Inland Norway
University of
Applied Sciences

Faculty of Applied Ecology, Agricultural Sciences and Biotechnology

Bindiya Bajracharya

Master's Thesis

Study of pathogenicity, virulence, and antimicrobial resistance in *Acinetobacter baumannii* clinical isolates from Norway and India using whole-genome sequence data

Master's Degree in Applied and Commercial Biotechnology

2022

Consent to lending by University College Library YES ☒ NO ☐

Consent to accessibility in digital archive Brage YES ☒ NO ☐

Acknowledgment

First of all, I would like to convey my sincere gratitude to my supervisor, Associate Professor Dr. Rafi Ahmad for believing me and providing me the opportunity to work on this project under his supervision. I had very little knowledge of bioinformatics prior to this study but this thesis has given me the chance to learn a lot about bioinformatics.

I would also like to express my special appreciation to the post-doctoral researcher, Dr. Abdolrahman Khezri, for his time, continuous guidance, and support throughout my thesis without whom my thesis would not have been completed.

In addition, I would like to acknowledge the administration of Inland Norway University of Applied Sciences (INN) Campus, Hamar, for providing me with the equipment and resources required to achieve the goals of this project.

I am also grateful to all the bioinformatics team members of INN: Yusuf Khan, Ekaterina Avershina, Jawad Ali, and Chidimma Phoebe Echebiri for their advice and assistance during the project as well as the writing of the thesis.

Lastly, I would like to thank my husband for his continuous support and motivation throughout my journey. I am also very grateful to my parents and family members for their unconditional love, support, and moral guidance.

Bindiya Bajracharya

1st June 2022

Abbreviations

ABC	ATP Binding Cassette
ACB	*Acinetobacter calcoaceticus-Acinetobacter baumannii*
ABySS	Assembly By Short Sequencing
AME	Aminoglycoside Modifying Enzyme
AMR	Antimicrobial Resistance
ANI	Average Nucleotide Identity
AP	Alignment Percentage
AST	Antimicrobial Susceptibility Testing
BAC	Bacterial Artificial Chromosome
Bandage	Bioinformatics Application for Navigating De novo Assembly Graphs Easily
BLAST	Basic Local Alignment Search Tool
BUSCO	Benchmarking Universal Single-Copy Orthologs
CARD	Comprehensive Antibiotic Resistance Database
CarO	Carbapenem resistance-associated Outer membrane protein
CDC	Centre for Disease Control and Prevention
CDS	Coding Sequences
CHDL	Carbapenem Hydrolyzing Class D β-lactamase
CLSI	Clinical and Laboratory Standards Institute
CRAB	Carbapenem Resistant *Acinetobacter baumannii*
DMT	Drug / Metabolite Transporter
DNA	Deoxyribonucleic acid
ECDC	European Centre for Disease Prevention and Control
HAI	Hospital-acquired infections
HGT	Horizontal Gene Transfer
ICU	Intensive Care Unit
LOS	Lipooligosaccharide
MATE	Multidrug and toxic compound extrusion
MBL	Metallo-β-lactamase
MDR	Multidrug-resistant

MFS	Major Facilitator Superfamily
MIC	Minimum Inhibitory Concentration
MLST	Multilocus Sequence Typing
NCBI	National Center for Biotechnology Information
NGS	Next-Generation Sequencing
OMP	Outer Membrane Protein
OmpA	Outer Membrane Protein A
OMV	Outer Membrane Vesicle
PBP	Penicillin Binding Protein
PCR	Polymerase chain reaction
PDR	Pan drug-resistant
PLC	Phospholipase C
PLD	Phospholipase D
PLSDB	Plasmid Database
QUAST	Quality Assessment Tool
RGI	Resistance Gene Identifier
RNA	Ribonucleic acid
RND	Resistance Nodulation Division
rRNA	ribosomal RNA
SMR	Small Multidrug Resistance
SPAdes	St. Petersburg genome assembler
tRNA	transfer RNA
tmRNA	transfer messenger RNA
UTI	Urinary Tract Infection
VF	Virulence Factor
VFDB	Virulence Factor Database
WGA	Whole Genome Alignment
WGS	Whole Genome Sequencing
WHO	World Health Organization
XDR	Extremely drug-resistant
YAC	Yeast Artificial Chromosome

Table of Contents

Abstract

Acinetobacter baumannii is an emerging pathogen worldwide that mainly causes nosocomial infections and has become a threat for healthcare systems due to its multidrug resistance (MDR) nature. The advancements in affordable and fast DNA sequencing technologies and bioinformatic tools have made it easier to study pathogenicity, virulence, and antimicrobial resistance. In this study whole genome sequence (WGS) data obtained from *A. baumannii* clinical isolates from Norway and India were used to study the important factors related to its pathogenicity, virulence and antimicrobial resistance using bioinformatic tools.

In total, WGS data from Illumina sequencing of 96 *A. baumannii* clinical isolates were provided. To fulfil the objective of the study, first, genome assembly of the WGS data was created after choosing the best suited trimmer and assembler. Later, the assembled genomes which were not *A. baumannii*, were excluded using Multilocus sequence typing (MLST) and Whole genome alignment (WGA). Then, the assembled genomes were annotated using Prokka to identify the CDS, rRNA and tRNA. The plasmids, AMR genes and virulence factors were predicted using different bioinformatic tools and databases including PLSDB, CARD and VFDB. Finally, the genotypic (detected AMR genes) and phenotypic (AST results) resistance data were compared to find the correlation between them.

In this study, the Trimmomatic and Unicycler were the chosen trimmer and assembler. The QUAST, BUSCO and Bandage results showed that the genomes assembled using these tools were compatible with the reference genome. MLST and WGA indicated that 8 out of 96 isolates were not *A. baumannii*. The number of CDS, rRNA and tRNA obtained were comparable to the reference genome. The plasmid pVB11737_6, AMR gene *AdeK*, efflux pump resistance mechanism and acinetobactin virulence gene cluster were found in majority of both Norwegian and Indian *A. baumannii* clinical isolates. The comparison between genotypic and phenotypic resistance data showed less concordance in Indian isolates. The AST results showed the MDR nature of *A. baumannii*. The occurrence of antibiotic resistance in *A. baumannii* was found to be more in India than in Norway.

In conclusion, the selection of tools for performing genome assembly and to study the other factors related to the pathogenicity, is a prerequisite. Overall, this study presented the potential of WGS to investigate the bacterial pathogenicity, virulence, and antimicrobial resistance of different population.

1 Introduction

1.1 *Acinetobacter baumannii*

1.1.1 History

The genus *Acinetobacter* was first isolated by a Dutch microbiologist Beijerinck in 1911 from soil and it was named as *Micrococcus calcoaceticus* (Beijerinck, 1911). The current designation of the genus *Acinetobacter* (derived from Greek word akinetos, meaning nonmotile) was proposed by Brisou and Prevot in 1954, to separate the nonmotile microorganisms from the motile microorganisms within the genus *Achromobacter* (Brisou & Prevot, 1954). The designation was accepted only in 1968 after publication of a comprehensive study of a similar group of organisms concluding that they could not be further sub-classified into different species based on phenotypical characteristics and they belonged to a single genus (Baumann et al., 1968). Finally, in 1974, this designation was included in Bergey's Manual of Systematic Bacteriology, where it was described as having only one species: *Acinetobacter calcoaceticus* (Bergey et al., 1975).

Later, in 1986, Bouvet and Grimont observed inconsistencies in the application of phenotypic tests to determine the genus and species of *Acinetobacter* because the members of this genus have different catabolic pathways that allow them to adapt to most substrates (Bouvet & Grimont, 1986). DNA hybridization studies were then introduced to determine the different species, and the homology groups with more than 70% DNA-DNA relatedness were called genomic species. Currently, there are 32 genospecies known. The *Acinetobacter calcoaceticus – Acinetobacter baumannii* (ACB complex) includes four genospecies: genospecies 1 (*A. calcoaceticus*), genospecies 2 (*A. baumannii*), genospecies 3 (*A. pittii*) and genospecies 13TU (*A. nosocomialis*) (Peleg et al., 2008). Of these, *A. baumannii* is the most important in clinical context since it is the species associated with hospital outbreaks and nosocomial infections (Cerqueira & Peleg, 2011; Chu et al., 1999; Chuang et al., 2011; Munoz-Price & Weinstein, 2008). The timeline showing brief history of genus *Acinetobacter* is presented in Figure 1.

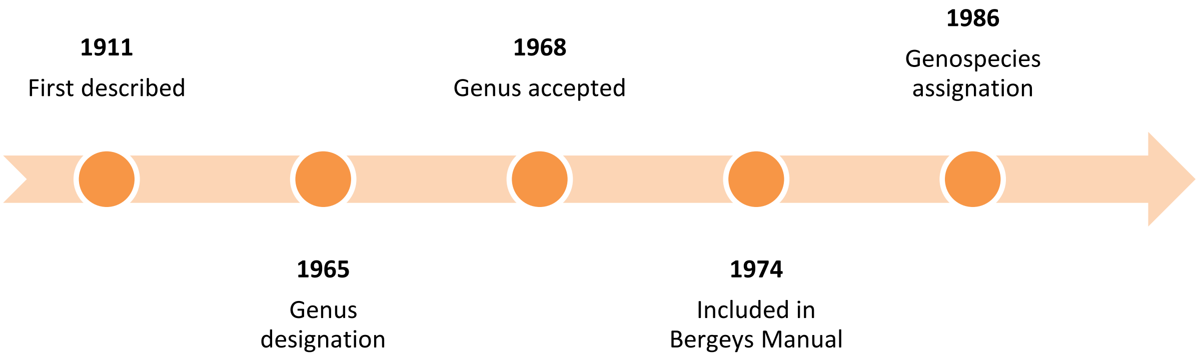


Figure 1: Timeline showing brief history of genus *Acinetobacter*.

1.1.2 Taxonomy

The taxonomic hierarchy of *A. baumannii* is as follow:

Domain: Bacteria
  Phylum: Proteobacteria
    Class: Gammaproteobacteria
      Order: Pseudomonadales
        Family: Moraxellaceae (Rossau et al., 1991)
          Genus: *Acinetobacter* (Brisou & Prevot, 1954)
            Species: *A. baumannii* (Bouvet & Grimont, 1986)

1.1.3 Phenotypic characteristics

Acinetobacter is a gram-negative, strictly aerobic, non-fermenting, non-fastidious, non-motile, catalase-positive, oxidase-negative coccobacilli (Peleg et al., 2008) as can be seen in Figure 2. Although *Acinetobacter* is non-motile, *A. baumannii* is capable of surface-associated and twitching motility (Clemmer et al., 2011; Harding et al., 2018).

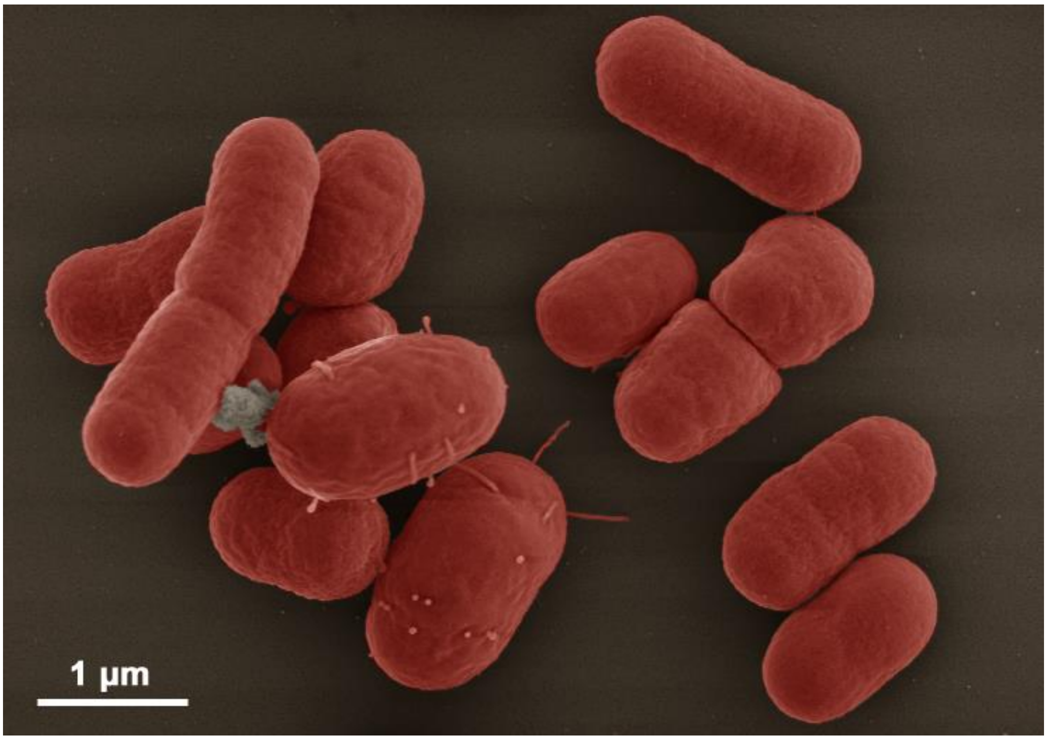


Figure 2: Scanning electron microscopy of *A. baumannii* (Retrieved from: © Gudrun Holland; Coloring: Michael Laue/RKI)

1.1.4 Genotypic characteristics

A. baumannii genome consists of a single circular chromosome and plasmids (Salgado-Camargo et al., 2020). Currently there are 6541 assembled genomes and 703 plasmids of *A. baumannii* in NCBI. The median total length, median protein count and median GC (%) of *A. baumannii* genome is 3,974,730 base pairs (bp), 3,681 and 39% respectively. The genome size ranges from 2,950,000 bp to 10,860,000 bp and the plasmid size ranges from 359 bp to 1020000 bp (NCBI Genome ID 403).

Plasmids are small, usually circular, extrachromosomal DNA molecules that can exist independently of the chromosome and can replicate on their own. They have the potential to be transferred frequently, but not exclusively by conjugation among bacteria (same or different species) (Smillie et al., 2010; Salgado-Camargo et al., 2020). These plasmids play an important role in the spread of antibiotic resistance genes and virulence factors among pathogenic bacteria that cause hospital acquired or community acquired infections (Salgado-Camargo et al., 2020) through a process called horizontal gene transfer (HGT) (Burmeister, 2015). HGT occurs by three mechanisms, i.e., transformation (AMR genes released by one bacterium are taken up by the other), conjugation (AMR genes transfer directly from one cell to another through contact) and transduction (AMR genes transfer from one cell to another via bacteriophages (Burmeister, 2015). Plasmids are considered to be specialized vehicle for HGT as they are able to self-replicate, transfer, persist and even acquire new genes. So, research on the plasmids have become important to develop new strategies to control antimicrobial resistance dissemination (Salto et al., 2018).

1.1.5 Habitat

Different species of genus *Acinetobacter* are thought to be ubiquitous as they can be isolated from almost all soil and surface water samples (Baumann, 1968) but not all the species have their natural habitat in the environment (Peleg et al., 2008). There is little evidence that *A. baumannii* can be found frequently in the environment and available data show that it has a low prevalence in the community (Dijkshoorn et al., 2007). However, it has been found in vegetables, fish, meat, and soil (Berlau et al., 1999; Houang et al., 2001).

A. baumannii is rarely found as the faecal flora of individuals in the community (Dijkshoorn et al., 2005) and as the normal microflora of the skin (Aucken et al., 1999; Seifert et al., 1997). However, as a pathogen, it specifically targets moist tissues like mucous membranes or the skin areas that are exposed through injury (Sebeny et al., 2008). *A. baumannii* is found frequently in human clinical specimens (Dijkshoorn et al., 2007). It is also found in the field hospitals due to the contamination of the environment of field hospitals and infection transmission in healthcare facilities (Scott et al., 2007). It shows an incredible ability to survive on dry surfaces for prolonged periods, which enhances its capacity to spread in the nosocomial environment (Fournier et al., 2006; Jawad et al., 1998; Wendt et al., 1997).

1.1.6 Clinical Significance

Nosocomial (Hospital-acquired) infections:

Hospital-acquired infections, also known as healthcare-associated infections (HAI) or nosocomial infections are the one which is not present at the time of admission in hospital but are acquired after hospitalization (Monegro et al., 2022).

A. baumannii is an opportunistic pathogen that causes various infections mainly in critically ill patients in intensive care units (ICUs). Hospital-acquired infections caused by *A. baumannii* are ventilator-associated pneumonia; skin and soft-tissue infections; wound infections; urinary-tract infections (UTIs); secondary meningitis; and bloodstream infections (Morris et al., 2019). Nosocomial *A. baumannii* is also found to cause wound infection in people injured with natural or man-made disasters (Dijkshoorn et al., 2007). *A. baumannii* were commonly isolated from wounds of the military from Iraq or Afghanistan (Calhoun et al., 2008; Petersen et al., 2007; Scott et al., 2007; Yun et al., 2006). The most common nosocomial infection caused by *A. baumannii* are ventilator-associated pneumonia and bloodstream infection (bacteraemia), both of which are linked to high morbidity and mortality rates (Cisneros et al., 1996; Seifert et al., 1995).

The different modes for transmission of nosocomial (hospital-acquired) infections caused by *A. baumannii* are illustrated in Figure 3. The host-related risk factors that make individuals susceptible to the infection with *A. baumannii* are major surgery or trauma (in particular, burn trauma), immunosuppression, aging, and prematurity in new-borns (Dijkshoorn et al., 2007). The exposure-related risk factors are previous or prolonged stay in a hospital or ICU, residence in a unit in which *A. baumannii* is endemic and exposure to contaminated medical equipment (Dijkshoorn et al., 2007). The medical treatment-related risk factors are mechanical ventilation, the presence of indwelling devices (such as intravascular catheters, urinary catheters, and drainage tubes), the number of invasive procedures that are performed and previous antimicrobial therapy (Dijkshoorn et al., 2007; García-Garmendia et al., 2001).

Community-acquired infection:

A. baumannii is a rare but serious cause of community-acquired pneumonia in tropical regions of the world with a mortality rate reported as high as 64%. This infection is common in individuals with conditions like alcoholism, diabetes mellitus, smoking and chronic lung disease (Anstey et al., 1992; Dexter et al., 2015). However, it is not clear if the host factors or virulence factors of the bacteria are responsible for the infections (Dijkshoorn et al., 2007; Morris et al., 2019).

