	1.30	1.30	1.30	0.00
Frozen SO BF	3	120	120	120	2.08	2.08	2.08	0.00
Frozen SO BF	3	10	20	15	1.00	1.30	1.15	0.21
Frozen SO BF	3	420	370	395	2.62	2.57	2.60	0.04

Table E3 Raw data of viable counts of *S. aureus* enumerated from Fresh MSM (CFU/g), Inside MDM (CFU/swab), MDM Conveyor (CFU/swab) and MSM carcass (CFU/g) during 6-h processing time.

Product Name	Batch no.	*S. aureus* counts (CFU/g)			*S. aureus* counts (Log 10 CFU/g)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
MSM (1h)	1	220	130	175	2.34	2.11	2.24	0.16
MSM (2h)	1	280	210	245	2.45	2.32	2.39	0.09
MSM (3h)	1	1700	1100	1400	3.23	3.04	3.15	0.13
MSM (4h)	1	390	350	370	2.59	2.54	2.57	0.03
MSM (5h)	1	2100	1900	2000	3.32	3.28	3.30	0.03
MSM (6h)	1	3200	2500	2850	3.51	3.40	3.45	0.08
MSM (1h)	2	80	40	60	1.90	1.60	1.75	0.11
MSM (2h)	2	30	40	35	1.48	1.60	1.54	0.04
MSM (3h)	2	20	40	30	1.30	1.60	1.45	0.11
MSM (4h)	2	200	30	115	2.30	1.48	1.89	0.29
MSM (5h)	2	60	200	130	1.78	2.30	2.04	0.18
MSM (6h)	2	110	120	115	2.04	2.08	2.06	0.01
MSM (1h)	3	900	430	665	2.95	2.63	2.79	0.23
MSM (2h)	3	20	60	40	1.30	1.78	1.54	0.34
MSM (3h)	3	470	470	470	2.67	2.67	2.67	0.00
MSM (4h)	3	10	80	45	1.00	1.90	1.45	0.64
MSM (5h)	3	110	40	75	2.04	1.60	1.82	0.31
MSM (6h)	3	300	900	600	2.48	2.95	2.72	0.34
Inside MDM	1	400	600	500	2.60	2.78	2.70	0.12
Inside MDM	1	300	200	250	2.48	2.30	2.40	0.12
Inside MDM	1	140	60	100	2.15	1.78	2.00	0.26
Inside MDM	1	400	230	315	2.60	2.36	2.50	0.17
Inside MDM	1	100	50	75	2.00	1.70	1.88	0.21
Inside MDM	1	200	200	200	2.30	2.30	2.30	0.00
Inside MDM	2	10	10	5	1.00	1.00	1.00	0.00
Inside MDM	2	50	60	55	1.70	1.78	1.74	0.03
Inside MDM	2	550	510	530	2.74	2.71	2.72	0.01
Inside MDM	2	240	270	255	2.38	2.43	2.41	0.02
Inside MDM	2	10	10	10	1.00	1.00	1.00	0.00
Inside MDM	2	30	40	35	1.48	1.60	1.54	0.09
Inside MDM	3	10	10	10	1.00	1.00	1.00	0.00
Inside MDM	3	40	10	25	1.60	1.00	1.30	0.43

Inside MDM	3	120	250	185	2.08	2.40	2.24	0.23
Inside MDM	3	30	30	30	1.48	1.48	1.48	0.00
Inside MDM	3	20	20	20	1.30	1.30	1.30	0.00
Inside MDM	3	250	270	260	2.40	2.43	2.41	0.02
MDM Conveyor (1h)	1	30	10	15	1.48	1.00	1.24	0.17
MDM Conveyor (2h)	1	10	10	5	1.00	1.00	1.00	0.00
MDM Conveyor (3h)	1	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (4h)	1	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (5h)	1	10	10	5	1.00	1.00	1.00	0.00
MDM Conveyor (6h)	1	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (1h)	2	20	30	25	1.30	1.48	1.39	0.06
MDM Conveyor (2h)	2	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (3h)	2	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (4h)	2	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (5h)	2	50	40	45	1.70	1.60	1.65	0.03
MDM Conveyor (6h)	2	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (1h)	3	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (2h)	3	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (3h)	3	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (4h)	3	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (5h)	3	10	10	10	1.00	1.00	1.00	0.00
MDM Conveyor (6h)	3	10	10	10	1.00	1.00	1.00	0.00

Carcass MSM (1h)	1	200	100	150	2.30	2.00	2.18	0.21
MSM Carcass (2h)	1	40	60	50	1.60	1.78	1.70	0.12
MSM Carcass (3h)	1	100	100	100	2.00	2.00	2.00	0.00
MSM Carcass (4h)	1	130	130	130	2.11	2.11	2.11	0.00
MSM Carcass (5h)	1	70	80	75	1.85	1.90	1.88	0.04
MSM Carcass (6h)	1	10	100	55	1.00	2.00	1.74	0.71
MSM Carcass (1h)	2	10	20	15	1.00	1.30	1.15	0.21
MSM Carcass (2h)	2	10	30	20	1.00	1.48	1.24	0.17
MSM Carcass (3h)	2	100	100	100	2.00	2.00	2.00	0.00
MSM Carcass (4h)	2	10	10	10	1.00	1.00	1.00	0.00
MSM Carcass (5h)	2	70	90	80	1.85	1.95	1.90	0.04
MSM Carcass (6h)	2	10	50	30	1.00	1.70	1.35	0.25
MSM Carcass (1h)	3	40	40	40	1.60	1.60	1.60	0.00
MSM Carcass (2h)	3	20	40	30	1.30	1.60	1.45	0.21
MSM Carcass (3h)	3	10	20	15	1.00	1.30	1.15	0.21
MSM Carcass (4h)	3	10	10	10	1.00	1.00	1.00	0.00
MSM Carcass (5h)	3	40	50	45	1.60	1.70	1.65	0.07
MSM Carcass (6h)	3	40	70	55	1.60	1.85	1.72	0.17

Data in red indicate the viable counts of *S. aureus* of less than 10 colonies.

Table E4 Raw data of viable counts of *S. aureus* enumerated from Fresh Skin (CFU/g) and Skinner Conveyor (CFU/swab) during 6-h processing.

Product Name	Batch no.	*S. aureus* counts (CFU/g)			*S. aureus* counts (Log 10 CFU/g)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Fresh Skin (1h)	1	30	30	30	1.48	1.48	1.48	0.00
Fresh Skin (2h)	1	20	20	20	1.30	1.30	1.30	0.00
Fresh Skin (3h)	1	80	90	85	1.90	1.95	1.93	0.04
Fresh Skin (4h)	1	60	110	85	1.78	2.04	1.93	0.19
Fresh Skin (5h)	1	300	100	200	2.48	2.00	2.30	0.34
Fresh Skin (6h)	1	100	100	100	2.00	2.00	2.00	0.00
Fresh Skin (1h)	2	10	10	10	1.00	1.00	1.00	0.00
Fresh Skin (2h)	2	500	180	340	2.70	2.26	2.48	0.31
Fresh Skin (3h)	2	10	10	10	1.00	1.00	1.00	0.00
Fresh Skin (4h)	2	120	100	110	2.08	2.00	2.04	0.03
Fresh Skin (5h)	2	40	300	170	1.60	2.48	2.04	0.31
Fresh Skin (6h)	2	30	100	65	1.48	2.00	1.74	0.18
Fresh Skin (1h)	3	90	120	105	1.95	2.08	2.02	0.09
Fresh Skin (2h)	3	120	160	140	2.08	2.20	2.14	0.09
Fresh Skin (3h)	3	300	500	400	2.48	2.70	2.59	0.16
Fresh Skin (4h)	3	110	130	120	2.04	2.11	2.08	0.05
Fresh Skin (5h)	3	13700	12700	13200	4.14	4.10	4.12	0.02
Fresh Skin (6h)	3	140	150	145	2.15	2.18	2.16	0.02
Skinner Conveyor (1h)	1	10	10	5	1.00	1.00	1.00	0.00
Skinner Conveyor (2h)	1	190	10	95	2.28	1.00	1.64	0.45
Skinner Conveyor (3h)	1	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (4h)	1	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (5h)	1	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (6h)	1	50	100	75	1.70	2.00	1.85	0.11
Skinner Conveyor (1h)	2	10	10	5	1.00	1.00	1.00	0.00
Skinner Conveyor (2h)	2	30	30	30	1.48	1.48	1.48	0.00
Skinner Conveyor (3h)	2	20	10	15	1.30	1.00	1.15	0.11
Skinner Conveyor (4h)	2	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (5h)	2	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (6h)	2	40	10	20	1.60	1.00	1.30	0.21
Skinner Conveyor (1h)	3	30	60	45	1.48	1.78	1.63	0.11
Skinner Conveyor (2h)	3	20	10	15	1.30	1.00	1.15	0.11

Skinner Conveyor (3h)	3	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (4h)	3	10	10	10	1.00	1.00	1.00	0.00
Skinner Conveyor (5h)	3	10	50	30	1.00	1.70	1.35	0.26
Skinner Conveyor (6h)	3	10	10	10	1.00	1.00	1.00	0.00

Data in red indicate the viable counts of *S. aureus* of less than 10 colonies.

Table E5 Raw data of viable counts of *S. aureus* enumerated from Fresh Skin-on Breast Fillet (CFU/g) during 6-h processing time.

Product Name	Batch no.	*S. aureus* counts (CFU/g)			*S. aureus* counts (Log 10 CFU/g)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Fresh SO BF (1h)	1	120	80	100	2.08	1.90	1.99	0.06
Fresh SO BF (2h)	1	40	70	55	1.60	1.85	1.72	0.09
Fresh SO BF (3h)	1	350	450	400	2.54	2.65	2.60	0.04
Fresh SO BF (4h)	1	70	90	80	1.85	1.95	1.90	0.04
Fresh SO BF (5h)	1	100	150	125	2.00	2.18	2.09	0.06
Fresh SO BF (6h)	1	110	120	115	2.04	2.08	2.06	0.01
Fresh SO BF (1h)	2	130	80	105	2.11	1.90	2.01	0.07
Fresh SO BF (2h)	2	50	70	60	1.70	1.85	1.77	0.05
Fresh SO BF (3h)	2	900	800	850	2.95	2.90	2.93	0.02
Fresh SO BF (4h)	2	60	100	80	1.78	2.00	1.89	0.08
Fresh SO BF (5h)	2	690	700	695	2.84	2.85	2.84	0.00
Fresh SO BF (6h)	2	600	200	400	2.78	2.30	2.54	0.17
Fresh SO BF (1h)	3	30	50	40	1.48	1.70	1.59	0.08
Fresh SO BF (2h)	3	50	70	60	1.70	1.85	1.77	0.05
Fresh SO BF (3h)	3	400	400	400	2.60	2.60	2.60	0.00
Fresh SO BF (4h)	3	50	90	70	1.70	1.95	1.83	0.09
Fresh SO BF (5h)	3	10	10	10	1.00	1.00	1.00	0.00
Fresh SO BF (6h)	3	200	220	210	2.30	2.34	2.32	0.01

Table E6 Raw data of viable counts of *S. aureus* enumerated from Rubber Fingers (CFU/swab) in the three pluckers.

Product Name	Plucker No.	Day	*S. aureus* counts (CFU/swab)			*S. aureus* counts (Log 10 CFU/swab)			
			Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Rubber Finger	1	1	140	150	145	2.15	2.18	2.16	0.02
Rubber Finger	1	1	240	260	250	2.38	2.41	2.40	0.02
Rubber Finger	2	1	10	20	15	1.00	1.30	1.15	0.21
Rubber Finger	2	1	10	10	10	1.00	1.00	1.00	0.00
Rubber Finger	3	1	700	530	615	2.85	2.72	2.78	0.09
Rubber Finger	3	1	50	60	55	1.70	1.78	1.74	0.06
Rubber Finger	1	2	2450	2520	2485	3.39	3.40	3.40	0.01
Rubber Finger	1	2	120	90	105	2.08	1.95	2.02	0.09
Rubber Finger	2	2	10	10	10	1.00	1.00	1.00	0.00
Rubber Finger	2	2	190	200	195	2.28	2.30	2.29	0.02
Rubber Finger	3	2	10	10	10	1.00	1.00	1.00	0.00
Rubber Finger	3	2	530	520	525	2.72	2.72	2.72	0.01
Rubber Finger	1	3	190	150	170	2.28	2.18	2.23	0.07
Rubber Finger	1	3	470	280	375	2.67	2.45	2.56	0.16
Rubber Finger	2	3	40	30	35	1.60	1.48	1.54	0.09
Rubber Finger	2	3	20	20	20	1.30	1.30	1.30	0.00
Rubber Finger	3	3	220	200	210	2.34	2.30	2.32	0.03
Rubber Finger	3	3	100	90	95	2.00	1.95	1.98	0.03

Data in red indicate the viable counts of *S. aureus* of less than 10 colonies.

Table E7 Raw data of viable counts of *S. aureus* (CFU/swab) enumerated from the Nostrils of live chickens in the farm.

Sampling site	Chicken age	*S. aureus* counts (CFU/swab)			*S. aureus* counts (Log 10 CFU/swab)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Nostril	One week	80	40	60	1.90	1.60	1.75	0.21
Nostril	One week	10	10	10	1.00	1.00	1.00	0.00
Nostril	One week	10	10	10	1.00	1.00	1.00	0.00
Nostril	One week	10	10	10	1.00	1.00	1.00	0.00
Nostril	One week	10	30	20	1.00	1.48	1.24	0.34
Nostril	One week	10	10	10	1.00	1.00	1.00	0.00

Nostril	Three weeks	10	10	10	1.00	1.00	1.00	0.00
Nostril	Three weeks	40	40	40	1.60	1.60	1.60	0.00
Nostril	Three weeks	10	10	10	1.00	1.00	1.00	0.00
Nostril	Three weeks	10	10	10	1.00	1.00	1.00	0.00
Nostril	Three weeks	1240	1380	1310	3.09	3.14	3.12	0.03
Nostril	Three weeks	20	20	20	1.30	1.30	1.30	0.00
Nostril	Six weeks	30	10	20	1.48	1.00	1.24	0.34
Nostril	Six weeks	3580	204	1892	3.55	2.31	2.93	0.88
Nostril	Six weeks	90	30	60	1.95	1.48	1.72	0.34
Nostril	Six weeks	70	10	40	1.85	1.00	1.42	0.60
Nostril	Six weeks	30	10	20	1.48	1.00	1.24	0.34
Nostril	Six weeks	10	10	10	1.00	1.00	1.00	0.00

Table E8 Raw data of viable counts of *S. aureus* (CFU/swab) enumerated from the Skin of live chickens in the farm.

Sampling site	Chicken age	*S. aureus* counts (CFU/swab)			*S. aureus* counts (Log 10 CFU/swab)			
		Duplicate 1	Duplicate 2	Mean	Log 10 Duplicate 1	Log 10 Duplicate 2	Log 10 Mean	SD
Skin	One week	10	10	10	1.00	1.00	1.00	0.00
Skin	One week	10	10	10	1.00	1.00	1.00	0.00
Skin	One week	10	10	10	1.00	1.00	1.00	0.00
Skin	One week	10	10	10	1.00	1.00	1.00	0.00
Skin	One week	60	70	65	1.78	1.85	1.81	0.05
Skin	One week	10	10	10	1.00	1.00	1.00	0.00
Skin	Three weeks	10	30	20	1.00	1.48	1.24	0.34
Skin	Three weeks	10	10	10	1.00	1.00	1.00	0.00
Skin	Three weeks	80	120	100	1.90	2.08	1.99	0.12
Skin	Three weeks	10	20	15	1.00	1.30	1.15	0.21
Skin	Three weeks	10	10	10	1.00	1.00	1.00	0.00
Skin	Three weeks	20	10	15	1.30	1.00	1.15	0.21
Skin	Six weeks	140	150	145	2.15	2.18	2.16	0.02
Skin	Six weeks	10	10	10	1.00	1.00	1.00	0.00
Skin	Six weeks	30	60	45	1.48	1.78	1.63	0.21
Skin	Six weeks	30	10	20	1.48	1.00	1.24	0.34
Skin	Six weeks	20	10	15	1.30	1.00	1.15	0.21
Skin	Six weeks	10	10	10	1.00	1.00	1.00	0.00

Data in red indicate the viable counts of *S. aureus* of less than 10 colonies.

Appendix F. PCR results of staphylococcal enterotoxin detection

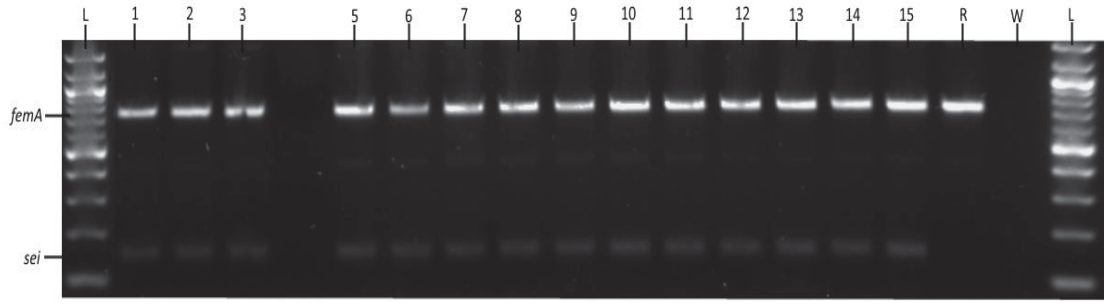


Figure F1 Multiplex PCR results of staphylococcal enterotoxin detection (Set 1). L: 100bp DNA ladder; Lane 2-16: colony 1-15 (*femA*, *sei*); R: negative control (strain RN4220); W: negative control (distilled water).

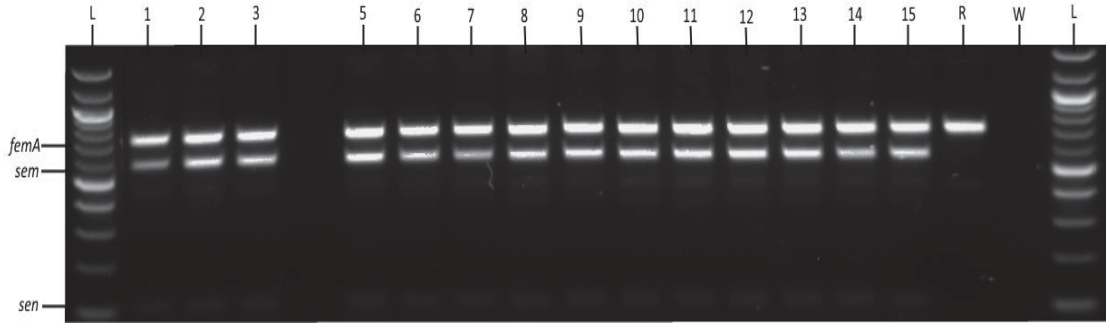


Figure F2 Multiplex PCR results of staphylococcal enterotoxin detection (Set 2). L: 100bp DNA ladder; Lane 2-16: colony 1-15 (*femA*, *sen, sem*); R: negative control (strain RN4220); W: negative control (distilled water).

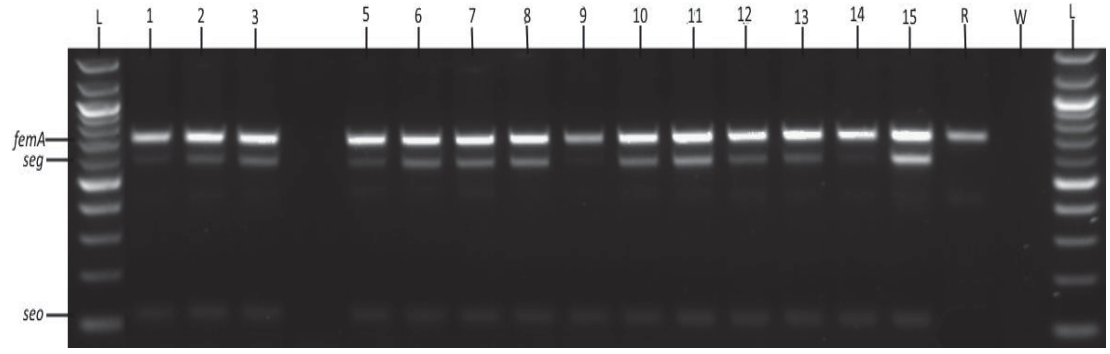


Figure F3 Multiplex PCR results of staphylococcal enterotoxin detection (Set 3). L: 100bp DNA ladder; Lane 2-16: colony 1-15 (*femA*, *seg, seo*); R: negative control (strain RN4220); W: negative control (distilled water).

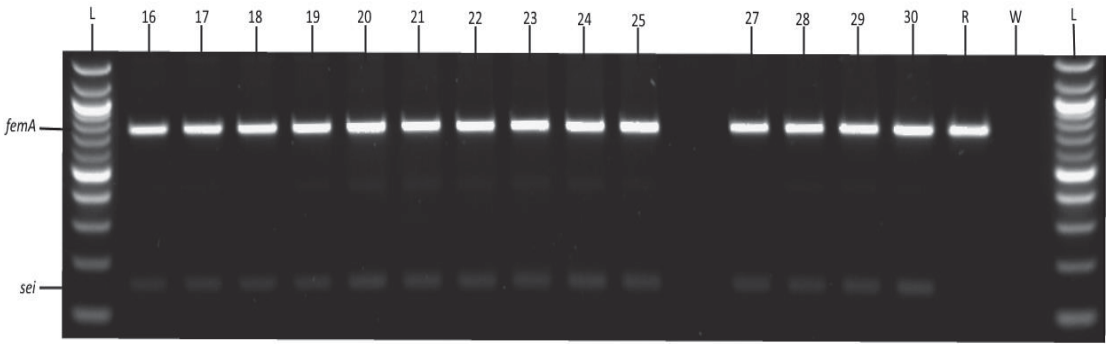


Figure F4 Multiplex PCR results of staphylococcal enterotoxin detection (Set 1). L: 100bp DNA ladder; Lane 2-16: colony 16-30 (*femA*, *sei*); R: negative control (strain RN4220); W: negative control (distilled water).

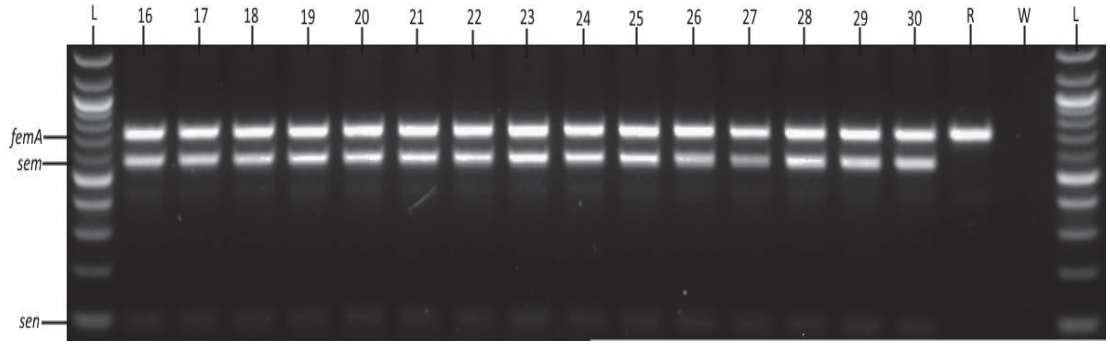


Figure F5 Multiplex PCR results of staphylococcal enterotoxin detection (Set 2). L: 100bp DNA ladder; Lane 2-16: colony 16-30 (femA, sem, sen); R: negative control (strain RN4220); W: negative control (distilled water).

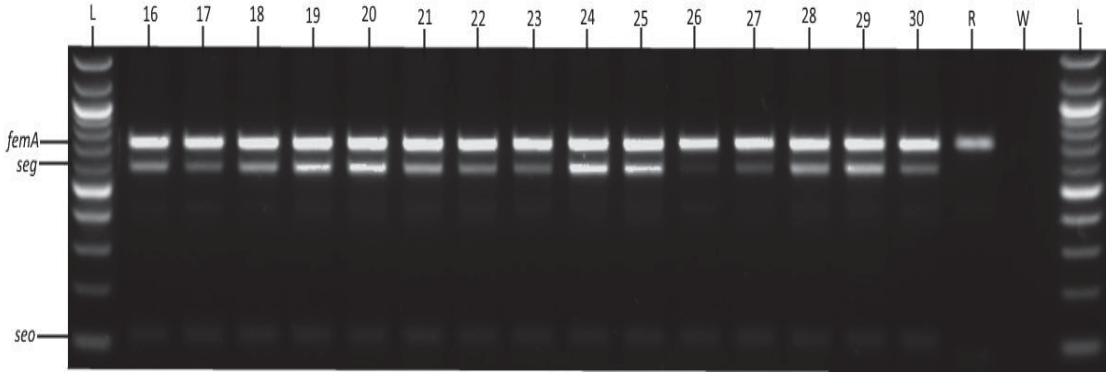


Figure F6 Multiplex PCR results of staphylococcal enterotoxin detection (Set 3). L: 100bp DNA ladder; Lane 2-16: colony 16-30 (femA, seg, seo); R: negative control (strain RN4220); W: negative control (distilled water).

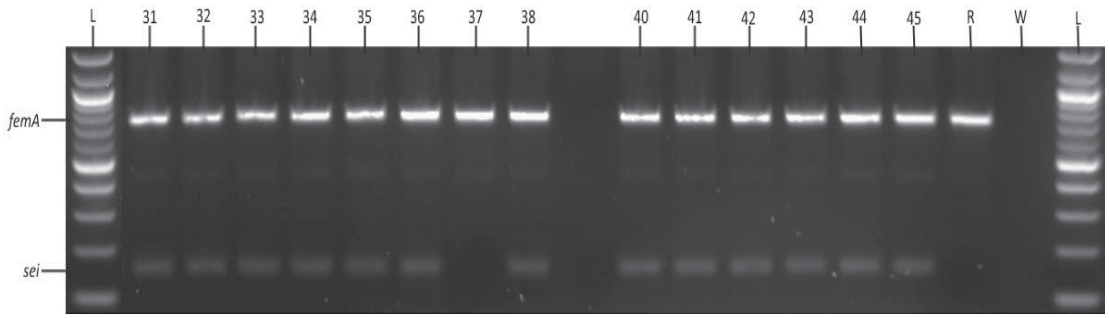


Figure F7 Multiplex PCR results of staphylococcal enterotoxin detection (Set 1). L: 100bp DNA ladder; Lane 2-16: colony 31-45 (femA, sei); R: negative control (strain RN4220); W: negative control (distilled water).

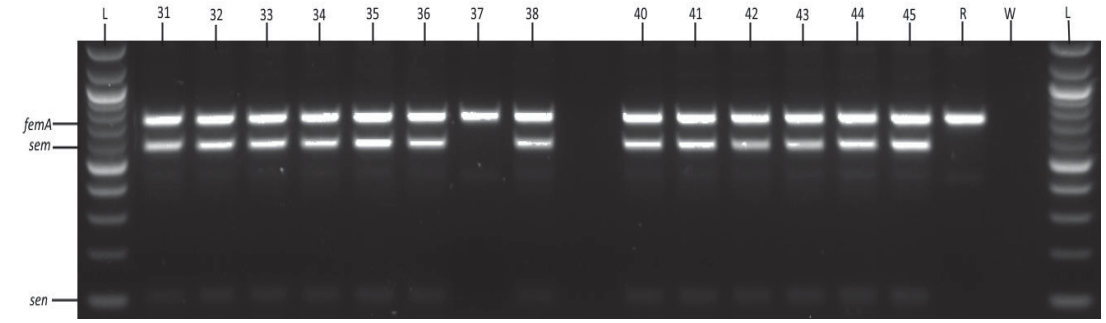


Figure F8 Multiplex PCR results of staphylococcal enterotoxin detection (Set 2). L: 100bp DNA ladder; Lane 2-16: colony 31-45 (femA, sem, sen); R: negative control (strain RN4220); W: negative control (distilled water).