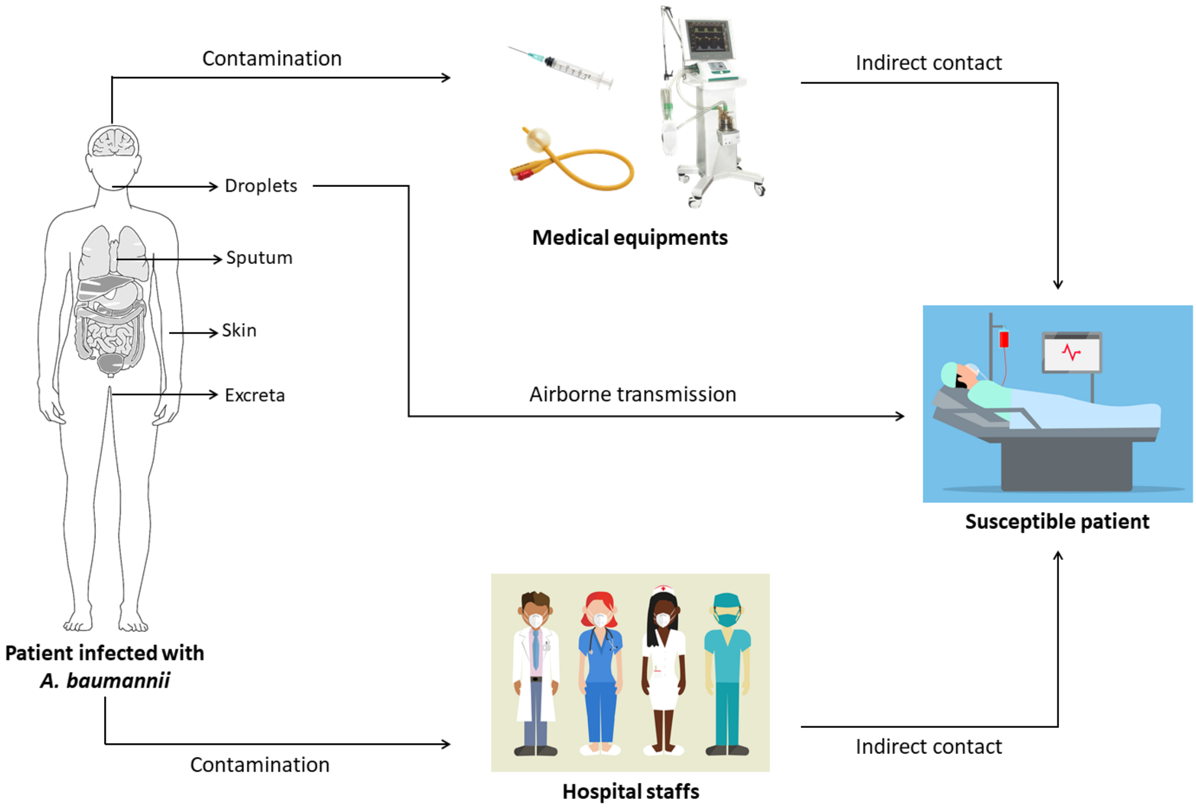


Figure 3: Different modes for transmission of nosocomial (hospital-acquired) infections caused by *A. baumannii*.

1.1.7 Virulence factors (VFs)

Bacterial pathogenesis depends on different factors that aid in the colonization of the bacterium, development of infection and its persistence on biotic or abiotic surfaces (Rumbo et al., 2014). The molecular features used by a bacterium that enable successful interaction followed by colonization in the human host are called virulence factors (Harding et al., 2018). The important virulence factors in *A. baumannii* are described below:

Glycoconjugates:

In *A. baumannii*, lipooligosaccharide (LOS) contributes to drug and desiccation resistance (Boll et al., 2015). The capsular polysaccharide protects cells from complement-mediated killing (Russo et al., 2010). The glycoproteins contribute to virulence by enhancing biofilm formation and maintenance (Iwashkiw et al., 2012) and glycosylated type IV pili (Harding et al., 2015) have been implied to function in immune evasion, shielding the antigenic protein from antibody recognition (Piepenbrink et al., 2016).

Porins:

Porins are outer membrane proteins that regulate cellular permeability (Lee et al., 2017). Outer membrane protein A (OmpA) is a porin that is responsible for the adherence and invasion of *A. baumannii* in epithelial cells (C. H. Choi et al., 2008) and induce apoptosis through mitochondrial (C. H. Choi et al., 2005) and nuclear targeting (C. H. Choi et al., 2007) in the early stage of infection. It also plays a limited role in biofilm formation on plastic (Gaddy et al., 2009). OmpA can bind to factor H in human serum which prevents *A. baumannii* from complement-mediated killing (Kim et al., 2009).

Outer Membrane Vesicles (OMVs):

OMVs are small, round-shaped, and double membrane-bound vesicles produced by the outer membrane of all gram-negative bacteria (Beveridge, 1999). *A. baumannii* OMVs act as a vehicle to deliver OmpA, after which OmpA packaged in OMVs induce cytotoxicity (Jin et al., 2011) and deliver several putative virulence-associated proteins to the host cells (Kwon et al., 2009).

Biofilm formation:

Biofilms are bacterial community comprised of a heterogeneous protein matrix, nucleic acids, polysaccharides, and bacterial microcolonies, dispersed with water channels. *A. baumannii* forms biofilms on both biotic and abiotic surfaces, promoting survival on indwelling medical devices, hospital surfaces, or in otherwise unfavorable conditions (Hall-Stoodley et al., 2004). Biofilm formation on abiotic surfaces has contributed to the success of this pathogen in hospital environments, with their ability to adhere to medically relevant surfaces, such as titanium and polystyrene (Espinal et al., 2012; Loehfelm et al., 2008).

Phospholipase:

A. baumannii encodes two phospholipase C (PLC) and three phospholipase D (PLD) enzymes having specific hydrolytic properties towards a eukaryotic membrane component called phosphatidylcholine (Fiester et al., 2016). PLD is required for epithelial cell invasion, resistance to human serum and in-vivo pathogenesis (Jacobs et al., 2010; Stahl et al., 2015) and PLC plays an important role in haemolytic and cytolytic activities towards host cells (Fiester et al., 2016).

Iron Acquisition System:

A. baumannii has developed an iron acquisition system to adapt in the iron-limited (as it is bound to heme) host environment (Eijkelkamp et al., 2011; Sheldon & Skaar, 2020; Wandersman & Delepelaire, 2004). *A. baumannii* has 8 gene clusters in this system. Among them, one is involved in iron acquisition, two in heme uptake and five in siderophore biosynthesis and utilization (Sheldon & Skaar, 2020). Siderophores are high-affinity iron chelator proteins which compete with host cells for iron (Wandersman & Delepelaire, 2004). There are ten structurally distinct siderophores expressed in *A. baumannii* including acinetobactin, baumannoferrins and fimsbactins (Sheldon & Skaar, 2020). Among them, acinetobactin has been the most extensively studied and structurally characterized. (Eijkelkamp et al., 2011).

Efflux Pumps:

Bacterial efflux systems are membrane crossing systems that show broad substrate specificity and expel potentially toxic compounds from the periplasm to the extracellular environment. In gram-negative pathogens, efflux pumps play critical roles in the extrusion of bile salts and antimicrobial fatty acids and peptides or actively secrete virulence factors such as siderophores (Morris et al., 2019). There are six families of bacterial efflux pumps: the ATP binding cassette (ABC) family, the major facilitator superfamily (MFS), the resistance-nodulation-division (RND) family, the multidrug and toxin extrusion (MATE) family, the small multidrug resistance (SMR) family and the drug/metabolite transporter (DMT) superfamily (Morris et al., 2019; Vila et al., 2007).

1.2 Antibiotic resistance

According to World Health Organization (WHO), antimicrobial resistance (AMR) occurs when microorganisms including bacteria, viruses, fungi, and parasites no longer respond to the medications that once impacted them (Antimicrobial Resistance, 2021). Antibiotic resistance is a subset of AMR that occurs when bacteria becomes unaffected by an antibiotic which was once effective (Antibiotic Resistance, 2020).

1.2.1 Categories of antibiotic resistance pattern

The joint initiative by the European Centre for Disease Prevention and Control (ECDC) and the Centers for Disease Control and Prevention (CDC) created definition for the following three categories of resistance pattern (Magiorakos et al., 2012):

Multidrug-resistant (MDR): MDR was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial categories.

Extensively drug-resistant (XDR): XDR was defined as non-susceptibility to at least one agent in all except two or fewer antimicrobial categories i.e., bacterial isolates remain susceptible to only one or two categories.

Pan drug-resistant (PDR): PDR was defined as non-susceptibility to all agents in all antimicrobial categories.

1.2.2 Mechanisms of antibiotic resistance

Antibiotic resistance can occur by various processes. The main categories of mechanisms (depicted in Figure 4) by which *A. baumannii* acquire antibiotic resistance are described below (Blair et al., 2015; C Reygaert, 2018; Maragakis & Perl, 2008; Tooke et al., 2019):

1. **Antibiotic efflux:** Efflux pump proteins are the transport proteins capable of extruding the toxic substances (antibiotics) out of the cell. Bacteria can acquire antibiotic resistance through over-expression of these efflux pump proteins and keep the intracellular concentration below toxic levels.
2. **Antibiotic inactivation:** Bacteria can produce various antibiotic inactivating enzymes. These enzymes inactivate the antibiotics directly by modifying or degrading the antibiotics structure, hence preventing their action.
3. **Antibiotic target modification:** There are components in the bacterial cell that may be targets of antibiotics to kill them. Bacteria can modify those antibiotic targets through genetic mutation or expression of alternative Penicillin Binding Proteins (PBPs) or post-translational modification, eventually protecting the action of the antibiotic.
4. **Reduced permeability to antibiotic:** Antibiotics enters the bacterial cell through porin channels. The decrease in the number of porins or the mutations that change the selectivity of the porin channel**,** can reduce the cell membrane permeability to antibiotics. Thus, preventing the action of the antibiotics.

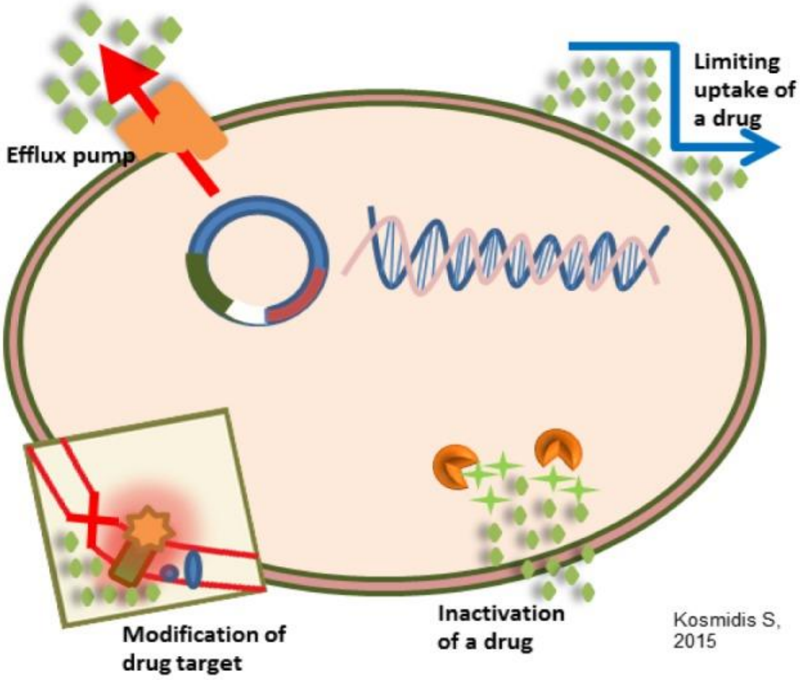


Figure 4: Mechanism of antibiotic resistance. Retrieved from: (C Reygaert, 2018)

1.3 Antibiotic resistance in *A. baumannii*

It was possible to treat *Acinetobacter* infections before 1970s with a wide range of antibiotics including β-lactams, aminoglycosides, and tetracyclines. However, *A. baumannii* with a wide range of both intrinsic and acquired resistance determinants have emerged causing resistance to all known antibiotics. Thus, making it difficult to treat *A.* baumannii infections (Peleg et al., 2008).

There are differences in antimicrobial susceptibility between *A. baumannii* and other *Acinetobacter spp*, with *A. baumannii* being the most resistant one (Van Looveren & Goossens, 2004). High frequencies of MDR bacteria have been grouped under the acronym ESKAPE: *Enterococcus faecium*, *Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa* and *Enterobacter spp* which includes *A. baumannii*. The ESKAPE pathogens are responsible for the majority of nosocomial infections and capable of 'escaping' the biocidal action of antimicrobial agents (Navidinia, 2016; Rice, 2008). In 2017, WHO published a list of pathogens for which urgent global action is needed. WHO has ranked carbapenem resistant *A. baumannii* (CRAB) as a critical priority (priority 1) pathogen of the list of antibiotic-resistant bacteria to guide drug research and development (Tacconelli et al., 2018).

The mechanisms by which *A. baumannii* develop resistance to some antimicrobials are described below:

1.3.1 Resistance to β-lactam antibiotics

β-lactam antibiotics comprise penicillins, cephalosporins, carbapenems, monobactams, and β-lactamase inhibitors. Resistance to beta-lactam antibiotics can be conferred through various mechanisms (Kyriakidis et al., 2021). The main mechanisms of β-lactam resistance in *A. baumannii* are described below:

β-lactamases:

The enzyme-mediated resistance to β-lactam antibiotics occurs from the activity of β-lactamases, the enzymes produced by bacteria that can hydrolyze the β-lactam antibiotics (Kyriakidis et al., 2021; Tooke et al., 2019). β-lactamases can be divided into four classes based on sequence motifs and differences in hydrolytic mechanism as class A, B, C and D (Ambler, 1980). Three of these classes: A, C, and D are active-site serine enzymes called serine β-lactamases (SBLs) and class B are zinc-dependent enzymes called metallo-β-lactamases (MBLs) (Massova & Mobashery, 1998). Class D β-lactamases are also called oxicillinases or carbapenem-hydrolyzing class D β-lactamases (CHDLs). They can inactivate all β-lactams and account for the main mechanism of carbapenem resistance (Antunes & Fisher, 2014).

Outer membrane protein (OmpA):

OmpA is the most abundant non-specific porin that provide resistance to *A. baumannii* by allowing slower diffusion of negatively charged β-lactam antibiotics (Uppalapati et al., 2020), whose collaboration with β-lactamases and efflux pumps, enhances antibiotic resistance (Sugawara & Nikaido, 2012). It participates in the transport of antibiotics out from the periplasmic space through outer membrane (Smani et al., 2014).

Carbapenem resistance-associated outer membrane protein (CarO):

CarO is an OMP found in family *Moraxellaceae* of class *Gammaproteobacteria* that participates in the influx of carbapenem (selectively imipenem) into *A. baumannii* (Mussi et al., 2005). CarO was first found in imipenem sensitive *A. baumannii* that acquired imipenem resistance upon the loss of this 29 kDa OMP (Limansky et al., 2002). Mutation of CarO gene can cause structural modification of CarO, reducing outer membrane permeability and hence causing antibiotic resistance in *A. baumannii* (Zhu et al., 2019).

1.3.2 Resistance to aminoglycosides antibiotics

Resistance to aminoglycosides in *A. baumannii* can occur through three mechanisms: aminoglycoside modifying enzymes (AMEs) that weaken aminoglycoside binding capacity, target site alteration by 16S rRNA methyltransferases, and limited aminoglycoside uptake after loss of permeability or overactivity of efflux pumps (Kyriakidis et al., 2021). AMEs are further categorized as acetyl-, adenyl-, and phospho-transferases, depending on the site of aminoglycoside modification (primarily by N-acetylation, O-nucleotidylation, and O-phosphorylation, respectively) (Kyriakidis et al., 2021).

1.4 Epidemiology of *A. baumannii*

Formerly, *Acinetobacter spp.* had been thought to be opportunistic pathogens that were rare and less serious. However, since 1980s, an increase in both the incidence and seriousness of *A. baumannii* infection has been observed, with the main targets being patients in ICUs (Gootz & Marra, 2008; Zhao et al., 2019). Since then, the prevalence of *A. baumannii* infections have been reported worldwide including Europe, especially the UK, Germany, Italy, Spain and the US by transmission of MDR strains (Akrami & Namvar, 2019). The prevalence of nosocomial infections in ICUs due to *A. baumannii* ranges from 2% to 10% of all gram-negative bacterial infections in Europe and account for about 2.5% of them in the United States (Fournier et al., 2006). The main source for spread of *A. baumannii* infections are the hospital environment, medical equipment and hospital staffs (Akrami & Namvar, 2019; Maragakis & Perl, 2008). The incidence of *A. baumannii* infections can also be affected by person to person contact and antimicrobial resistance acquired by the bacteria (Allen & Green, 1987; Munoz-Price & Weinstein, 2008). Study done in US have shown that summer season and higher outdoor temperature are associated with increased frequency of *Acinetobacter* nosocomial infections (Eber et al., 2011). The rate of MDR (82%) and XDR (51.1%) *Acinetobacter spp.* were very high in Asian countries. Especially, imipenem resistance rates of *Acinetobacter spp.* isolates from Thailand, Malaysia, and India were higher than 80% and that of China was 58.9%. (Chung et al., 2011). Few studies conducted in India reported 26-38% carbapenem resistance among *Acinetobacter* isolates from ICUs (Chaudhary & Payasi, 2013; Hans et al., 2015). The prevalence of *Acinetobacter* among nosocomial infections in Bosnia was 51.4%, in which

74.1% belonged to respiratory infections (Custovic et al., 2014). In general, studies show that the community-acquired *A. baumannii* infections are often detected in tropical and subtropical regions such as Singapore, Hong Kong, and Taiwan mostly in rainy seasons (Davis et al., 2014; Leung et al., 2006; Ong et al., 2009; Wang et al., 2002). It has been reported that about 65% of *A. baumannii* pneumonia in the United States and Europe was caused by carbapenem-resistant *A. baumannii* (CRAB) (Zhao et al., 2019). The highest resistance percentages of *Acinetobacter spp.* were reported from the Baltic countries and from southern and south-eastern Europe (Antimicrobial Resistance in the EU/EEA (EARS-Net) - Annual Epidemiological Report 2019, 2020).

1.5 Sequencing technology

DNA sequencing is the process of determining the sequence of nucleotide bases – Adenine (A), Thymine (T), Cytosine (C), and Guanine (G) in DNA molecule using sequencing machines (Griffiths, 2012; Kchouk et al., 2017). It plays an important role in study and analysis of genomic sequences of organisms. There are three main types of DNA sequencing technologies as described below:

1.5.1 First generation sequencing

The first generation sequencing technologies were developed by (Sanger et al., 1977) from Cambridge University and (Maxam & Gilbert, 1977) from Harvard University. Sanger sequencing technology uses chain termination method while Maxam-Gilbert sequencing technology uses chemical degradation method. The sanger sequencing was widely used for three decades for single or low-throughput DNA sequencing; however, it is expensive, time consuming and does not allow the sequencing of complex genomes (Kchouk et al., 2017). Maxam-Gilbert sequencing method is considered dangerous because it uses toxic and radioactive chemicals (Kchouk et al., 2017).

1.5.2 Second generation sequencing

The second-generation sequencing technologies are also known as Next generation sequencing (NGS) or High throughput sequencing technologies. It was first developed in 2005 and continued to develop in the following years. The NGS technology can generate millions of short reads in parallel with high speed and low cost, thus overcome the limitations of first-generation sequencing technologies. Some common NGS platforms are Roche/454 sequencing, Ion torrent sequencing, Illumina/Solexa sequencing, ABI/SOLiD sequencing, etc (Kchouk et al., 2017).

1.5.3 Third generation sequencing

NGS technologies generally require PCR amplification step which takes long time and is expensive. In addition, NGS produces short reads which makes genome assembly difficult as genomes are complex with many repetitive areas. So, to solve this problem, third generation sequencing technology was developed. The third-generation sequencing require no PCR amplification and can produce long reads in less time and low cost. Two common third generation sequencing platforms are Pacific biosciences sequencing and Oxford nanopore sequencing (Kchouk et al., 2017).

1.6 Whole-genome sequencing (WGS)

Whole genome sequencing is a procedure that determines the order of bases in the genome of an organism in one process (Whole Genome Sequencing (WGS), 2019). The two major approaches for whole genome sequencing are the shotgun and the hierarchical (illustrated in Figure 5) (Xiong, 2006).

In the shotgun approach, the cloned DNA is sequenced randomly from both ends and many sequenced DNA fragments are generated that can overlap sufficiently to cover the entire genome. Since this approach is based on direct sequencing, it can produce draft sequences very rapidly but requires a powerful computer assembly program to assemble those sequences into a single, whole-genome sequence. This approach can be employed in sequencing small microbial genomes (Choudhuri & Kotewicz, 2014; Xiong, 2006).