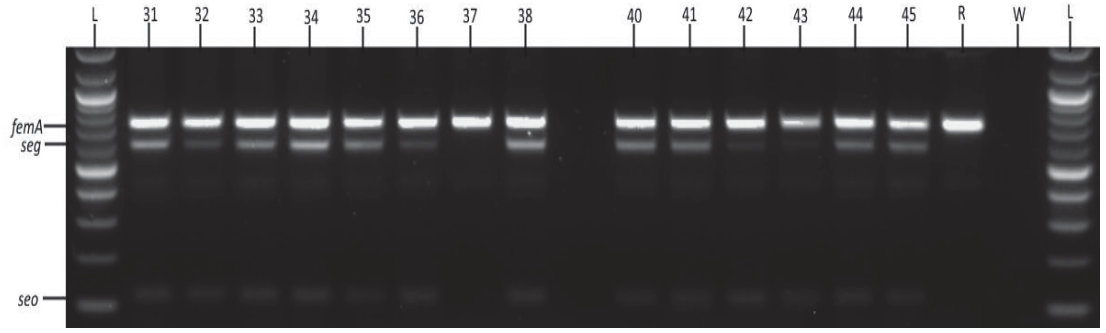


Figure F9 Multiplex PCR results of staphylococcal enterotoxin detection (Set 3). L: 100bp DNA ladder; Lane 2-16: colony 31-45 (femA, seg, seo); R: negative control (strain RN4220); W: negative control (distilled water).

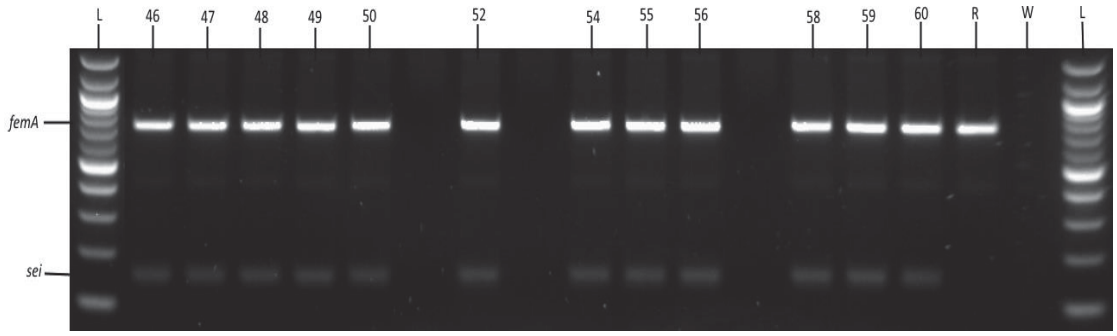


Figure F10 Multiplex PCR results of staphylococcal enterotoxin detection (Set 1). L: 100bp DNA ladder; Lane 2-16: colony 46-60 (femA, sei); R: negative control (strain RN4220); W: negative control (distilled water).

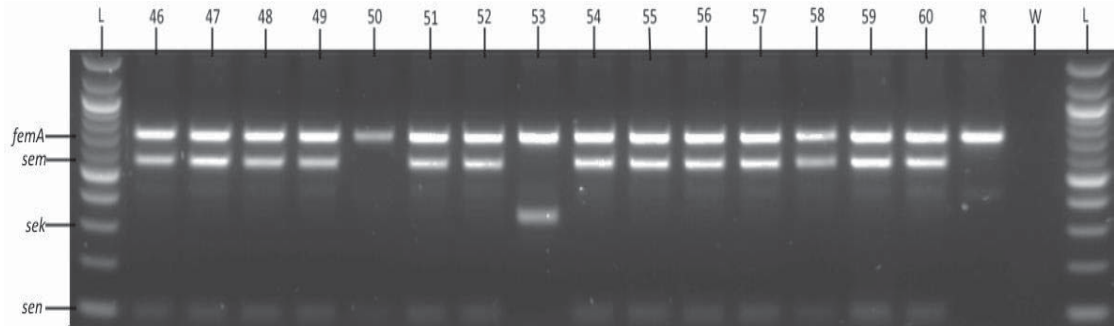


Figure F11 Multiplex PCR results of staphylococcal enterotoxin detection (Set 2). L: 100bp DNA ladder; Lane 2-16: colony 46-60 (femA, sem, sek, sen); R: negative control (strain RN4220); W: negative control (distilled water).

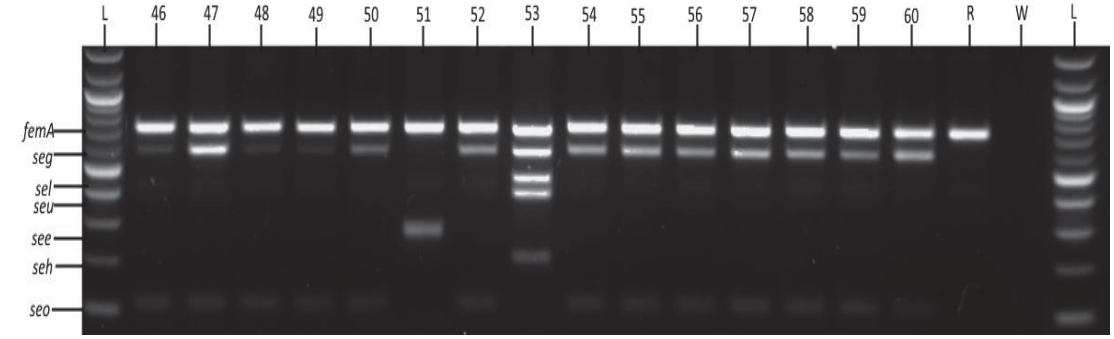


Figure F12 Multiplex PCR results of staphylococcal enterotoxin detection (Set 3). L: 100bp DNA ladder; Lane 2-16: colony 46-60 (femA, seg, sel, seu, see, seh, seo); R: negative control (strain RN4220); W: negative control (distilled water).

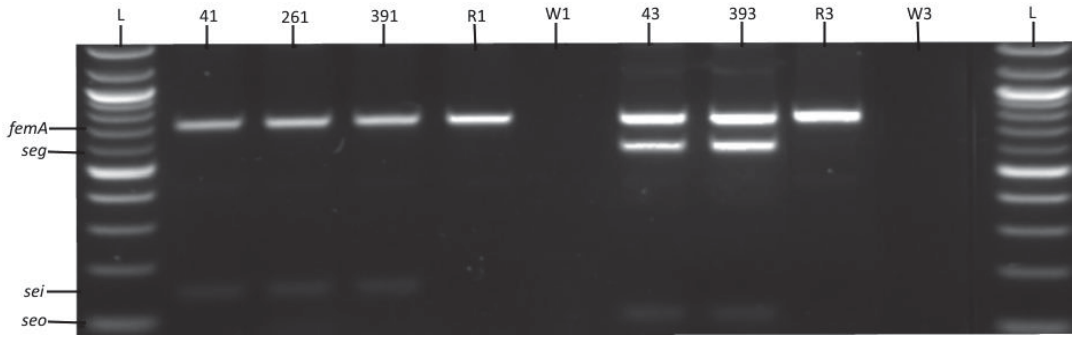


Figure F13 Multiplex PCR results of staphylococcal enterotoxin detection (Set 2 and Set 3). L: 100bp DNA ladder; Lane 2-4: colony 4, 26, 39 (femA, seg, sei, seo); Lane 7-8: colony 4, 39; R1: Set1, negative control (strain RN4220); W1: Set1, negative control (distilled water); R2: Set1, negative control (strain RN4220); W2: Set1, negative control (distilled water).

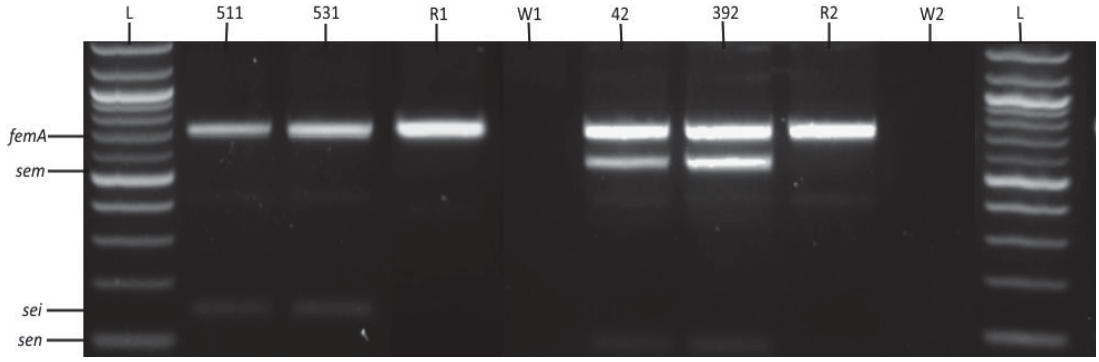


Figure F14 Multiplex PCR results of staphylococcal enterotoxin detection (Set 1 and Set 2). L: 100bp DNA ladder; Lane 2-3: colony 51, 53 (femA, seg, sei, seo); Lane 6-7: colony 4, 39; R1: Set1, negative control (strain RN4220); W1: Set1, negative control (distilled water); R2: Set1, negative control (strain RN4220); W2: Set1, negative control (distilled water).

Appendix G. Results of PCR and purified PCR products in terms of MLST of each *S. aureus* isolates

a. MLST PCR results

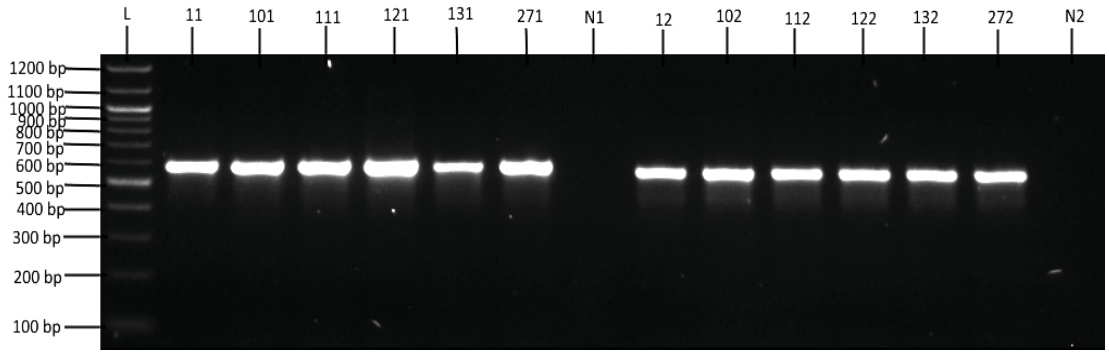


Figure G1 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first and second numbers of each lane represent the number of *S. aureus* isolates (1: colony 1, 10: colony 10, 11: colony 11, 12: colony 12, 13: colony 13, 27: colony 27). The last number of each lane represents the genes being amplified (1: *yqi* 516bp, 2: *arc* 456bp). N1 and N2: negative controls (distilled water).

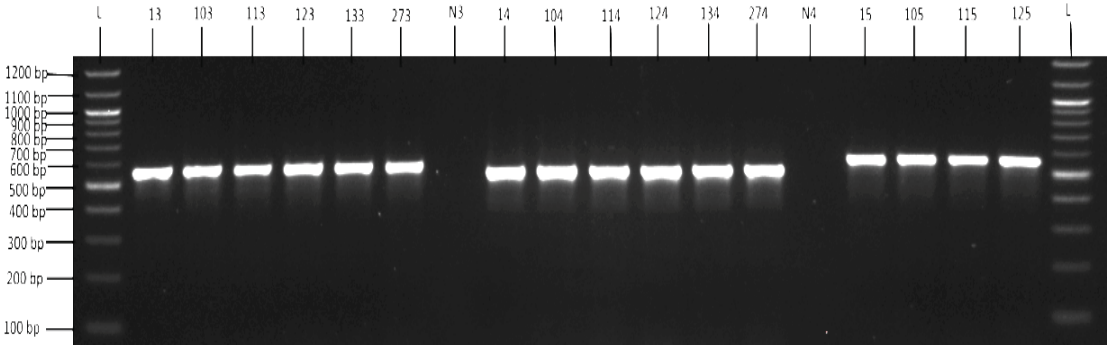


Figure G2 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first or first two numbers of each lane represent the number of S. aureus isolates (1: colony 1, 10: colony 10, 11: colony 11, 12: colony 12, 13: colony 13, 27: colony 27). The last number of each lane represents the genes being amplified (3: pta 474bp, 4: aro 456bp, 5: glp 465bp). N3 and N4: negative controls (distilled water).

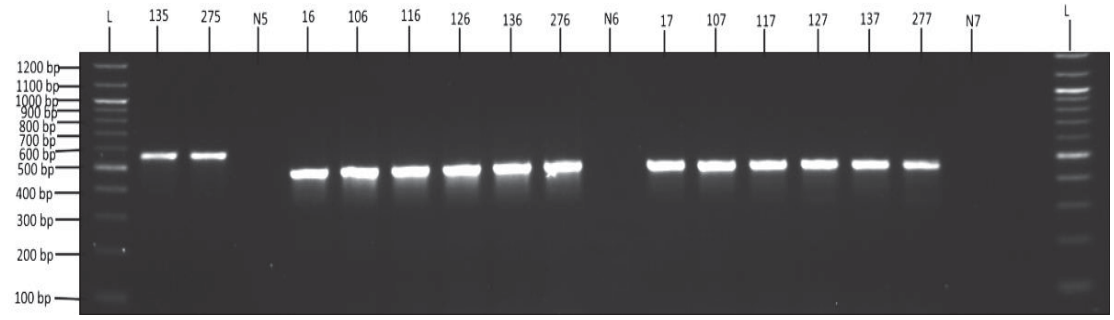


Figure G3 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first or first two numbers of each lane represent the number of S. aureus isolates (1: colony 1, 10: colony 10, 11: colony 11, 12: colony 12, 13: colony 13, 27: colony 27). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N5, N6 and N7: negative controls (distilled water).

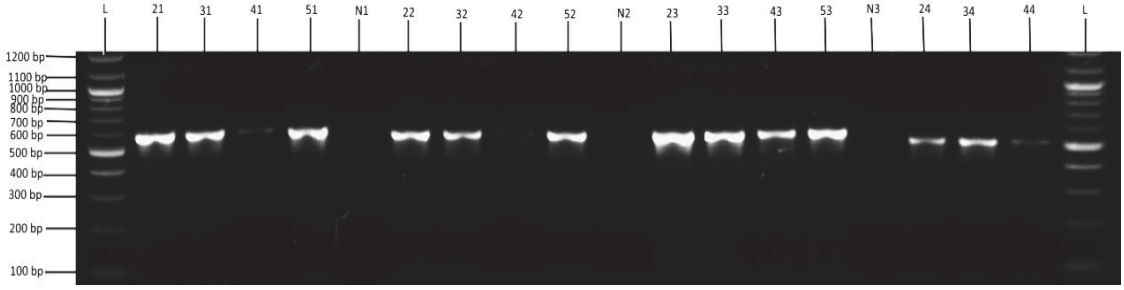


Figure G4 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (2: colony 2, 3: colony 3, 4: colony 4, 5: colony 5). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

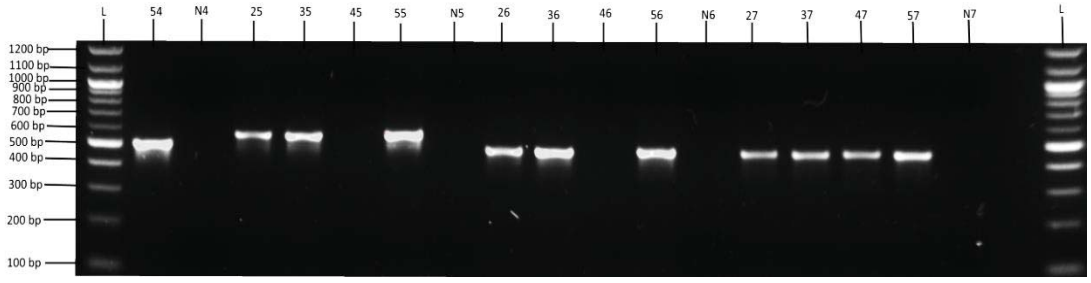


Figure G5 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (2: colony 2, 3: colony 3, 4: colony 4, 5: colony 5). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

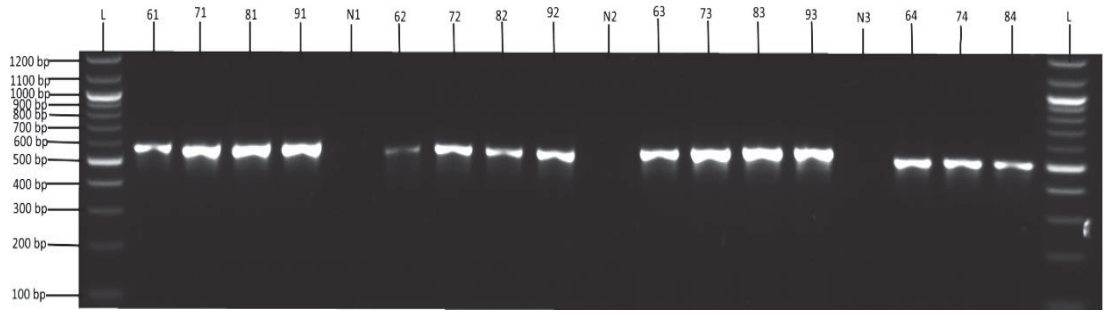


Figure G6 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (6: colony 6, 7: colony 7, 8: colony 8, 9: colony 9). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

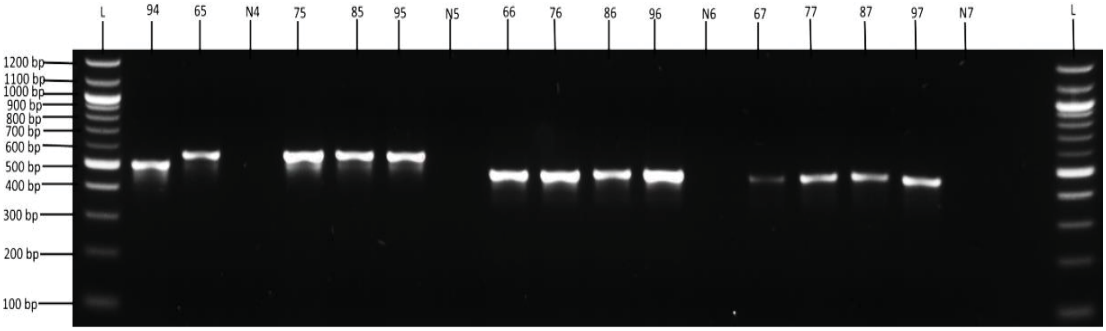


Figure G7 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (6: colony 6, 7: colony 7, 8: colony 8, 9: colony 9). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

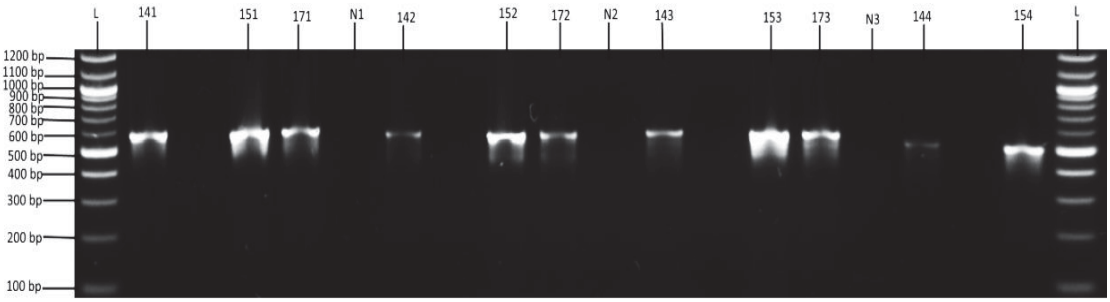


Figure G8 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (14: colony 14, 15: colony 15, 17: colony 17). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

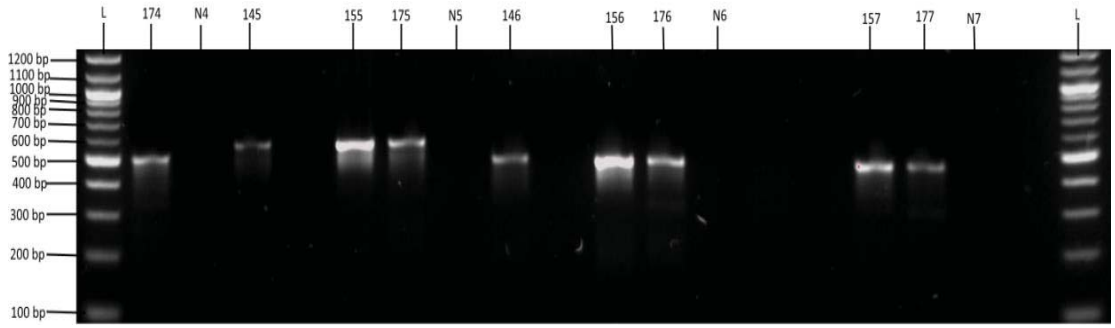


Figure G9 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of *S. aureus* isolates (14: colony 14, 15: colony 15, 17: colony 17). The last number of each lane represents the genes being amplified (5: *glp* 465bp, 6: *gmk* 417bp, 7: *tpi* 402bp). N4, N5, N6 and N7: negative controls (distilled water).

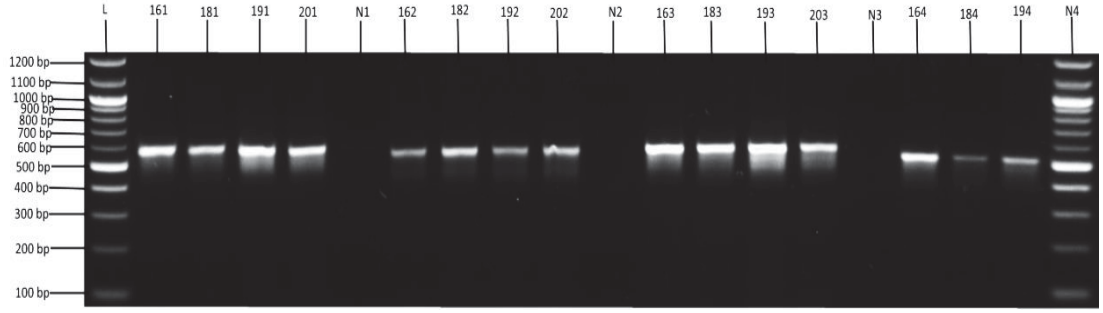


Figure G10 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (16: colony 16, 18: colony 18, 19: colony 19, 20: colony 20). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

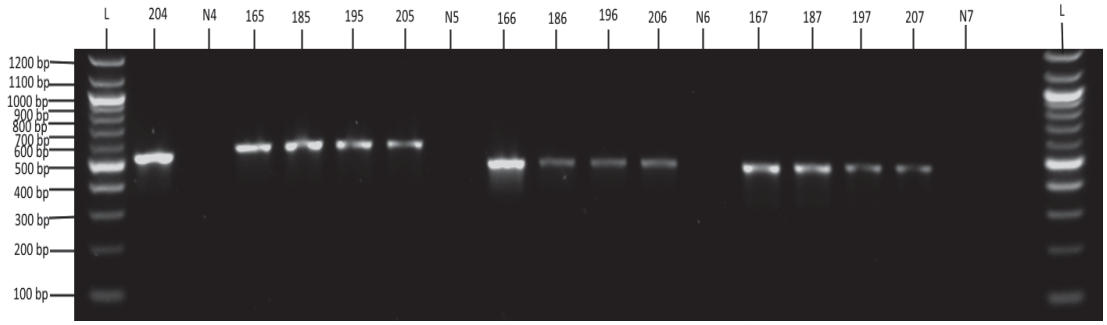


Figure G11 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (16: colony 16, 18: colony 18, 19: colony 19, 20: colony 20). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

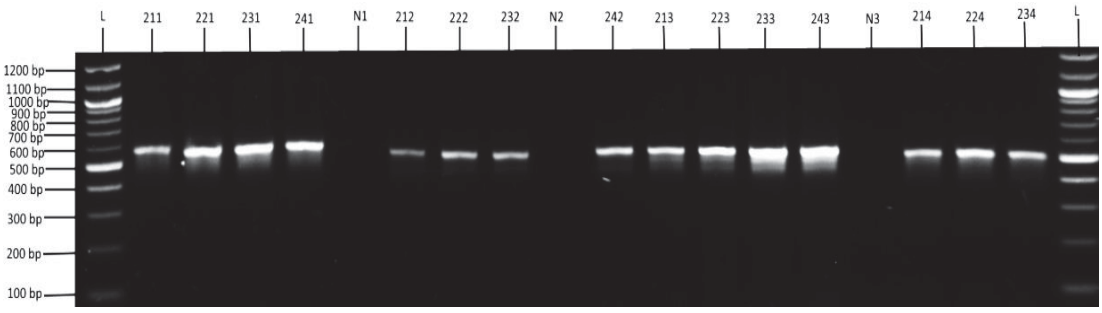


Figure G12 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (21: colony 21, 22: colony 22, 23: colony 23, 24: colony 24). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

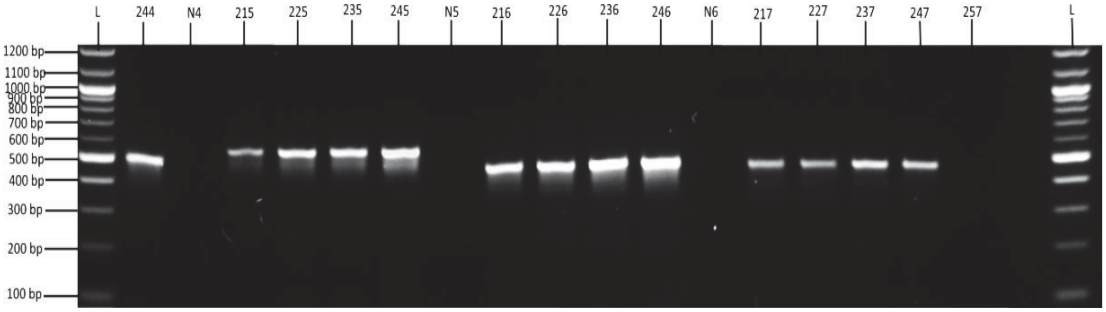


Figure G13 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (21: colony 21, 22: colony 22, 23: colony 23, 24: colony 24). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

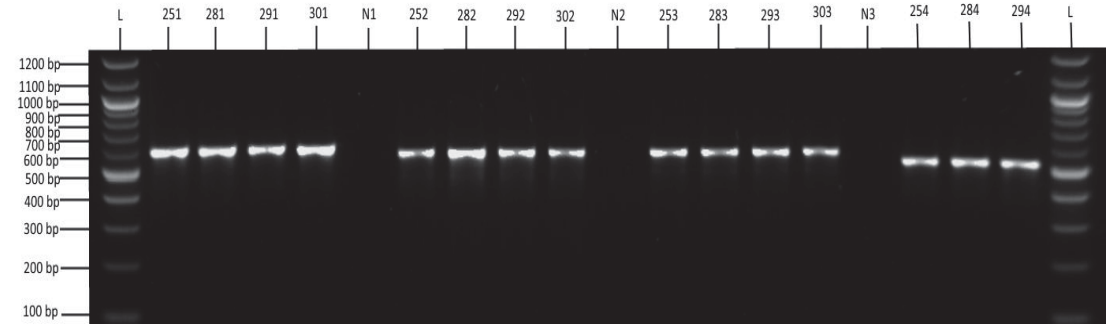


Figure G14 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (25: colony 25, 28: colony 28, 29: colony 29, 30: colony 30). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

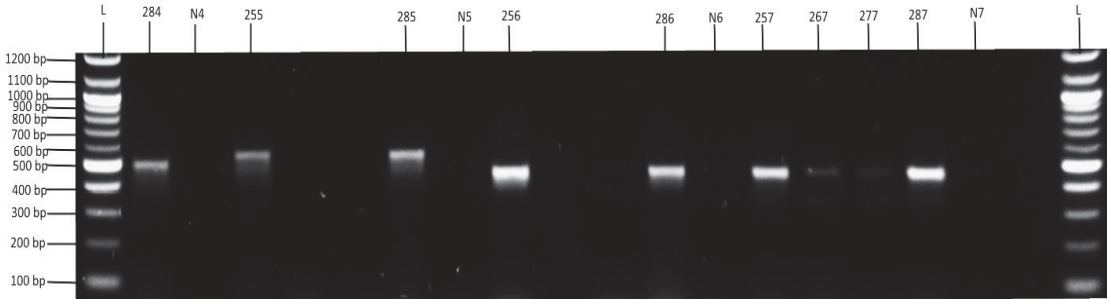


Figure G15 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of *S. aureus* isolates (25: colony 25, 28: colony 28, 27: colony 27). The last number of each lane represents the genes being amplified (5: *glp* 465bp, 6: *gmk* 417bp, 7: *tpi* 402bp). N4, N5, N6 and N7: negative controls (distilled water).