In the hierarchical approach, firstly, the chromosomes are mapped using the physical mapping strategy, broken into longer fragments, and cloned into a high-capacity vector-like bacterial artificial chromosome (BAC) or yeast artificial chromosomes (YACs). Once the locations and orders of the BAC clones on a chromosome are determined based on the results of the physical mapping, the larger fragments in these clones are broken down into smaller fragments and then sequenced using a shotgun sequencing strategy. This approach is slow and expensive but less error prone. This approach can be used in sequencing a complex eukaryotic genome that contains high levels of repetitive sequences because the shotgun approach is less accurate and tends to leave more "holes" in the final assembled sequence in such cases (Choudhuri & Kotewicz, 2014; Xiong, 2006).

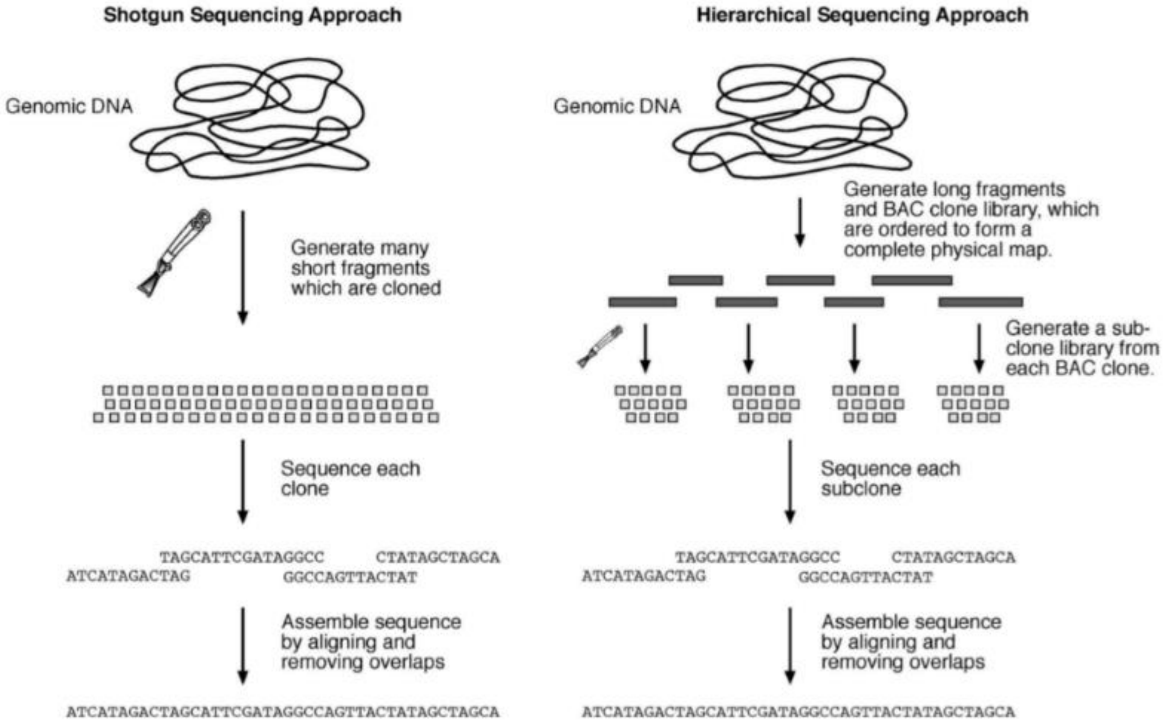


Figure 5: Comparison of two approaches of whole-genome sequencing. A: Shotgun approach B: Hierarchical approach (Xiong, 2006).

1.7 Genome assembly and relevant tools

Genome assembly is a computational process done after sequencing, in order to connect millions and billions of generated reads, to form a genome of an organism (Kalyanaraman et al., 2011; Pop, 2009; Wajid & Serpedin, 2016; Xiong, 2006). Genome assemblies offer a consensus representation of a genome, spanning all the chromosomes and extrachromosomal elements such as organellar genomes and plasmids (Pevsner, 2015).

Sequencing technologies generate reads (~500 to 2000 bases long) from DNA clones. The length of the reads varies according to the sequencing platform from which they are derived (as described in section 1.5). According to sequencing approaches, there are three different types of reads generated by sequencers, i.e., single-end read (read from only one sequence end of a fragment), paired-end reads (read from both sequence ends of a fragment) and mate pairs (read from both sequence ends of a fragment but larger than paired-end reads) (Ekblom & Wolf, 2014; He et al., 2013).

The reads are put together by a sequence assembler. The process of assembling the genome is shown in Figure 6. Firstly, these reads are overlapped and merged to form larger fragments called contigs (~5,000 to 10,000 bases long). Furthermore, several contigs are connected together in the correct orientation and order (based on the available information) to form longer scaffolds or supercontigs (~30,000 to 50,000 bases long) (Choudhuri & Kotewicz, 2014; He et al., 2013; Xiong, 2006). Usually, scaffold represents discontinuous region of genome consisting of contigs and the gaps between them. A scaffold linkage is represented by a directed graph where a node is a contig and a directed edge represents the order of two contigs (He et al., 2013).

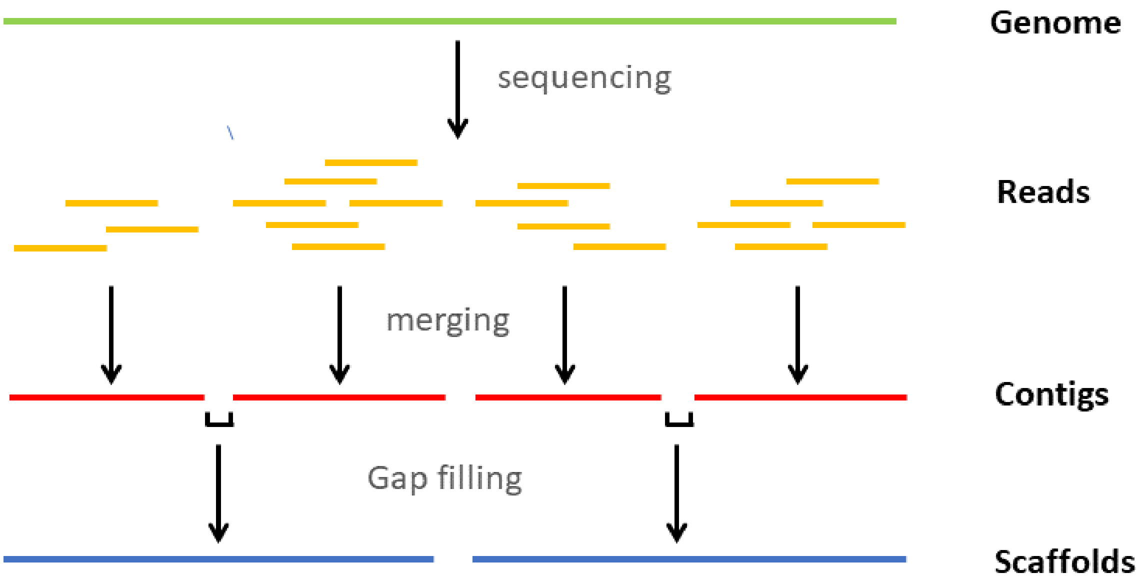


Figure 6: Process of genome assembly. Firstly, the genome is sequenced resulting in short reads. The assemblers merge the overlapping reads to form longer contigs, which are further joined by gap filling to form scaffolds. Finally, the scaffolds are linked together to form a consensus sequence.

There are two approaches for genome assembly: the *de novo* approach (for constructing genomes that are not similar to any previously sequenced genome) and the reference-based assembly approach (for assembling a genome using the sequence of a closely related organism as a guide). In the *de novo* assembly approach, sequence reads are aligned to each other and then overlapped to build longer contiguous sequences. In the reference-based assembly approach, each read is mapped to a reference genome sequence to form a complete genome

(Ng & Kirkness, 2010; Pop, 2009). The *de novo* genome assembly can be difficult while reference-based assembly can be easier. However, the two approaches are not exclusive because even if a reference genome is available, regions of the sequenced genome that differ significantly from the reference can only be reconstructed through *de novo* assembly (Pop, 2009).

There are various bioinformatic tools available for performing genome assembly. In early days, Newbler, Celera assembler, MIRA were used for assembling bacterial genomes that analysed overlaps between whole sequence reads to build a consensus (Segerman, 2020). Recent assemblers uses methods that divides the reads into k-mers and creates de Bruijn graphs (Pevzner et al., 2001). The first de Bruijn graphs-based assembler was VELVET. However, in the recent years SPAdes has become the most frequently used assembler. The de Bruijn graph assemblers with low but relatively consistent usage are SOAPdenovo, MEGAHIT, ABYSS, etc. For long PacBio reads, HGA and Canu assemblers are used but for long Oxford Nanopore reads Unicycler and Canu are used. Unicycler can process Illumina data using SPAdes so it can also be used for Illumina data alone (Segerman, 2020).

1.8 Study of antibiotic resistance in bacteria

1.8.1 Antimicrobial Susceptibility Testing (AST)

Antimicrobial susceptibility testing (AST) is a laboratory procedure performed by clinical laboratory technicians to identify which antimicrobial agent is effective for the treatment of individual patient. It helps in the phenotypic identification of susceptibility of a bacterium towards the antimicrobial agents (Bayot & Bragg, 2022; Jorgensen & Ferraro, 2009). It helps in the evaluation of treatment services provided by hospitals, clinics, and national programs for the control and prevention of infectious diseases (Bayot & Bragg, 2022). Currently, clinical laboratories use various methods of AST depending on the laboratory test menu. The commonly used AST test methods are broth dilution tests, antimicrobial gradient method, disk diffusion test and automated instrument systems (Jorgensen & Ferraro, 2009). The measurement and interpretation of results of these approaches depends upon the zone diameters in case of disk diffusion and minimal inhibitory concentration (MIC) in case of other methods, the interpretive criteria for both has been published in CLSI guideline (Jorgensen & Ferraro, 2009). MIC refers to the minimal concentration of drug that will inhibit growth of the bacteria. The susceptibility is a range of the average MICs for any given drug across the same bacterial species. If the average MIC for a species is in the resistant part of the range, the species is considered to have intrinsic resistance to that drug (C Reygaert, 2018).

1.8.2 Antimicrobial resistance (AMR) gene detection

The common molecular methods used for detection of AMR genes include PCR, DNA microarray, whole-genome sequencing (WGS), and matrix-assisted laser desorption ionization–time of flight mass spectrometry, among which, PCR and WGS seems to be the popular and easier methods in present context (Anjum et al., 2017). The PCR method includes PCR amplification of target DNA followed by amplicon confirmation by gel electrophoresis, probe hybridization techniques, or DNA sequencing (Cockerill, 1999).

Because of the recent advancement in fast and cost effective sequencing technologies, WGS has become easily accessible and an effective tool in prediction of antibiotic resistance gene (Galhano et al., 2021; Hendriksen et al., 2019). There are many freely accessible bioinformatics tools and databases for detection of AMR genes in DNA or amino acid sequence data like ARG-ANNOT, CARD, SRST2, MEGARes, Genefinder, ARIBA, KmerResistance, AMRFinder, ResFinder, etc (Hendriksen et al., 2019). The search for resistance genes is mostly done by methods (for instance, BLAST) that consider the similarity of the contigs to the genes contained in reference databases and the choice of database depends on both the purpose of each study and on the sequence deposited in each database (Galhano et al., 2021). The databases differ in several ways including type of accepted input data, presence/absence of software for search within a database, and the search approach employed which may be mapping or alignment. As a consequence, each tool has strengths and limitations in sensitivity and specificity of detection of AMR genes (Hendriksen et al., 2019).

1.9 Detection of plasmids and VF genes in bacteria using WGS

Various tools and databases for the detection of plasmids (that could harbour potential AMR or virulence genes) using WGS are available like PlasmidFinder, PGD, pATLAS, PLSDB, etc (Galata et al., 2019; Quainoo et al., 2017). The PlasmidFinder contains markers specific to Enterobacteriaceae plasmids and some gram-positive-organism-associated plasmids only

(Quainoo et al., 2017) whereas PLSDB is a set of complete bacterial plasmids from the NCBI database covering records from RefSeq and INSDC (which includes DDBJ, EMBL-EBI and GenBank) (Galata et al., 2019).

The detection of VF genes using conventional method like qPCR requires huge investment in primers and probe design. Also, the rapid evolution of bacteria leads to mutations in targets which could lead to negative qPCR results and redesigning of primers and probes delay diagnostics during outbreak analyses. So, WGS with VF detection tools and curated databases can be used to overcome these issues. VirulenceFinder and Virulence Factor Database (VFDB) are two web-based tool and resources. However, VirulenceFinder has genes for only *Listeria, S. aureus, E. coli*, or *Enterococcus*. Compared to VirulenceFinder, VFDB contains more VF genes (Quainoo et al., 2017).

2 Objective of the study

2.1.1 General Objective

This study aimed to perform genome assembly using whole genome sequence data obtained from *Acinetobacter baumannii* clinical isolates and then use the assembled genome to study the important factors related to its pathogenicity, virulence, and antimicrobial resistance between Norway and India using bioinformatic tools.

2.1.2 Specific Objectives

To achieve the main objective of the study, the following secondary objectives were implemented:

1. Test several bioinformatics tools on a subset of samples to find the best-suited trimmer and assembler and perform the genome assembly of all the samples using the selected tools.
2. Perform the downstream analyses of the assembled genome that belonged to *A. baumannii* to detect and identify the CDS, rRNA, tRNA, plasmids, AMR genes and virulence factors.
3. Analyze the detected AMR genes with the AST data provided by the hospitals to find the correlation between genotypic and phenotypic antimicrobial resistance.
4. Compare the prevalence of antimicrobial resistance of *A. baumannii* between Norway and India.

3 Material and methods

3.1 Illumina sequencing datasets

The Illumina reads obtained from MiSeq sequencer for 96 (94 paired-end and 2 single-end) *Acinetobacter baumannii* clinical isolates were provided in fastq format. Among them, 11 samples were from the Norwegian clinical isolates and 85 were from the Indian clinical isolates. The isolates were from different clinical samples collected from different hospitals of Norway and India. The AST result for the isolates were also provided. The WGS was done by Stephan A. Frye at Oslo universitetssykehus (OUS) and AST was done by Helene Bouras at Folkehelseinstituttet (FHI).

3.2 Design for bioinformatic analyses

The method for the bioinformatic study of the WGS data from *A. baumannii* clinical isolates is divided into the following parts (as shown in Figure 7):

A. Quality Control: Inspecting the quality of raw reads before performing genome assembly.

B. Genome assembly: The genome assembly part is further divided into two parts. Firstly, testing the bioinformatics tools on a subset of samples to find the best suited trimmer and assembler. Secondly, performing trimming and genome assembly of all the samples using the selected tools.

C. Exclusion of samples that was not *A. baumannii*: Excluding the assembled genomes that was not *A. baumannii* before performing the downstream analyses.

D. Downstream analyses of selected assembled genomes: Performing the downstream analyses of assembled genomes to detect and identify the CDS, rRNA, tRNA, plasmids, AMR genes and virulence factors.

E. Comparison of the detected AMR genes with the AST data: Comparing the AMR genes detected using bioinformatic tools with the AST data provided by the hospital.

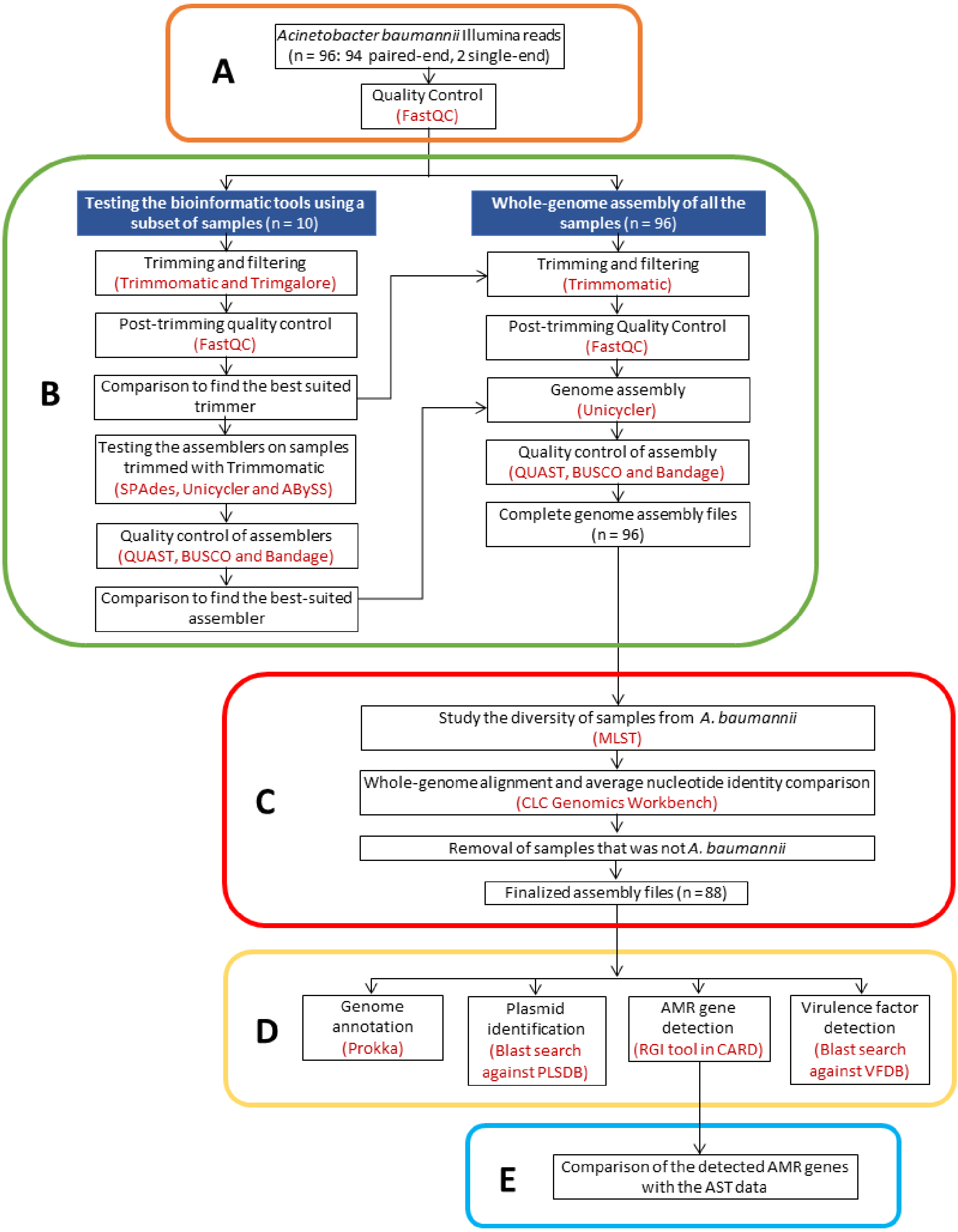


Figure 7: Flow chart showing the experimental design to study the whole genome sequence data from *A. baumannii* clinical isolates; A: Quality Control; B: Genome assembly; C: Exclusion of assembled genomes that was not *A. baumannii*. D: Downstream analyses of assembled genomes; E: Comparison of the detected AMR genes with the AST data (The black font indicates the method, and the red font indicates the tool(s) which were used).

3.3 Methods

3.3.1 Quality control

Quality control of the reads was performed using FastQC v0.11.9 (Andrews, 2019) in Linux. Number of sequences reads, GC (%), per base sequence quality, per sequence quality scores and adapter contamination for each sample were checked.

Furthermore, the number of base pairs (bp) for each sample were found using the following command in Linux terminal:

```
cat filename.fastq | paste - - - - | cut -f 2 | tr -d ‘\n’; | wc –c
```

The total sequence length of *A. baumannii* assembly with accession number: GCA_003264295.1 was retrieved from GenBank (Benson et al., 2015). This sample from now on is reference genome. The reference sample was chosen by comparing the median total sequence length and GC (%) from the available database to find the closest one. Then it was used to calculate the coverage of all the samples using the following formula:

$$\text{Coverage} = \frac{\text{Average number of basepairs in both reads}}{\text{total sequence length in reference genome}}$$

3.3.2 Testing the bioinformatic tools using a subset of samples

3.3.2.1 Selection of a subset of samples

A subset of 10 samples, 5 with low coverage (first 5 samples among the 11 samples with least coverage between 24x to 86x) and 5 with high coverage (first 5 samples among the 85 samples with high coverage between 86x to 355x) was chosen for testing the bioinformatic tools for trimming and genome assembly.

3.3.2.2 Testing the trimming tool

For trimming the low-quality reads and Illumina adapters, two bioinformatic tools, i.e., Trimmomatic v2.0.29 (Bolger et al., 2014) integrated with OmicsBox (*OmicsBox - Bioinformatics Made Easy*, 2019) and Trim Galore v0.6.6 (Krueger, 2020) both in Linux were tested on the subset of samples.

The default parameters used for trimming paired-end reads with Trimmomatic in OmicsBox are shown in Table 1.

Table 1: Default parameters used for trimming the paired-end reads with Trimmomatic in OmicsBox.

Parameter	**Value**
Upstream Files Pattern	_R1
Downstream Files Pattern	_R2
Quality Encoding	Autodetection
Remove Adapters	true
Use Adapters From	Default Adapter Sequences
Adapter Sequences	TruSeq3
Seed Mismatches	2
Palindrome Clip Threshold	30
Simple Clip Threshold	15
Minimum Adapter Length	8
Keep Both Reads	true
Trimming	true
Trimming Option	Sliding Window Trimming
Window Size	4
Required Quality	15
Filter By Quality	true
Average Quality	25
Filter By Length	True
Minimum Length	36
Output Prefix	Trimmed_

The trimming with Trim Galore was done using the following commands in the Linux terminal:

```
trim_galore --paired filename1.fastq filename2.fastq -o output_directory
```

The default parameters used for trimming with Trim Galore are shown in Table 2.

Table 2: Default parameters used for trimming the paired-end reads with Trim Galore.

Parameter	**Value**
Input filename	filename.fastq
Trimming mode	Paired-end
Trim Galore version	0.6.6
Cutadapt version	3.4
Number of cores used for trimming	1
Quality Phred score cutoff	20
Quality encoding type selected	ASCII+33
Adapter sequence	‘AGATCGGAAGAGC’ (Illumina TruSeq, Sanger iPCR; auto-detected)
Maximum trimming error rate	0.1 (default)
Minimum required adapter overlap (stringency)	1 bp
Minimum required sequence length for both reads before a sequence pair gets removed	20 bp

3.3.2.3 Post-trimming quality control

Quality control of the trimmed subset of samples was performed using FastQC v0.11.9 (Andrews, 2019) in Linux to confirm the complete removal of low-quality reads and adapter contaminants. Number of sequences reads, GC percentage, coverage, per base sequence quality, per sequence quality scores and adapter contamination for each sample after trimming were evaluated.

The number of base pairs (bp) was found and evaluated using the following command in the Linux terminal. The command is different from the one used in 2.3.1.1 because the raw data were in fastq.qz (compressed) format after trimming.

```
zcat filename.fastq.gz | paste - - - - | cut -f2 | wc –c
```

Finally, the parameters including number of sequences reads, GC percentage, coverage, per base sequence quality, per sequence quality scores, adapter content and number of base pairs of trimmed reads were compared with the pre-trimmed reads to confirm the improvement in the quality of reads and choosing the best suited trimming tool.

3.3.2.4 Testing the short reads assemblers

To find the best assembler for genome assembly, three bioinformatic tools, i.e., SPAdes v3.13.0 (Prjibelski et al., 2020), Unicycler v0.4.9 (Wick et al., 2017) and ABySS v2.0.36 (Simpson et al., 2009) integrated with OmicsBox (*OmicsBox - Bioinformatics Made Easy*, 2019) were used to assemble the trimmed subset of reads (trimmed with best suited trimmer).

The genome assembly with SPAdes was done using the following commands in Linux terminal:

```
spades.py -1 filename1_trimmed.fastq.gz -2 filename2_trimmed.fastq.gz -o
output_directory
```

The genome assembly with Unicycler was done using the following commands in the Linux terminal:

```
unicycler -1 filename1_trimmed.fastq.gz -2 filename2_trimmed.fastq.gz -o
output_directory
```

The genome assembly using ABySS integrated with OmicsBox was done with the parameters shown in Table 3 using five different k-mer values: 55 (default), 75, 95, 115 and 125.

Table 3: Parameters used for genome assembly using ABySS in OmicsBox.

Parameter	**Value**
Upstream Files Pattern	_R1_001
Downstream Files Pattern	_R2_001
Use additional Data	false
k-mer size	55 (default) or 75 or 95 or 115 or 125
Use Paired de Bruijn graph	false
Minimum Alignment length	40
Hash functions	1
k-mer Count Threshold	2
Save Graph Files	true

3.3.2.5 Quality control of assembled genomes created using different assemblers

In order to compare the quality of assembled genomes and choose the best tool, the quality of assembled genomes was evaluated using QUAST v5.1.Orc1(Gurevich et al., 2013) in Linux. Using QUAST different parameters such as number of contigs, N50, GC percentage and total length were obtained. Furthermore, to obtain genomic fraction (percentage of reference genome length, which is covered by assembled genomes, QUAST tool was run with reference genome option (an assembly with accession number: GCA_003264295.1 which was also used before for quality control in 2.3.1) using following command line:

```
python quast.py -r reference_genome assembly.fasta -o output_directory
```

The completeness of assembled genomes (created by different assemblers) was evaluated using BUSCO (Benchmarking Universal Single-Copy Orthologs) v5.2.2 (Simão et al., 2015) in online platform Galaxy v21.09.rc1(Afgan et al., 2018). BUSCO tested the assemblies for the completed, fragmented, and missing housekeeping genes in *A. baumannii*.

The assembly graph and number of dead ends of 10 assemblies (created by different assemblers) were visualized using Bandage (Wick et al., 2015). Dead ends are the termination found in genome which should not be present in a circular DNA of *A. baumannii*.

Finally, to find out the best assembly tool, parameters including number of contigs, N50, percentage GC, total length and genomic fraction (%) obtained from QUAST, in addition to BUSCO result and the dead ends obtained from Bandage were compared.

3.3.3 Whole genome assembly of all the samples

3.3.3.1 Trimming and filtering

According to the analysis performed in step 3.3.2.2, all the raw Illumina reads were trimmed using Trimmomatic integrated with OmicsBox with the parameters mentioned in step 3.3.2.2.

3.3.3.2 Post-trimming quality control

The post-trimming quality control for all the samples was performed as mentioned in step 3.3.2.3.

3.3.3.3 Genome assembly

According to the analysis performed in step 3.3.2.4, Unicycler was able to create the best assembly among other assemblers. Therefore, assembly of all other samples was performed using Unicycler as described in step 3.3.2.4.

3.3.3.4 Quality control of the assembly

The quality control of all the assemblies was performed as mentioned in step 3.3.2.5.

3.3.4 Exclusion of samples that was not *A. baumannii*

Assembled genomes were used for Multilocus sequence typing (MLST) analyses. Two MLST schemes, Oxford and Pasteur in MLST v2.0.1 (Larsen et al., 2012) integrated with OmicsBox were used to study the diversity of the *A. baumannii* clinical isolates.

Whole genome alignment and average nucleotide identity comparison of all the assembled genomes was performed using QIAGEN CLC Genomics Workbench v21.0.3 in Linux to find the level of similarity between the genome of all the samples with each other.

Then, the samples from the MLST result as well as the average nucleotide identity comparison were compared. The isolates having no match or partial match in either Oxford or Pasteur scheme with alignment percentage (AP) ≤ 70% and average nucleotide identity (ANI) ≤ 90%, were removed before further analysis.

Finally, the taxonomic classification of the samples to be removed was done using Kraken v2.1.2 (Wood et al., 2019; Wood & Salzberg, 2014) in OmicsBox with the default parameters (Enable Filter = Yes, Kraken Confidence Filter = 0.05 and Minimum Hit Groups = 2).

3.3.5 Bioinformatic analyses of all the assembled genomes

3.3.5.1 Genome annotation

Using Prokka v1.14.6 (Seemann, 2014) in Linux, all the assembled genomes were annotated to find the number of coding sequences (CDS), ribosomal RNA (rRNA), transfer RNA (tRNA) and transfer messenger RNA (tmRNA). The following command was used in terminal for annotation:

```
prokka assembly.fasta --outdir output_directory --prefix Prokka_
```

The Prokka results were saved in .tsv file and to calculate the number of hypothetical proteins and putative proteins, the following commands were used in terminal:

`grep -wc ‘hypothetical protein’ filename.tsv` (to find the hypothetical protein)

`grep -wc ‘putative protein’ filename.tsv` (to find the putative protein)

3.3.5.2 Plasmid identification

For identifying plasmids in the assembly files, PLSDB database v0.4.1 (Galata et al., 2019) was downloaded in the ready for BLAST format (containing .nin, .nsq, .nhr files). The assembly files were BLAST searched against the PLSDB database using Local BLAST (BLAST+) v2.2.25 (Camacho et al., 2009) in Linux with the following command in the terminal:

```
blastn -query assembly.fasta -db plsdb.fna -outfmt "6 qseqid sseqid salltitles qstart qend sstart send qcovs qlen slen length pident evalue" -perc_identity 95 -word_size 28 -out filename.tsv
```

In the above command, the output of BLAST search was formatted according to the need. The meaning of the options used in the output format are as follows:

qseqid: Query Sequence-id

sseqid: Subject Sequence-id

salltitles: All subject titles

qstart: Start of alignment in query

qend: End of alignment in query

sstart: Start of alignment in subject

send: End of alignment in subject

qcovs: Query coverage per subject

qlen: Query sequence length

slen: Subject sequence length

length: Alignment length evalue: Expect value

pident: Percentage of identical matches

BLAST results revealed several plasmids hits per each assembly file. Only hits passing the criteria mentioned in Table 4 were considered as true plasmid hits.

Table 4: Selection criteria for filtration of plasmids from blast search.

Parameter	**Value**
Percentage identity	≥ 95%
e-value	0
Query sequence length / Subject length	100± 10%
Alignment length / Query sequence length	100± 10%
Alignment length / Subject sequence length	100± 10%

In case of multiple plasmid hits per contig, further selection of one plasmid per one contig was done by comparing and selecting the plasmid with best parameters among the multiple plasmid hits within single contig. If all the parameters among the multiple plasmid hits were same, all of them were selected even if they belonged to a single contig.

Later the occurrence of different plasmids in the whole dataset was counted.

3.3.5.3 Antimicrobial resistance (AMR) gene detection

All the assembled genomes were submitted to RGI v5.2.0 tool in CARD v3.1.4 (Alcock et al., 2019) for the prediction of resistance gene.

The results obtained from RGI (.tsv file) for all the assemblies were filtered for the Cut_Off value “Perfect” using the following command in Linux terminal:

```
grep ‘Perfect’ *.txt > new_filename.ods
```

The occurrence of each resistance gene, drug class and resistance mechanism were counted based on RGI output. Furthermore, to identify the AMR genes carried by plasmids, the contig ID of AMR genes and plasmids were compared. If both shared the same contig ID, it was concluded that the gene is carried by the plasmid.

3.3.5.4 Virulence factor (VF) detection

For VF gene prediction, VFDB database (B. Liu et al., 2019) was downloaded in fasta format. Downloaded fasta file was used to create the BLAST database (.nin, .nsq, .nhr) with the following commands in the Linux terminal:

```
makeblastdb -in downloaded_VFDB.fasta -dbtype nucl -out filename
```

The assembly files were blast searched against the VFDB database using Local BLAST (BLAST+) v2.2.25 (Camacho et al., 2009) in Linux with the following command in the terminal:

```
blastn -query assembly.fasta -db vldb -outfmt "6 qseqid sseqid salltitles
qstart qend sstart send qcovs qlen slen length pident evalue" -perc_identity
95 -word_size 28 -out filename.tsv
```

The description of the command line options is provided in 3.3.5.2.

Among several VF genes obtained per each assembly files, only VF genes having the percentage identity ≥ 95%, e-value = 0 and Alignment length / Subject sequence length = 100± 10%, were considered as true VF genes.

At the end, the occurrence of different VF genes in the whole dataset were counted. The contig ID of VF genes and plasmids were compared to find the VF genes carried by plasmids. If both shared the same contig (same contig ID), it was concluded that the gene is carried by the plasmid.

3.3.6 Comparison of detected AMR genes with the Antimicrobial sensitivity test (AST) data

The antimicrobial susceptibility test (AST) result for 6 antibiotics (Amikacin, Ceftazidime, Aztreonam, Piperacillin, Imipenem and Ciprofloxacin) was available for 73 out of total 77 Indian *A. baumannii* isolates. Furthermore, AST result for 9 antibiotics (Amikacin, Imipenem, Ciprofloxacin, Meropenem, Gentamicin, Tobramycin, Trimethoprim, Tigecycline and Colistin) was available for all the 11 Norwegian *A. baumannii* isolates. The AST for the Indian and Norwegian isolates were done by Kirby-Bauer disk diffusion method (Bauer et al., 1966) and broth dilution method respectively.

The antibiotic class for which the detected AMR genes confer resistance was obtained via CARD database. Then, to compare the resistance conferred by the detected AMR genes (genotypic data) with the AST result (phenotypic data), the antibiotic class in which the above-mentioned antibiotics belonged was determined. After that, the genotypic and the phenotypic data was compared to check the similarity and differences in the susceptibility and resistance towards the antibiotic/antibiotic class. While comparing, the samples with intermediate resistance in AST was considered as resistant.

4 Results

4.1 Statistics of illumina sequencing datasets

The summary of sequencing statistics for *A. baumannii* clinical isolates obtained by the Illumina sequencing platform is shown in Appendix A. A total of 96 (94 paired-end and 2 single-end) reads generated by the Illumina sequencing platform was provided in fastq format. Among them, 11 reads were from the Norwegian isolates and 85 reads were from the Indian isolates.

The average number of base pairs (bp), average number of reads and mean coverage, of all the 96 samples was found to be 549,362,884, 3,567,913 and 138.21 respectively. A clear difference was observed between the Norwegian and the Indian datasets. The file size of Norwegian datasets was comparatively less (200 MB – 750 MB) while that of Indian dataset was high (800 MB – 3.5 GB) before trimming. In the Norwegian dataset, the number of base pairs (bp) was comparatively lower (ranging from 325,896 to 1,124,724) than that of the Indian dataset (ranging from 2,283,995 to 9,356,696). Also, the mean coverage was comparatively low for the Norwegian dataset (between 24x to 86x) than that of the Indian dataset (between 86x to 355x).

The FastQC report also displayed the difference in the quality of these two datasets. The Norwegian dataset had low per base sequence quality (phred score ≤ 20) (Figure 8A) and high degree of adapter contamination (Figure 8C). But the Indian dataset displayed good per base sequence quality (phred score ≥ 20) (Figure 9A) and very less degree of adapter contamination (Figure 9C).

4.2 Trimmomatic was choosen for trimming of the reads

Within the 10 samples chosen for testing the trimming tools, all the 5 samples with low coverage were from Norwegian isolates and all the 5 samples with high coverage were from Indian isolates.

The average of post-trimming quality control results obtained after trimming the subset of samples with Trimmomatic and Trim Galore are shown in Table 5. After trimming the reads with Trimmomatic, the GC percentage and the retained average number of reads sequenced for all the 10 samples were almost similar to the one before trimming. However, the average base pairs (bp) retained for Norwegian samples after trimming was found to be 55.61% which is very low as compared to Indian samples which was 96.25%. The mean coverage (after trimming) for Norwegian samples was found to be 24.61x which is also low as compared to Indian samples which is 146.06x.

To improve the trimming output for the Norwegian isolates, the Trim galore was tested. The average base pairs (bp) retained after trimming was found to be 56.92% and the average coverage was found to be 25.19x. Trimming using Trim Galore resulted in 2.42% higher recovered sequence reads and a marginal increase in base pair retained (1.31%) as well as coverage (0.58%) in dataset from Norway. A similar trend was observed for the dataset from India. Considering neglectable improvement and previous experience with Trimmomatic in the bioinformatics group at INN, it was decided to use Trimmomatic for trimming all the samples.

Table 5: Results of post-trimming quality control obtained after trimming the subset of samples with Trimmomatic and Trim Galore.

Parameters	**Trimmomatic**		**Trim Galore**	
	Norwegian samples	**Indian samples**	**Norwegian samples**	**Indian samples**
GC (%)	40	38.2	40	38.2
Average retained number of reads sequenced after trimming	96.86%	97.02%	99.28%	99.91%
Average base pairs (bp) retained after trimming	55.61%	96.25%	56.92%	99.29%
Average coverage after trimming	24.61x	146.06x	25.19x	150.68x

4.3 Quality of reads was improved after trimming with Trimmomatic

Figure 8 and Figure 9 show the FastQC report before and after trimming of low-quality reads and adapters, for the reads having low coverage (from Norwegian isolates) and high coverage (from Indian isolates) respectively. In both Figure 8 and 9, the box and whisker plot of per base sequence quality of reads before (A) and after (B) trimming and the graph showing adapter content of reads before (C) and after (D) trimming can be observed. In box and whisker plot of per base sequence quality, the yellow box plots (box: interquartile ranges 25-75%, red bar: median, and whisker: 10-90% percentile) show the base-calling quality scores across all sequencing reads and the blue line indicates the mean quality score. In graph of adapter content, the curve line shows the amount of adapter contamination, and the colour of the curve indicates the type of adapter.

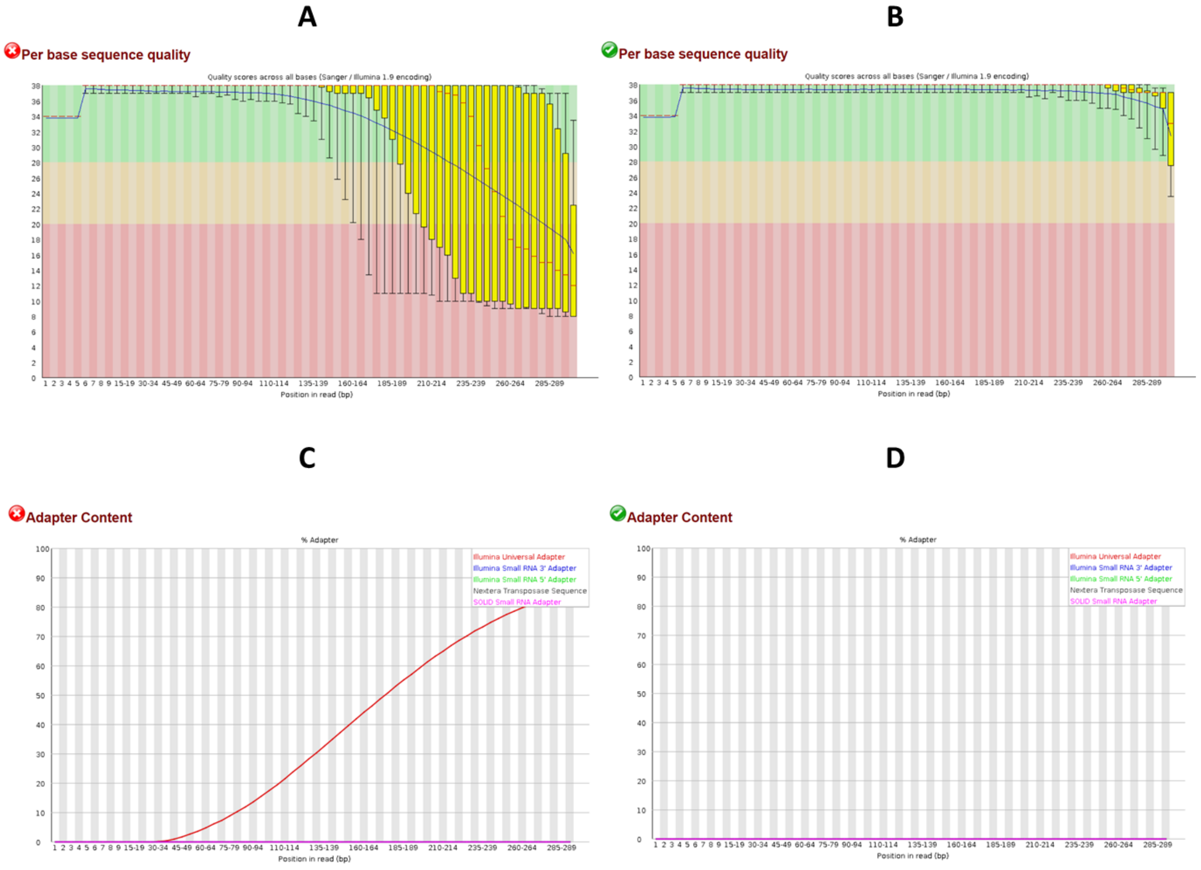


Figure 8: FastQC report generated for low coverage reads before and after trimming with Trimmomatic in Norwegian dataset. Box and whisker plot showing a considerable higher phred scores across the reads after trimming (B) compared to before trimming (A). Graph showing high amount of adapter contamination before trimming (C) which was removed successfully after trimming (D).