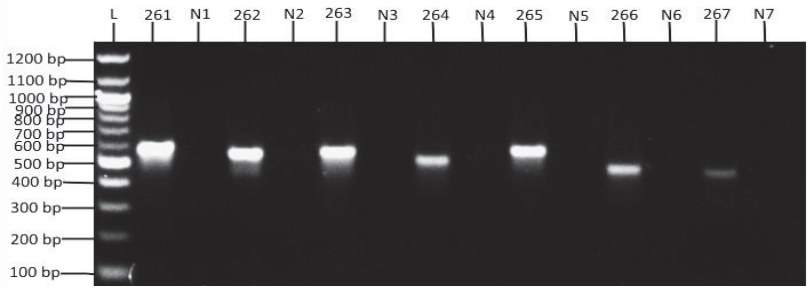


Figure G16 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (26: colony 26). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N1, N2, N3, N4, N5, N6 and N7: negative controls (distilled water).

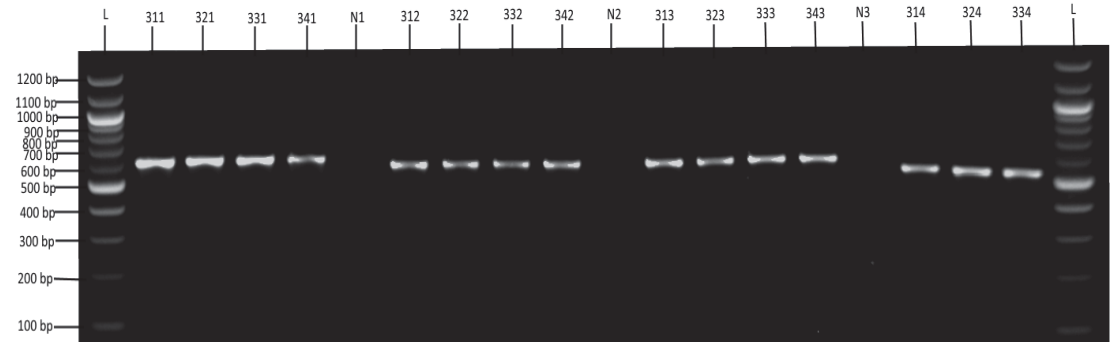


Figure G17 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (31: colony 31, 32: colony 32, 33: colony 33, 34: colony 34). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

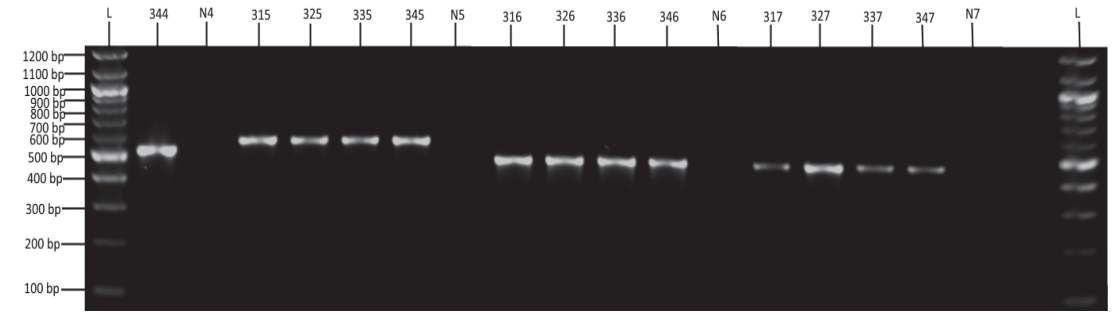


Figure G18 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (31: colony 31, 32: colony 32, 33: colony 33, 34: colony 34). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

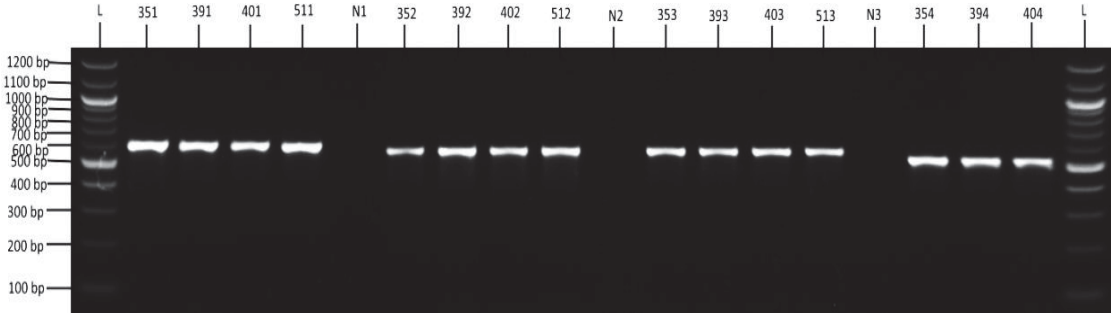


Figure G19 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (35: colony 35, 39: colony 39, 40: colony 40, 51: colony 51). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp). N1, N2 and N3: negative controls (distilled water).

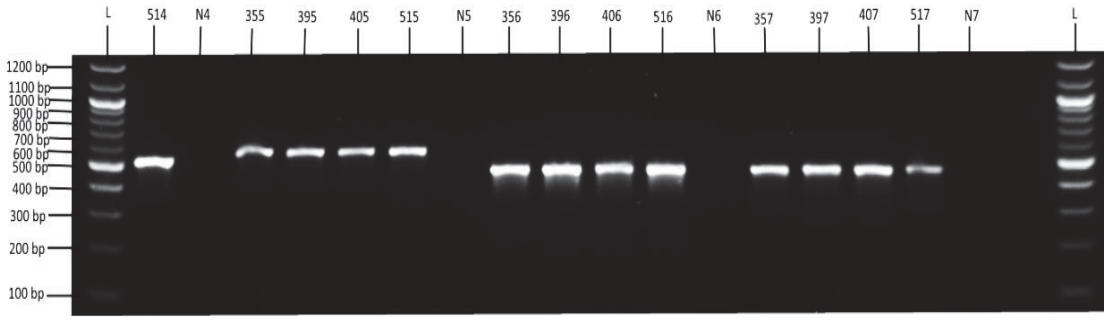


Figure G20 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (35: colony 35, 39: colony 39, 40: colony 40, 51: colony 51). The last number of each lane represents the genes being amplified (5: glp 465bp, 6: gmk 417bp, 7: tpi 402bp). N4, N5, N6 and N7: negative controls (distilled water).

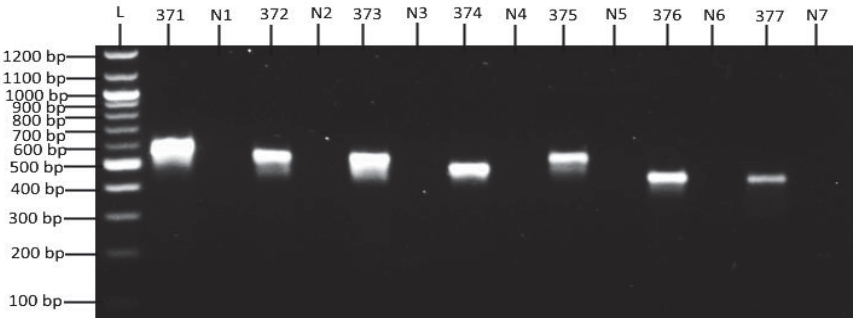


Figure G21 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of *S. aureus* isolates (37: colony 37). The last number of each lane represents the genes being amplified (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp, 6: *gmk* 417bp, 7: *tpi* 402bp). N1, N2, N3, N4, N5, N6 and N7: negative controls (distilled water).

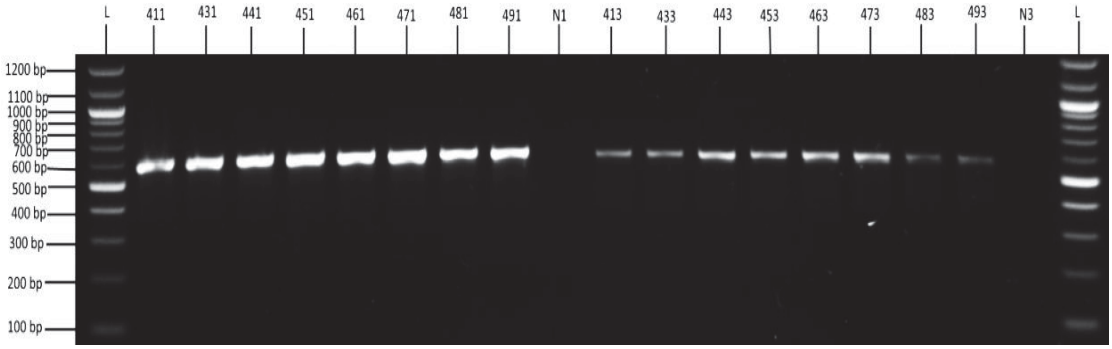


Figure G22 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (41: colony 41, 43: colony 43, 44: colony 44, 45: colony 45, 46: colony 46, 47: colony 47, 48: colony 48, 49: colony 49). The last number of each lane represents the genes being amplified (1: yqi 516bp, 3: pta 474bp). N1 and N3: negative controls (distilled water).

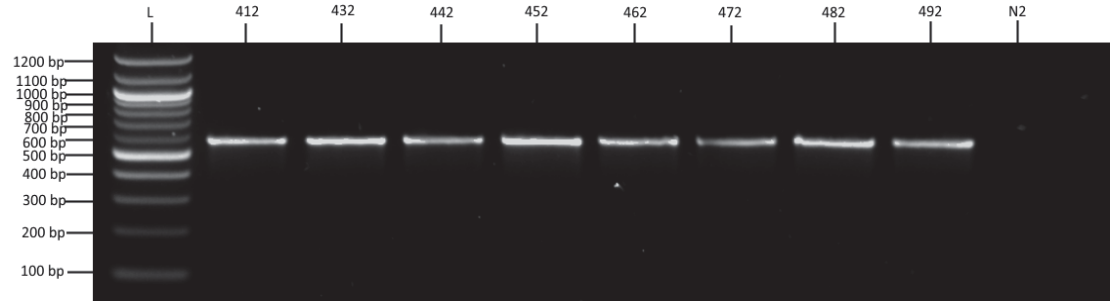


Figure G23 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (41: colony 41, 43: colony 43, 44: colony 44, 45: colony 45, 46: colony 46, 47: colony 47, 48: colony 48, 49: colony 49). The last number of each lane represents the genes being amplified (2: arc 456bp). N2: negative controls (distilled water).

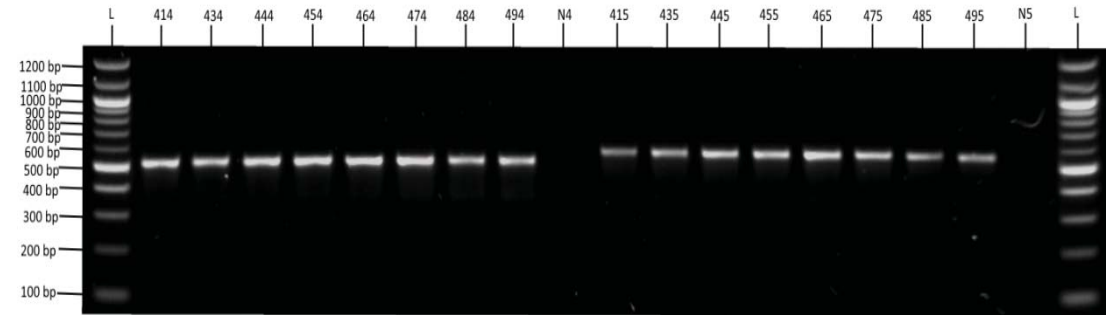


Figure G24 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of *S. aureus* isolates (41: colony 41, 43: colony 43, 44: colony 44, 45: colony 45, 46: colony 46, 47: colony 47, 48: colony 48, 49: colony 49). The last number of each lane represents the genes being amplified (4: *aro* 456bp, 5: *glp* 465bp). N4 and N5: negative controls (distilled water).

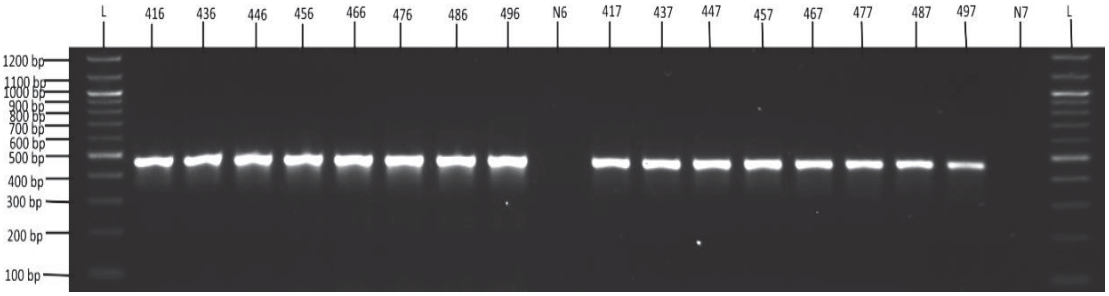


Figure G25 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first number of each lane represents the number of S. aureus isolates (41: colony 41, 43: colony 43, 44: colony 44, 45: colony 45, 46: colony 46, 47: colony 47, 48: colony 48, 49: colony 49). The last number of each lane represents the genes being amplified (6: gmk 417bp, 7: tpi 402bp). N6 and N7: negative controls (distilled water).

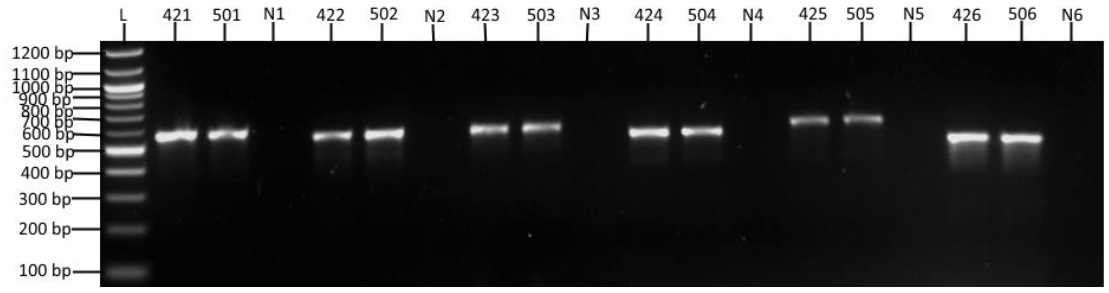


Figure G26 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (42: colony 42, 50: colony 50). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp). N1, N2, N3, N4, N5 and N6: negative controls (distilled water).

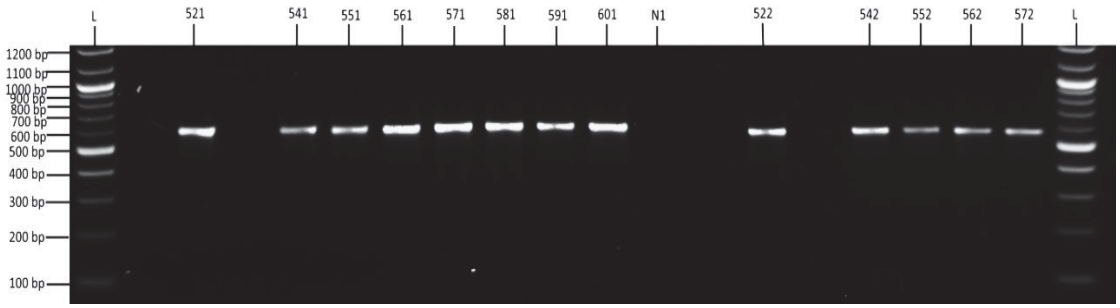


Figure G27 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (52: colony 52, 54: colony 54, 55: colony 55, 56: colony 56, 57: colony 57, 58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the genes being amplified (1: yqi 516bp, 2: arc 456bp). N1: negative controls (distilled water).

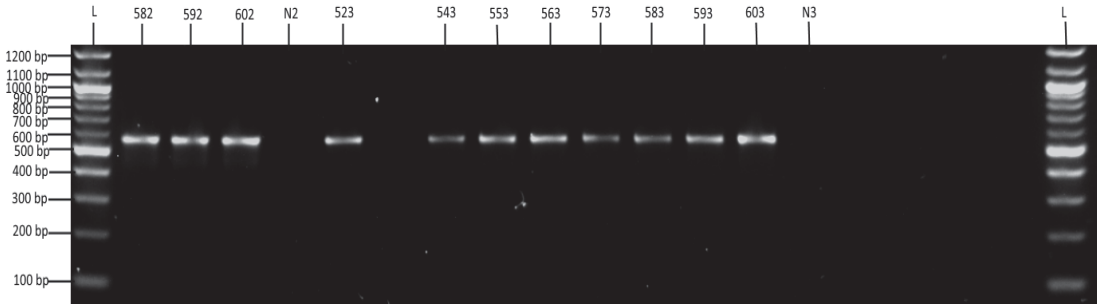


Figure G28 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (54: colony 54, 55: colony 55, 56: colony 56, 57: colony 57, 58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the genes being amplified (2: arc 456bp, 3: pta 474bp). N2 and N3: negative controls (distilled water).

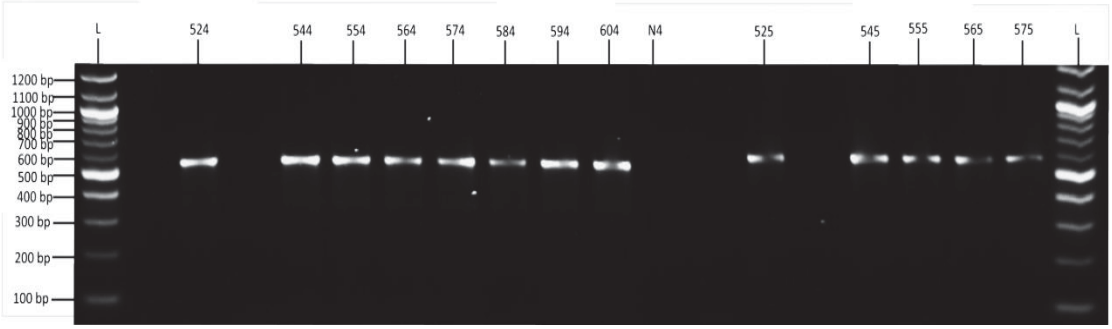


Figure G29 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (52: colony 52, 54: colony 54, 55: colony 55, 56: colony 56, 57: colony 57, 58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the genes being amplified (4: aro 456bp, 5: glp 465bp). N4: negative controls (distilled water).

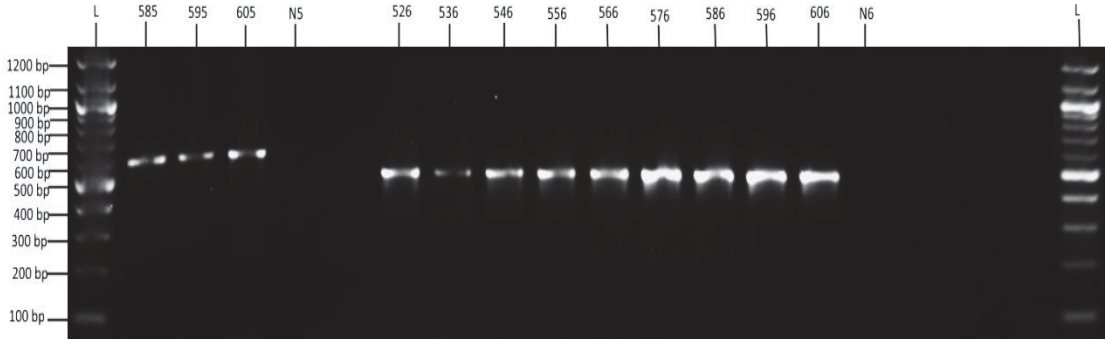


Figure G30 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of *S. aureus* isolates (52: colony 52, 54: colony 54, 55: colony 55, 56: colony 56, 57: colony 57, 58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the genes being amplified (5: *glp* 465bp, 6: *gmk* 417bp). N5 and N6: negative controls (distilled water).

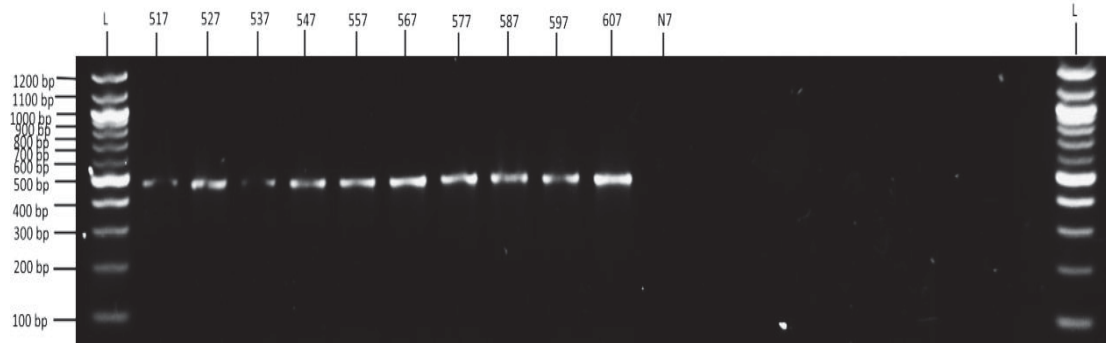


Figure G31 Agarose gel electrophoresis of MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first two numbers of each lane represent the number of S. aureus isolates (52: colony 52, 54: colony 54, 55: colony 55, 56: colony 56, 57: colony 57, 58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the genes being amplified (7: tpi 402bp). N7: negative controls (distilled water).

b. Results of purified PCR products

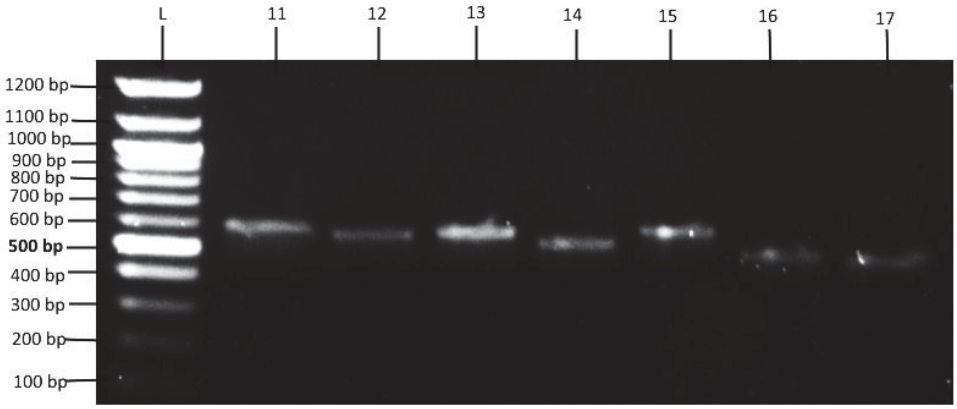


Figure G32 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolate. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (1: colony 1). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

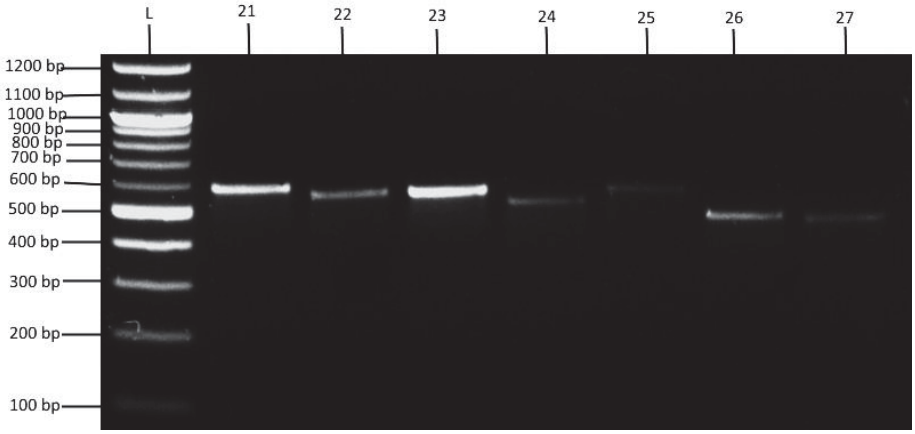


Figure G33 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolate. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (2: colony 2). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

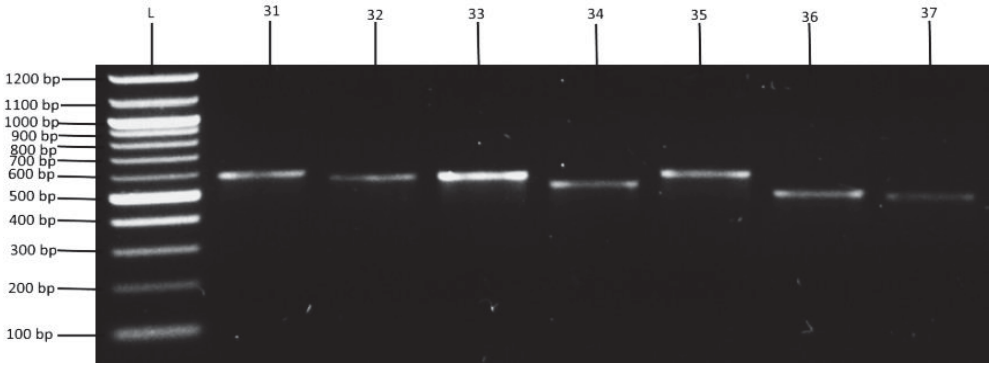


Figure G34 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolate. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of *S. aureus* isolate (3: colony 3). The last number of each lane represents the seven house-keeping genes of *S. aureus* isolate (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp, 6: *gmk* 417bp).

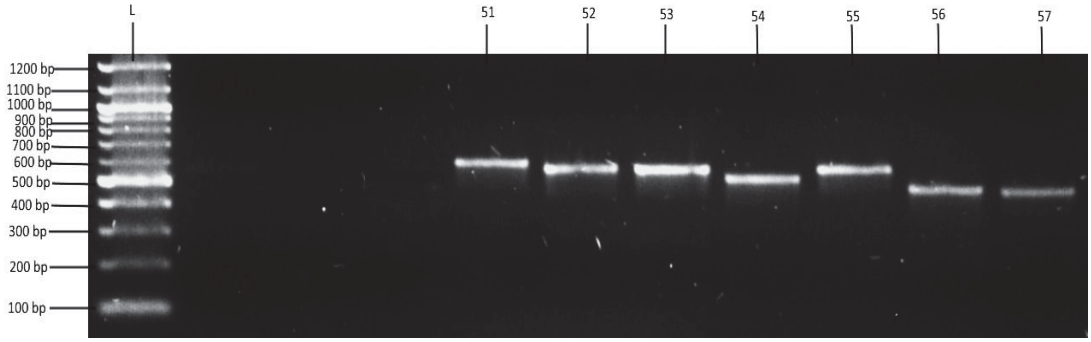


Figure G35 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolate. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (5: colony 5). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

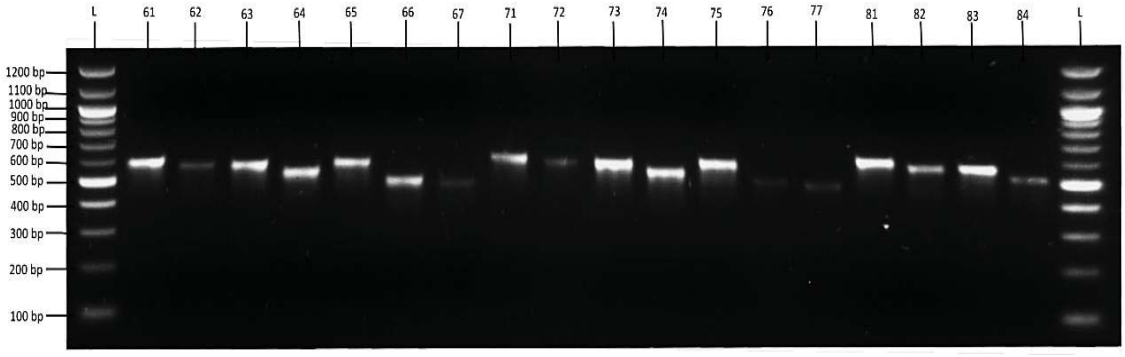


Figure G36 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (6: colony 6, 7: colony 7, 8: colony 8). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

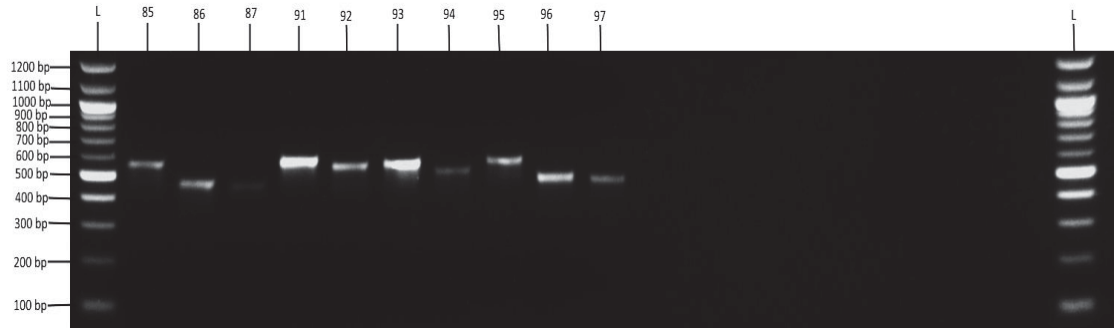


Figure G37 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (8: colony 8, 9: colony 9). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

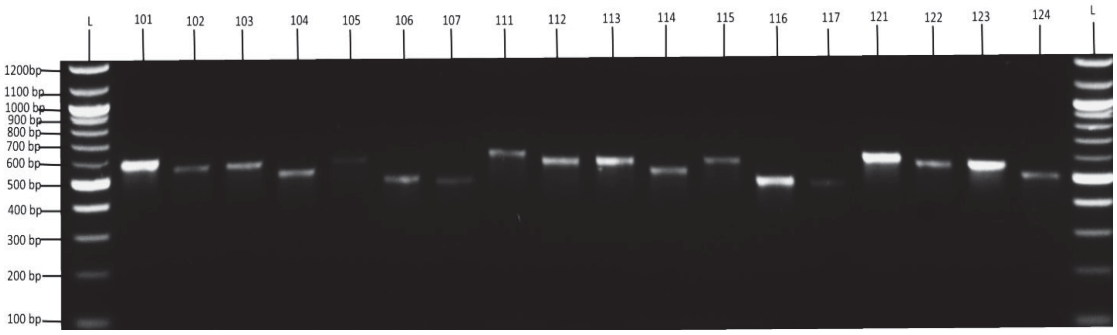


Figure G38 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (10: colony 10, 11: colony 11, 12: colony 12). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

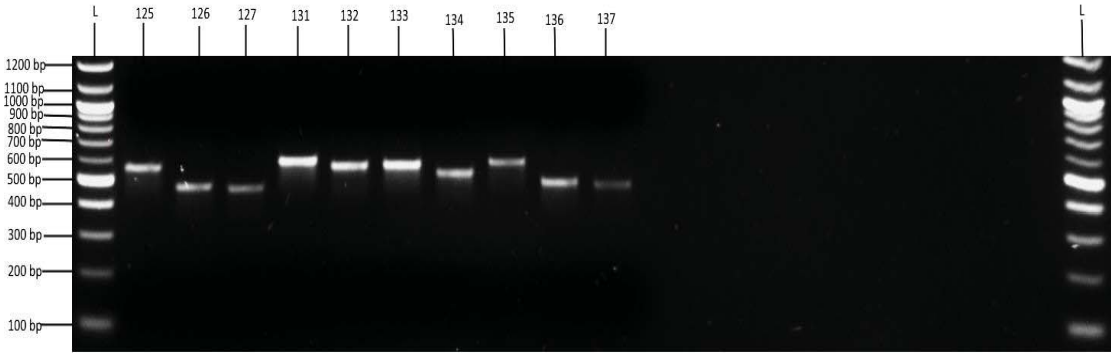


Figure G39 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (12: colony 12, 13: colony 13). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

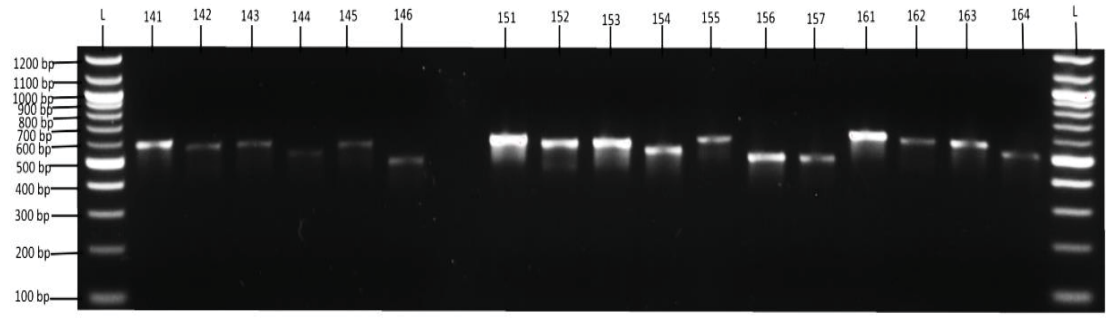


Figure G40 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of *S. aureus* isolate (14: colony 14, 15: colony 15, 16: colony 16). The last number of each lane represents the seven house-keeping genes of *S. aureus* isolate (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp, 6: *gmk* 417bp).

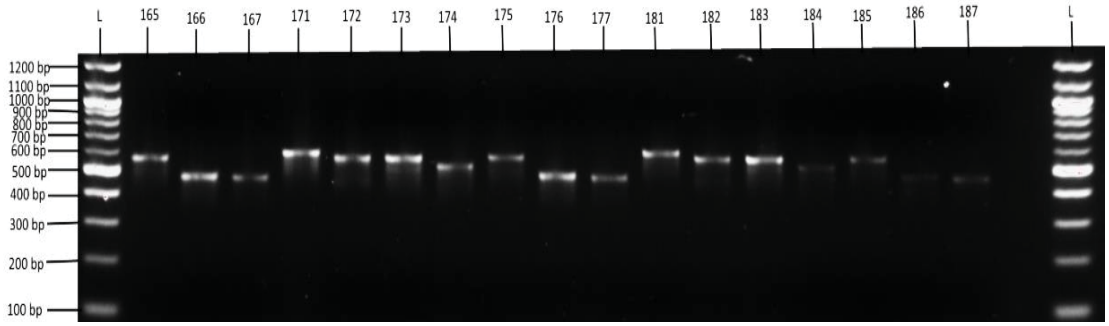


Figure G41 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (16: colony 16, 17: colony 17, 18: colony 18). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

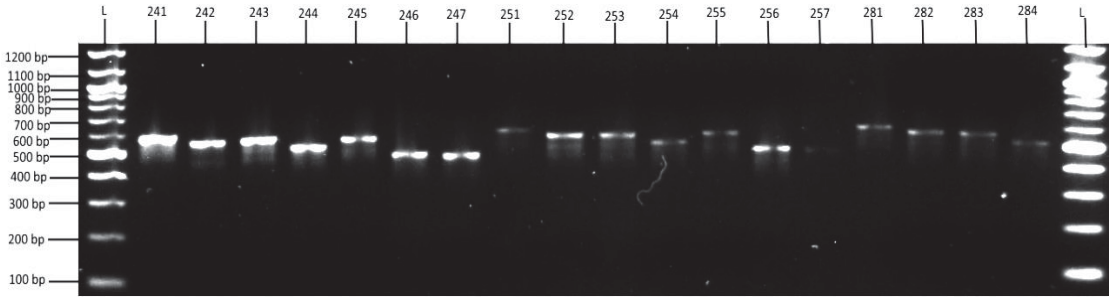


Figure G42 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (24: colony 24, 25: colony 25, 28: colony 28). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

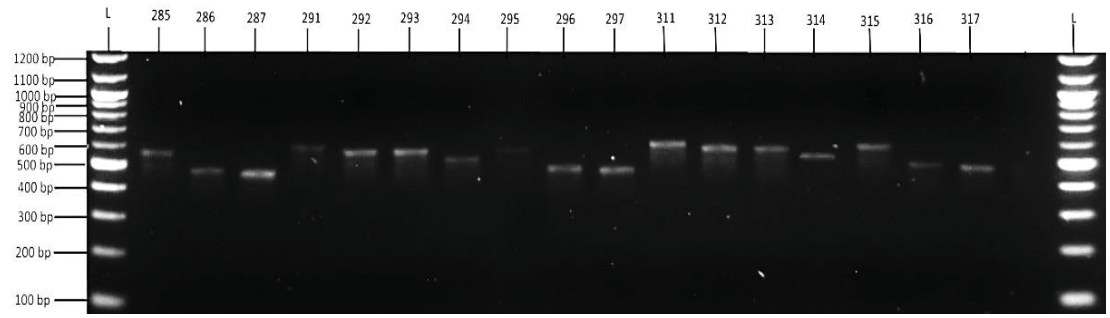


Figure G43 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (28: colony 28, 29: colony 29, 31: colony 31). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

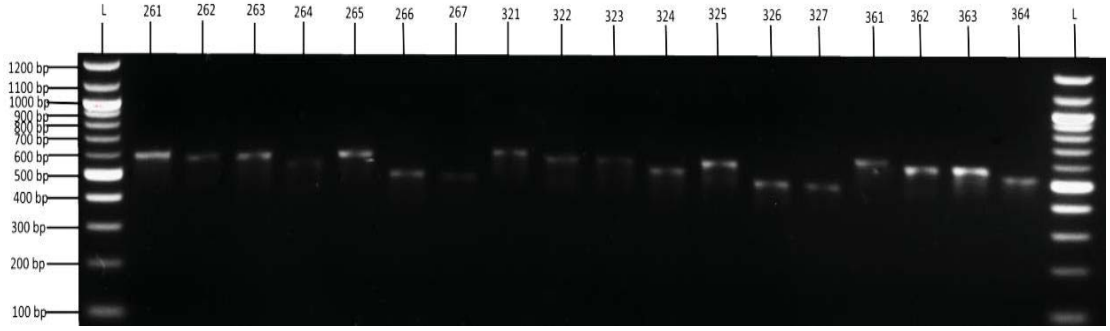


Figure G44 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (26: colony 26, 32: colony 32, 36: colony 36). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

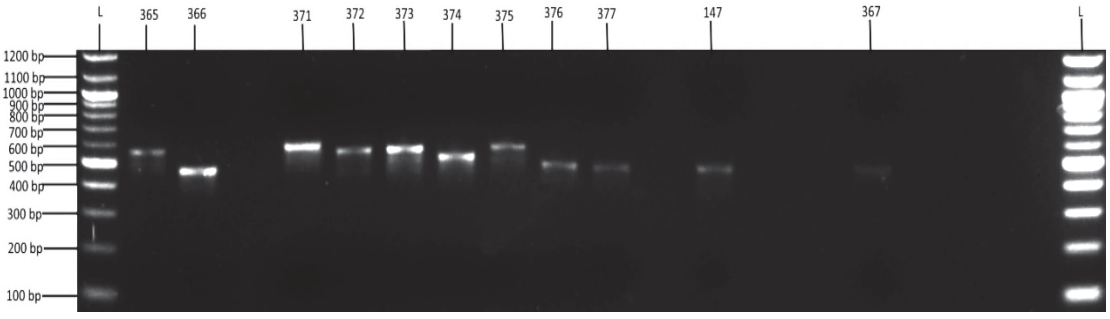


Figure G45 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (36: colony 36, 37: colony 37, 14: colony 14). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

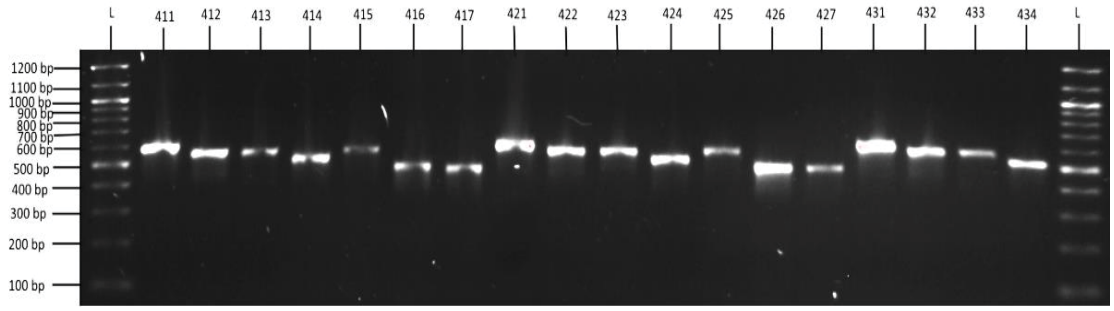


Figure G46 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of *S. aureus* isolate (41: colony 41, 42: colony 42, 43: colony 43). The last number of each lane represents the seven house-keeping genes of *S. aureus* isolate (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp, 6: *gmk* 417bp).

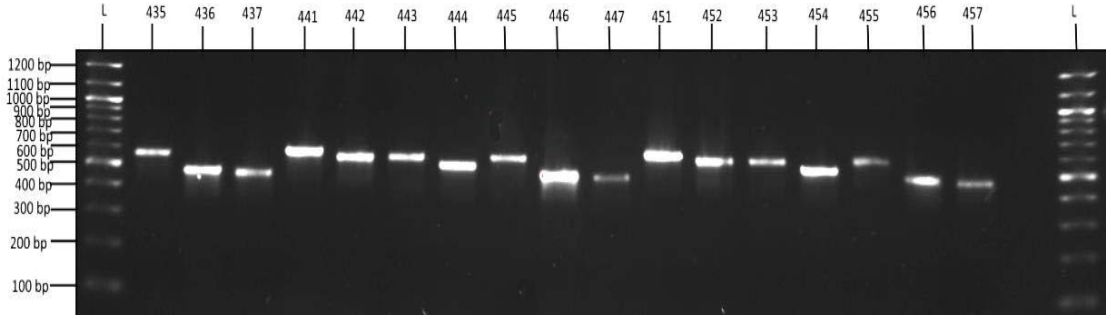


Figure G47 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (43: colony 43, 44: colony 44, 45: colony 45). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

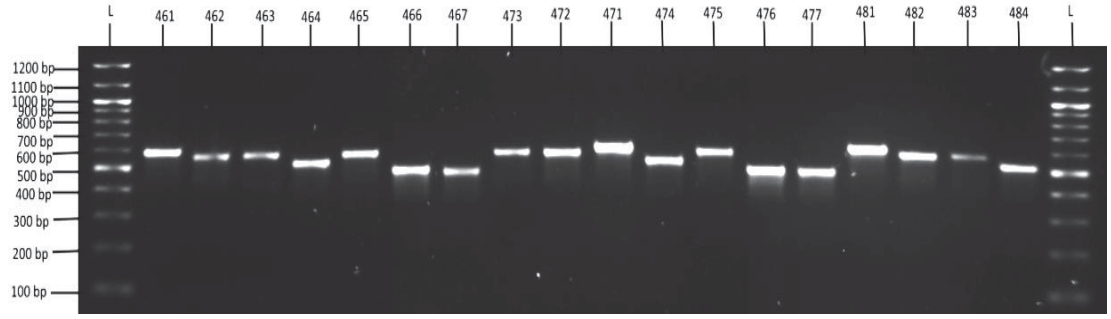


Figure G48 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (46: colony 46, 47: colony 47, 48: colony 48). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

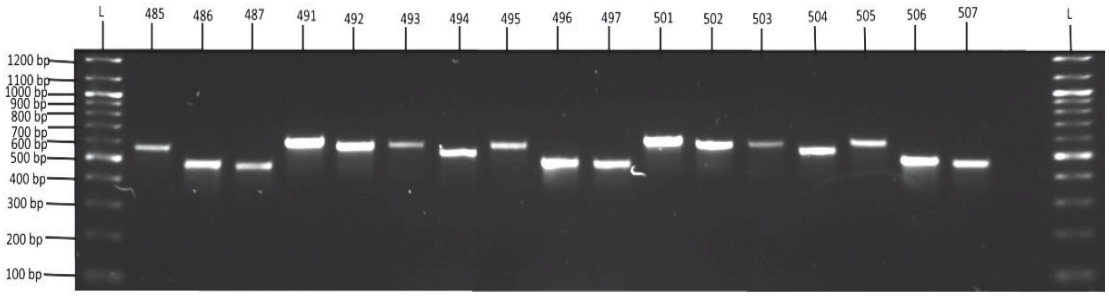


Figure G49 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of *S. aureus* isolate (46: colony 46, 47: colony 47, 48: colony 48). The last number of each lane represents the seven house-keeping genes of *S. aureus* isolate (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: *glp* 465bp, 6: *gmk* 417bp).

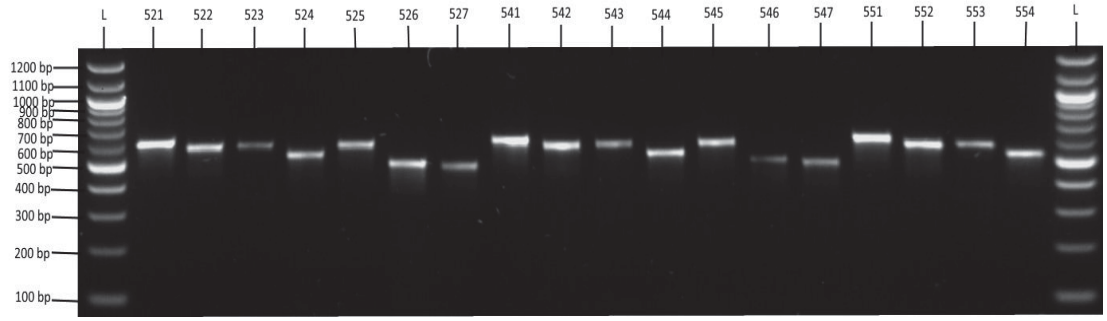


Figure G50 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (52: colony 52, 54: colony 54, 55: colony 55). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

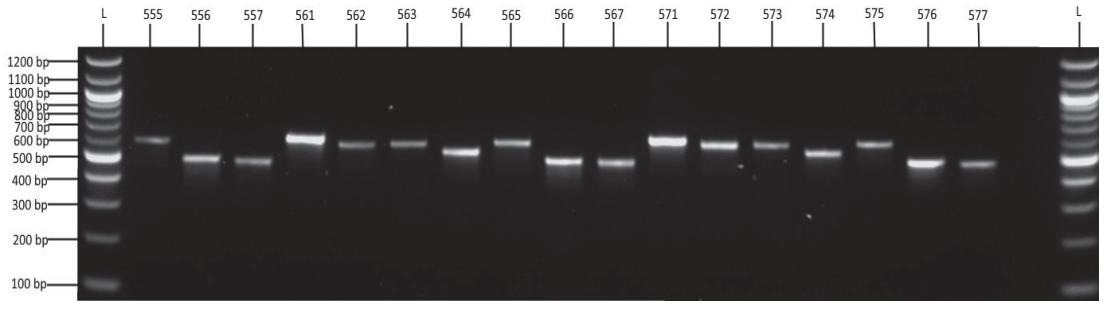


Figure G51 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (55: colony 55, 56: colony 56, 57: colony 57). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

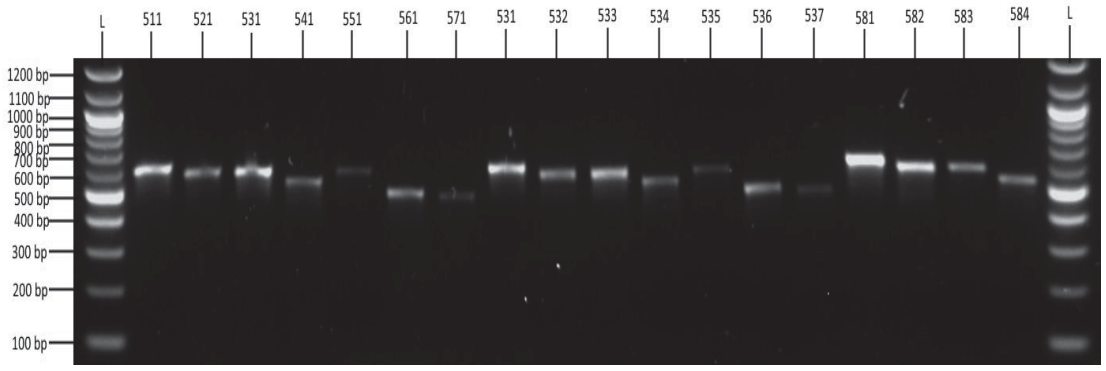


Figure G52 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of *S. aureus* isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of *S. aureus* isolate (51: colony 51, 56: colony 56, 53: colony 53, 58: colony 58). The last number of each lane represents the seven house-keeping genes of *S. aureus* isolate (1: *yqi* 516bp, 2: *arc* 456bp, 3: *pta* 474bp, 4: *aro* 456bp, 5: g*lp* 465bp, 6: *gmk* 417bp).

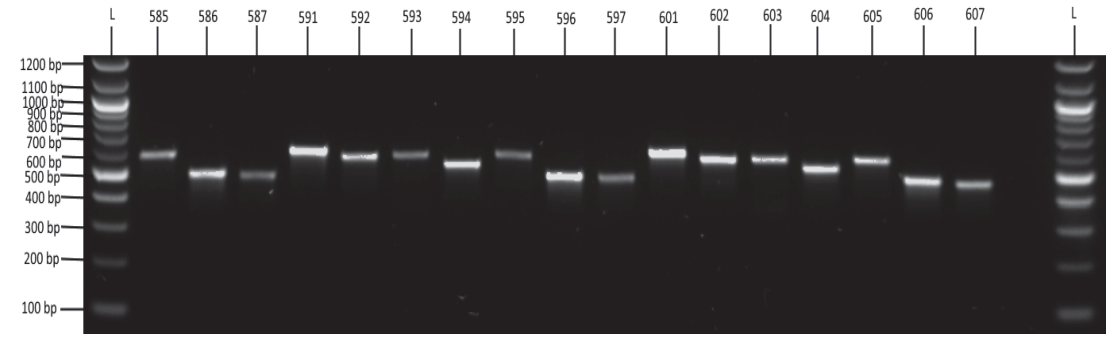


Figure G53 Agarose gel electrophoresis of purified MLST PCR products amplified with seven house-keeping genes of S. aureus isolates. Lane L: 100bp DNA ladder. The first numbers of each lane represent the number of S. aureus isolate (58: colony 58, 59: colony 59, 60: colony 60). The last number of each lane represents the seven house-keeping genes of S. aureus isolate (1: yqi 516bp, 2: arc 456bp, 3: pta 474bp, 4: aro 456bp, 5: glp 465bp, 6: gmk 417bp).

Appendix H. Sequencing results of the seven house-keeping genes of each *S. aureus* isolates

Colony 1:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAAYAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 1\YQI.txt

```
                 ....|....|....|....|....|....|....|....|....|....|....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 2:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\arc.txt

```
                 ....|....|....|....|....|....|....|....|....|....|....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   485        495        505        515        525        535
Consensus        .......... .......... .......... .......... .......... ..........

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   545        555        565        575        585        595
Consensus
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\aro.txt

```
                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                     5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                    65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   485        495        505        515        525        535
Consensus       .......... .......... .......... .......... .......... ..........

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   545        555        565        575        585        595
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\glp.txt

```
                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                     5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                    65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\gmk.txt

```
                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                     5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                    65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....|    ....|....|    ....|....|    ....|....|    ....|....|    ....|....|
                   365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\tpi.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 2\yqi.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 3:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 3\yqi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 4:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consenusu    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consenusu    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consenusu    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consenusu    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consenusu    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consenusu    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consenusu    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consenusu    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 4\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 5:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... ......... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA....... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 5\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 6:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 6\yqi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 7:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....||
                  185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC |

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 7\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .....
```

Colony 8:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 8\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 9:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 9\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 10:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 10\yqi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 11:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA.....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 11\yqi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 12:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\tpi.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 12\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 13:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\glp.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\pta.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 13\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..........
```

Colony 14:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\glp.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\gmk.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 14\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 15:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTTCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 15\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 16:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 16\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 17:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT |

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 17\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 18:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\tpi.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 18\yqi.txt

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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensusu   GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensusu   GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensusu   GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensusu   CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensusu   CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensusu   CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensusu   GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensusu   ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                485        495        505        515        525        535
Consensusu   GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 19:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\glp.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\pta.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 19\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 20:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 20\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 21:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 21\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 22:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\aro.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\pta.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 22\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 23:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\aro.txt

```
                 ....|....|....|....|....|....|....|....|....|....|....|....|
                     5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                    65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\glp.txt

```
                 ....|....|....|....|....|....|....|....|....|....|....|....|
                     5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                    65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\gmk.txt

```
                 ....|....|....|....|....|....|....|....|....|....|....|....|
                     5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                    65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....|....|....|....|....|....|....|....|....|....|....|
                   365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 23\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 24:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA.....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 24\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 25:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensusu   AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensusu   TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensusu   CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensusu   GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensusu   ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensusu   ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensusu   CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensusu   AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 25\yqi.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 26:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 26\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 27:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 27\yqi.txt

```
                ....|....|....|....|....|....|....|....|....|....|....|....|
                    5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                   65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 28:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\arc.txt

```
                ....|....|....|....|....|....|....|....|....|....|....|....|
                    5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                   65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\aro.txt

```
                ....|....|....|....|....|....|....|....|....|....|....|....|
                    5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                   65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....|....|....|....|....|....|....|....|....|....|....|
                  425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 28\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..........  ..........
```

Colony 29:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..........  ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA.....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 29\yqi.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
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Colony 30:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\glp.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\gmk.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\tpi.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 30\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 31:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA|

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\gmk.tx

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
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```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu    CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu    GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu    GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 31\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consenusu    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consenusu    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 32:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consenusu    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consenusu    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consenusu    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consenusu    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consenusu    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consenusu    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consenusu    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consenusu    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consenusu    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consenusu    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consenusu    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consenusu    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consenusu    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consenusu    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consenusu    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 32\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..........  ..........
```

Colony 33:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\arc.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 33\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 34:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\aro.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 34\yqi.txt