It can be observed in Figure 8 (A) that the quality score of low coverage data is less, which can be seen to be improved in Figure 8 (B) after trimming. In Figure 9 (A), the quality score of the high coverage data can be observed, which is not low as compared to the low coverage data. However, slight improvement in the quality score can be observed after trimming in Figure 9 (B).

In Figure 8 (C) there is high degree of adapter (Illumina Universal adapter) contamination present in the low coverage reads before trimming, which can be observed to be successfully removed after trimming with Trimmomatic in Figure 8 (D). However, there was less degree of adapter contamination in high coverage data as shown is Figure 9 (C) that has also been removed after trimming which can be seen in Figure 9 (D). Overall, these results indicate that the quality of the reads was improved after trimming the raw reads using Trimmomatic.

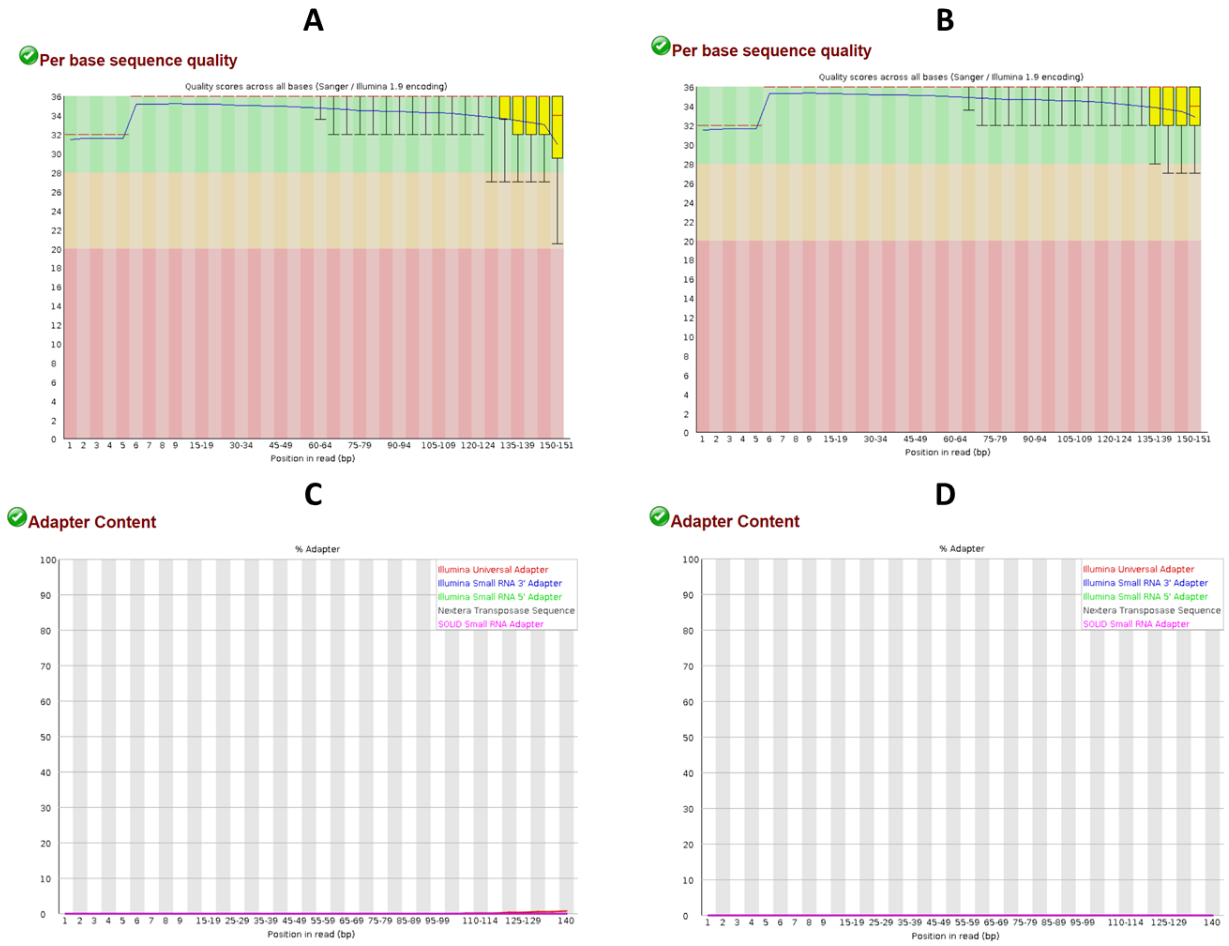


Figure 9: FastQC report generated for high coverage reads before and after trimming using Trimmomatic in Indian dataset. Box and whisker plot showing a considerable higher phred scores across the reads after trimming (B) compared to before trimming (A). Graph showing high amount of adapter contamination before trimming (C) which was removed successfully after trimming (D).

4.4 Unicycler was choosen as a short read assembler

Table 6 represents the mean and median value (in parentheses) of different parameters obtained using QUAST, Bandage and BUSCO on the subset of assemblies created using different tools.

It can be observed that the average values for number of contigs was least, the value of N50 was highest and the number of dead ends was less for assemblies created using Unicycler but the total sequence length and genome fraction (%) seems to be highest for the assemblies created using SPAdes. Similarly, the median values for number of contigs was least, genome fraction was highest, and the number of dead ends was less for assemblies created using Unicycler whereas the value of N50 and total sequence length was highest for assemblies created using SPAdes. There is not much difference in both the mean and median value of GC (%) among the assemblies created using different assemblers. The value of completed, fragmented and missing BUSCO was best for assemblies created using Unicycler. Considering the best value of N50, dead ends and BUSCO obtained using Unicycler and only slight difference in the value of other parameters, it was concluded that Unicycler was the best suited assembler to carry out the assembly of all the genome.

Table 6: The mean and median value (in parentheses) of different parameters obtained using QUAST, Bandage and BUSCO on the subset of assemblies created with ABySS (using five different k-mer values), SPAdes and Unicycler. The values in bold font represent the best among all.

Parameters	**ABySS**					**SPAdes**	**Unicycler**
	55 k-mer (default)	**75 k-mer**	**95 k-mer**	**115 k-mer**	**125 k-mer**		
No. of contigs	976 (830)	687 (546)	651 (649)	767 (441)	859 (549)	246 (118)	**98 (98)**
N50	18276 (15644)	45768 (45590)	62995 (61321)	67957 (61139)	65820 (62296)	136350 (**138314)**	**137900** (124782)
GC (%)	38.90 (38.90)	38.95 (38.97)	38.99 (39.02)	39.04 (39.03)	39.07 (39.04)	39.20 (38.98)	38.96 (38.96)
Total sequence length	3954116 (3987636)	4035004 (4006553)	4076113 (4038152)	4038727 (3958236)	4001474 (3940137)	**4198808 (4229386)**	4053189 (3993921)
Genome fraction	86.22% (87.18%)	88.37% (88.82%)	88.74% (88.48%)	87.86% (89.17%)	87.01% (89.16%)	**90.38%** (89.81%)	89.72% (**91.55%)**
Dead ends	-	-	-	-	-	1503	**24**
BUSCO Completed	84.39 (85.80%)	90.73 (92.30)	93.16 (94.16)	92.52 (94.90)	91.21 (96.25)	98.25 (98.25)	**98.4 (98.30)**
BUSCO Fragmented	12.25 (11.20%)	7.18 (6.15)	5.32 (3.95)	5.73 (3.80)	6.71 (2.85)	0.89 (0.95)	**0.84 (0.80)**
BUSCO Missing	3.36 (2.45%)	2.09 (1.55)	1.52 (1.40)	1.75 (1.30)	2.08 (1.15)	0.86 **(0.90)**	**0.78 (0.90)**

4.5 Assembled genomes were found to be compatible with the reference genome

Table 7 presents the mean and median value of different parameters obtained after assessment of all the assembled genome using QUAST and BUSCO.

The median value for assembled genome size (3,990,212) and GC percentage (38.93) in this study were close to the reported median values for reference genome (GCF_003464295.1) in NCBI which was 3,974,327 and 38.9107 respectively. Similarly, it was also close to the median values for all the *A. baumannii* isolates in NCBI which was 3,974,730 and 39% respectively. However, the median value for number of contigs was higher and the median value for N50 was lower than that of the reference genome which was 2 and 3,909,773 respectively.

It is clear from the table that the number of completed BUSCO is high and the number of fragmented and missing BUSCO is low indicating the completeness of the assembled genome.

Table 7: Mean and median value of different parameters obtained after quality assessment of all the assembled genome using QUAST and BUSCO.

Parameters	**Mean value**	**Median value**
Contigs	120	89
Total sequence length	4208023	3990212
GC (%)	39.26	38.93
N50	155265	137379
Genome fraction	82.57%	86.06%
BUSCO Completed	98.07	98.30
BUSCO Fragmented	1.02	0.80
BUSCO Missing	0.92	0.90

Figure 10 represents the Bandage assembly graph with the lowest and highest number of dead ends for the assemblies created using Unicycler.

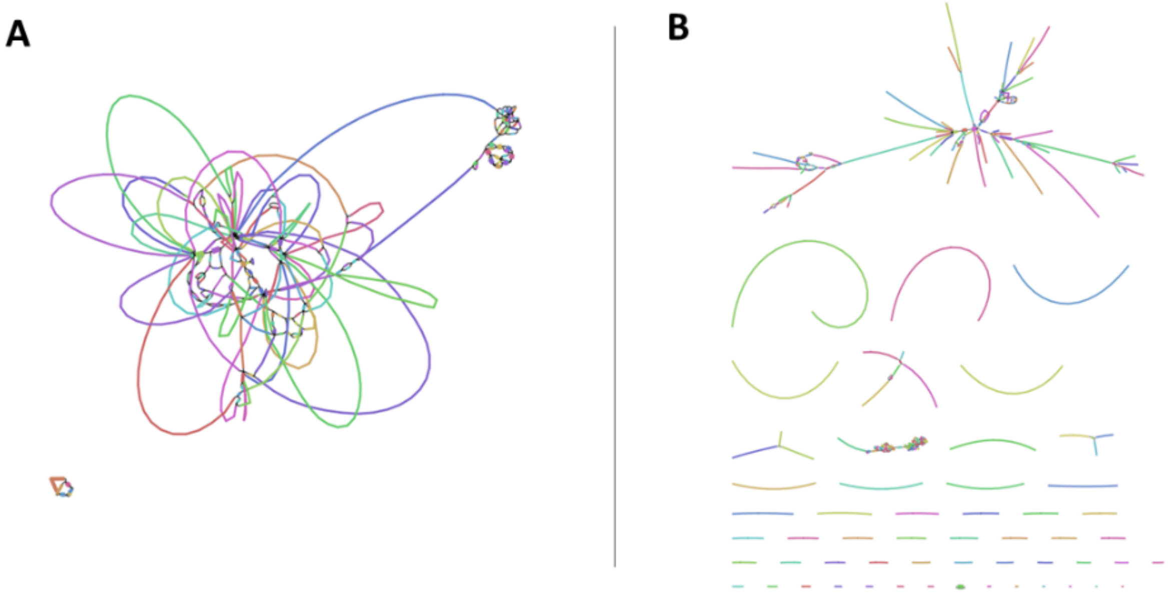


Figure 10: Representative assembly graphs for assemblies created using Unicycler; A: Graph with the lowest number of dead ends; B: Graph with the highest number of dead ends

4.6 Eight assemblies were found to be not *A. baumannii*

According to the Oxford scheme of MLST, out of total 96 isolates, 80 were matched, 14 were partially matched and 2 were not matched to *A. baumannii*. In case of Pasteur scheme, 88 were matched, 5 were partially matched and 3 were not matched to *A. baumanii*.

The result of WGA of all the 96 isolates is shown in Appendix B. It can be observed that 3 isolates (Lot1_P6, Lot2_P21 and Lot3_P33) indicated with blue gradient, have very low ANI and AP showing less identity with the other samples.

After comparing the results of MLST and WGA, 8 of the isolates did not match (having no match or partial match in Oxford or Pasteur scheme with AP ≤ 70 and ANI ≤ 90) to the *A. baumannii* and were decided to be excluded before performing the downstream analyses. The average ANI and average AP for all the samples after excluding these 8 isolates were 96.31% and 74.37% respectively. Table 8 show the eight isolates that were excluded before downstream analyses with the respective average ANI, average AP, and taxonomic classification.

Table 9 shows the occurrence of isolates that belong to a particular sequence type according to the Oxford and Pasteur schemes of MLST. According to the Oxford scheme, the majority of *A. baumanni* isolates were found to be matched with sequence type 2 followed by sequence type 149. For the Pasteur scheme, the majority of *A. baumanni* isolates were matched with unknown sequence type followed by sequence type 451!, 1809!, 848!, 1956! and 1051.

Table 8: Results obtained from MLST (Oxford and Pasteur) and WGA (average ANI and average AP) for the isolates that were not *A. baumannii* with their taxonomic classification.

Isolates	**OXFORD**	**PASTUER**	**Average ANI**	**Average AP**	**Taxonomic classification**
Lot1_P6	No match	No match	2.70	2.04	*Proteus mirabilis*
Lot1_P17	Partial match	Partial match	88.46	49.06	*A. pittii*
Lot1_P18	Partial match	Partial match	88.46	49.04	*A. pittii*
Lot2_P21	Partial match	No match	82.98	12.29	*A. haemolyticus*
Lot3_P33	No match	No match	2.70	2.04	*Proteus mirabilis*
Lot3_P45	Partial match	Partial match	88.46	49.04	*A. pittii*
Lot3_P46	Partial match	Partial match	88.46	49.07	*A. pittii*
Lot4_P53	Partial match	Match	96.30	59.41	*A. pittii*

Table 9: Number of isolates having particular sequence type found using Oxford and Pasteur scheme of MLST. The asterisk (*) sign indicates that the Sequence Type number is not a 100% match.

OXFORD scheme		**PASTEUR scheme**			
Sequence Type	**No. of isolates**	**Sequence Type**	**No. of isolates**	**Sequence Type**	**No. of isolates**
2	39	Unknown	16	1390	2
149	11	451!, 1809!	10	691	1
Unknown	10	848!, 1956!	10	452!	1
575	8	1051	10	191!	1
1	6	1053	7	348!, 1808!	1
575*	6	1506	6	218!	1
94	4	1050	5	236	1
10	3	2062!, 2063!	4	1388	1
25	2	195!, 1816!	3	784!, 1852!	1
52	2	582	2	1313	1
149*	2	349!, 1838!	2	1052	1
15	1	231!, 1604!	2	1503!	1
45	1	447	2	192!	1
338	1	861	2	369!, 1837!	1

4.7 Results of genome annotation was found comparable to the *A. baumannii* reference genome

Table 10 illustrates the mean and standard deviation (SD) of the number of CDS, rRNA, tRNA, tmRNA, hypothetical protein, putative protein and the CDS excluding hypothetical and putative protein found in the assemblies using Prokka and the same in the reference sample. Higher CDS and lower rRNA and tRNA can be observed in mean value of samples as compared with that of the reference sample.

Table 10: The mean and standard deviation (SD) of the number of CDS, rRNA, tRNA, tmRNA, hypothetical protein, putative protein and the CDS excluding hypothetical and putative protein found in the assemblies using Prokka and the same in the reference genome.

	Samples (n=88) Mean (SD)	**Reference genome (GCF_003464295.1)**
CDS	3966 (854.61)	3724
rRNA	3 (0.67)	18
tRNA	62 (14.43)	73
tmRNA	1 (0.32)	1
Hypothetical protein	1737 (356.59)	1585
Putative protein	22 (6.97)	20
CDS – (hypothetical protein + putative protein)	2207 (514.18)	2119

4.8 Plasmid pVB11737_6 was found in majority of *A. baumannii* isolates

In total, 40 unique plasmids were identified from all the isolates. The details of all the 40 unique plasmids identified is shown in Appendix C. Among them, the top ten mostly occurring plasmids in *A. baumannii* with their name, accession number, source organism and occurrence (in descending order) are shown in Table 11. The most frequently occurring plasmid in both Norwegian (4 out of 16 plasmids) and Indian (56 out of 161 plasmids) isolates was found to be pVB11737_6 (60 out of 177 plasmids in total). Six out of forty detected plasmids were common between both Indian and Norwegian isolates. The plasmids that belong to the other *Acinetobacter* species (than *A. baumannii*) i.e., *A. serfertii* and *A. schindleri* were detected in both Norwegian and Indian isolates and the plasmids from the genus other than *Acinetobacter*, i.e., *Klebsiella pneumoniae* and *Klebsiella oxytoca* were also detected in the Indian isolates.

Table 11: List of top 10 mostly occurring plasmids in *A. baumannii* isolates with their name, accession number, source organism and occurrence.

Name of the plasmid	**Accession Number**	**Source organism**	**Occurrence in**		
			Norwegian isolates	**Indian isolates**	**Total**
pVB11737_6	NZ_CP050397.1	*A. baumannii*	4	56	60
p2AB5075	NZ_CP008708.1	*A. baumannii*	1	10	11
pABAUUSACASD_frag2	CP064294.1	*A. baumannii*	0	11	11
pAS5-3	NZ_CP061686.1	*A. seifertii*	0	8	8
pVB2486_4	NZ_CP050407.1	*A. baumannii*	2	6	8
pYQ12450	NZ_KR059864.1	*Klebsiella pneumoniae*	0	8	8
pVB11737_4	NZ_CP050395.1	*A. baumannii*	0	7	7
p3KSK1	NZ_CP072125.1	*A. baumannii*	0	6	6
pVB473_1	NZ_CP050389.1	*A. baumannii*	0	6	6
pPM193665_3	NZ_CP050418.1	*A. baumannii*	0	5	5

4.9 *adeK* gene and efflux pump resistance mechanism were found in majority of *A. baumannii* isolates

In total, 57 unique AMR genes were identified from all the *A. baumannii* isolates. The details on the antibiotics to which these genes confer resistance and their occurrence are shown in Appendix D. Among them, the list of top ten mostly occurring AMR genes are presented in Table 12. The AMR genes found in majority of *A. baumannii* isolates were *adeK* (87 out of 88 total isolates) followed by *adeI* (85 out of 88 total isolates). The highest occurring gene was same for both the Norwegian and Indian isolates. Both of the genes confer resistance to macrolide, fluoroquinolone, lincosamide, carbapenem, cephalosporin, tetracycline, rifamycin, diaminopyrimidine, phenicol and penem.