```
                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                       5         15         25         35         45         55
 Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      65         75         85         95        105        115
 Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     125        135        145        155        165        175
 Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     185        195        205        215        225        235
 Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     245        255        265        275        285        295
 Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     305        315        325        335        345        355
 Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     365        375        385        395        405        415
 Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     425        435        445        455        465        475
 Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                  ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     485        495        505        515        525        535
 Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 35:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\aro.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\glp.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\pta.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 35\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 36:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\gmk.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\tpi.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 36\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consenusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consenusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consenusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consenusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consenusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consenusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consenusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consenusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 485        495        505        515        525        535
Consenusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 37:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\aro.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATCATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GACAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       AACCAAATTT CATTAGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu      GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu      GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu      GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu      ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu      GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu      TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu      AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu      TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\gmk.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu      CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu      ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu      GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu      ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu      GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu      GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu      GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTAATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTC CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCGCA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGCGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....
                   425        435        445        455        465
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAACCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 37\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CGGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAATCACCAA TGCTTGTCAA CAACAGTCGC TTTGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACAAAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 38:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensusu   AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensusu   TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensusu   CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensusu   GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensusu   ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensusu   ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensusu   CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensusu   AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\glp.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensusu   GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensusu   GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensusu   GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensusu   ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensusu   GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensusu   TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensusu   AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensusu   TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\gmk.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensusu   CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensusu   ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensusu   GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensusu   ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensusu   GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensusu   GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensusu   GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\pta.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\tpi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 38\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 39:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consenusu        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consenusu        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensusu   CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensusu   ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensusu   GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensusu   ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensusu   GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensusu   GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensusu   GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensusu   GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensusu   GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensusu   GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensusu   GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensusu   GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensusu   GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensusu   TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               425        435        445        455        465        475
Consensusu   CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensusu   CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensusu   CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensusu   GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensusu   GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensusu   GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensusu   TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensusu   ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 39\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consenusu    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consenusu    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consenusu    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consenusu    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consenusu    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consenusu    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consenusu    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consenusu    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consenusu    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 40:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consenusu    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consenusu    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consenusu    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consenusu    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consenusu    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consenusu    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consenusu    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consenusu    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\glp.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\pta.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 40\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..........  .........
```

Colony 41:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..........  .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA |

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 41\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 42:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 42\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 43:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\aro.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 43\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 44:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\aro.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\glp.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 44\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 45:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensusu   AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensusu   TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensusu   CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensusu   GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensusu   ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensusu   ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensusu   CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensusu   AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensusu   GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensusu   GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensusu   GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensusu   ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensusu   GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensusu   TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensusu   AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensusu   TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 45\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensusu    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 46:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus     TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus     TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus     TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus     AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus     GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus     GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus     CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus     ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\aro.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus     AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus     TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus     CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus     GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus     ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus     ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus     CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus     AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\gmk.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\tpi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 46\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .....  .....
```

Colony 47:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .....  .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA.....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 47\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 48:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\aro.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\glp.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu      GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu      ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu      GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu      TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu      AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu      TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\gmk.txt

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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\pta.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\tpi.txt

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 48\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consenusu    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consenusu    GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consenusu    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consenusu    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consenusu    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consenusu    CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consenusu    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consenusu    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                485        495        505        515        525        535
Consenusu    GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 49:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consenusus   TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consenusus   TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consenusus   TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consenusus   AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consenusus   GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consenusus   GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consenusus   CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consenusus   ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\aro.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consenusu    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consenusu    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consenusu    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consenusu    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consenusu    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consenusu    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consenusu    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consenusu    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\glp.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\pta.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\tpi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       ATGGCACAAA CTGATATAGA TGGGGCATTA GTAGGTGGCG CA..... .........
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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 49\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 50:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAACGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 50\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 51:

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\aro.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       CCTCATAAAG AACGTATCAT ACCGTATTTA GATCATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GACAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       AACCAAATTT CATTAGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\glp.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensus       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensus       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensus       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensus       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensus       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensus       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensus       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensus       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\gmk.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GCTTTAATCA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGCTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GCACCTCCAA GTTTAGAACA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCTGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\pta.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       TTCTTTATGA TTAAAGGTGA TGTACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\tpi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA........ ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 51\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTGGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensus        GTAAACTCAC AACAAAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 52:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\glp.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\gmk.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 52\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..........
```

Colony 53:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTTGA TAACCCAACT AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        AATTTTAATT CTTTGGGATT AGATGATAGT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCAAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        CCTCATAAAG AGCGTATCAT ACCGTATTTA GATCATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        GGTGCAGTTA ATACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        ATTGGTTATG TAAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        ATTTTGGGAG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGTTG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        AATCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCAGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCTGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        GAGAAAATAC AAAGTCGTAT TAACGAAGCA CGTAAAGAAG TCGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\pta.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GTTCAATCTT TAGCGCAAAA ACTTAATCTT GATATTTCTA ATATTGAATT AATTAATCCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GTTTATGCTG GTAAAGCAGA TGGCTTAGTT AGTGGTGCAG CACATTCAAC AGGCGACACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    GTGCGTCCAG CATTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\tpi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCATGCTA TTTTCAAACA TGGTATGACA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    CCAATTATTT GTGTTGGTGA AACAGATGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGAGCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    GTAATTGCTT ATGAACCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    GCGAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 53\yqi.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus    GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus    GAGACGGGTT TGAATCCAAG TGAGATTAAT GAAGTCATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus    GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus    CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus    CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus    CAATCACCAA TGCTTGTCAA CAACAGTCGC TTTGGTTTTA AAATGGGACA TCAGTCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus    GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus    ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              485        495        505        515        525        535
Consensus    GTAAACTCAC AACAAAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 54:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\arc.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\aro.txt

```
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55
Consensus    AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 65         75         85         95        105        115
Consensus    TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
Consensus    CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
Consensus    GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                245        255        265        275        285        295
Consensus    ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
Consensus    ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
Consensus    CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                425        435        445        455        465        475
Consensus    AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\glp.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\gmk.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\pta.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 54\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consenusu        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consenusu        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consenusu        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consenusu        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consenusu        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consenusu        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consenusu        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consenusu        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consenusu        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 55:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA.....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 55\yqi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 56:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\arc.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consenusu        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consenusu        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consenusu        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consenusu        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consenusu        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consenusu        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consenusu        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consenusu        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consenusu        GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consenusu        GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consenusu        GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consenusu        ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consenusu        GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consenusu        TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consenusu        AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consenusu        TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\tpi.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 56\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  485        495        505        515        525        535
Consensus        GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 57:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\arc.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\aro.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensus        AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensus        TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensus        CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensus        GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensus        ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensus        ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensus        CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensus        AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\pta.txt

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\tpi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensusu   CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensusu   CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensusu   GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensusu   GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensusu   GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensusu   TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensusu   ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 57\yqi.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensusu   GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensusu   GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensusu   GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensusu   CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensusu   CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensusu   CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensusu   GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               425        435        445        455        465        475
Consensusu   ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               485        495        505        515        525        535
Consensusu   GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 58:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\arc.txt

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
Consensus    TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                65         75         85         95        105        115
Consensus    TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               125        135        145        155        165        175
Consensus    TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               185        195        205        215        225        235
Consensus    AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               245        255        265        275        285        295
Consensus    GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               305        315        325        335        345        355
Consensus    GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               365        375        385        395        405        415
Consensus    CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               425        435        445        455        465        475
Consensus    ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... ..... .....
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\aro.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\pta.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 58\yqi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                      5         15         25         35         45         55
Consensusu       GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     65         75         85         95        105        115
Consensusu       GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    125        135        145        155        165        175
Consensusu       GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    185        195        205        215        225        235
Consensusu       CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    245        255        265        275        285        295
Consensusu       CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    305        315        325        335        345        355
Consensusu       CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    365        375        385        395        405        415
Consensusu       GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    425        435        445        455        465        475
Consensusu       ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    485        495        505        515        525        535
Consensusu       GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Colony 59:

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\arc.txt

```
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus   TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus   TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus   TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus   AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus   GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus   GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus   CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus   ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\aro.txt

```
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus   AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus   TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus   CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus   GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus   ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus   ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus   CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus   AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\glp.txt

```
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                5         15         25         35         45         55
Consensus   GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
               65         75         85         95        105        115
Consensus   GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              125        135        145        155        165        175
Consensus   GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              185        195        205        215        225        235
Consensus   ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              245        255        265        275        285        295
Consensus   GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              305        315        325        335        345        355
Consensus   TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              365        375        385        395        405        415
Consensus   AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
              425        435        445        455        465        475
Consensus   TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

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Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\gmk.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\pta.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\tpi.txt

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 59\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... .......... ..........
```

Colony 60:

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\arc.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensus       TTATTAATCC AACAAGCTAA ATCGAACAGT GACACAACGC CGGCAATGCC ATTGGATACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensus       TGTGGTGCAA TGTCACAGGG TATGATAGGC TATTGGTTGG AAACTGAAAT CAATCGCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensus       TTAACTGAAA TGAATAGTGA TAGAACTGTA GGCACAATCG TTACACGTGT GGAAGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensus       AAAGATGATC CACGATTCAA TAACCCAACC AAACCAATTG GTCCTTTTTA TACGAAAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensus       GAAGTTGAAG AATTACAAAA AGAACAGCCA GACTCAGTCT TTAAAGAAGA TGCAGGACGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensus       GGTTATAGAA AAGTAGTTGC GTCACCACTA CCTCAATCTA TACTAGAACA CCAGTTAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensus       CGAACTTTAG CAGACGGTAA AAATATTGTC ATTGCATGCG GTGGTGGCGG TATTCCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensus       ATAAAAAAAG AAAATACCTA TGAAGGTGTT GAAGCG.... .......... ..........
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\aro.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5         15         25         35         45         55
Consensusu      AATTTTAATT CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTCC AATTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    65         75         85         95        105        115
Consensusu      TTTCATTTAA TTAAAGAAAT TATTTCGAAA AAAGAATTAG ATGGCTTTAA TATCACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   125        135        145        155        165        175
Consensusu      CCTCATAAAG AACGTATCAT ACCGTATTTA GATTATGTTG ATGAACAAGC GATTAATGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   185        195        205        215        225        235
Consensusu      GGTGCAGTTA ACACTGTTTT GATAAAAGAT GGCAAGTGGA TAGGGTATAA TACAGATGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   245        255        265        275        285        295
Consensusu      ATTGGTTATG TTAAAGGATT GCACAGCGTT TATCCAGATT TAGAAAATGC ATACATTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   305        315        325        335        345        355
Consensusu      ATTTTGGGCG CAGGTGGTGC AAGTAAAGGT ATTGCTTATG AATTAGCAAA ATTTGTAAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   365        375        385        395        405        415
Consensusu      CCCAAATTAA CTGTTGCGAA TAGAACGATG GCTCGTTTTG AATCTTGGAA TTTAAATATA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475
Consensusu      AACCAAATTT CATTGGCAGA TGCTGAAAAG TATTTA.... .......... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\glp.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GGTGCTGATT GGATTGTCAT CACAGCTGGA TGGGGATTAG CGGTTACAAT GGGTGTGTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GCTGTCGGTC AATTCTCAGG TGCACATTTA AACCCAGCGG TGTCTTTAGC TCTTGCATTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GACGGAAGTT TTGATTGGTC ATTAGTTCCT GGTTATATTG TTGCTCAAAT GTTAGGTGCA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ATTGTCGGAG CAACAATTGT ATGGTTAATG TACTTGCCAC ATTGGAAAGC GACAGAAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GCTGGCGCGA AATTAGGTGT TTTCTCTACA GCACCGGCTA TTAAGAATTA CTTTGCCAAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       TTTTTAAGTG AGATTATCGG AACAATGGCA TTAACTTTAG GTATTTTATT TATCGGTGTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       AACAAAATTG CCGATGGTTT AAATCCTTTA ATTGTCGGAG CATTAATTGT TGCAATCGGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       TTAAGTTTAG GCGGTGCTAC TGGTTATGCA ATCAACCCAG CACGT..... ..........
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\gmk.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       CGAATATTTG AAGATCCAAG TACATCATAT AAGTATTCTA TTTCAATGAC AACACGTCAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       ATGCGTGAAG GTGAAGTTGA TGGCGTAGAT TACTTTTTTA AAACTAGGGA TGCGTTTGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCTTTAATTA AAGATGACCA ATTTATAGAA TATGCTGAAT ATGTAGGCAA CTATTATGGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       ACACCAGTTC AATATGTTAA AGATACAATG GACGAAGGTC ATGATGTATT TTTAGAAATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GAAGTAGAAG GTGCAAAGCA AGTTAGAAAG AAATTTCCAG ATGCGTTATT TATTTTCTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GCACCTCCAA GTTTAGATCA CTTGAGAGAG CGATTAGTAG GTAGAGGAAC AGAATCCAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       GAGAAAATAC AAAGTCGTAT TAACGAAGCG CGTAAAGAAG TTGAAATGAT GAATTTA...
```

Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\pta.txt

```
                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    5         15         25         35         45         55
Consensusu       GCAACACAAT TACAAGCAAC AGATTATGTT ACACCAATCG TGTTAGGTGA TGAGACTAAG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   65         75         85         95        105        115
Consensusu       GTTCAATCTT TAGCGCAAAA ACTTGATCTT GATATTTCTA ATATTGAATT AATTAATCCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  125        135        145        155        165        175
Consensusu       GCGACAAGTG AATTGAAAGC TGAATTAGTT CAATCATTTG TTGAACGACG TAAAGGTAAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  185        195        205        215        225        235
Consensusu       GCGACTGAAG AACAAGCACA AGAATTATTA AACAATGTGA ACTACTTCGG TACAATGCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  245        255        265        275        285        295
Consensusu       GTTTATGCTG GTAAAGCAGA TGGTTTAGTT AGTGGTGCAG CACATTCAAC AGGAGACACT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  305        315        325        335        345        355
Consensusu       GTGCGTCCAG CTTTACAAAT CATCAAAACG AAACCAGGTG TATCAAGAAC ATCAGGTATC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  365        375        385        395        405        415
Consensusu       TTCTTTATGA TTAAAGGTGA TGAACAATAC ATCTTTGGTG ATTGTGCAAT CAATCCAGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475
Consensusu       CTTGATTCAC AAGGACTTGC AGAAATTGCA GTAGAAAGTG CAAAATCAGC ATTA......
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\tpi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      CACGAAACAG ATGAAGAAAT TAACAAAAAA GCGCACGCTA TTTTCAAACA TGGAATGACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      CCAATTATTT GTGTTGGTGA AACAGACGAA GAGCGTGAAA GTGGTAAAGC TAACGATGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GTAGGTGAGC AAGTTAAGAA AGCTGTTGCA GGTTTATCTG AAGATCAACT TAAATCAGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      GTAATTGCTT ATGAGCCAAT CTGGGCAATC GGAACTGGTA AATCATCAAC ATCTGAAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      GCAAATGAAA TGTGTGCATT TGTACGTCAA ACTATTGCTG ACTTATCAAG CAAAGAAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      TCAGAAGCAA CTCGTATTCA ATATGGTGGT AGTGTTAAAC CTAACAACAT TAAAGAATAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      ATGGCACAAA CTGATATTGA TGGGGCATTA GTAGGTGGCG CA..... .....
```

```
Alignment: D:\Study\Master\sequencing result\consensus sequences\colony 60\yqi.txt

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55
Consensusu      GCGTTTAAAG ACGTGCCAGC CTATGATTTA GGTGCGACTT TAATAGAACA TATTATTAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
Consensusu      GAGACGGGTT TGAATCCAAG TGAGATTGAT GAAGTTATCA TCGGTAACGT ACTACAAGCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 125        135        145        155        165        175
Consensusu      GGACAAGGAC AAAATCCAGC ACGAATTGCT GCTATGAAAG GTGGCTTGCC AGAAACAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 185        195        205        215        225        235
Consensusu      CCTGCATTTA CAGTGAATAA AGTATGTGGT TCTGGGTTAA AGTCGATTCA ATTAGCATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
Consensusu      CAATCTATTG TGACTGGTGA AAATGACATC GTGCTAGCTG GCGGTATGGA GAATATGTCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 305        315        325        335        345        355
Consensusu      CAGTCACCAA TGCTTGTCAA CAACAGTCGC TTCGGTTTTA AAATGGGACA TCAATCAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 365        375        385        395        405        415
Consensusu      GTTGATAGCA TGGTATATGA TGGTTTAACA GATGTATTTA ATCAATATCA TATGGGTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 425        435        445        455        465        475
Consensusu      ACTGCTGAAA ATTTAGTAGA GCAATATGGT ATTTCAAGAG AAGAACAAGA TACATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 485        495        505        515        525        535
Consensusu      GTAAACTCAC AACATAAAGC AGTACGTGCA CAGCAA.... ..... .....
```

Appendix I. Summary of MLST results

Table I The allelic profile• ssequence types and source of the sixty *S. aureus* isolate.

Colony Code	Sequence Type	arc	aro	glp	gmk	pta	tpi	yqi	Sampling sites
1	ST5	1	4	1	4	12	1	10	Final Products
2	ST5	1	4	1	4	12	1	10	Final Products
3	ST5	1	4	1	4	12	1	10	Final Products
4	ST5	1	4	1	4	12	1	10	Final Products
5	ST5	1	4	1	4	12	1	10	Final Products
6	ST5	1	4	1	4	12	1	10	Final Products
7	ST5	1	4	1	4	12	1	10	Final Products
8	ST5	1	4	1	4	12	1	10	Final Products
9	ST5	1	4	1	4	12	1	10	Final Products
10	ST5	1	4	1	4	12	1	10	Final Products
11	ST5	1	4	1	4	12	1	10	Fresh MSM
12	ST5	1	4	1	4	12	1	10	Fresh MSM
13	ST5	1	4	1	4	12	1	10	Fresh MSM
14	ST5	1	4	1	4	12	1	10	Fresh MSM
15	ST5	1	4	1	4	12	1	10	Fresh MSM
16	ST5	1	4	1	4	12	1	10	Fresh MSM
17	ST5	1	4	1	4	12	1	10	Fresh MSM
18	ST5	1	4	1	4	12	1	10	Fresh MSM
19	ST5	1	4	1	4	12	1	10	Fresh MSM
20	ST2594	1	4	320	4	12	1	10	Fresh MSM
21	ST5	1	4	1	4	12	1	10	Fresh Skin
22	ST5	1	4	1	4	12	1	10	Fresh Skin
23	ST5	1	4	1	4	12	1	10	Fresh Skin
24	ST5	1	4	1	4	12	1	10	Fresh Skin
25	ST5	1	4	1	4	12	1	10	Fresh Skin
26	ST5	1	4	1	4	12	1	10	Fresh Skin
27	ST5	1	4	1	4	12	1	10	Fresh Skin
28	ST5	1	4	1	4	12	1	10	Fresh Skin
29	ST5	1	4	1	4	12	1	10	Fresh Skin
30	ST5	1	4	1	4	12	1	10	Fresh Skin
31	ST5	1	4	1	4	12	1	10	Fresh SO BF
32	ST5	1	4	1	4	12	1	10	Fresh SO BF
33	ST5	1	4	1	4	12	1	10	Fresh SO BF
34	ST5	1	4	1	4	12	1	10	Fresh SO BF
35	ST5	1	4	1	4	12	1	10	Fresh SO BF
36	ST5	1	4	1	4	12	1	10	Fresh SO BF
37	ST5	1	4	1	4	12	1	10	Fresh SO BF
38	ST5	1	4	1	4	12	1	10	Fresh SO BF
39	ST5	1	4	1	4	12	1	10	Fresh SO BF
40	ST101	3	1	14	15	11	19	3	Fresh SO BF
41	ST5	1	4	1	4	12	1	10	Rubber Fingers
42	ST5	1	4	1	4	12	1	10	Rubber Fingers
43	ST5	1	4	1	4	12	1	10	Rubber Fingers
44	ST5	1	4	1	4	12	1	10	Rubber Fingers

45	ST5	1	4	1	4	12	1	10	Rubber Fingers
46	ST5	1	4	1	4	12	1	10	Rubber Fingers
47	ST5	1	4	1	4	12	1	10	Rubber Fingers
48	ST5	1	4	1	4	12	1	10	Rubber Fingers
49	ST83	1	4	1	4	12	41	10	Rubber Fingers
50	ST2777	1	4	348	4	12	1	10	Rubber Fingers
51	ST5	1	4	1	4	12	1	10	Live Chickens
52	ST5	1	4	1	4	12	1	10	Live Chickens
53	ST5	1	4	1	4	12	1	10	Live Chickens
54	ST5	1	4	1	4	12	1	10	Live Chickens
55	ST5	1	4	1	4	12	1	10	Live Chickens
56	ST5	1	4	1	4	12	1	10	Live Chickens
57	ST5	1	4	1	4	12	1	10	Live Chickens
58	ST5	1	4	1	4	12	1	10	Live Chickens
59	ST398	3	35	19	2	20	26	39	Live Chickens
60	ST1	1	1	1	1	1	1	1	Live Chickens

Appendix J. eBURST analysis outputs

eBURST Report - Sat Feb 21 18:26:33 NZDT 2015
No. isolates = 60 | No. STs = 6 | No. re-samplings for bootstrapping = 1000
No. loci per isolate = 7 | No. identical loci for group def = 5 | No. groups = 1

Group 1: No. Isolates = 57 | No. STs = 3 | Predicted Founder = 5

ST	FREQ	SLV	DLV	TLV	SAT	Average Distance
5	55	2	0	0	0	1.0
83	1	1	1	0	0	1.5
2594	1	1	1	0	0	1.5

Singletons: size 3
101
1
398

Figure J eBURST analysis outputs

Appendix K. Statistical outputs

A. Final Products

Explore
Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%
	Batch 4	6	100.0%	0	0.0%	6	100.0%
	Batch 5	6	100.0%	0	0.0%	6	100.0%
	Batch 6	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		2.0960	.31885
		95% Confidence Interval for Mean	Lower Bound	1.2763	
			Upper Bound	2.9156	
		5% Trimmed Mean		2.0773	
		Median		1.8601	
		Variance		.610	
		Std. Deviation		.78103	
		Minimum		1.40	
		Maximum		3.13	
		Range		1.73	
		Interquartile Range		1.58	
		Skewness		.528	.845
		Kurtosis		-2.121	1.741
	Batch 2	Mean		1.8523	.09266
		95% Confidence Interval for Mean	Lower Bound	1.6141	
			Upper Bound	2.0905	
		5% Trimmed Mean		1.8517	
		Median		1.8290	
		Variance		.052	
		Std. Deviation		.22697	
		Minimum		1.54	
		Maximum		2.17	
		Range		.63	
		Interquartile Range		.41	
		Skewness		.161	.845
		Kurtosis		-.657	1.741
	Batch 3	Mean		1.6039	.14277
		95% Confidence Interval for Mean	Lower Bound	1.2369	
			Upper Bound	1.9709	
		5% Trimmed Mean		1.5889	
		Median		1.5000	
		Variance		.122	
		Std. Deviation		.34970	

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum		1.30	
		Maximum		2.18	
		Range		.88	
		Interquartile Range		.63	
		Skewness		.962	.845
		Kurtosis		-.202	1.741
		Mean		2.1561	.18797
		95% Confidence Interval for Mean	Lower Bound	1.6729	
			Upper Bound	2.6393	
		5% Trimmed Mean		2.1400	
		Median		2.0880	
		Variance		.212	
	Batch 4	Std. Deviation		.46044	
		Minimum		1.70	
		Maximum		2.90	
		Range		1.20	
		Interquartile Range		.75	
		Skewness		.797	.845
		Kurtosis		-.259	1.741
		Mean		2.0649	.20853
		95% Confidence Interval for Mean	Lower Bound	1.5289	
			Upper Bound	2.6010	
		5% Trimmed Mean		2.0505	
		Median		1.8580	
		Variance		.261	
	Batch 5	Std. Deviation		.51080	
		Minimum		1.54	
		Maximum		2.85	
		Range		1.30	
		Interquartile Range		.93	
		Skewness		.876	.845
		Kurtosis		-.979	1.741
	Batch 6	Mean		2.0100	.11479

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 6	95% Confidence Interval for Mean	Lower Bound	1.7149	
			Upper Bound	2.3050	
		5% Trimmed Mean		2.0057	
		Median		1.9418	
		Variance		.079	
		Std. Deviation		.28117	
		Minimum		1.70	
		Maximum		2.40	
		Range		.70	
		Interquartile Range		.57	
		Skewness		.538	.845
		Kurtosis		-1.532	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]	Shapiro-Wilk

		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.260	6	.200*	.839	6	.128
	Batch 2	.179	6	.200*	.979	6	.947
	Batch 3	.222	6	.200*	.880	6	.267
	Batch 4	.229	6	.200*	.908	6	.420
	Batch 5	.291	6	.123	.878	6	.259
	Batch 6	.245	6	.200*	.906	6	.410

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	2.0960	.78103	.31885	1.2763	2.9156	1.40
Batch 2	6	1.8523	.22697	.09266	1.6141	2.0905	1.54
Batch 3	6	1.6039	.34970	.14277	1.2369	1.9709	1.30
Batch 4	6	2.1561	.46044	.18797	1.6729	2.6393	1.70
Batch 5	6	2.0649	.51080	.20853	1.5289	2.6010	1.54
Batch 6	6	2.0100	.28117	.11479	1.7149	2.3050	1.70
Total	36	1.9638	.47605	.07934	1.8028	2.1249	1.30

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	3.13
Batch 2	2.17
Batch 3	2.18
Batch 4	2.90
Batch 5	2.85
Batch 6	2.40
Total	3.13

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	1.253	5	.251	1.125	.368
Within Groups	6.679	30	.223		
Total	7.932	35			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	.24369	.27242	.945	-.5849	1.0723
	Batch 3	.49209	.27242	.477	-.3365	1.3207
	Batch 4	-.06012	.27242	1.000	-.8887	.7685
	Batch 5	.03103	.27242	1.000	-.7975	.8596
	Batch 6	.08601	.27242	1.000	-.7426	.9146
Batch 2	Batch 1	-.24369	.27242	.945	-1.0723	.5849
	Batch 3	.24840	.27242	.940	-.5802	1.0770

	Batch 4	-.30381	.27242	.871	-1.1324	.5248
	Batch 5	-.21266	.27242	.969	-1.0412	.6159
	Batch 6	-.15768	.27242	.992	-.9863	.6709
	Batch 1	-.49209	.27242	.477	-1.3207	.3365
	Batch 2	-.24840	.27242	.940	-1.0770	.5802
Batch 3	Batch 4	-.55221	.27242	.351	-1.3808	.2764
	Batch 5	-.46106	.27242	.547	-1.2896	.3675
	Batch 6	-.40608	.27242	.673	-1.2347	.4225
	Batch 1	.06012	.27242	1.000	-.7685	.8887
	Batch 2	.30381	.27242	.871	-.5248	1.1324
Batch 4	Batch 3	.55221	.27242	.351	-.2764	1.3808
	Batch 5	.09115	.27242	.999	-.7374	.9197
	Batch 6	.14613	.27242	.994	-.6825	.9747
	Batch 1	-.03103	.27242	1.000	-.8596	.7975
	Batch 2	.21266	.27242	.969	-.6159	1.0412
Batch 5	Batch 3	.46106	.27242	.547	-.3675	1.2896
	Batch 4	-.09115	.27242	.999	-.9197	.7374
	Batch 6	.05497	.27242	1.000	-.7736	.8836
	Batch 1	-.08601	.27242	1.000	-.9146	.7426
	Batch 2	.15768	.27242	.992	-.6709	.9863
Batch 6	Batch 3	.40608	.27242	.673	-.4225	1.2347
	Batch 4	-.14613	.27242	.994	-.9747	.6825
	Batch 5	-.05497	.27242	1.000	-.8836	.7736

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 3	6	1.6039
Batch 2	6	1.8523
Batch 6	6	2.0100
Batch 5	6	2.0649
Batch 1	6	2.0960
Batch 4	6	2.1561
Sig.		.351

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 6.000.

Custom Tables

Table 1

Batch No.																							
Batch 1				Batch 2				Batch 3				Batch 4				Batch 5				Batch 6			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	50.0 %	3	50.0 %	5	83.3 %	1	16.7 %	5	83.3 %	1	16.7 %	3	50.0 %	3	50.0 %	4	66.7 %	2	33.3 %	4	66.7 %	2	33.3 %

B. Frozen MSM

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		2.4961	.19806
		95% Confidence Interval for Mean	Lower Bound	1.9870	
			Upper Bound	3.0053	
		5% Trimmed Mean		2.5043	
		Median		2.6178	
		Variance		.235	
		Std. Deviation		.48513	
		Minimum		1.70	
		Maximum		3.15	
		Range		1.45	
		Interquartile Range		.67	
		Skewness		-.632	.845
		Kurtosis		1.175	1.741
	Batch 2	Mean		1.9759	.41626
		95% Confidence Interval for Mean	Lower Bound	.9059	
			Upper Bound	3.0460	
		5% Trimmed Mean		1.9231	
		Median		1.6004	
		Variance		1.040	
		Std. Deviation		1.01963	
		Minimum		1.15	
		Maximum		3.75	
		Range		2.60	
		Interquartile Range		1.74	
		Skewness		1.304	.845
		Kurtosis		.923	1.741
	Batch 3	Mean		2.3348	.23866
		95% Confidence Interval for Mean	Lower Bound	1.7213	
			Upper Bound	2.9483	
		5% Trimmed Mean		2.3622	
		Median		2.4693	
		Variance		.342	
		Std. Deviation		.58459	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum	1.30	
		Maximum	2.87	
		Range	1.57	
		Interquartile Range	.92	
		Skewness	-1.262	.845
		Kurtosis	1.437	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.253	6	.200*	.934	6	.611
	Batch 2	.288	6	.131	.841	6	.133
	Batch 3	.179	6	.200*	.891	6	.326

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	2.4961	.48513	.19806	1.9870	3.0053	1.70
Batch 2	6	1.9759	1.01963	.41626	.9059	3.0460	1.15
Batch 3	6	2.3348	.58459	.23866	1.7213	2.9483	1.30
Total	18	2.2690	.72496	.17087	1.9084	2.6295	1.15

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	3.15
Batch 2	3.75
Batch 3	2.87
Total	3.75

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.851	2	.425	.789	.472
Within Groups	8.084	15	.539		
Total	8.935	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)

Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	.52020	.42384	.456	-.5807	1.6211
	Batch 3	.16138	.42384	.924	-.9395	1.2623
Batch 2	Batch 1	-.52020	.42384	.456	-1.6211	.5807
	Batch 3	-.35882	.42384	.681	-1.4597	.7421
Batch 3	Batch 1	-.16138	.42384	.924	-1.2623	.9395
	Batch 2	.35882	.42384	.681	-.7421	1.4597

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 2	6	1.9759
Batch 3	6	2.3348
Batch 1	6	2.4961
Sig.		.456

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 6.000.

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
1	16.7%	5	83.3%	4	66.7%	2	33.3%	1	16.7%	5	83.3%

C. Frozen Skin

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		1.8712	.29387
		95% Confidence Interval for Mean	Lower Bound	1.1158	
			Upper Bound	2.6266	
		5% Trimmed Mean		1.8569	
		Median		1.9771	
		Variance		.518	
		Std. Deviation		.71983	
		Minimum		1.00	
		Maximum		3.00	
		Range		2.00	
		Interquartile Range		1.19	
		Skewness		.366	.845
		Kurtosis		.101	1.741
	Batch 2	Mean		2.3377	.37998
		95% Confidence Interval for Mean	Lower Bound	1.3609	
			Upper Bound	3.3145	
		5% Trimmed Mean		2.3073	
		Median		2.2358	
		Variance		.866	
		Std. Deviation		.93076	
		Minimum		1.30	
		Maximum		3.92	
		Range		2.62	
		Interquartile Range		1.52	
		Skewness		.930	.845
		Kurtosis		1.013	1.741
	Batch 3	Mean		1.7184	.21845
		95% Confidence Interval for Mean	Lower Bound	1.1569	
			Upper Bound	2.2800	
		5% Trimmed Mean		1.7104	
		Median		1.6391	
		Variance		.286	
		Std. Deviation		.53509	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum	1.15	
		Maximum	2.43	
		Range	1.28	
		Interquartile Range	.96	
		Skewness	.255	.845
		Kurtosis	-2.313	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.213	6	.200*	.925	6	.546
	Batch 2	.200	6	.200*	.936	6	.626
	Batch 3	.282	6	.146	.878	6	.260

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	1.8712	.71983	.29387	1.1158	2.6266	1.00
Batch 2	6	2.3377	.93076	.37998	1.3609	3.3145	1.30
Batch 3	6	1.7184	.53509	.21845	1.1569	2.2800	1.15
Total	18	1.9758	.75158	.17715	1.6020	2.3495	1.00

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	3.00
Batch 2	3.92
Batch 3	2.43
Total	3.92

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	1.249	2	.624	1.121	.352
Within Groups	8.354	15	.557		
Total	9.603	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)

Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	-.46652	.43086	.539	-1.5857	.6526
	Batch 3	.15276	.43086	.933	-.9664	1.2719
Batch 2	Batch 1	.46652	.43086	.539	-.6526	1.5857
	Batch 3	.61928	.43086	.348	-.4999	1.7384
Batch 3	Batch 1	-.15276	.43086	.933	-1.2719	.9664
	Batch 2	-.61928	.43086	.348	-1.7384	.4999

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 3	6	1.7184
Batch 1	6	1.8712
Batch 2	6	2.3377
Sig.		.348

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 6.000.

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Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
4	66.7%	2	33.3%	2	33.3%	4	66.7%	4	66.7%	2	33.3%

D. Frozen SO BF

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	5	100.0%	0	0.0%	5	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
LogMean2	Batch 1	Mean		.4621	.16669
		95% Confidence Interval for Mean	Lower Bound	.0336	
			Upper Bound	.8906	
		5% Trimmed Mean		.4550	
		Median		.5156	
		Variance		.167	
		Std. Deviation		.40831	
		Minimum		.00	
		Maximum		1.05	
		Range		1.05	
		Interquartile Range		.78	
		Skewness		.092	.845
		Kurtosis		-.818	1.741
	Batch 2	Mean		.3152	.18250
		95% Confidence Interval for Mean	Lower Bound	-.1540	
			Upper Bound	.7843	
		5% Trimmed Mean		.2934	
		Median		.0701	
		Variance		.200	
		Std. Deviation		.44703	
		Minimum		.00	
		Maximum		1.02	
		Range		1.02	
		Interquartile Range		.80	
		Skewness		1.089	.845
		Kurtosis		-.831	1.741
	Batch 3	Mean		.4178	.18188
		95% Confidence Interval for Mean	Lower Bound	-.0871	
			Upper Bound	.9228	
		5% Trimmed Mean		.4113	
		Median		.2632	
		Variance		.165	
		Std. Deviation		.40669	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
LogMean2	Batch 3	Minimum	.00	
		Maximum	.95	
		Range	.95	
		Interquartile Range	.77	
		Skewness	.539	.913
		Kurtosis	-2.093	2.000

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	Batch 1	.205	6	.200*	.914	6	.463
	Batch 2	.319	6	.056	.764	6	.028
	Batch 3	.248	5	.200*	.912	5	.480

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	1.7011	.69666	.28441	.9700	2.4322	1.00
Batch 2	6	1.5003	.75287	.30736	.7102	2.2904	1.00
Batch 3	5	1.6253	.68361	.30572	.7765	2.4741	1.00
Total	17	1.6079	.67329	.16330	1.2617	1.9541	1.00

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	2.87
Batch 2	2.78
Batch 3	2.60
Total	2.87

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.123	2	.062	.121	.887
Within Groups	7.130	14	.509		
Total	7.253	16			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)

Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	.20082	.41202	.878	-.8776	1.2792
	Batch 3	.07581	.43213	.983	-1.0552	1.2068
Batch 2	Batch 1	-.20082	.41202	.878	-1.2792	.8776
	Batch 3	-.12501	.43213	.955	-1.2560	1.0060
Batch 3	Batch 1	-.07581	.43213	.983	-1.2068	1.0552
	Batch 2	.12501	.43213	.955	-1.0060	1.2560

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 2	6	1.5003
Batch 3	5	1.6253
Batch 1	6	1.7011
Sig.		.885

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 5.625.

b. The group sizes are unequal. The harmonic mean of the group sizes is used. Type I error levels are not guaranteed.

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Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
5	83.3%	1	16.7%	4	66.7%	2	33.3%	3	60.0%	2	40.0%

E. Fr Se Mh M

Explore
Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		2.8504	.20953
		95% Confidence Interval for Mean	Lower Bound	2.3118	
			Upper Bound	3.3890	
		5% Trimmed Mean		2.8506	
		Median		2.8572	
		Variance		.263	
		Std. Deviation		.51325	
		Minimum		2.24	
		Maximum		3.45	
		Range		1.21	
		Interquartile Range		.99	
		Skewness		-.014	.845
		Kurtosis		-2.517	1.741
	Batch 2	Mean		1.7888	.10389
		95% Confidence Interval for Mean	Lower Bound	1.5217	
			Upper Bound	2.0558	
		5% Trimmed Mean		1.7924	
		Median		1.8208	
		Variance		.065	
		Std. Deviation		.25449	
		Minimum		1.45	
		Maximum		2.06	
		Range		.61	
		Interquartile Range		.53	
		Skewness		-.311	.845
		Kurtosis		-1.863	1.741
	Batch 3	Mean		2.1657	.25651
		95% Confidence Interval for Mean	Lower Bound	1.5064	
			Upper Bound	2.8251	
		5% Trimmed Mean		2.1705	
		Median		2.2469	
		Variance		.395	
		Std. Deviation		.62831	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum	1.45	
		Maximum	2.79	
		Range	1.34	
		Interquartile Range	1.22	
		Skewness	-.129	.845
		Kurtosis	-2.923	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.218	6	.200*	.896	6	.349
	Batch 2	.171	6	.200*	.913	6	.458
	Batch 3	.290	6	.126	.815	6	.080

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	2.8504	.51325	.20953	2.3118	3.3890	2.24
Batch 2	6	1.7888	.25449	.10389	1.5217	2.0558	1.45
Batch 3	6	2.1657	.62831	.25651	1.5064	2.8251	1.45
Total	18	2.2683	.64583	.15222	1.9471	2.5895	1.45

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	3.45
Batch 2	2.06
Batch 3	2.79
Total	3.45

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	3.476	2	1.738	7.212	.006
Within Groups	3.615	15	.241		
Total	7.091	17			

post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	1.06162*	.28342	.005	.3254	1.7978
	Batch 3	.68465	.28342	.070	-.0515	1.4208
Batch 2	Batch 1	-1.06162*	.28342	.005	-1.7978	-.3254
	Batch 3	-.37697	.28342	.401	-1.1132	.3592
Batch 3	Batch 1	-.68465	.28342	.070	-1.4208	.0515
	Batch 2	.37697	.28342	.401	-.3592	1.1132

*. The mean difference is significant at the 0.05 level.

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05	
		1	2
Batch 2	6	1.7888	
Batch 3	6	2.1657	2.1657
Batch 1	6		2.8504
Sig.		.401	.070

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 6.000.

Explore
Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/g)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3
	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/g)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	1 hour	Mean		2.2632	.30076
		95% Confidence Interval for Mean	Lower Bound	.9691	
			Upper Bound	3.5572	
		5% Trimmed Mean		.	
		Median		2.2430	
		Variance		.271	
		Std. Deviation		.52093	
		Minimum		1.75	
		Maximum		2.79	
		Range		1.04	
		Interquartile Range		.	
		Skewness		.174	1.225
		Kurtosis		.	.
	2 hour	Mean		1.8228	.28319
		95% Confidence Interval for Mean	Lower Bound	.6043	
			Upper Bound	3.0413	
		5% Trimmed Mean		.	
		Median		1.5396	
		Variance		.241	
		Std. Deviation		.49050	
		Minimum		1.54	
		Maximum		2.39	
		Range		.85	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
	3 hour	Mean		2.4233	.50476
		95% Confidence Interval for Mean	Lower Bound	.2515	
			Upper Bound	4.5951	
		5% Trimmed Mean		.	
		Median		2.6721	
		Variance		.764	
		Std. Deviation		.87427	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	3 hour	Minimum		1.45	
		Maximum		3.15	
		Range		1.69	
		Interquartile Range		.	
		Skewness		-1.177	1.225
		Kurtosis		.	.
	4 hour	Mean		1.9696	.32486
		95% Confidence Interval for Mean	Lower Bound	.5719	
			Upper Bound	3.3674	
		5% Trimmed Mean		.	
		Median		1.8891	

		Variance		.317	
		Std. Deviation		.56267	
		Minimum		1.45	
		Maximum		2.57	
		Range		1.12	
		Interquartile Range		.	
		Skewness		.631	1.225
		Kurtosis		.	.
		Mean		2.3874	.46110
		95% Confidence Interval for Mean	Lower Bound	.4035	
			Upper Bound	4.3714	
		5% Trimmed Mean		.	
		Median		2.0396	
		Variance		.638	
	5 hour	Std. Deviation		.79865	
		Minimum		1.82	
		Maximum		3.30	
		Range		1.48	
		Interquartile Range		.	
		Skewness		1.588	1.225
		Kurtosis		.	.
	6 hour	Mean		2.7436	.40282

Descriptives Statistics

Processing Time (h)				Statistic	Std. Error
Mean (Log CFU/g)	6 hour	95% Confidence Interval for Mean	Lower Bound	1.0104	
			Upper Bound	4.4768	
		5% Trimmed Mean		.	
		Median		2.7157	
		Variance		.487	
		Std. Deviation		.69770	
		Minimum		2.06	
		Maximum		3.45	
		Range		1.39	
		Interquartile Range		.	
		Skewness		.180	1.225
		Kurtosis		.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/g)	1 hour	.182	3	.	.999	3
	2 hour	.385	3	.	.750	3
	3 hour	.279	3	.	.939	3
	4 hour	.224	3	.	.985	3
	5 hour	.335	3	.	.858	3
	6 hour	.183	3	.	.999	3

Tests of Normality

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/g)	1 hour	.936
	2 hour	.000
	3 hour	.524
	4 hour	.763
	5 hour	.261
	6 hour	.934

a. Lilliefors Significance Correction

Explore
Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	1 hour	3	100.0%	0	0.0%	3	100.0%
	2 hour	3	100.0%	0	0.0%	3	100.0%
	3 hour	3	100.0%	0	0.0%	3	100.0%
	4 hour	3	100.0%	0	0.0%	3	100.0%
	5 hour	3	100.0%	0	0.0%	3	100.0%
	6 hour	3	100.0%	0	0.0%	3	100.0%

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	1 hour	Mean		.7988	.13470
		95% Confidence Interval for Mean	Lower Bound	.2192	
			Upper Bound	1.3783	
		5% Trimmed Mean		.	
		Median		.8078	
		Variance		.054	
		Std. Deviation		.23330	
		Minimum		.56	
		Maximum		1.03	
		Range		.47	
		Interquartile Range		.	
		Skewness		-.174	1.225
		Kurtosis		.	.
	2 hour	Mean		.5780	.14648
		95% Confidence Interval for Mean	Lower Bound	-.0522	
			Upper Bound	1.2082	
		5% Trimmed Mean		.	
		Median		.4315	
		Variance		.064	
		Std. Deviation		.25370	
		Minimum		.43	

		Maximum		.87	
		Range		.44	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
		Mean		.8339	.23540
		95% Confidence Interval for Mean	Lower Bound	-.1790	
			Upper Bound	1.8467	
	3 hour	5% Trimmed Mean		.	
		Median		.9829	
		Variance		.166	
		Std. Deviation		.40772	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	3 hour	Minimum		.37	
		Maximum		1.15	
		Range		.77	
		Interquartile Range		.	
		Skewness		-1.425	1.225
		Kurtosis		.	.
		Mean		.6506	.16487
		95% Confidence Interval for Mean	Lower Bound	-.0587	
			Upper Bound	1.3600	
		5% Trimmed Mean		.	
		Median		.6361	
		Variance		.082	
	4 hour	Std. Deviation		.28557	
		Minimum		.37	
		Maximum		.94	
		Range		.57	
		Interquartile Range		.	
		Skewness		.229	1.225
		Kurtosis		.	.
		Mean		.8356	.18226
		95% Confidence Interval for Mean	Lower Bound	.0514	
			Upper Bound	1.6198	
		5% Trimmed Mean		.	
		Median		.7127	
		Variance		.100	
	5 hour	Std. Deviation		.31569	
		Minimum		.60	
		Maximum		1.19	
		Range		.59	
		Interquartile Range		.	
		Skewness		1.486	1.225
		Kurtosis		.	.
	6 hour	Mean		.9872	.14934

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	6 hour	95% Confidence Interval for Mean	Lower Bound	.3447	
			Upper Bound	1.6298	
		5% Trimmed Mean		.	
		Median		.9990	
		Variance		.067	
		Std. Deviation		.25867	
		Minimum		.72	
		Maximum		1.24	
		Range		.52	
		Interquartile Range		.	
		Skewness		-.205	1.225
		Kurtosis		.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	1 hour	.182	3	.	.999	3	.936
	2 hour	.385	3	.	.750	3	.000
	3 hour	.309	3	.	.900	3	.385
	4 hour	.187	3	.	.998	3	.916
	5 hour	.318	3	.	.886	3	.344
	6 hour	.185	3	.	.998	3	.924

a. Lilliefors Significance Correction

NPar Tests

Descriptive Statistics

	N	Mean	Std. Deviation	Minimum	Maximum
Mean (Log CFU/g)	18	2.2683	.64583	1.45	3.45
Processing Time (h)	18	3.50	1.757	1	6

Kruskal-Wallis Test

Ranks

	Processing Time (h)	N	Mean Rank
Mean (Log CFU/g)	1 hour	3	10.00
	2 hour	3	6.00
	3 hour	3	10.17
	4 hour	3	6.83
	5 hour	3	10.33
	6 hour	3	13.67
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/g)
Chi-Square	4.020
df	5
Asymp. Sig.	.547

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
0	0.0%	6	100.0%	5	83.3%	1	16.7%	3	50.0%	3	50.0%

Custom Tables

Table 1

Processing Time (h)																							
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
1	33.3 %	2	66.7 %	2	66.7 %	1	33.3 %	1	33.3 %	2	66.7 %	2	66.7 %	1	33.3 %	2	66.7 %	1	33.3 %	0	0.0 %	3	100.0 %

F. MDM Conveyor

Explore

Warnings

Mean (Log CFU/swab) is constant when Batch No. = Batch 3. It will be included in any boxplots produced but other output will be omitted.

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/swab)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics[a]

	Batch No.			Statistic	Std. Error
Mean (Log CFU/swab)	Batch 1	Mean		1.0398	.03976
		95% Confidence Interval for Mean	Lower Bound	.9376	
			Upper Bound	1.1420	
		5% Trimmed Mean		1.0309	
		Median		1.0000	
		Variance		.009	
		Std. Deviation		.09739	
		Minimum		1.00	
		Maximum		1.24	
		Range		.24	
		Interquartile Range		.06	
		Skewness		2.449	.845
		Kurtosis		6.000	1.741
	Batch 2	Mean		1.1733	.11466
		95% Confidence Interval for Mean	Lower Bound	.8785	
			Upper Bound	1.4680	
		5% Trimmed Mean		1.1564	
		Median		1.0000	
		Variance		.079	
		Std. Deviation		.28086	
		Minimum		1.00	
		Maximum		1.65	
		Range		.65	
		Interquartile Range		.45	
		Skewness		1.326	.845
		Kurtosis		.235	1.741

a. Mean (Log CFU/swab) is constant when Batch No. = Batch 3. It has been omitted.

Tests of Normality[b]

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/swab)	Batch 1	.492	6	.000	.496	6	.000
	Batch 2	.398	6	.003	.705	6	.007

a. Lilliefors Significance Correction
b. Mean (Log CFU/swab) is constant when Batch No. = Batch 3. It has been omitted.

Explore

Warnings

LogMean2 is constant when Batch No. = Batch 3. It will be included in any boxplots produced but other output will be omitted.

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics[a]

Batch No.			Statistic	Std. Error
LogMean2	Batch 1	Mean	.0357	.03566