Table 12: List of top 10 mostly occurring AMR genes in *A. baumannii* isolates with their name, antibiotic class to which it confers resistance and occurrence (in descending order).

AMR gene	**Antibiotic class to which resistance is conferred**	**Occurrence in**		
		Norwegian isolates	**Indian isolates**	**Total**
adeK	macrolide; fluoroquinolone; lincosamide; carbapenem; cephalosporin; tetracycline; rifamycin; diaminopyrimidine; phenicol; penem	11	76	87
adeI	macrolide; fluoroquinolone; lincosamide; carbapenem; cephalosporin; tetracycline; rifamycin; diaminopyrimidine; phenicol; penem	11	74	85
AbaQ	fluoroquinolone	10	70	80
OXA-23	carbapenem; cephalosporin; penam	9	69	78
adeL	fluoroquinolone; tetracycline	7	67	74
msrE	macrolide; lincosamide; streptogramin; tetracycline; oxazolidinone; phenicol; pleuromutilin	8	65	73
mphE	macrolide	8	64	72
abeS	macrolide; aminocoumarin	11	59	70
armA	aminoglycoside	4	60	64
AbaF	fosfomycin	6	52	58

Table 13 represents the occurrence of AMR genes with respective AMR gene class/family and resistance mechanism (in descending order) in *A. baumannii* isolates. In total, 21 unique AMR gene class/family and 6 unique resistance mechanisms were identified in *A. baumannii* isolates. It is apparent from Table 13 that the antibiotic efflux pumps (693 out of 1450 genes) followed by antibiotic inactivation (511 out of 1450 genes) were the two most dominant resistance mechanisms in *A. baumannii*. This is true for both the Norwegian and Indian isolates. Among the antibiotic efflux pump genes, resistance-nodulation-cell division (RND) (393 out of total 693) was the highest occurring AMR gene family in *A. baumannii* followed by major facilitator superfamily (MFS) (228 out of total 693) and Small Multidrug Resistance (SMR) (70 out of total 693). The result was same for independent Norwegian and Indian isolates. Regarding the antibiotic inactivation causing enzymes, β-lactamases (295 out of 511 enzymes) are the one having highest occurrence in *A. baumannii*. Comparison among the β-lactamases showed that Class D β-lactamases/oxacillinases (particularly OXA-23) were the most abundant β-lactamases.

Table 13: List of detected AMR genes with the respective AMR gene class/family, resistance mechanism and occurrence.

Resistance Mechanism	**AMR gene Class / Family**	**AMR genes (Occurrence in total isolates)**	**Occurrence in**		
			Norwegian isolates	**Indian isolates**	**Total**
Antibiotic efflux pumps	Resistance Nodulation Cell Division (RND)	*adeA* (38), *adeC* (40), *adeF* (10), *adeG* (49), *adeI* (85), *adeK* (87), *adeL* (74), *adeR* (10)	59	334	393
	Major Facilitator Superfamily (MFS)	*AbaF* (58), *AbaQ* (80), *AmvA* (10), *cmlA5* (31), *qacEdelta1* (48), *tet(39)* (1)	27	201	228
	Small Multidrug Resistance (SMR)	*abeS*	11	59	70
	Multidrug And Toxic Compound Extrusion (MATE)	*abeM*	0	2	2
Antibiotic inactivation	Class D β-lactamases (oxacillinases)	*OXA-104* (13), *OXA-120* (1), *OXA-129* (2), *OXA-144* (14), *OXA-20* (1), *OXA-23* (78), *OXA-51* (1), *OXA-58* (1), *OXA-64* (2), *OXA-66* (40), *OXA-68* (3), *OXA-69* (10), *OXA-72* (1), *OXA-98* (2)	23	146	169
	Macrolide phosphotransferases (MPH)	*mphE*	8	64	72
	Class C β-lactamases	*ADC-11* (2), *ADC-115* (1), *ADC-158* (2), *ADC-185* (1), *ADC-191* (2), *ADC-30* (20), *ADC-73* (17), *ADC-76* (18)	6	57	63
	APH(3') aminoglycoside phosphotransferase	*APH(3')-Ia* (39), *APH(3')-VIa* (21)	5	55	60
	Class A β-lactamases	*TEM-1* (19), *PER-7* (37)	6	50	56
	rifampin ADP-ribosyltransferase (Arr)	*arr-2*	1	32	33
	chloramphenicol acetyltransferase (CAT)	*catB8* (18), *catI* (2)	3	17	20
	ANT(3") aminoglycoside nucleotidyltransferase	*aadA*	1	10	11
	Bleomycin resistant protein	*BRP(MBL)*	0	10	10
	streptothricin acetyltransferase (SAT)	*SAT-2*	0	8	8
	Class B β-lactamases	*NDM-1*	0	7	7
	AAC(6') aminoglycoside acetyltransferase	*AAC(6')-Ian*	0	2	2
Antibiotic target replacement	Sulfonamide resistant sul	*sul1* (57), *sul2* (48)	11	94	105
	trimethoprim resistant dihydrofolate reductase dfr	*dfrB5*	0	2	2
Antibiotic target protection	ABC-F ATP-binding cassette ribosomal protection protein	*msrE*	8	65	73
Antibiotic target alteration	16S rRNA methyltransferase	*armA*	4	60	64
Reduced permeability to antibiotic	Intrinsic peptide antibiotic resistant Lps	*LpsB*	0	2	2
		Total	173	1277	1450

4.10 Four AMR genes were found to be associated with plasmids

Table 14 presents an overview of the occurrence of AMR genes associated with the respective plasmids and the antibiotic class to which it confers resistance. Out of 40 unique plasmids detected, only 3 plasmids, i.e., pVB11737_5, pYQ12450 and pPM192696_1 were found to contain AMR genes *sul2*, *BRP(MBL)* & *NDM-1* and *APH(3')-VIa* respectively (as the plasmids and the ARG shared the same contig). *BRP (MBL)* and *NDM-1* are the two AMR genes (both carried by plasmid pYQ12450) having the highest occurrence. The source organism for plasmid pYQ12450 was found to be *Klebsiella pneumoniae* while the other two AMR genes associated plasmids were originally from *A. baumannii.* Most of the AMR genes associated with plasmids were found in Indian isolates and *sul2* was the only plasmid associated AMR gene found in Norwegian isolates.

Table 14: AMR genes associated with plasmids, with their occurrence and the drug class for which it causes resistance.

Plasmid (Source organism)	**Associated ARG**	**Antibiotic class to which resistance is conferred**	**Occurrence in**		
			Norwegian isolates	**Indian isolates**	**Total**
pVB11737_5 *(A. baumannii)*	*sul2*	sulphonamide	1	2	3
pYQ12450 (*Klebsiella pneumoniae)*	*BRP(MBL)*	glycopeptide	0	8	8
	NDM-1	carbapenem, cephalosporin, cephamycin, penam	0	6	6
pPM192696_1 (*A. baumannii)*	*APH(3')-VIa*	aminoglycoside	0	1	1

4.11 Acinetobactin virulence gene cluster was found in majority of *A. baumanniii* isolates

Table 15 illustrates the VF genes detected with the corresponding virulence factors they confer and their occurrence in the order from highest to lowest. As can be seen from the table, *bas* genes are the VF genes having highest occurrence followed by *bau* genes, both of which belong to the acinetobactin gene cluster. This is true for both Norwegian and Indian isolates. The *bar* and *ent* genes involved in this cluster were also detected.

Table 15: Detected virulence factor genes with the respective virulence factor they confer and their occurrence. The numbers in the bracket indicate the occurrence of each gene.

Virulence factor genes	**Virulence factor**	**Occurrence in**		
		Norwegian isolates	**Indian isolates**	**Total**
basA (68), *basB* (88), *basC* (87), *basD* (87), *basF* (87), *basG* (87), *basH* (87), *basI* (85), *basJ* (86)	Acinetobactin (siderophore)	98	664	762
bauA (55), *bauB* (87), *bauC* (88), *bauD* (86), *bauE* (87), *bauF* (88)	siderophore receptor / transporter	62	429	491
csuA (68), *csuA/B* (68), *csuB* (69), *csuC* (69), *csuD* (69), *csuE* (70)	Csu pili; Biofilm; Biofilm formation	62	351	413
pgaA (72), *pgaB* (87), *pgaC* (87), *pgaD* (87)	Poly-beta-1,6 N-acetyl-D-glucosamine	42	291	333
adeF (87), *adeG* (87), *adeH* (84)	Biofilm; Biofilm formation	31	227	258
bfmR (88), *bfmS* (87)	biofilm-controlling response regulator, signal transduction histidine kinase	22	153	175
plc (88), *plcD* (86)	phospholipase	21	153	174
barA (87), *barB* (86)	siderophore efflux system of the ABC superfamily	21	152	173
abaI (77), *abaR* (73)	Biofilm; Quorum sensing	22	128	150
entE (88)	non-ribosomal peptide synthetase adenylate-forming enzyme of acinetobactin synthesis	89	90	88
ompA (80)	Outer membrane protein A	81	82	80
bap (22)	Biofilm associated protein	23	24	22
	Total	574	2744	3119

4.12 No plasmid associated VF gene was found

In the study, none of the identified VF genes shared the same contig with the plasmids. Therefore, no plasmid associated VF genes was found.

4.13 AST showed resistance to all the antibiotics except colistin (polymyxin)

Figure 11 represents the AST pattern acquired by 11 Norwegian *A. baumannii* isolates. It can be observed that most of the isolates acquire resistance to 5 antibiotic classes, i.e., aminoglycosides, carbapenems, fluroquinolones, tetracycline, and diaminopyrimidine. However, all the isolates seem to be sensitive towards the antibiotic class polymyxin (colistin).

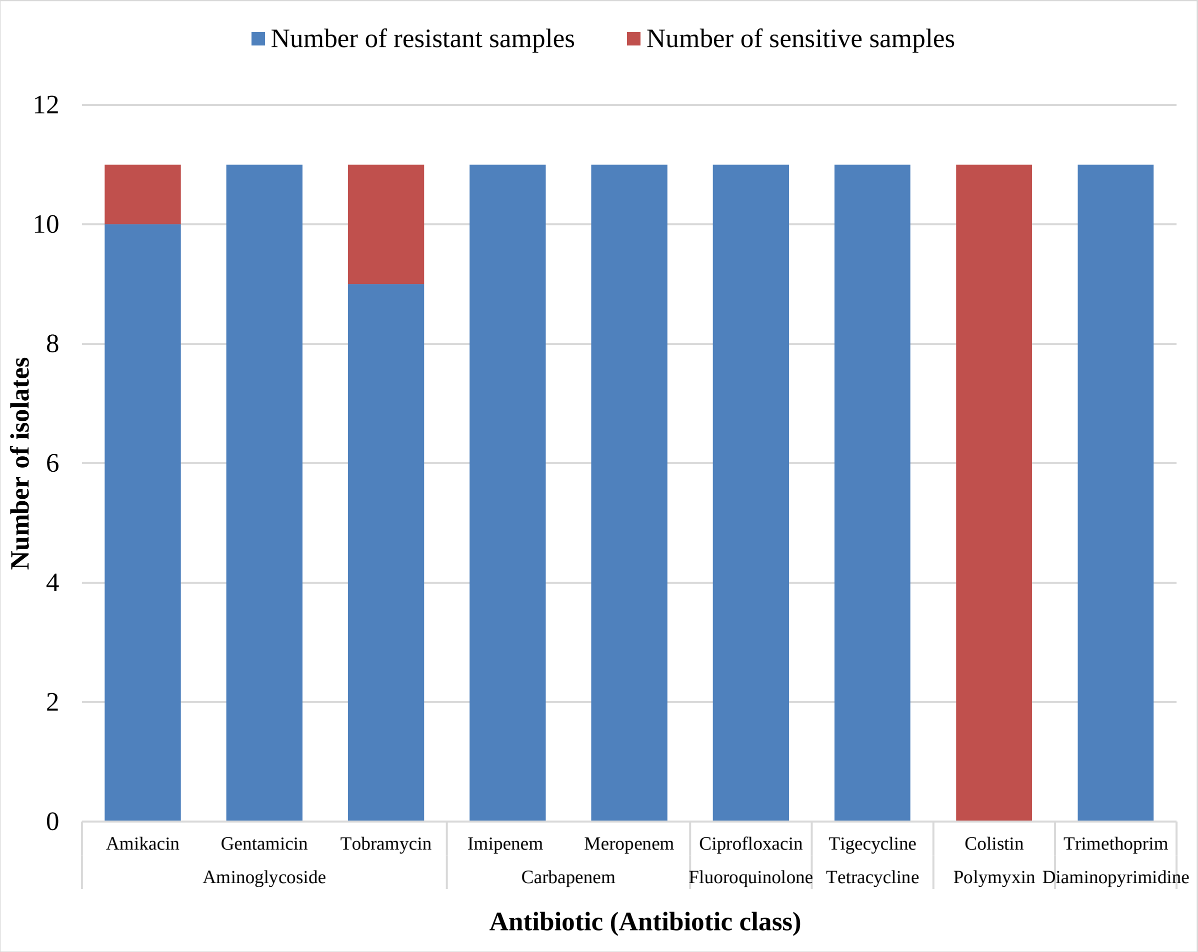


Figure 11: Bar graph showing the pattern of antimicrobial susceptibility test (AST) acquired by the 11 Norwegian *A. baumannii* isolates, for nine different antibiotics that fall under six different antibiotic classes.

Figure 12 illustrates the antibiotic susceptibility test (AST) pattern acquired by 73 Indian *A. baumannii* isolates. It can be observed that most of the isolates acquire resistance to all the six antibiotic classes, i.e., aminoglycosides, cephalosporins, monobactams, penicillin/penams, carbapenems, and fluoroquinolones. The highest number of the isolates have resistance against penicillin/penam (piperacillin) followed by monobactam (aztreonam), cephalosporin (ceftazidime) and aminoglycoside (Amikacin).

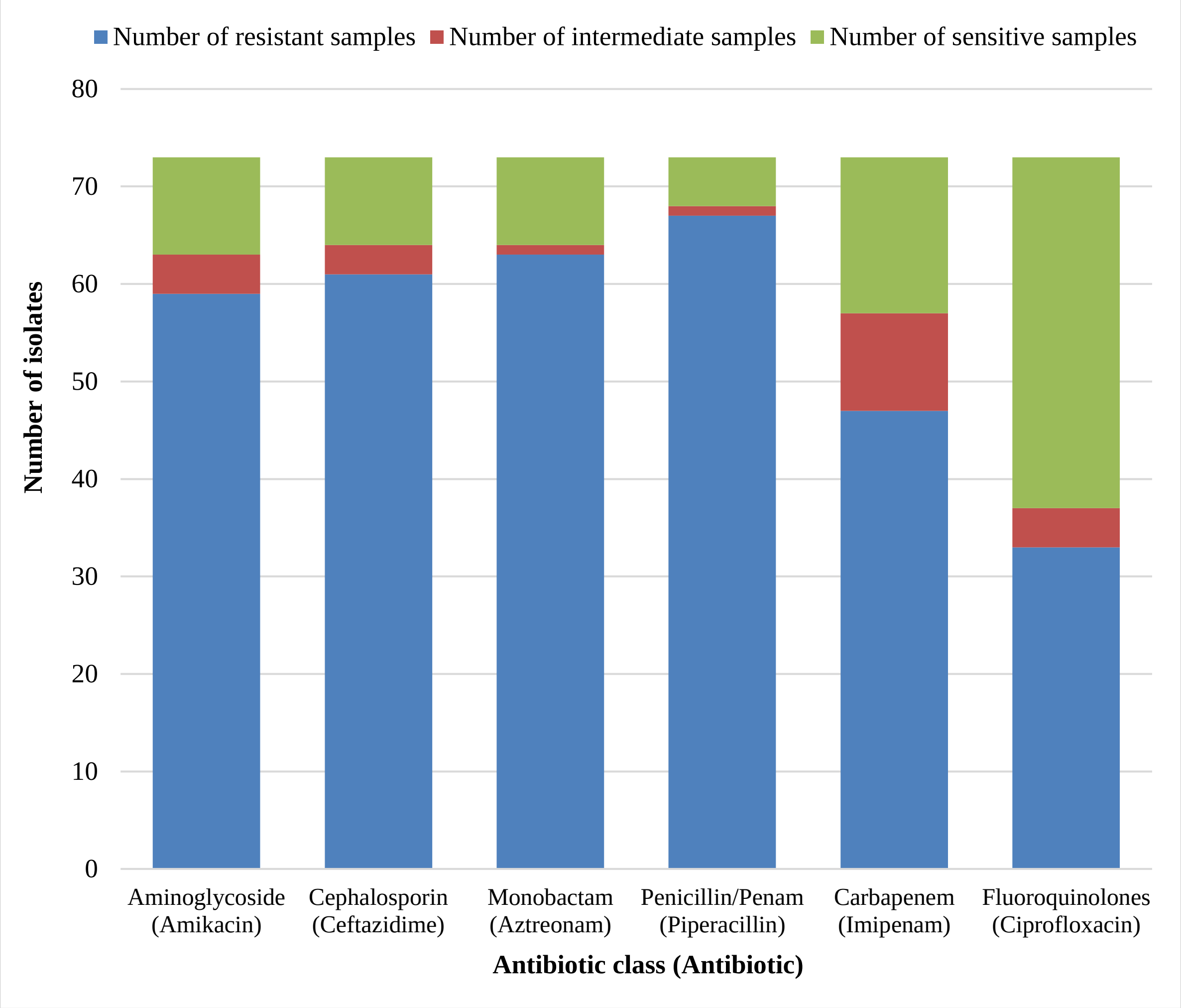


Figure 12: Bar graph showing the pattern of antimicrobial susceptibility test (AST) acquired by the 73 Indian *A. baumannii* isolates, for six different antibiotic class and antibiotics (in parentheses).

4.14 Minimal concordance between genotypic and phenotypic resistance in Indian isolates

Comparing the AST results and AMR genes for the 84 isolates (73 Indian and 11 Norwegian), only 32.14% (27 out of 84) of isolates showed exact concordance between genotypic and phenotypic results while 67.86% (57 out of 84) had different genotypic and phenotypic results.

However, comparing the genotypic and phenotypic data for the 11 Norwegian isolates showed that all of them (100%) had exactly same phenotypic and genotypic results which is apparent from the bar graph in Figure 13.

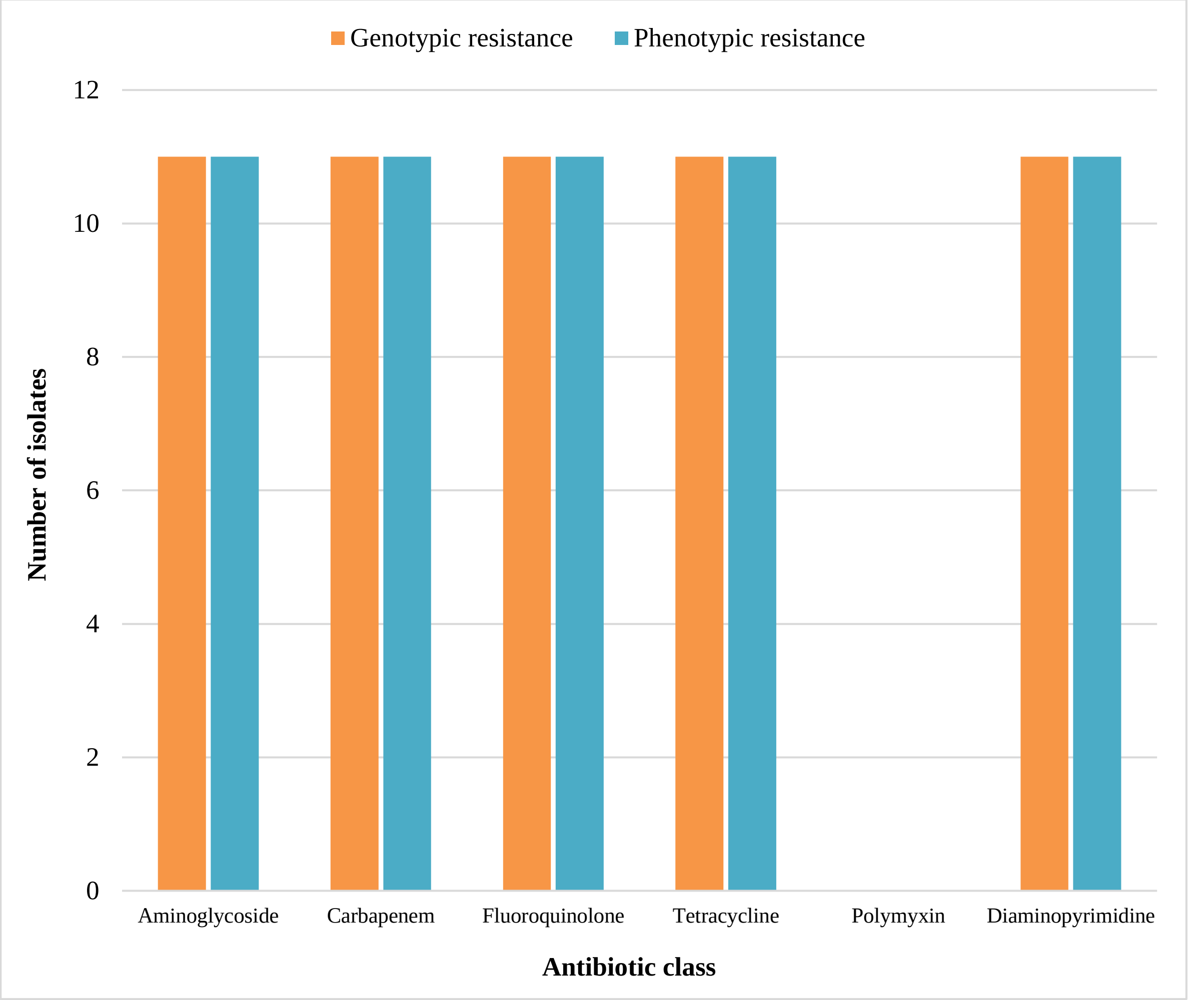


Figure 13: Bar graph showing the comparison of genotypic and phenotypic resistance patterns of 11 Norwegian *A. baumannii* isolates.

Figure 14 represents the comparison of genotypic and phenotypic resistance pattern for six different antibiotic classes for 73 Indian *A. baumannii* isolates. Only 22.22% (16 out of 73) of Indian isolates appeared to have exactly same genotypic and phenotypic results. It can be observed in Figure 14 that some isolates carrying resistance gene have not shown phenotypic resistance. Similarly, some isolates have shown phenotypic resistance while no genes that confer resistance to the antibiotic has been detected.

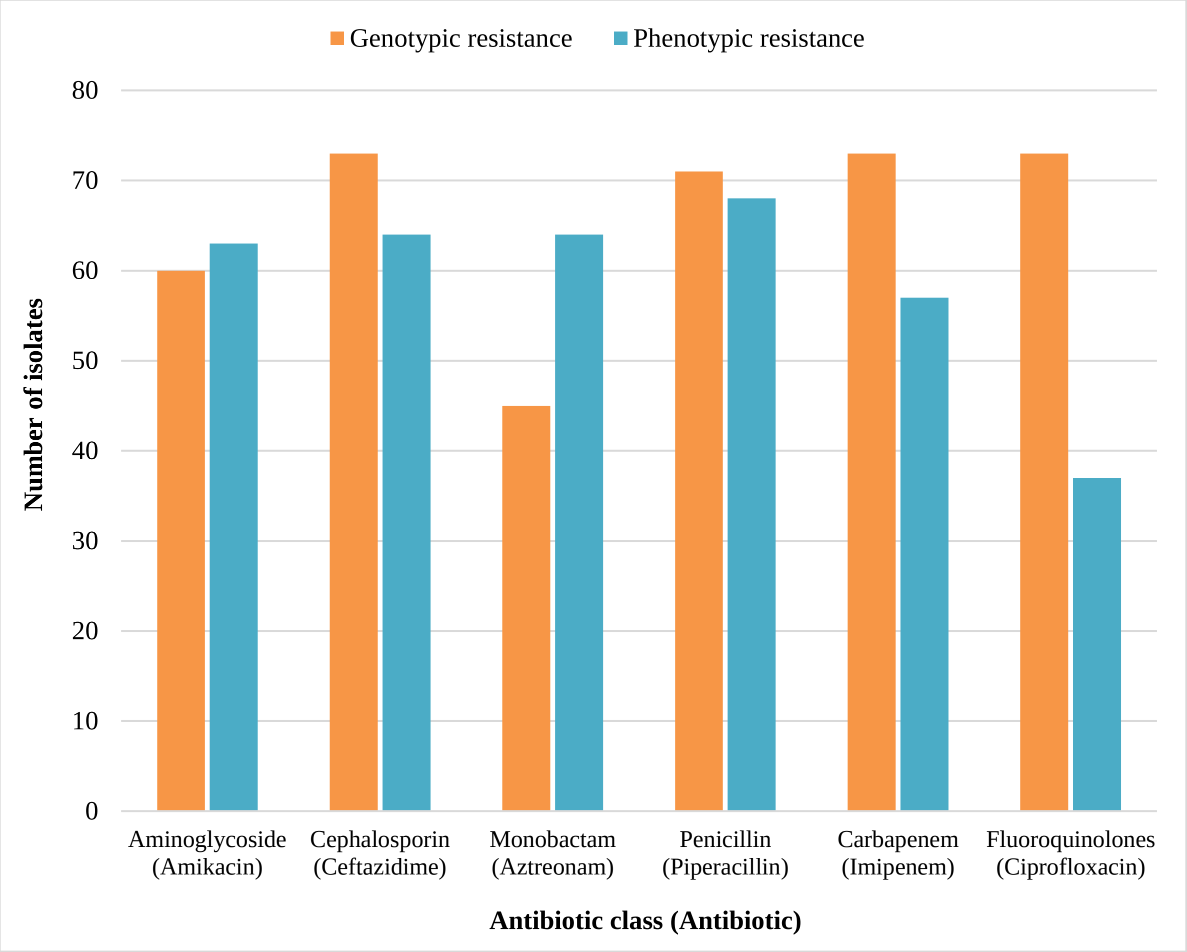


Figure 14: Bar graph showing the comparison of genotypic and phenotypic resistance patterns of 73 Indian *A. baumannii* isolates.

4.15 AMR genes for all the classes of antibiotics were detected except polymyxin

Figure 15 illustrates the occurrence of AMR genes in 11 Norwegian *A. baumannii* isolates that confer resistance to respective antibiotics. The AMR genes that confer resistance to five different antibiotics class was found but no AMR gene for polymyxin was detected. Similar phenotypic result was observed in Figure 11 where the isolates were sensitive towards colistin (polymyxin).

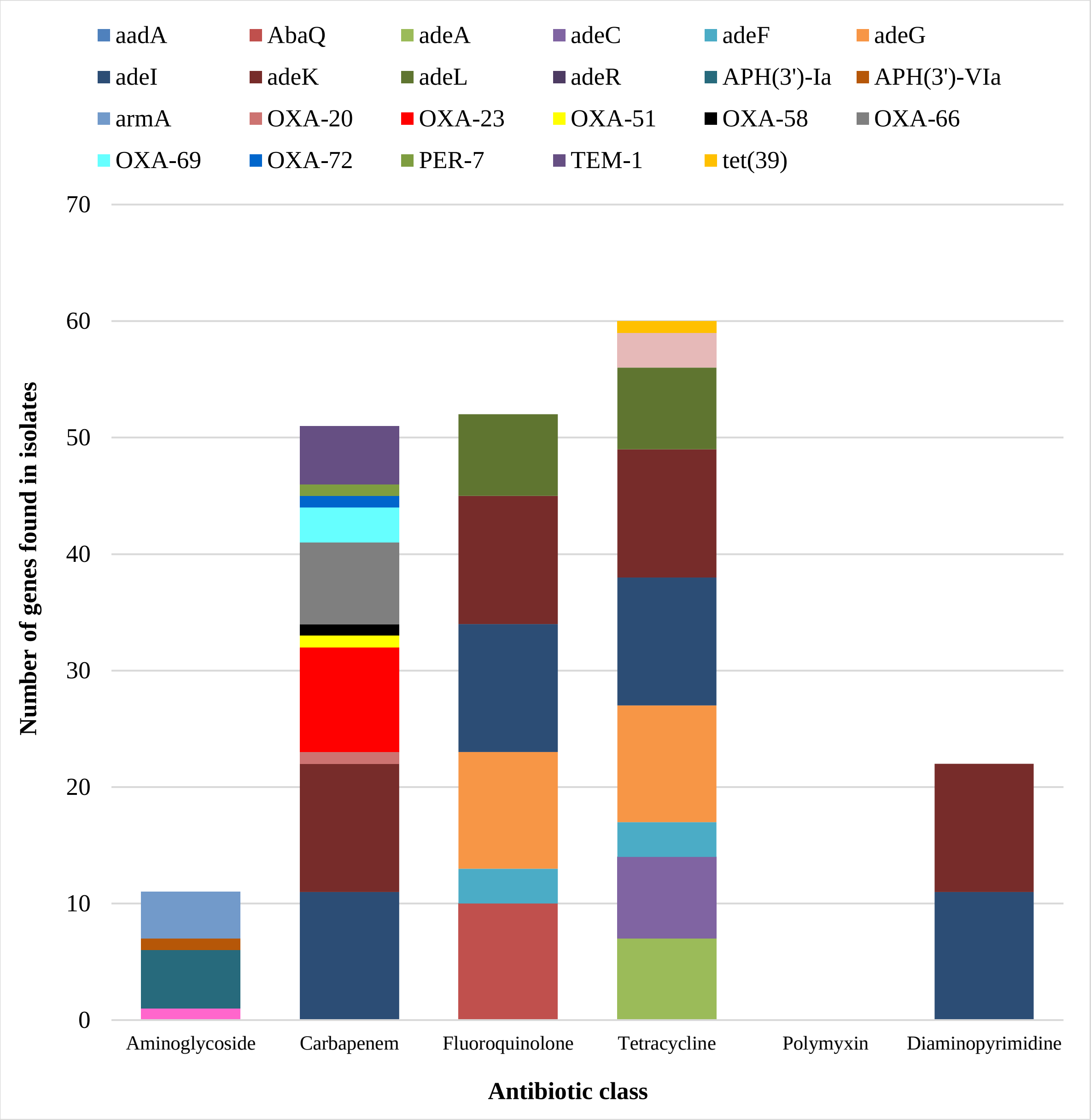


Figure 15: Bar graph showing the occurrence of AMR genes (in y-axis) that confer resistance to respective antibiotic class (in x-axis) for the 11 Norwegian *A. baumannii* isolates

Figure 16 illustrates the occurrence of AMR genes in 73 Indian *A. baumannii* isolates that confer resistance to respective antibiotics. The AMR genes that confer resistance to all six antibiotic classes was detected. Some AMR genes were common between cephalosporin, monobactam, penam and carbapenem.

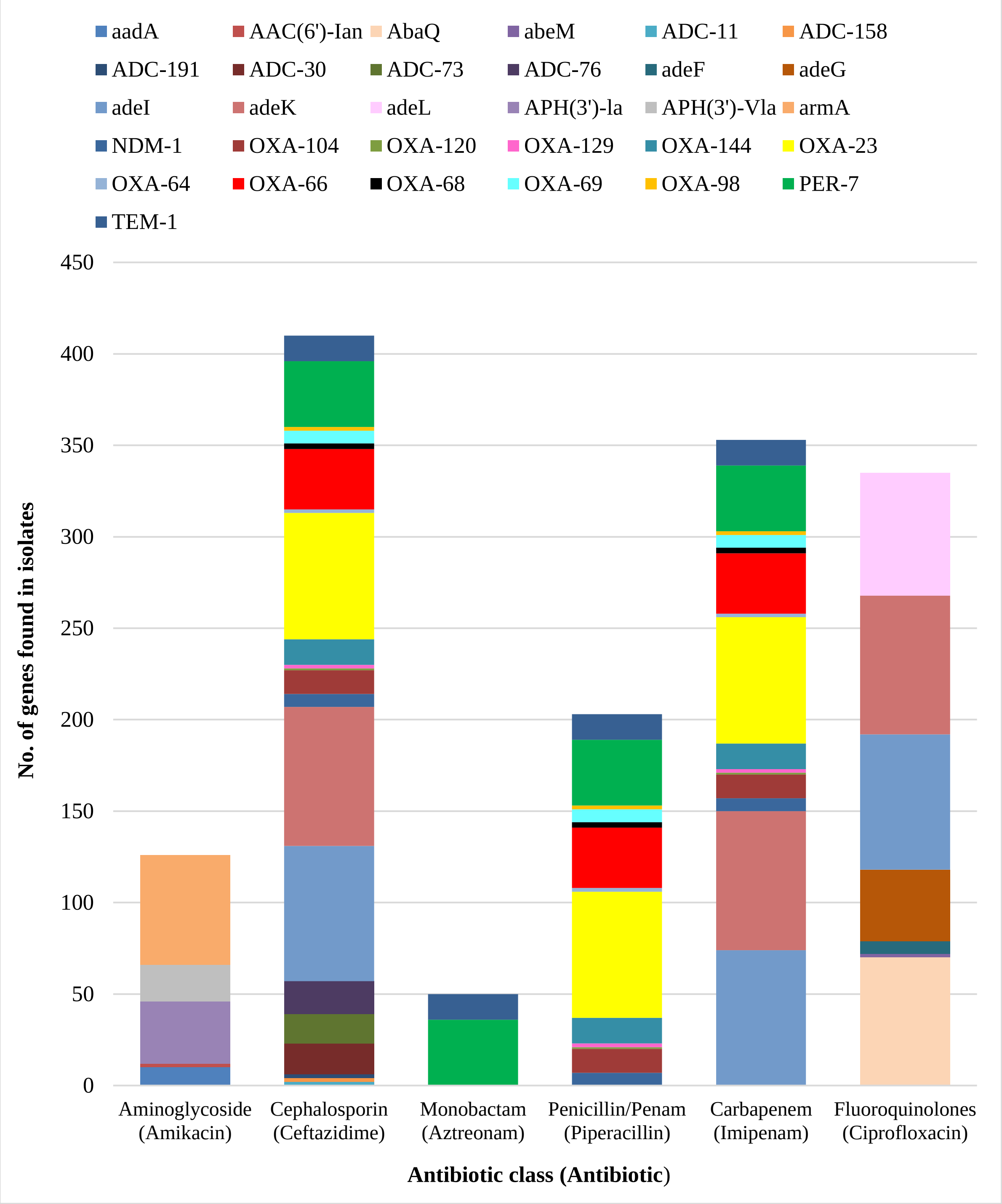


Figure 16: Bar graph showing the occurrence of AMR genes (in y-axis) that confer resistance to respective antibiotics / antibiotic classes (in x-axis) for the 73 *A. baumannii* isolates from the Indian hospital.

5 Discussion

5.1 Quality of datasets

The Illumina sequencing statistics showed clear difference between the Norwegian and the Indian datasets. The Norwegian datasets showed lower Phred score and higher amount of adapter contamination than the Indian datasets. The explanation for the low quality of Norwegian dataset could be the errors in NGS during sample preparation or the sequencing process.

5.2 Best suited trimmer and short read assembler

It was observed that both Trimmomatic and Trim galore performed well during trimming and filtering of the subset of Indian dataset, but considerate number of base pairs were lost, and the coverage was also decreased (lower compared to Indian dataset) in the subset of Norwegian dataset after trimming with both the tools. A possible explanation for this might be the difference in the quality of reads of the Norwegian and Indian datasets before trimming. Comparatively, the number of sequences reads, coverage, per base sequence quality and file size of reads obtained from the Norwegian datasets were lower, and the adapter contamination was higher than that of the Indian datasets before trimming. This difference might be the reason for difference in the performance of the trimming for the different datasets. Comparatively, slightly more data was retained by Trim galore than Trimmomatic. However, it was decided to use Trimmomatic for trimming all the datasets because the data retained was negligible and, also previous experience with Trimmomatic in the bioinformatics group at INN proved it to be an optimal trimmer.

The comparison of QUAST metrics of the three assemblers (ABySS, SPAdes and Unicycler) indicated that both SPAdes and Unicycler seemed to perform consistently similar and better than AbySS. This result is in agreement with the result obtained by Khezri et al., (2021) in which Unicycler and SPAdes performed similarly and better than ABySS. The consistent performance of SPAdes and Unicycler might be due to the reason that Unicycler also uses SPAdes to construct the initial De Bruijn assembly graph (Wick et al., 2017). A considerable difference was only seen in the number of dead ends between the assemblies created by SPAdes and Unicycler, i.e, Unicycler produced fewer dead ends than SPAdes. This result also supports the result of Khezri et al., (2021) in which assemblies created using Unicycler had fewer dead ends than that created using SPAdes. In SPAdes, large k-mers result in larger contigs, but excessively large k-mers causes a fragmented graph with dead ends, but Unicycler assigns a score to each k-mer graph based on the number of contigs and the number of dead ends and the highest scoring graph is selected as a balance between minimizing both contig count and dead ends (Wick et al., 2017). This might be the reason for occurrence of a smaller number of dead ends in the assemblies created by Unicycler than SPAdes. The number of dead ends in the assemblies created by ABySS could not be determined because the assembly files obtained from ABySS were in .dot format which was not supported by the Bandage.

Eventually, Unicycler was chosen to be the best suited assembler in this study. This finding is consistent with the finding done by Khezri et al., (2021) in which Unicycler performed better than SPAdes and ABySS for the assembly of short reads. Similar result was also obtained by Wick et al., (2015) in which Unicycler performed better than the other short read assemblers in each QUAST metrics.

5.3 Genome assembly

Before trimming, the FastQC report indicated very low per base sequence quality and high adapter contamination in the low coverage (Norwegian) reads. The post trimming FastQC report displayed that the per base sequence quality was good and the adapter was also removed indicating the improvement in the quality of the low coverage reads. Thus, indicating that the reads were ready to be assembled.

The evaluation of assembled genome (created with Unicycler) using QUAST indicated that the median total length and GC percentage were similar to the reported median values for the reference genome (GCF_003464295.1) as well as all the *A. baumannii* assemblies in NCBI. Similar values for total length and GC percentage was observed in assemblies created by Unicycler in studies done by Chapartegui-González et al., (2019) and Farrow et al., (2021). The median value for number of contigs was lower and median value for N50 was higher than that of the reference genome indicating that the assembled genomes were not contiguous.

Finally, BUSCO was used to assess the assembled genomes for the presence of highly conserved genes among *A. baumannii*. It produced a median BUSCO completeness score of 98.3% indicating the presence of high percentage of highly conserved genes in the assembled genomes. It also generated median BUSCO fragmentation and missing score of 0.80% and

0.90%. In summary, the results indicated that the genome assembly was performed successfully.