		95% Confidence Interval for Mean — Lower Bound	-.0560	
		95% Confidence Interval for Mean — Upper Bound	.1273	
		5% Trimmed Mean	.0277	
		Median	.0000	
		Variance	.008	
		Std. Deviation	.08734	
		Minimum	.00	
		Maximum	.21	
		Range	.21	
		Interquartile Range	.05	
		Skewness	2.449	.845
		Kurtosis	6.000	1.741
	Batch 2	Mean	.1383	.09025
		95% Confidence Interval for Mean — Lower Bound	-.0937	
		95% Confidence Interval for Mean — Upper Bound	.3703	
		5% Trimmed Mean	.1258	
		Median	.0000	
		Variance	.049	
		Std. Deviation	.22107	
		Minimum	.00	
		Maximum	.50	
		Range	.50	

	Interquartile Range	.37	
	Skewness	1.224	.845
	Kurtosis	-.359	1.741

a. LogMean2 is constant when Batch No. = Batch 3. It has been omitted.

Tests of Normality[b]

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	Batch 1	.492	6	.000	.496	6	.000
	Batch 2	.401	6	.003	.703	6	.007

a. Lilliefors Significance Correction
b. LogMean2 is constant when Batch No. = Batch 3. It has been omitted.

NPar Tests
Kruskal-Wallis Test

Ranks

	Batch No.	N	Mean Rank
Mean (Log CFU/swab)	Batch 1	6	9.33
	Batch 2	6	11.17
	Batch 3	6	8.00
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/swab)
Chi-Square	2.522
df	2
Asymp. Sig.	.283

a. Kruskal Wallis Test
b. Grouping Variable: Batch No.

Explore

Warnings

Mean (Log CFU/swab) is constant when Processing Time (h) = 2 hour. It will be included in any boxplots produced but other output will be omitted.
Mean (Log CFU/swab) is constant when Processing Time (h) = 3 hour. It will be included in any boxplots produced but other output will be omitted.
Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It will be included in any boxplots produced but other output will be omitted.
Mean (Log CFU/swab) is constant when Processing Time (h) = 6 hour. It will be included in any boxplots produced but other output will be omitted.

Processing Time (h)

Case Processing Summary

Processing Time (h)	Cases		
	Valid	Missing	Total

		N	Percent	N	Percent	N
Mean (Log CFU/swab)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3
	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/swab)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics[a,b,c,d]

Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/swab)	1 hour	Mean	1.2092	.11327
		95% Confidence Interval for Mean — Lower Bound	.7218	
		95% Confidence Interval for Mean — Upper Bound	1.6966	
		5% Trimmed Mean	.	
		Median	1.2386	
		Variance	.038	
		Std. Deviation	.19619	
		Minimum	1.00	
		Maximum	1.39	
		Range	.39	
		Interquartile Range	.	
		Skewness	-.658	1.225
		Kurtosis	.	.
	5 hour	Mean	1.2168	.21684
		95% Confidence Interval for Mean — Lower Bound	.2839	
		95% Confidence Interval for Mean — Upper Bound	2.1498	
		5% Trimmed Mean	.	
		Median	1.0000	
		Variance	.141	
		Std. Deviation	.37558	
		Minimum	1.00	
		Maximum	1.65	
		Range	.65	
		Interquartile Range	.	
		Skewness	1.732	1.225
		Kurtosis	.	.

a. Mean (Log CFU/swab) is constant when Processing Time (h) = 2 hour. It has been omitted.
b. Mean (Log CFU/swab) is constant when Processing Time (h) = 3 hour. It has been omitted.

c. Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It has been omitted.
d. Mean (Log CFU/swab) is constant when Processing Time (h) = 6 hour. It has been omitted.

Tests of Normality[b,c,d,e]

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/swab)	1 hour	.226	3	.	.983	3
	5 hour	.385	3	.	.750	3

Tests of Normality[b,c,d,e]

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/swab)	1 hour	.752
	5 hour	.000

a. Lilliefors Significance Correction
b. Mean (Log CFU/swab) is constant when Processing Time (h) = 2 hour. It has been omitted.
c. Mean (Log CFU/swab) is constant when Processing Time (h) = 3 hour. It has been omitted.
d. Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It has been omitted.
e. Mean (Log CFU/swab) is constant when Processing Time (h) = 6 hour. It has been omitted.

Oneway

Descriptives Statistics

Mean (Log CFU/swab)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
1 hour	3	1.2092	.19619	.11327	.7218	1.6966	1.00
2 hour	3	1.0000	.00000	.00000	1.0000	1.0000	1.00
3 hour	3	1.0000	.00000	.00000	1.0000	1.0000	1.00
4 hour	3	1.0000	.00000	.00000	1.0000	1.0000	1.00
5 hour	3	1.2168	.37558	.21684	.2839	2.1498	1.00
6 hour	3	1.0000	.00000	.00000	1.0000	1.0000	1.00
Total	18	1.0710	.17834	.04204	.9823	1.1597	1.00

Descriptives Statistics

Mean (Log CFU/swab)

	Maximum
1 hour	1.39
2 hour	1.00
3 hour	1.00
4 hour	1.00
5 hour	1.65
6 hour	1.00
Total	1.65

ANOVA

Mean (Log CFU/swab)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.182	5	.036	1.214	.360
Within Groups	.359	12	.030		

Total	.541	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/swab)
Tukey HSD

(I) Processing Time (h)	(J) Processing Time (h)	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval
					Lower Bound
	2 hour	.20921	.14124	.681	-.2652
	3 hour	.20921	.14124	.681	-.2652
1 hour	4 hour	.20921	.14124	.681	-.2652
	5 hour	-.00763	.14124	1.000	-.4821
	6 hour	.20921	.14124	.681	-.2652
	1 hour	-.20921	.14124	.681	-.6836
	3 hour	.00000	.14124	1.000	-.4744
2 hour	4 hour	.00000	.14124	1.000	-.4744
	5 hour	-.21684	.14124	.651	-.6913
	6 hour	.00000	.14124	1.000	-.4744
	1 hour	-.20921	.14124	.681	-.6836
	2 hour	.00000	.14124	1.000	-.4744
3 hour	4 hour	.00000	.14124	1.000	-.4744
	5 hour	-.21684	.14124	.651	-.6913
	6 hour	.00000	.14124	1.000	-.4744
	1 hour	-.20921	.14124	.681	-.6836
	2 hour	.00000	.14124	1.000	-.4744
4 hour	3 hour	.00000	.14124	1.000	-.4744
	5 hour	-.21684	.14124	.651	-.6913
	6 hour	.00000	.14124	1.000	-.4744
	1 hour	.00763	.14124	1.000	-.4668
	2 hour	.21684	.14124	.651	-.2576
5 hour	3 hour	.21684	.14124	.651	-.2576
	4 hour	.21684	.14124	.651	-.2576
	6 hour	.21684	.14124	.651	-.2576
	1 hour	-.20921	.14124	.681	-.6836
	2 hour	.00000	.14124	1.000	-.4744
6 hour	3 hour	.00000	.14124	1.000	-.4744
	4 hour	.00000	.14124	1.000	-.4744
	5 hour	-.21684	.14124	.651	-.6913

Multiple Comparisons

Dependent Variable: Mean (Log CFU/swab)
Tukey HSD

(I) Processing Time (h)	(J) Processing Time (h)	95% Confidence Interval
		Upper Bound
	2 hour	.6836
	3 hour	.6836
1 hour	4 hour	.6836
	5 hour	.4668
	6 hour	.6836
	1 hour	.2652
2 hour	3 hour	.4744
	4 hour	.4744

	5 hour	.2576
	6 hour	.4744
	1 hour	.2652
	2 hour	.4744
3 hour	4 hour	.4744
	5 hour	.2576
	6 hour	.4744
	1 hour	.2652
	2 hour	.4744
4 hour	3 hour	.4744
	5 hour	.2576
	6 hour	.4744
	1 hour	.4821
	2 hour	.6913
5 hour	3 hour	.6913
	4 hour	.6913
	6 hour	.6913
	1 hour	.2652
	2 hour	.4744
6 hour	3 hour	.4744
	4 hour	.4744
	5 hour	.2576

Homogeneous Subsets

Mean (Log CFU/swab)

Tukey HSD

Processing Time (h)	N	Subset for alpha = 0.05
		1
2 hour	3	1.0000
3 hour	3	1.0000
4 hour	3	1.0000
6 hour	3	1.0000
1 hour	3	1.2092
5 hour	3	1.2168
Sig.		.651

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 3.000.

Custom Table

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
6	100.0%	0	0.0%	6	100.0%	0	0.0%	6	100.0%	0	0.0%

Custom Table

Table 1

Processing Time (h)																			
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%

G. MSM carcass

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		1.9341	.07991
		95% Confidence Interval for Mean	Lower Bound	1.7287	
			Upper Bound	2.1395	
		5% Trimmed Mean		1.9337	
		Median		1.9375	
		Variance		.038	
		Std. Deviation		.19573	
		Minimum		1.70	
		Maximum		2.18	
		Range		.48	
		Interquartile Range		.40	
		Skewness		-.007	.845
		Kurtosis		-1.971	1.741
	Batch 2	Mean		1.4397	.16843
		95% Confidence Interval for Mean	Lower Bound	1.0067	
			Upper Bound	1.8727	
		5% Trimmed Mean		1.4330	
		Median		1.2940	
		Variance		.170	
		Std. Deviation		.41257	
		Minimum		1.00	
		Maximum		2.00	
		Range		1.00	
		Interquartile Range		.81	
		Skewness		.663	.845
		Kurtosis		-1.674	1.741
	Batch 3	Mean		1.4297	.11943
		95% Confidence Interval for Mean	Lower Bound	1.1227	
			Upper Bound	1.7367	
		5% Trimmed Mean		1.4372	
		Median		1.5268	
		Variance		.086	
		Std. Deviation		.29254	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum	1.00	
		Maximum	1.72	
		Range	.72	
		Interquartile Range	.56	
		Skewness	-.717	.845
		Kurtosis	-1.386	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.172	6	.200*	.933	6	.601
	Batch 2	.253	6	.200*	.875	6	.248
	Batch 3	.222	6	.200*	.895	6	.346

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	1.9341	.19573	.07991	1.7287	2.1395	1.70
Batch 2	6	1.4397	.41257	.16843	1.0067	1.8727	1.00
Batch 3	6	1.4297	.29254	.11943	1.1227	1.7367	1.00
Total	18	1.6012	.38104	.08981	1.4117	1.7906	1.00

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	2.18
Batch 2	2.00
Batch 3	1.72
Total	2.18

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.998	2	.499	5.089	.021
Within Groups	1.471	15	.098		
Total	2.468	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	.49437*	.18077	.038	.0248	.9639
	Batch 3	.50437*	.18077	.035	.0348	.9739
Batch 2	Batch 1	-.49437*	.18077	.038	-.9639	-.0248
	Batch 3	.01000	.18077	.998	-.4595	.4796
Batch 3	Batch 1	-.50437*	.18077	.035	-.9739	-.0348
	Batch 2	-.01000	.18077	.998	-.4796	.4595

*. The mean difference is significant at the 0.05 level.

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05	
		1	2
Batch 3	6	1.4297	
Batch 2	6	1.4397	
Batch 1	6		1.9341
Sig.		.998	1.000

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 6.000.

Explore

Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/g)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3
	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/g)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	1 hour	Mean		1.6429	.29676
		95% Confidence Interval for Mean	Lower Bound	.3660	
			Upper Bound	2.9197	
		5% Trimmed Mean		.	
		Median		1.6021	
		Variance		.264	
		Std. Deviation		.51401	
		Minimum		1.15	
		Maximum		2.18	
		Range		1.03	
		Interquartile Range		.	
		Skewness		.355	1.225
		Kurtosis		.	.
	2 hour	Mean		1.4630	.13303
		95% Confidence Interval for Mean	Lower Bound	.8906	
			Upper Bound	2.0354	
		5% Trimmed Mean		.	
		Median		1.4515	
		Variance		.053	
		Std. Deviation		.23042	
		Minimum		1.24	
		Maximum		1.70	
		Range		.46	
		Interquartile Range		.	
		Skewness		.224	1.225
		Kurtosis		.	.
	3 hour	Mean		1.7168	.28316
		95% Confidence Interval for Mean	Lower Bound	.4985	
			Upper Bound	2.9352	
		5% Trimmed Mean		.	
		Median		2.0000	
		Variance		.241	
		Std. Deviation		.49045	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	3 hour	Minimum		1.15	
		Maximum		2.00	
		Range		.85	
		Interquartile Range		.	
		Skewness		-1.732	1.225
		Kurtosis		.	.
	4 hour	Mean		1.3713	.37131
		95% Confidence Interval for Mean	Lower Bound	-.2263	
			Upper Bound	2.9690	
		5% Trimmed Mean		.	
		Median		1.0000	

		Variance		.414	
		Std. Deviation		.64314	
		Minimum		1.00	
		Maximum		2.11	
		Range		1.11	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
		Mean		1.8084	.07927
		95% Confidence Interval for Mean	Lower Bound	1.4673	
			Upper Bound	2.1495	
		5% Trimmed Mean		.	
		Median		1.8751	
		Variance		.019	
	5 hour	Std. Deviation		.13730	
		Minimum		1.65	
		Maximum		1.90	
		Range		.25	
		Interquartile Range		.	
		Skewness		-1.670	1.225
		Kurtosis		.	.
	6 hour	Mean		1.6045	.12759

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	6 hour	95% Confidence Interval for Mean	Lower Bound	1.0555	
			Upper Bound	2.1534	
		5% Trimmed Mean		.	
		Median		1.7236	
		Variance		.049	
		Std. Deviation		.22099	
		Minimum		1.35	
		Maximum		1.74	
		Range		.39	
		Interquartile Range		.	
		Skewness		-1.721	1.225
		Kurtosis		.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/g)	1 hour	.198	3	.	.995	3
	2 hour	.187	3	.	.998	3
	3 hour	.385	3	.	.750	3
	4 hour	.385	3	.	.750	3
	5 hour	.353	3	.	.823	3
	6 hour	.372	3	.	.782	3

Tests of Normality

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/g)	1 hour	.869
	2 hour	.918
	3 hour	.000
	4 hour	.000
	5 hour	.171
	6 hour	.073

a. Lilliefors Significance Correction

NPar Tests

Descriptive Statistics

	N	Mean	Std. Deviation	Minimum	Maximum
Mean (Log CFU/g)	18	1.6012	.38104	1.00	2.18
Processing Time (h)	18	3.50	1.757	1	6

Kruskal-Wallis Test

Ranks

	Processing Time (h)	N	Mean Rank
Mean (Log CFU/g)	1 hour	3	5.17
	2 hour	3	4.33
	3 hour	3	5.50
	Total	9	

Test Statistics[a,b]

	Mean (Log CFU/g)
Chi-Square	.294
df	2
Asymp. Sig.	.863

a. Kruskal Wallis Test
b. Grouping Variable: Processing Time (h)

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
4	66.7%	2	33.3%	6	100.0%	0	0.0%	6	100.0%	0	0.0%

Custom Tables

Table 1

Processing Time (h)																							
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
2	66.7%	1	33.3%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	2	66.7%	1	33.3%	3	100.0%	0	0.0%	3	100.0%	0	0.0%

H. Inside MDM

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/swab)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/swab)	Batch 1	Mean		2.2952	.12630
		95% Confidence Interval for Mean	Lower Bound	1.9706	
			Upper Bound	2.6199	
		5% Trimmed Mean		2.2961	
		Median		2.3495	
		Variance		.096	
		Std. Deviation		.30936	
		Minimum		1.88	
		Maximum		2.70	
		Range		.82	
		Interquartile Range		.58	
		Skewness		-.249	.845
		Kurtosis		-1.119	1.741
	Batch 2	Mean		1.7347	.29136
		95% Confidence Interval for Mean	Lower Bound	.9857	
			Upper Bound	2.4836	
		5% Trimmed Mean		1.7205	
		Median		1.6391	
		Variance		.509	
		Std. Deviation		.71367	
		Minimum		1.00	
		Maximum		2.72	
		Range		1.72	
		Interquartile Range		1.49	
		Skewness		.388	.845
		Kurtosis		-1.542	1.741
	Batch 3	Mean		1.6221	.23255
		95% Confidence Interval for Mean	Lower Bound	1.0243	
			Upper Bound	2.2199	
		5% Trimmed Mean		1.6126	
		Median		1.3891	
		Variance		.324	

	Std. Deviation	.56962	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/swab)	Batch 3	Minimum	1.00	
		Maximum	2.41	
		Range	1.41	
		Interquartile Range	1.06	
		Skewness	.685	.845
		Kurtosis	-1.526	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/swab)	Batch 1	.174	6	.200*	.961	6	.828
	Batch 2	.182	6	.200*	.908	6	.423
	Batch 3	.267	6	.200*	.870	6	.228

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/swab)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	2.2952	.30936	.12630	1.9706	2.6199	1.88
Batch 2	6	1.7347	.71367	.29136	.9857	2.4836	1.00
Batch 3	6	1.6221	.56962	.23255	1.0243	2.2199	1.00
Total	18	1.8840	.60428	.14243	1.5835	2.1845	1.00

Descriptives Statistics

Mean (Log CFU/swab)

	Maximum
Batch 1	2.70
Batch 2	2.72
Batch 3	2.41
Total	2.72

ANOVA

Mean (Log CFU/swab)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	1.560	2	.780	2.518	.114
Within Groups	4.648	15	.310		
Total	6.208	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/swab)

Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	.56057	.32137	.222	-.2742	1.3953
	Batch 3	.67315	.32137	.125	-.1616	1.5079
Batch 2	Batch 1	-.56057	.32137	.222	-1.3953	.2742
	Batch 3	.11259	.32137	.935	-.7222	.9473
Batch 3	Batch 1	-.67315	.32137	.125	-1.5079	.1616
	Batch 2	-.11259	.32137	.935	-.9473	.7222

Homogeneous Subsets

Mean (Log CFU/swab)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 3	6	1.6221
Batch 2	6	1.7347
Batch 1	6	2.2952
Sig.		.125

Means for groups in homogeneous subsets are displayed.

a. Uses Harmonic Mean Sample Size = 6.000.

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
2	33.3%	4	66.7%	4	66.7%	2	33.3%	4	66.7%	2	33.3%

I. Fresh Skin

Explore
Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
LogMean2	Batch 1	Mean		.5824	.08667
		95% Confidence Interval for Mean	Lower Bound	.3596	
			Upper Bound	.8052	
		5% Trimmed Mean		.5862	
		Median		.6572	
		Variance		.045	
		Std. Deviation		.21229	
		Minimum		.26	
		Maximum		.83	
		Range		.57	
		Interquartile Range		.37	
		Skewness		-.678	.845
		Kurtosis		-.759	1.741
	Batch 2	Mean		.4809	.15884
		95% Confidence Interval for Mean	Lower Bound	.0726	
			Upper Bound	.8892	
		5% Trimmed Mean		.4840	
		Median		.6329	
		Variance		.151	
		Std. Deviation		.38907	
		Minimum		.00	
		Maximum		.91	
		Range		.91	
		Interquartile Range		.76	
		Skewness		-.610	.845
		Kurtosis		-1.797	1.741
	Batch 3	Mean		.8886	.11132
		95% Confidence Interval for Mean	Lower Bound	.6025	
			Upper Bound	1.1748	
		5% Trimmed Mean		.8697	
		Median		.7661	
		Variance		.074	
		Std. Deviation		.27268	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
LogMean2	Batch 3	Minimum	.70	
		Maximum	1.42	
		Range	.71	
		Interquartile Range	.34	
		Skewness	1.964	.845
		Kurtosis	3.830	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	Batch 1	.304	6	.086	.905	6	.407
	Batch 2	.240	6	.200*	.840	6	.131
	Batch 3	.334	6	.035	.732	6	.013

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

NPar Tests
Kruskal-Wallis Test

Ranks

	Batch No.	N	Mean Rank
Mean (Log CFU/g)	Batch 1	6	7.17
	Batch 2	6	7.50
	Batch 3	6	13.83
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/g)
Chi-Square	5.960
df	2
Asymp. Sig.	.051

a. Kruskal Wallis Test
b. Grouping Variable: Batch No.

Explore
Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/g)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3

	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/g)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics

Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	1 hour	Mean	1.4979	.29368
		95% Confidence Interval for Mean — Lower Bound	.2343	
		95% Confidence Interval for Mean — Upper Bound	2.7616	
		5% Trimmed Mean	.	
		Median	1.4771	
		Variance	.259	
		Std. Deviation	.50868	
		Minimum	1.00	
		Maximum	2.02	
		Range	1.02	
		Interquartile Range	.	
		Skewness	.184	1.225
		Kurtosis	.	.
	2 hour	Mean	1.9733	.34979
		95% Confidence Interval for Mean — Lower Bound	.4682	
		95% Confidence Interval for Mean — Upper Bound	3.4783	
		5% Trimmed Mean	.	
		Median	2.1417	
		Variance	.367	
		Std. Deviation	.60586	
		Minimum	1.30	
		Maximum	2.48	
		Range	1.18	
		Interquartile Range	.	
		Skewness	-1.154	1.225
		Kurtosis	.	.
	3 hour	Mean	1.8392	.46065
		95% Confidence Interval for Mean — Lower Bound	-.1428	
		95% Confidence Interval for Mean — Upper Bound	3.8212	
		5% Trimmed Mean	.	
		Median	1.9294	
		Variance	.637	

		Std. Deviation		.79786	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	3 hour	Minimum		1.00	
		Maximum		2.59	
		Range		1.59	
		Interquartile Range		.	
		Skewness		-.503	1.225
		Kurtosis		.	.
		Mean		2.0156	.04445
		95% Confidence Interval for Mean	Lower Bound	1.8243	
			Upper Bound	2.2068	
		5% Trimmed Mean		.	
		Median		2.0396	
		Variance		.006	
	4 hour	Std. Deviation		.07699	
		Minimum		1.93	
		Maximum		2.08	
		Range		.15	
		Interquartile Range		.	
		Skewness		-1.268	1.225
		Kurtosis		.	.
		Mean		2.8203	.65435
		95% Confidence Interval for Mean	Lower Bound	.0048	
			Upper Bound	5.6357	
		5% Trimmed Mean		.	
		Median		2.3010	
		Variance		1.285	
	5 hour	Std. Deviation		1.13337	
		Minimum		2.04	
		Maximum		4.12	
		Range		2.08	
		Interquartile Range		.	
		Skewness		1.629	1.225
		Kurtosis		.	.
	6 hour	Mean		1.9666	.12312

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	6 hour	95% Confidence Interval for Mean	Lower Bound	1.4368	
			Upper Bound	2.4963	
		5% Trimmed Mean		.	
		Median		2.0000	
		Variance		.045	
		Std. Deviation		.21325	
		Minimum		1.74	
		Maximum		2.16	
		Range		.42	
		Interquartile Range		.	

	Skewness	-.688	1.225
	Kurtosis	.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/g)	1 hour	.183	3	.	.999	3
	2 hour	.276	3	.	.942	3
	3 hour	.212	3	.	.990	3
	4 hour	.289	3	.	.927	3
	5 hour	.343	3	.	.843	3
	6 hour	.229	3	.	.982	3

Tests of Normality

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/g)	1 hour	.932
	2 hour	.536
	3 hour	.813
	4 hour	.477
	5 hour	.221
	6 hour	.740

a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
1 hour	3	1.4979	.50868	.29368	.2343	2.7616	1.00
2 hour	3	1.9733	.60586	.34979	.4682	3.4783	1.30
3 hour	3	1.8392	.79786	.46065	-.1428	3.8212	1.00
4 hour	3	2.0156	.07699	.04445	1.8243	2.2068	1.93
5 hour	3	2.8203	1.13337	.65435	.0048	5.6357	2.04
6 hour	3	1.9666	.21325	.12312	1.4368	2.4963	1.74
Total	18	2.0188	.68809	.16218	1.6766	2.3610	1.00

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
1 hour	2.02
2 hour	2.48
3 hour	2.59
4 hour	2.08
5 hour	4.12
6 hour	2.16
Total	4.12

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	2.852	5	.570	1.317	.321
Within Groups	5.197	12	.433		
Total	8.049	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Processing Time (h)	(J) Processing Time (h)	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval
					Lower Bound
	2 hour	-.47532	.53731	.943	-2.2801
	3 hour	-.34121	.53731	.986	-2.1460
1 hour	4 hour	-.51761	.53731	.921	-2.3224
	5 hour	-1.32235	.53731	.210	-3.1271
	6 hour	-.46861	.53731	.946	-2.2734
	1 hour	.47532	.53731	.943	-1.3295
	3 hour	.13411	.53731	1.000	-1.6707
2 hour	4 hour	-.04229	.53731	1.000	-1.8471
	5 hour	-.84703	.53731	.627	-2.6518
	6 hour	.00671	.53731	1.000	-1.7981
	1 hour	.34121	.53731	.986	-1.4636
	2 hour	-.13411	.53731	1.000	-1.9389
3 hour	4 hour	-.17640	.53731	.999	-1.9812
	5 hour	-.98114	.53731	.486	-2.7859
	6 hour	-.12740	.53731	1.000	-1.9322
	1 hour	.51761	.53731	.921	-1.2872
	2 hour	.04229	.53731	1.000	-1.7625
4 hour	3 hour	.17640	.53731	.999	-1.6284
	5 hour	-.80474	.53731	.672	-2.6095
	6 hour	.04900	.53731	1.000	-1.7558
	1 hour	1.32235	.53731	.210	-.4824
	2 hour	.84703	.53731	.627	-.9578
5 hour	3 hour	.98114	.53731	.486	-.8236
	4 hour	.80474	.53731	.672	-1.0000
	6 hour	.85374	.53731	.620	-.9510
	1 hour	.46861	.53731	.946	-1.3362
	2 hour	-.00671	.53731	1.000	-1.8115
6 hour	3 hour	.12740	.53731	1.000	-1.6774
	4 hour	-.04900	.53731	1.000	-1.8538
	5 hour	-.85374	.53731	.620	-2.6585

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Processing Time (h)	(J) Processing Time (h)	95% Confidence Interval
		Upper Bound
	2 hour	1.3295
1 hour	3 hour	1.4636
	4 hour	1.2872

	5 hour	.4824
	6 hour	1.3362
	1 hour	2.2801
	3 hour	1.9389
2 hour	4 hour	1.7625
	5 hour	.9578
	6 hour	1.8115
	1 hour	2.1460
	2 hour	1.6707
3 hour	4 hour	1.6284
	5 hour	.8236
	6 hour	1.6774
	1 hour	2.3224
	2 hour	1.8471
4 hour	3 hour	1.9812
	5 hour	1.0000
	6 hour	1.8538
	1 hour	3.1271
	2 hour	2.6518
5 hour	3 hour	2.7859
	4 hour	2.6095
	6 hour	2.6585
	1 hour	2.2734
	2 hour	1.7981
6 hour	3 hour	1.9322
	4 hour	1.7558
	5 hour	.9510

Homogeneous Subsets

Mean (Log CFU/g)

Tukey HSD

Processing Time (h)	N	Subset for alpha = 0.05
		1
1 hour	3	1.4979
3 hour	3	1.8392
6 hour	3	1.9666
2 hour	3	1.9733
4 hour	3	2.0156
5 hour	3	2.8203
Sig.		.210

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 3.000.

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
5	83.3%	1	16.7%	5	83.3%	1	16.7%	1	16.7%	5	83.3%

Custom Tables

Table 1

Processing Time (h)																			
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	100.0 %	0	0.0 %	1	33.3 %	2	66.7 %	2	66.7 %	1	33.3 %	2	66.7 %	1	33.3 %	1	33.3 %	2	66.7 %	2	66.7 %	1	33.3 %

J. Skinner Conveyor

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/swab)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/swab)	Batch 1	Mean		1.2481	.15927
		95% Confidence Interval for Mean	Lower Bound	.8387	
			Upper Bound	1.6576	
		5% Trimmed Mean		1.2285	
		Median		1.0000	
		Variance		.152	
		Std. Deviation		.39012	
		Minimum		1.00	
		Maximum		1.85	
		Range		.85	
		Interquartile Range		.69	
		Skewness		1.092	.845
		Kurtosis		-1.132	1.741
	Batch 2	Mean		1.1548	.08107
		95% Confidence Interval for Mean	Lower Bound	.9464	
			Upper Bound	1.3632	
		5% Trimmed Mean		1.1455	
		Median		1.0753	
		Variance		.039	
		Std. Deviation		.19859	
		Minimum		1.00	
		Maximum		1.48	
		Range		.48	
		Interquartile Range		.35	
		Skewness		.977	.845
		Kurtosis		-.410	1.741
	Batch 3	Mean		1.1046	.11159
		95% Confidence Interval for Mean	Lower Bound	.8178	
			Upper Bound	1.3915	
		5% Trimmed Mean		1.0897	
		Median		1.0000	
		Variance		.075	
		Std. Deviation		.27334	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/swab)	Batch 3	Minimum	.85	
		Maximum	1.63	
		Range	.78	
		Interquartile Range	.31	
		Skewness	1.809	.845
		Kurtosis	3.710	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/swab)	Batch 1	.404	6	.003	.692	6	.005
	Batch 2	.282	6	.147	.830	6	.108
	Batch 3	.316	6	.062	.788	6	.046

a. Lilliefors Significance Correction

Explore
Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
LogMean2	Batch 1	Mean		.1849	.11795
		95% Confidence Interval for Mean	Lower Bound	-.1183	
			Upper Bound	.4881	
		5% Trimmed Mean		.1713	
		Median		.0000	
		Variance		.083	
		Std. Deviation		.28893	
		Minimum		.00	
		Maximum		.61	
		Range		.61	
		Interquartile Range		.52	
		Skewness		1.043	.845
		Kurtosis		-1.424	1.741
	Batch 2	Mean		.1322	.06737
		95% Confidence Interval for Mean	Lower Bound	-.0409	
			Upper Bound	.3054	
		5% Trimmed Mean		.1253	
		Median		.0701	
		Variance		.027	
		Std. Deviation		.16502	
		Minimum		.00	

		Maximum		.39	
		Range		.39	
		Interquartile Range		.29	
		Skewness		.831	.845
		Kurtosis		-.933	1.741
		Mean		.0774	.09086
		95% Confidence Interval for Mean	Lower Bound	-.1562	
			Upper Bound	.3109	
	Batch 3	5% Trimmed Mean		.0680	
		Median		.0000	
		Variance		.050	
		Std. Deviation		.22255	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
LogMean2	Batch 3	Minimum	-.16	
		Maximum	.49	
		Range	.65	
		Interquartile Range	.27	
		Skewness	1.463	.845
		Kurtosis	2.784	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	Batch 1	.406	6	.003	.684	6	.004
	Batch 2	.289	6	.129	.834	6	.117
	Batch 3	.303	6	.091	.845	6	.143

a. Lilliefors Significance Correction

NPar Tests
Kruskal-Wallis Test

Ranks

	Batch No.	N	Mean Rank
Mean (Log CFU/swab)	Batch 1	6	10.17
	Batch 2	6	10.17
	Batch 3	6	8.17
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/swab)
Chi-Square	.677
df	2
Asymp. Sig.	.713

a. Kruskal Wallis Test
b. Grouping Variable: Batch No.

Explore

Warnings

Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It will be included in any boxplots produced but other output will be omitted.

Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/swab)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3
	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/swab)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics[a]

Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/swab)	1 hour	Mean	1.2092	.20921
		95% Confidence Interval for Mean — Lower Bound	.3090	
		95% Confidence Interval for Mean — Upper Bound	2.1094	
		5% Trimmed Mean	.	
		Median	1.0000	
		Variance	.131	
		Std. Deviation	.36237	
		Minimum	1.00	
		Maximum	1.63	
		Range	.63	
		Interquartile Range	.	
		Skewness	1.732	1.225
		Kurtosis	.	.
	2 hour	Mean	1.4223	.14376
		95% Confidence Interval for Mean — Lower Bound	.8038	
		95% Confidence Interval for Mean — Upper Bound	2.0409	
		5% Trimmed Mean	.	
		Median	1.4771	
		Variance	.062	

		Std. Deviation		.24899	
		Minimum		1.15	
		Maximum		1.64	
		Range		.49	
		Interquartile Range		.	
		Skewness		-.942	1.225
		Kurtosis		.	.
		Mean		1.0502	.05017
		95% Confidence Interval for Mean	Lower Bound	.8343	
			Upper Bound	1.2660	
	3 hour	5% Trimmed Mean		.	
		Median		1.0000	
		Variance		.008	
		Std. Deviation		.08690	

Descriptives Statistics[a]

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/swab)	3 hour	Minimum		1.00	
		Maximum		1.15	
		Range		.15	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
		Mean		.9498	.05017
		95% Confidence Interval for Mean	Lower Bound	.7340	
			Upper Bound	1.1657	
		5% Trimmed Mean		.	
		Median		1.0000	
		Variance		.008	
	5 hour	Std. Deviation		.08690	
		Minimum		.85	
		Maximum		1.00	
		Range		.15	
		Interquartile Range		.	
		Skewness		-1.732	1.225
		Kurtosis		.	.
		Mean		1.3835	.24867
		95% Confidence Interval for Mean	Lower Bound	.3136	
			Upper Bound	2.4534	
		5% Trimmed Mean		.	
		Median		1.3010	
		Variance		.186	
	6 hour	Std. Deviation		.43071	
		Minimum		1.00	
		Maximum		1.85	
		Range		.85	
		Interquartile Range		.	
		Skewness		.830	1.225
		Kurtosis		.	.

a. Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It has been omitted.

Tests of Normality[b]

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/swab)	1 hour	.385	3	.	.750	3
	2 hour	.254	3	.	.964	3
	3 hour	.385	3	.	.750	3
	5 hour	.385	3	.	.750	3
	6 hour	.243	3	.	.972	3

Tests of Normality[b]

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/swab)	1 hour	.000
	2 hour	.634
	3 hour	.000
	5 hour	.000
	6 hour	.682

a. Lilliefors Significance Correction
b. Mean (Log CFU/swab) is constant when Processing Time (h) = 4 hour. It has been omitted.

Explore

Warnings

LogMean2 is constant when Processing Time (h) = 4 hour. It will be included in any boxplots produced but other output will be omitted.

Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	1 hour	3	100.0%	0	0.0%	3	100.0%
	2 hour	3	100.0%	0	0.0%	3	100.0%
	3 hour	3	100.0%	0	0.0%	3	100.0%
	4 hour	3	100.0%	0	0.0%	3	100.0%
	5 hour	3	100.0%	0	0.0%	3	100.0%
	6 hour	3	100.0%	0	0.0%	3	100.0%

Descriptives Statistics[a]

	Processing Time (h)			Statistic	Std. Error
LogMean2	1 hour	Mean		.1624	.16238
		95% Confidence Interval for Mean	Lower Bound	-.5363	
			Upper Bound	.8610	
		5% Trimmed Mean		.	
		Median		.0000	
		Variance		.079	

		Std. Deviation		.28124	
		Minimum		.00	
		Maximum		.49	
		Range		.49	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
		Mean		.3415	.10507
		95% Confidence Interval for Mean	Lower Bound	-.1105	
			Upper Bound	.7936	
		5% Trimmed Mean		.	
		Median		.3901	
		Variance		.033	
	2 hour	Std. Deviation		.18198	
		Minimum		.14	
		Maximum		.49	
		Range		.35	
		Interquartile Range		.	
		Skewness		-1.115	1.225
		Kurtosis		.	.
		Mean		.0467	.04674
		95% Confidence Interval for Mean	Lower Bound	-.1544	
			Upper Bound	.2478	
	3 hour	5% Trimmed Mean		.	
		Median		.0000	
		Variance		.007	
		Std. Deviation		.08095	

Descriptives Statistics[a]

	Processing Time (h)			Statistic	Std. Error
LogMean2	3 hour	Minimum		.00	
		Maximum		.14	
		Range		.14	
		Interquartile Range		.	
		Skewness		1.732	1.225
		Kurtosis		.	.
		Mean		-.0544	.05437
		95% Confidence Interval for Mean	Lower Bound	-.2883	
			Upper Bound	.1796	
		5% Trimmed Mean		.	
		Median		.0000	
		Variance		.009	
	5 hour	Std. Deviation		.09418	
		Minimum		-.16	
		Maximum		.00	
		Range		.16	
		Interquartile Range		.	
		Skewness		-1.732	1.225
		Kurtosis		.	.
	6 hour	Mean		.2927	.17812

	95% Confidence Interval for Mean	Lower Bound	-.4737	
		Upper Bound	1.0591	
	5% Trimmed Mean		.	
	Median		.2632	
	Variance		.095	
	Std. Deviation		.30852	
	Minimum		.00	
	Maximum		.61	
	Range		.61	
	Interquartile Range		.	
	Skewness		.427	1.225
	Kurtosis		.	.

a. LogMean2 is constant when Processing Time (h) = 4 hour. It has been omitted.

Tests of Normality[b]

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	1 hour	.385	3	.	.750	3	.000
	2 hour	.272	3	.	.947	3	.555
	3 hour	.385	3	.	.750	3	.000
	5 hour	.385	3	.	.750	3	.000
	6 hour	.205	3	.	.993	3	.841

a. Lilliefors Significance Correction
b. LogMean2 is constant when Processing Time (h) = 4 hour. It has been omitted.

NPar Tests
Kruskal-Wallis Test

Ranks

	Processing Time (h)	N	Mean Rank
Mean (Log CFU/swab)	1 hour	3	9.67
	2 hour	3	14.83
	3 hour	3	8.50
	4 hour	3	6.50
	5 hour	3	4.67
	6 hour	3	12.83
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/swab)
Chi-Square	9.266
df	5
Asymp. Sig.	.099

a. Kruskal Wallis Test
b. Grouping Variable: Processing Time (h)

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
6	100.0%	0	0.0%	6	100.0%	0	0.0%	6	100.0%	0	0.0%

Custom Tables

Table 1

Processing Time (h)																			
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%	3	100.0%	0	0.0%

K. Fresh SO BF

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/g)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/g)	Batch 1	Mean		2.0602	.12035
		95% Confidence Interval for Mean	Lower Bound	1.7508	
			Upper Bound	2.3696	
		5% Trimmed Mean		2.0490	
		Median		2.0257	
		Variance		.087	
		Std. Deviation		.29480	
		Minimum		1.72	
		Maximum		2.60	
		Range		.88	
		Interquartile Range		.36	
		Skewness		1.329	.845
		Kurtosis		2.792	1.741
	Batch 2	Mean		2.3300	.20604
		95% Confidence Interval for Mean	Lower Bound	1.8003	
			Upper Bound	2.8596	
		5% Trimmed Mean		2.3277	
		Median		2.2741	
		Variance		.255	
		Std. Deviation		.50469	
		Minimum		1.77	
		Maximum		2.93	
		Range		1.16	
		Interquartile Range		1.00	
		Skewness		.153	.845
		Kurtosis		-2.533	1.741
	Batch 3	Mean		1.8517	.22992
		95% Confidence Interval for Mean	Lower Bound	1.2607	
			Upper Bound	2.4428	
		5% Trimmed Mean		1.8574	
		Median		1.7993	
		Variance		.317	
		Std. Deviation		.56318	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/g)	Batch 3	Minimum	1.00	
		Maximum	2.60	
		Range	1.60	
		Interquartile Range	.95	
		Skewness	-.186	.845
		Kurtosis	-.009	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/g)	Batch 1	.296	6	.110	.889	6	.314
	Batch 2	.238	6	.200*	.879	6	.265
	Batch 3	.184	6	.200*	.971	6	.898

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/g)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	2.0602	.29480	.12035	1.7508	2.3696	1.72
Batch 2	6	2.3300	.50469	.20604	1.8003	2.8596	1.77
Batch 3	6	1.8517	.56318	.22992	1.2607	2.4428	1.00
Total	18	2.0806	.48409	.11410	1.8399	2.3214	1.00

Descriptives Statistics

Mean (Log CFU/g)

	Maximum
Batch 1	2.60
Batch 2	2.93
Batch 3	2.60
Total	2.93

ANOVA

Mean (Log CFU/g)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.690	2	.345	1.571	.240
Within Groups	3.294	15	.220		
Total	3.984	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/g)
Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	-.26975	.27055	.590	-.9725	.4330
	Batch 3	.20848	.27055	.726	-.4943	.9112
Batch 2	Batch 1	.26975	.27055	.590	-.4330	.9725
	Batch 3	.47823	.27055	.214	-.2245	1.1810
Batch 3	Batch 1	-.20848	.27055	.726	-.9112	.4943
	Batch 2	-.47823	.27055	.214	-1.1810	.2245

Homogeneous Subsets

Mean (Log CFU/g)
Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 3	6	1.8517
Batch 1	6	2.0602
Batch 2	6	2.3300
Sig.		.214

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 6.000.

Explore

Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/g)	1 hour	3	100.0%	0	0.0%	3
	2 hour	3	100.0%	0	0.0%	3
	3 hour	3	100.0%	0	0.0%	3
	4 hour	3	100.0%	0	0.0%	3
	5 hour	3	100.0%	0	0.0%	3
	6 hour	3	100.0%	0	0.0%	3

Case Processing Summary

	Processing Time (h)	Cases
		Total
		Percent
Mean (Log CFU/g)	1 hour	100.0%
	2 hour	100.0%
	3 hour	100.0%
	4 hour	100.0%
	5 hour	100.0%
	6 hour	100.0%

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	1 hour	Mean		1.8626	.13735
		95% Confidence Interval for Mean	Lower Bound	1.2716	
			Upper Bound	2.4535	
		5% Trimmed Mean		.	
		Median		1.9911	
		Variance		.057	
		Std. Deviation		.23790	
		Minimum		1.59	
		Maximum		2.01	
		Range		.42	
		Interquartile Range		.	
		Skewness		-1.722	1.225
		Kurtosis		.	.
	2 hour	Mean		1.7559	.01615
		95% Confidence Interval for Mean	Lower Bound	1.6864	
			Upper Bound	1.8254	
		5% Trimmed Mean		.	
		Median		1.7720	
		Variance		.001	
		Std. Deviation		.02798	
		Minimum		1.72	
		Maximum		1.77	
		Range		.05	
		Interquartile Range		.	
		Skewness		-1.732	1.225
		Kurtosis		.	.
	3 hour	Mean		2.7098	.10944
		95% Confidence Interval for Mean	Lower Bound	2.2389	
			Upper Bound	3.1807	
		5% Trimmed Mean		.	
		Median		2.6021	
		Variance		.036	
		Std. Deviation		.18956	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	3 hour	Minimum		2.60	
		Maximum		2.93	
		Range		.33	
		Interquartile Range		.	
		Skewness		1.731	1.225
		Kurtosis		.	.
	4 hour	Mean		1.8718	.02280
		95% Confidence Interval for Mean	Lower Bound	1.7737	
			Upper Bound	1.9699	
		5% Trimmed Mean		.	
		Median		1.8891	
		Variance		.002	
		Std. Deviation		.03948	

		Minimum		1.83	
		Maximum		1.90	
		Range		.07	
		Interquartile Range		.	
		Skewness		-1.593	1.225
		Kurtosis		.	.
		Mean		1.9767	.53464
		95% Confidence Interval for Mean	Lower Bound	.3237	
			Upper Bound	4.2770	
		5% Trimmed Mean		.	
		Median		2.0880	
		Variance		.858	
	5 hour	Std. Deviation		.92602	
		Minimum		1.00	
		Maximum		2.84	
		Range		1.84	
		Interquartile Range		.	
		Skewness		-.533	1.225
		Kurtosis		.	.
	6 hour	Mean		2.3072	.13855

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
Mean (Log CFU/g)	6 hour	95% Confidence Interval for Mean	Lower Bound	1.7111	
			Upper Bound	2.9033	
		5% Trimmed Mean		.	
		Median		2.3217	
		Variance		.058	
		Std. Deviation		.23998	
		Minimum		2.06	
		Maximum		2.54	
		Range		.48	
		Interquartile Range		.	
		Skewness		-.271	1.225
		Kurtosis		.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/g)	1 hour	.372	3	.	.781	3
	2 hour	.385	3	.	.750	3
	3 hour	.382	3	.	.758	3
	4 hour	.336	3	.	.856	3
	5 hour	.215	3	.	.989	3
	6 hour	.191	3	.	.997	3

Tests of Normality

	Processing Time (h)	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/g)	1 hour	.070

	2 hour	.000
	3 hour	.017
	4 hour	.257
	5 hour	.801
	6 hour	.900

a. Lilliefors Significance Correction

Explore

Processing Time (h)

Case Processing Summary

	Processing Time (h)	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	1 hour	3	100.0%	0	0.0%	3	100.0%
	2 hour	3	100.0%	0	0.0%	3	100.0%
	3 hour	3	100.0%	0	0.0%	3	100.0%
	4 hour	3	100.0%	0	0.0%	3	100.0%
	5 hour	3	100.0%	0	0.0%	3	100.0%
	6 hour	3	100.0%	0	0.0%	3	100.0%

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	1 hour	Mean		.6162	.07689
		95% Confidence Interval for Mean	Lower Bound	.2854	
			Upper Bound	.9470	
		5% Trimmed Mean		.	
		Median		.6887	
		Variance		.018	
		Std. Deviation		.13318	
		Minimum		.46	
		Maximum		.70	
		Range		.23	
		Interquartile Range		.	
		Skewness		-1.724	1.225
		Kurtosis		.	.
	2 hour	Mean		.5629	.00924
		95% Confidence Interval for Mean	Lower Bound	.5231	
			Upper Bound	.6027	
		5% Trimmed Mean		.	
		Median		.5721	
		Variance		.000	
		Std. Deviation		.01601	
		Minimum		.54	
		Maximum		.57	
		Range		.03	
		Interquartile Range		.	
		Skewness		-1.732	1.225
		Kurtosis		.	.

		Mean		.9953	.03964
		95% Confidence Interval for Mean	Lower Bound	.8247	
			Upper Bound	1.1658	
	3 hour	5% Trimmed Mean		.	
		Median		.9563	
		Variance		.005	
		Std. Deviation		.06865	

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	3 hour	Minimum		.95	
		Maximum		1.07	
		Range		.12	
		Interquartile Range		.	
		Skewness		1.731	1.225
		Kurtosis		.	.
		Mean		.6267	.01225
		95% Confidence Interval for Mean	Lower Bound	.5740	
			Upper Bound	.6794	
		5% Trimmed Mean		.	
		Median		.6361	
		Variance		.000	
	4 hour	Std. Deviation		.02121	
		Minimum		.60	
		Maximum		.64	
		Range		.04	
		Interquartile Range		.	
		Skewness		-1.598	1.225
		Kurtosis		.	.
		Mean		.5936	.30984
		95% Confidence Interval for Mean	Lower Bound	-.7396	
			Upper Bound	1.9267	
		5% Trimmed Mean		.	
		Median		.7362	
		Variance		.288	
	5 hour	Std. Deviation		.53666	
		Minimum		.00	
		Maximum		1.04	
		Range		1.04	
		Interquartile Range		.	
		Skewness		-1.112	1.225
		Kurtosis		.	.
	6 hour	Mean		.8324	.06058

Descriptives Statistics

	Processing Time (h)			Statistic	Std. Error
LogMean2	6 hour	95% Confidence Interval for Mean	Lower Bound	.5717	
			Upper Bound	1.0931	
		5% Trimmed Mean		.	
		Median		.8423	
		Variance		.011	

	Std. Deviation	.10493	
	Minimum	.72	
	Maximum	.93	
	Range	.21	
	Interquartile Range	.	
	Skewness	-.422	1.225
	Kurtosis	.	.

Tests of Normality

	Processing Time (h)	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	1 hour	.374	3	.	.778	3	.062
	2 hour	.385	3	.	.750	3	.000
	3 hour	.382	3	.	.758	3	.018
	4 hour	.337	3	.	.854	3	.252
	5 hour	.271	3	.	.947	3	.556
	6 hour	.204	3	.	.993	3	.843

a. Lilliefors Significance Correction

NPar Tests

Descriptive Statistics

	N	Mean	Std. Deviation	Minimum	Maximum
Mean (Log CFU/g)	18	2.0806	.48409	1.00	2.93
Processing Time (h)	18	3.5000	1.75734	1.00	6.00

Kruskal-Wallis Test

Ranks

	Processing Time (h)	N	Mean Rank
Mean (Log CFU/g)	1 hour	3	7.00
	2 hour	3	4.00
	3 hour	3	16.33
	4 hour	3	7.00
	5 hour	3	10.00
	6 hour	3	12.67
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/g)
Chi-Square	10.508
df	5
Asymp. Sig.	.062

a. Kruskal Wallis Test
b. Grouping Variable: Processing Time (h)

Custom Tables

Table 1

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	50.0%	3	50.0%	3	50.0%	3	50.0%	4	66.7%	2	33.3%

Custom Tables

Table 1

Processing Time (h)																							
1 hour				2 hour				3 hour				4 hour				5 hour				6 hour			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	100.0 %	0	0.0 %	3	100.0 %	0	0.0 %	0	0.0 %	3	100.0 %	3	100.0 %	0	0.0 %	1	33.3 %	2	66.7 %	0	0.0 %	3	100.0 %

L. Rubber Fingers

Explore

Batch No.

Case Processing Summary

	Batch No.	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
Mean (Log CFU/swab)	Batch 1	6	100.0%	0	0.0%	6	100.0%
	Batch 2	6	100.0%	0	0.0%	6	100.0%
	Batch 3	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Batch No.			Statistic	Std. Error
Mean (Log CFU/swab)	Batch 1	Mean		1.8721	.28819
		95% Confidence Interval for Mean	Lower Bound	1.1313	
			Upper Bound	2.6129	
		5% Trimmed Mean		1.8698	
		Median		1.9498	
		Variance		.498	
		Std. Deviation		.70591	
		Minimum		1.00	
		Maximum		2.78	
		Range		1.78	
		Interquartile Range		1.38	
		Skewness		-.095	.845
		Kurtosis		-1.664	1.741
	Batch 2	Mean		2.0703	.38816
		95% Confidence Interval for Mean	Lower Bound	1.0725	
			Upper Bound	3.0681	
		5% Trimmed Mean		2.0562	
		Median		2.1533	
		Variance		.904	
		Std. Deviation		.95079	
		Minimum		1.00	
		Maximum		3.40	
		Range		2.40	
		Interquartile Range		1.89	
		Skewness		.055	.845
		Kurtosis		-1.207	1.741
	Batch 3	Mean		1.9878	.19736
		95% Confidence Interval for Mean	Lower Bound	1.4804	
			Upper Bound	2.4951	
		5% Trimmed Mean		1.9941	
		Median		2.1023	
		Variance		.234	
		Std. Deviation		.48344	

Descriptives Statistics

	Batch No.		Statistic	Std. Error
Mean (Log CFU/swab)	Batch 3	Minimum	1.30	
		Maximum	2.56	
		Range	1.26	
		Interquartile Range	.90	
		Skewness	-.467	.845
		Kurtosis	-1.311	1.741

Tests of Normality

	Batch No.	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Mean (Log CFU/swab)	Batch 1	.180	6	.200*	.946	6	.704
	Batch 2	.203	6	.200*	.927	6	.558
	Batch 3	.190	6	.200*	.945	6	.700

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Oneway

Descriptives Statistics

Mean (Log CFU/swab)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum
					Lower Bound	Upper Bound	
Batch 1	6	1.8721	.70591	.28819	1.1313	2.6129	1.00
Batch 2	6	2.0703	.95079	.38816	1.0725	3.0681	1.00
Batch 3	6	1.9878	.48344	.19736	1.4804	2.4951	1.30
Total	18	1.9767	.69870	.16469	1.6293	2.3242	1.00

Descriptives Statistics

Mean (Log CFU/swab)

	Maximum
Batch 1	2.78
Batch 2	3.40
Batch 3	2.56
Total	3.40

ANOVA

Mean (Log CFU/swab)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	.119	2	.060	.109	.897
Within Groups	8.180	15	.545		
Total	8.299	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/swab)
Tukey HSD

(I) Batch No.	(J) Batch No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Batch 1	Batch 2	-.19826	.42636	.889	-1.3057	.9092
	Batch 3	-.11568	.42636	.960	-1.2231	.9918
Batch 2	Batch 1	.19826	.42636	.889	-.9092	1.3057
	Batch 3	.08258	.42636	.980	-1.0249	1.1900
Batch 3	Batch 1	.11568	.42636	.960	-.9918	1.2231
	Batch 2	-.08258	.42636	.980	-1.1900	1.0249

Homogeneous Subsets

Mean (Log CFU/swab)

Tukey HSD

Batch No.	N	Subset for alpha = 0.05
		1
Batch 1	6	1.8721
Batch 3	6	1.9878
Batch 2	6	2.0703
Sig.		.889

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 6.000.

Oneway

Descriptives Statistics

Mean (Log CFU/swab)

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean	
					Lower Bound	Upper Bound
Plucker 1	6	2.4596	.49568	.20236	1.9394	2.9798
Plucker 2	6	1.3802	.49012	.20009	.8658	1.8945
Plucker 3	6	2.0904	.67197	.27433	1.3852	2.7956
Total	18	1.9767	.69870	.16469	1.6293	2.3242

Descriptives Statistics

Mean (Log CFU/swab)

	Minimum	Maximum
Plucker 1	2.02	3.40
Plucker 2	1.00	2.29
Plucker 3	1.00	2.78
Total	1.00	3.40

ANOVA

Mean (Log CFU/swab)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	3.612	2	1.806	5.779	.014
Within Groups	4.687	15	.312		
Total	8.299	17			

Post Hoc Tests

Multiple Comparisons

Dependent Variable: Mean (Log CFU/swab)
Tukey HSD

(I) Plucker No.	(J) Plucker No.	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Plucker 1	Plucker 2	1.07945*	.32274	.012	.2411	1.9178
	Plucker 3	.36925	.32274	.503	-.4691	1.2076
Plucker 2	Plucker 1	-1.07945*	.32274	.012	-1.9178	-.2411
	Plucker 3	-.71020	.32274	.104	-1.5485	.1281
Plucker 3	Plucker 1	-.36925	.32274	.503	-1.2076	.4691
	Plucker 2	.71020	.32274	.104	-.1281	1.5485

*. The mean difference is significant at the 0.05 level.

Homogeneous Subsets

Mean (Log CFU/swab)

Tukey HSD

Plucker No.	N	Subset for alpha = 0.05	
		1	2
Plucker 2	6	1.3802	
Plucker 3	6	2.0904	2.0904
Plucker 1	6		2.4596
Sig.		.104	.503

Means for groups in homogeneous subsets are displayed.
a. Uses Harmonic Mean Sample Size = 6.000.

Custom Tables

Table 1

Plucker No.											
Plucker 1				Plucker 2				Plucker 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
1	16.7%	5	83.3%	5	83.3%	1	16.7%	3	50.0%	3	50.0%

M. Nostrils of live chicken

Explore

Chicken Age

Case Processing Summary

	Chicken Age	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/swab)	One Week	6	100.0%	0	0.0%	6
	Three Weeks	6	100.0%	0	0.0%	6
	Six Weeks	6	100.0%	0	0.0%	6

Case Processing Summary

	Chicken Age	Cases
		Total
		Percent
Mean (Log CFU/swab)	One Week	100.0%
	Three Weeks	100.0%
	Six Weeks	100.0%

Descriptives Statistics

Chicken Age				Statistic	Std. Error
Mean (Log CFU/swab)	One Week	Mean		1.1652	.12377
		95% Confidence Interval for Mean	Lower Bound	.8470	
			Upper Bound	1.4833	
		5% Trimmed Mean		1.1417	
		Median		1.0000	
		Variance		.092	
		Std. Deviation		.30317	
		Minimum		1.00	
		Maximum		1.75	
		Range		.75	
		Interquartile Range		.37	
		Skewness		1.992	.845
		Kurtosis		3.863	1.741
	Three Weeks	Mean		1.5033	.33732
		95% Confidence Interval for Mean	Lower Bound	.6362	
			Upper Bound	2.3704	
		5% Trimmed Mean		1.4416	
		Median		1.1505	
		Variance		.683	
		Std. Deviation		.82626	
		Minimum		1.00	
		Maximum		3.12	
		Range		2.12	
		Interquartile Range		.98	
		Skewness		2.026	.845
		Kurtosis		4.217	1.741
	Six Weeks	Mean		1.5912	.28515
		95% Confidence Interval for Mean	Lower Bound	.8582	
			Upper Bound	2.3242	

	5% Trimmed Mean	1.5496	
	Median	1.3306	
	Variance	.488	
	Std. Deviation	.69846	

Descriptives Statistics

	Chicken Age		Statistic	Std. Error
Mean (Log CFU/swab)	Six Weeks	Minimum	1.00	
		Maximum	2.93	
		Range	1.93	
		Interquartile Range	.84	
		Skewness	1.859	.845
		Kurtosis	3.702	1.741

Tests of Normality

	Chicken Age	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/swab)	One Week	.374	6	.009	.660	6
	Three Weeks	.286	6	.137	.710	6
	Six Weeks	.263	6	.200*	.795	6

Tests of Normality

	Chicken Age	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/swab)	One Week	.002
	Three Weeks	.008
	Six Weeks	.053

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

Explore

Chicken Age

Case Processing Summary

	Chicken Age	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	One Week	6	100.0%	0	0.0%	6	100.0%
	Three Weeks	6	100.0%	0	0.0%	6	100.0%
	Six Weeks	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Chicken Age			Statistic	Std. Error
LogMean2	One Week	Mean		.1292	.09318
		95% Confidence Interval for Mean	Lower Bound	-.1104	
			Upper Bound	.3687	
		5% Trimmed Mean		.1124	
		Median		.0000	
		Variance		.052	
		Std. Deviation		.22824	

		Minimum		.00	
		Maximum		.56	
		Range		.56	
		Interquartile Range		.30	
		Skewness		1.831	.845
		Kurtosis		3.027	1.741
		Mean		.3119	.18258
		95% Confidence Interval for Mean	Lower Bound	-.1575	
			Upper Bound	.7812	
		5% Trimmed Mean		.2834	
		Median		.1316	
		Variance		.200	
	Three Weeks	Std. Deviation		.44722	
		Minimum		.00	
		Maximum		1.14	
		Range		1.14	
		Interquartile Range		.64	
		Skewness		1.591	.845
		Kurtosis		2.360	1.741
		Mean		.3993	.15357
		95% Confidence Interval for Mean	Lower Bound	.0045	
			Upper Bound	.7940	
	Six Weeks	5% Trimmed Mean		.3839	
		Median		.2832	
		Variance		.141	
		Std. Deviation		.37616	

Descriptives Statistics

	Chicken Age		Statistic	Std. Error
LogMean2	Six Weeks	Minimum	.00	
		Maximum	1.08	
		Range	1.08	
		Interquartile Range	.51	
		Skewness	1.328	.845
		Kurtosis	2.050	1.741

Tests of Normality

	Chicken Age	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	One Week	.381	6	.007	.680	6	.004
	Three Weeks	.257	6	.200*	.786	6	.044
	Six Weeks	.216	6	.200*	.894	6	.340

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

NPar Tests
Kruskal-Wallis Test

Ranks

	Chicken Age	N	Mean Rank

Mean (Log CFU/swab)	One Week	6	7.33
	Three Weeks	6	9.58
	Six Weeks	6	11.58
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/swab)
Chi-Square	2.094
df	2
Asymp. Sig.	.351

a. Kruskal Wallis Test
b. Grouping Variable: Chicken Age

Custom Tables

Table 1

Chicken Age											
One Week				Three Weeks				Six Weeks			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
6	100.0%	0	0.0%	5	83.3%	1	16.7%	5	83.3%	1	16.7%

N. Skin of live chickens

Explore

Chicken Age

Case Processing Summary

	Chicken Age	Cases				
		Valid		Missing		Total
		N	Percent	N	Percent	N
Mean (Log CFU/swab)	One Week	6	100.0%	0	0.0%	6
	Three Weeks	6	100.0%	0	0.0%	6
	Six Weeks	6	100.0%	0	0.0%	6

Case Processing Summary

	Chicken Age	Cases
		Total
		Percent
Mean (Log CFU/swab)	One Week	100.0%
	Three Weeks	100.0%
	Six Weeks	100.0%

Descriptives Statistics

Chicken Age			Statistic	Std. Error
Mean (Log CFU/swab)	One Week	Mean	1.1353	.13527
		95% Confidence Interval for Mean — Lower Bound	.7875	
		95% Confidence Interval for Mean — Upper Bound	1.4830	
		5% Trimmed Mean	1.1052	
		Median	1.0000	
		Variance	.110	
		Std. Deviation	.33134	
		Minimum	1.00	
		Maximum	1.81	
		Range	.81	
		Interquartile Range	.20	
		Skewness	2.449	.845
		Kurtosis	6.000	1.741
	Three Weeks	Mean	1.2551	.15210
		95% Confidence Interval for Mean — Lower Bound	.8641	
		95% Confidence Interval for Mean — Upper Bound	1.6461	
		5% Trimmed Mean	1.2284	
		Median	1.1505	
		Variance	.139	
		Std. Deviation	.37257	
		Minimum	1.00	
		Maximum	1.99	
		Range	.99	
		Interquartile Range	.43	
		Skewness	2.107	.845
		Kurtosis	4.728	1.741

		Mean		1.3630	.18540
		95% Confidence Interval for Mean	Lower Bound	.8864	
			Upper Bound	1.8396	
	Six Weeks	5% Trimmed Mean		1.3388	
		Median		1.1945	
		Variance		.206	
		Std. Deviation		.45413	

Descriptives Statistics

	Chicken Age		Statistic	Std. Error
Mean (Log CFU/swab)	Six Weeks	Minimum	1.00	
		Maximum	2.16	
		Range	1.16	
		Interquartile Range	.76	
		Skewness	1.345	.845
		Kurtosis	1.118	1.741

Tests of Normality

	Chicken Age	Kolmogorov-Smirnov[a]			Shapiro-Wilk	
		Statistic	df	Sig.	Statistic	df
Mean (Log CFU/swab)	One Week	.492	6	.000	.496	6
	Three Weeks	.351	6	.020	.715	6
	Six Weeks	.275	6	.177	.840	6

Tests of Normality

	Chicken Age	Shapiro-Wilk[a]
		Sig.
Mean (Log CFU/swab)	One Week	.000
	Three Weeks	.009
	Six Weeks	.130

a. Lilliefors Significance Correction

Explore

Chicken Age

Case Processing Summary

	Chicken Age	Cases					
		Valid		Missing		Total	
		N	Percent	N	Percent	N	Percent
LogMean2	One Week	6	100.0%	0	0.0%	6	100.0%
	Three Weeks	6	100.0%	0	0.0%	6	100.0%
	Six Weeks	6	100.0%	0	0.0%	6	100.0%

Descriptives Statistics

	Chicken Age			Statistic	Std. Error
LogMean2	One Week	Mean		.0990	.09904
		95% Confidence Interval for Mean	Lower Bound	-.1555	
			Upper Bound	.3536	

		5% Trimmed Mean		.0770	
		Median		.0000	
		Variance		.059	
		Std. Deviation		.24259	
		Minimum		.00	
		Maximum		.59	
		Range		.59	
		Interquartile Range		.15	
		Skewness		2.449	.845
		Kurtosis		6.000	1.741
		Mean		.1972	.10426
		95% Confidence Interval for Mean	Lower Bound	-.0708	
			Upper Bound	.4652	
		5% Trimmed Mean		.1808	
		Median		.1402	
		Variance		.065	
	Three Weeks	Std. Deviation		.25539	
		Minimum		.00	
		Maximum		.69	
		Range		.69	
		Interquartile Range		.33	
		Skewness		1.856	.845
		Kurtosis		3.855	1.741
		Mean		.2687	.12430
		95% Confidence Interval for Mean	Lower Bound	-.0509	
			Upper Bound	.5882	
	Six Weeks	5% Trimmed Mean		.2557	
		Median		.1771	
		Variance		.093	
		Std. Deviation		.30448	

Descriptives Statistics

	Chicken Age		Statistic	Std. Error
LogMean2	Six Weeks	Minimum	.00	
		Maximum	.77	
		Range	.77	
		Interquartile Range	.56	
		Skewness	1.019	.845
		Kurtosis	-.022	1.741

Tests of Normality

	Chicken Age	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
LogMean2	One Week	.492	6	.000	.496	6	.000
	Three Weeks	.307	6	.080	.775	6	.035
	Six Weeks	.238	6	.200*	.880	6	.270

*. This is a lower bound of the true significance.
a. Lilliefors Significance Correction

NPar Tests

Kruskal-Wallis Test

Ranks

	Chicken Age	N	Mean Rank
Mean (Log CFU/swab)	One Week	6	6.83
	Three Weeks	6	10.42
	Six Weeks	6	11.25
	Total	18	

Test Statistics[a,b]

	Mean (Log CFU/swab)
Chi-Square	2.662
df	2
Asymp. Sig.	.264

a. Kruskal Wallis Test
b. Grouping Variable: Chicken Age

Custom Tables

Table 1

Chicken Age											
One Week				Three Weeks				Six Weeks			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
6	100.0%	0	0.0%	6	100.0%	0	0.0%	5	83.3%	1	16.7%

Custom Tables

Batch No.											
Batch 1				Batch 2				Batch 3			
LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)				LogMean > StandardlevelLog10CFUg (FILTER)			
Not Selected		Selected		Not Selected		Selected		Not Selected		Selected	
Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %	Count	Row N %
3	50.0%	3	50.0%	3	50.0%	3	50.0%	3	50.0%	3	50.0%