5.4 MLST and WGA

Before performing the downstream analyses, the isolates that were not *A. baumannii* had to be removed for which MLST and WGA was performed. Comparing the results of both MLST and WGA, eight of the isolates were found to be different than *A. baumannii*. Two out of eight belonged to a completely different genus (*Proteus mirabilis*) while the other six were *Acinetobacter* but belonged to different species. The reason for this might be the error in the identification of the bacteria from the clinical isolates. Other possible explanation for this could be the contamination that occurred during sample collection or while taking colonies for library preparation before sequencing.

According to the Oxford scheme, the most dominant sequence type of *A. baumanni* isolates was found to be sequence type 2 among all the isolates. This result supports the results from previous studies done by Adjei et al., (2021) and Nawfal Dagher et al., (2019). For the Pasteur scheme, the majority of *A. baumanni* isolates were matched with unknown sequence type. Even if the alleles in the query are matching the alleles in templates sequences in the MLST database for Pasteur scheme, the combination of the alleles does not have any MLST number assigned yet. This is the reason for majority of isolates to be matched to unknown sequence type. The most dominant sequence type with assigned MLST number according to Pasteur scheme was sequence type 451!, 1809!.

5.5 Plasmid identification

There is a reliable tool for detecting plasmids called PlasmidFinder that could identify the plasmids in assembled genome using homology search between the query and the subject sequences in the database. However, this tool could not be used in this study because it works only for the family Enterobacteriaceae and *A. baumannii* does not belong to this family. Therefore, the PLSDB database was downloaded and then the query sequences were BLAST searched manually. This took more time and effort to detect the plasmids.

In the study, the plasmid pVB11737_6 was found in majority of both the Indian and Norwegian isolates. The plasmid was initially isolated in India (NCBI Reference Sequence: NZ_CP050397.1) which seems to have been disseminated to Norway. The CDS of this plasmid codes for IS4 family transposase (NCBI Reference Sequence: NZ_CP050397.1) which is responsible for transposition processes at the origin of acquisition of *OXA-23* β-lactamase gene (Corvec et al., 2007).

In the current study, most of the detected plasmids were originated in *A. baumannii* but it was interesting to find some plasmids that belonged to other *Acinetobacter* species (*A. seifertii and A. schindleri*) and other genus (*Klebsiella*) in *A. baumannii* clinical isolates indicating the inter-species and inter-genus transfer of plasmid. It seems possible that these results are due to Horizontal gene transfer (HGT). Similar result was found in a study done by Salgado-Camargo et al. (2020), in which plasmids very similar in sequence and gene content to plasmids of *K. pneumoniae* were detected in *A. baumannii*. Studies have shown that some clinical *A. baumannii* strains are naturally competent for the uptake of genetic material (Ramirez et al., 2010) and *Acinetobacter spp.* do not discriminate between their own and foreign DNA (de Vries & Wackernagel, 2002), which could be the reasons for finding the plasmids from other genus and species in *A. baumannii*.

5.6 AMR gene identification

The AMR genes found in majority of *A. baumannii* isolates were *AdeK* (87 out of 88 total isolates) followed by *AdeJ*, (85 out of 88 total isolates) both of which belonged to the RND efflux pumps and confer resistance to macrolide, fluoroquinolone, lincosamide, carbapenem, cephalosporin, tetracycline, rifamycin, diaminopyrimidine, phenicol and penem. Similar result was observed in a study where *adeIJK* genes were detected in all the strains of *A. baumannii* used in the study (Damier-Piolle et al., 2008). A recent study has proposed that overexpression of *adeIJK* might contribute to MDR in *A. baumannii* clinical isolates (J. A. Choi et al., 2020).

The most prevalent resistance mechanisms in both the Norwegian and Indian *A. baumannii* isolates were the antibiotic efflux pumps. Among the antibiotic efflux pumps, RND family was the most dominant one followed by MFS and SMR. This result support the idea of Coyne et al. (2011) in which RND systems were the most prevalent efflux pumps in MDR *A. baumannii*. It has also been mentioned in a previous review that RND, the MFS and SMR families are the major efflux pumps involved in MDR in *A. baumannii* (Vila et al., 2007). Three RND efflux systems (AdeABC regulated by AdeRS, AdeIJK and AdeFGH) were found in this study. Among them, overexpression of AdeABC and AdeFGH efflux pumps contribute to MDR in *A. baumannii*, but AdeIJK contributes more to natural resistance than acquired resistance (Coyne et al., 2011; Damier-Piolle et al., 2008).

The second most dominant resistance mechanism in both the Norwegian and Indian *A. baumannii* isolates included enzymes that inactivated the antibiotics. Among various enzymes causing antibiotic inactivation, Class D β-lactamases/oxacillinases or carbapenem-hydrolyzing class D β-lactamases (CHDLs) (particularly OXA-23) was the most abundant ones. This result is in agreement with the statements mentioned in the previous reviews done by Hsu et al., (2017) and Rodríguez et al., (2018), that OXA-23 was the most prevalent OXA-type β-lactamase. The high occurrence of CHDL genes in *A. baumannii* isolates explains the fact of it being carbapenem resistant. Most of the CHDL genes including OXA-23 gene (first identified in an imipenem resistant Scottish clinical *A. baumannii* isolate), are usually associated with plasmids but can be present in chromosomes (Antunes & Fisher, 2014). However, none of the CHDL genes in this study was found to be associated with plasmids.

5.7 AMR genes associated with plasmids

In this study, only 7.5% of the total plasmids possessed antibiotic resistance genes. This result is lower compared to the study done by Salgado-Camargo et al., (2020) in which 35.2% of the plasmids possessed resistance genes. Out of total three resistant plasmids detected in this study, only one plasmid had two resistance gene. The rest of them had only one resistance gene. These results reflect those of Salgado-Camargo et al., (2020) who also found that highest number of plasmids contained only one resistance gene and second highest number of plasmids contained two resistance genes. However, in (Salgado-Camargo et al., 2020) plasmids containing 3 or more resistance genes were also found which was not found in the current study. The most frequent AMR gene associated with plasmids in this study were those involved in resistance to β-lactams followed by sulphonamide and aminoglycosides. In contrast to that, (Salgado-Camargo et al., 2020) found that the most frequent plasmid associated AMR gene were the one that confer resistance to aminoglycosides followed by β-lactams and sulphonamides.

One of the interesting findings of the study was the presence of resistance plasmid (pYQ12450) in *A. baumannii* possessing β-lactam resistant genes, which was originally detected in *K. pneumoniae*. This finding suggests that the inter-genus transfer of antibiotic resistance genes is possible through plasmid. The two β-lactam resistant genes transferred via this plasmid were *BRP(MBL)* and New Delhi metallo-β-lactamase 1 (*NDM-1)* and both the genes were found in the Indian isolates. It has been shown in previous study that these two genes were associated with each other as part of the same operon (Dortet et al., 2012, 2017) which might be the reason for these genes to occur in the same plasmid. The *NDM-1* gene was initially found in *Klebsiella pneumoniae* which was isolated from a Swedish patient hospitalized in India (Yong et al., 2009). This gene has been found to be disseminated to *A. baumannii* in several countries (Chen et al., 2011; Espinal et al., 2011; Kaase et al., 2011; Karthikeyan et al., 2010). Prior study as also shown the intra- and inter-species transfer of plasmid carrying this gene in *A. baumannii* via OMVs with high transformation frequency (Chatterjee et al., 2017).

5.8 VF gene identification

The VF genes found in majority of *A. baumannii* isolates were *bas* genes (that codes for acinetobactin, a siderophore) followed by bau genes (that codes for siderophore receptors and transporters) in both Norwegian and Indian isolates. Both these genes belong to the acinetobactin gene cluster which forms the iron acquisition system. Moreover, *bar* and *ent* genes associated with the siderophore system were also detected in both Norwegian and Indian isolates. It has been mentioned in Conde-Pérez et al., (2021) and Sheldon & Skaar, (2020) that acinetobactin is considered as the major siderophore in *A. baumannii* clinical isolates. This statement matches the results of this study. *A. baumannii* produces various iron chelators but only acinetobactin is the critical virulence factor needed for the growth of the pathogen on host with limited iron (Sheldon & Skaar, 2020). It was found in a previous study that *basG*, *basC*, *basD*, *basB* and *bauA* play an important role in virulence and pathogenicity of *A. baumannii* (Conde-Pérez et al., 2021). In a study done by (C. Liu et al., 2018), the *bap* (biofilm associated protein) gene was found to be the most dominant one but in the current study, *bap* was found to be the least occurring VF gene.

No plasmid associated VF genes was found in this study. This might be because, most of the VF genes were present on the chromosome but not on the plasmids.

5.9 Comparison between genotypic and phenotypic antibiotic resistance pattern

The comparison of AST data with detected AMR genes in Indian isolates showed less concordance in Indian isolates. Similar result was found in a study done for genomic investigation of antimicrobial resistance determinants and virulence factors in *Salmonella enterica* serovars, in which more than half of isolates showed disagreement between genotypic and phenotypic characteristics (de Melo et al., 2021). A possible explanation for this difference might be the difference in the expression of the gene which cannot be detected through analysis of WGS. Even the most suited bioinformatics tool and sequencing technologies cannot avoid gaps in the genome during assembly which might show the presence of resistance genes. This could be the other reason for the disagreement between genotypic and phenotypic antimicrobial resistance. However, comparison of the genotypic and phenotypic data for the Norwegian isolates in this study showed exact same results. Similar result was found in a study where antibiotic resistance profile was in agreement with the original clinical laboratory susceptibility profile in a study done on methicillin-resistant *Staphylococcus aureus* (Leopold et al., 2014).

The AST data of the Indian *A. baumannii* isolates showed resistance to all the six antibiotics/antibiotic classes while the AST result of Norwegian *A. baumannii* isolates showed resistance to all the antibiotic class except colistin (polymyxin). Similar result was found in a study where polymyxin B was found to be sensitive towards all the *A. baumannii* isolates (C. Liu et al., 2018). The sensitivity of *A. baumannii* isolates only towards colistin (polymyxin) indicated that it is the only antibiotic effective for the treatment. This finding supports the statements mentioned in review done by (Kyriakidis et al., 2021; Mulani et al., 2019) that the only remaining antibiotic treatment for MDR *A. baumannii* was colistin and tigecycline. Since only two antibiotics were remaining for the treatment, MDR *A. baumannii* had also been proposed as being extremely drug resistant (XDR) (Kengkla et al., 2018; J. Liu et al., 2021). Unfortunately, pan drug resistant (PDR) *A. baumannii* strains have also been reported to resist colistin and tigecycline (Cai et al., 2012; Gottig et al., 2014; Hernan et al., 2009; López-Rojas et al., 2013; O'Hara et al., 2013). The resistance to colistin has also been reported all over the world with the highest resistance rate reported in Asia followed by Europe (Cai et al., 2012).

The resistance of *A. baumannii* towards all the antibiotics except colistin also reveals its MDR nature. One of the major explanations for the MDR *A. baumannii* could be the overexpression of efflux pumps that includes RND and MFS transporters with wide substrate specificity (Coyne et al., 2011; Wongsuk et al., 2022; Yoon et al., 2015), which is found in majority in this study. However, one of the studies claim that it is doubtful that the clinical levels of antibiotic resistance in *A. baumannii* isolates are caused solely by the overproduction of RND efflux pumps (Leus et al., 2018). So the other explanation for MDR could be the acquisition of resistance gene through the mobile genetic elements like plasmid (Ghaly et al., 2020). It was found in a study that colistin was not a substrate for the RND efflux pumps (Yoon et al., 2015), which might be the reason for the sensitivity of *A baumannii* towards this antibiotic.

Among the detected AMR genes in both Indian and Norwegian isolates, some AMR genes were common between different antibiotic classes which means the same gene can confer resistance towards many antibiotic classes. In case of Indian isolates, common AMR genes were found for cephalosporin, monobactam, penam and carbapenem while in case of Norwegian isolates, common AMR genes were detected for carbapenem, fluoroquinolone, tetracycline and diaminopyrimidine.

5.10 Difference in the resistance pattern of *A. baumannii* between India and Norway

Out of total detected plasmids, six were common between both Indian and Norwegian isolates. Among these six plasmids, three were originated from India (NCBI Reference Sequence: NZ_CP050397.1, NZ_CP050407.1 and NZ_CP050396.1) and the others were originated from USA (NCBI Reference Sequence: NZ_CP008708.1), Taiwan (NCBI Reference Sequence: NZ_CP061638.1) and Australia (NCBI Reference Sequence: NZ_CP012953.1) but none of them were originated in Norway. This indicates that the plasmids originated from other countries had been disseminated to Norway. Among these plasmids, one of the plasmids (pVB11737_5) originated in India, carried *sul2* gene. It is possible, therefore, that this plasmid has been disseminated from India to Norway along with the resistance gene. In the current study, the most abundant plasmid (pVB11737_6) found in both Norwegian and Indian isolates was also originated from India. The presence of this plasmid in Norwegian isolates also suggests its transfer from India to Norway.

It can be observed that more AMR gene family was found in Indian isolates than the Norwegian isolates. In addition to that, most of the resistant plasmid were found in the Indian isolates while only one resistant plasmid was found in Norwegian isolates. Overall, these results reveal that, the occurrence of antibiotic resistance is higher in India than in Norway. It has been found that carbapenem resistance rates in *A. baumannii* have exceeded 40% throughout all of India (Hsu et al., 2017). The reason for this might be the overuse or misuse of antibiotics in India as compared to Norway. In India, it was reported that physicians were compensated by pharmaceutical companies and pharmacies for prescribing antibiotics (Laxminarayan & Chaudhury, 2016) which has caused the overuse and misuse of antibiotics. This result is also amplified by the fact of the unequal number of isolates (11 Norwegian and 77 Indian) between Norway and India used in this study.

6 Conclusion

To obtain reliable result from genome assembly, selection of suitable bioinformatics tools is a prerequisite. Therefore, the first objective of the study was to determine the best suited trimmer and short read assembler and then to use those tools to perform genome assembly. In the study, the chosen tools (Trimmomatic as trimmer and Unicycler as assembler) were found to perform well and resulted in producing good quality of assembled genome which could be used for downstream analyses.

The main objective of the study was to use *A. baumannii* assembled genomes for prediction of plasmids, AMR genes and VF genes. The plasmid pVB11737_6, AMR gene *AdeK*, efflux pump resistance mechanism and acinetobactin virulence gene cluster were found in majority of both Norwegian and Indian *A. baumannii* clinical isolates. Some plasmids from the species other than *A. baumannii* as well as genus other than *Acinetobacter* were also detected, indicating the inter-species and inter-genus HGT. Also, some plasmids carrying resistance gene that originated from *Klebsiella* were found in *A. baumannii* indicating the acquisition of resistance gene from this genus through HGT. The dominant occurrence of CHDL (particularly *OXA-23* gene) explains the occurrence of carbapenem resistance in the isolates.

The next objective was to compare the AST results with the detected AMR genes. The comparison showed less concordance between genotypic and phenotypic data in Indian isolates. So, the prediction of resistance phenotype using the NGS data cannot be done precisely. The AST results also showed the MDR nature of *A. baumanii* which could be due to the dominant expression of efflux pumps that actively pump drugs out of the cell or due to the acquisition of mobile genetic elements like plasmid containing resistance gene.

The final approach was to compare the prevalence of antimicrobial resistance of *A. baumannii* between Norway and India which indicated the occurrence of resistance is more in India than in Norway. It might be due to the overuse or misuse of antibiotics in India as compared to Norway.

Overall, the study revealed the potential of WGS to investigate the pathogenicity and antimicrobial resistance of the bacteria. With the decreased cost of sequencing and improved analyses methods, WGS could be used in future for detecting infections.

7 Future Perspective

A limitation of this study was low-quality reads from the Norwegian isolates which might have affected the whole genome assembly of those reads. Also, there was less number of Norwegian samples in the study, which might have affected the comparison of different factors between Indian and Norwegian isolates. Thus, the study could be repeated using higher number of samples and good quality reads for the Norwegian isolates.

In this study, the PLSDB was downloaded, and BLAST searched manually to identify putative plasmids. A plasmid detector tool like PlasmidFinder could be developed which could works for all the family of bacteria (not only Enterobacteriaceae) including *A. baumannii.*

A disagreement between the genotypic and phenotypic resistance pattern was found in this study. Thus, a question is raised by this study on the reason for these differences. So, further research should be carried out to answer this question. Also, for the prediction of resistance phenotype using the WGS data needs more research. The research on application of machine or deep learning could be done for the prediction of resistance phenotype using NGS.

The epidemiology of antibiotic resistance was found higher in India than in Norway which might be due to the overuse or misuse of antibiotics in India as compared to Norway. Therefore, antibiotic stewardship programs must be conducted in India to promote appropriate use of the antibiotics and reduce the antibiotic resistance.

8 References

Adjei, A. Y., Vasaikar, S. D., Apalata, T., Okuthe, E. G., & Songca, S. P. (2021). Phylogenetic analysis of carbapenem-resistant Acinetobacter baumannii isolated from different sources using Multilocus Sequence Typing Scheme. *Infection, Genetics and Evolution*, *96*, 105132. https://doi.org/10.1016/j.meegid.2021.105132

Afgan, E., Baker, D., Batut, B., van den Beek, M., Bouvier, D., Čech, M., Chilton, J., Clements, D., Coraor, N., Grüning, B. A., Guerler, A., Hillman-Jackson, J., Hiltemann, S., Jalili, V., Rasche, H., Soranzo, N., Goecks, J., Taylor, J., Nekrutenko, A., & Blankenberg, D. (2018). The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Research*, *46*(W1), W537–W544. https://doi.org/10.1093/nar/gky379

Akrami, F., & Namvar, A. E. (2019). Acinetobacter baumannii as Nosocomial Pathogenic Bacteria. *Molecular Genetics, Microbiology and Virology*, *34*(2), 84–96. https://doi.org/10.3103/S0891416819020046

Alcock, B. P., Raphenya, A. R., Lau, T. T. Y., Tsang, K. K., Bouchard, M., Edalatmand, A., Huynh, W., Nguyen, A.-L. V., Cheng, A. A., Liu, S., Min, S. Y., Miroshnichenko, A., Tran, H.-K., Werfalli, R. E., Nasir, J. A., Oloni, M., Speicher, D. J., Florescu, A., Singh, B., … McArthur, A. G. (2019). CARD 2020: Antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Research*, gkz935. https://doi.org/10.1093/nar/gkz935

Allen, K. D., & Green, H. T. (1987). Hospital outbreak of multi-resistant Acinetobacter anitratus: An airborne mode of spread? *Journal of Hospital Infection*, *9*(2), 110–119. https://doi.org/10.1016/0195-6701(87)90048-X

Ambler, R. P. (1980). The structure of β-lactamases. *Philosophical Transactions of the Royal Society of London. B, Biological Sciences*, *289*(1036), 321–331. https://doi.org/10.1098/rstb.1980.0049

Andrews, S. (2019). *FastQC: A Quality Control Tool for High Throughput Sequence Data* (0.11.9) [Java]. Babraham Institute. https://www.bioinformatics.babraham.ac.uk/projects/fastqc/

Anjum, M. F., Zankari, E., & Hasman, H. (2017). Molecular Methods for Detection of Antimicrobial Resistance. *Microbiology Spectrum*, *5*(6), 5.6.02. https://doi.org/10.1128/microbiolspec.ARBA-0011-2017

Anstey, N. M., Currie, B. J., & Withnall, K. M. (1992). Community-Acquired Acinetobacter Pneumonia in the Northern Territory of Australia. *Clinical Infectious Diseases*, *14*(1), 83–91. https://doi.org/10.1093/clinids/14.1.83

Antibiotic resistance. (2020, July 31). [Non profit]. World Health Organization (WHO). https://www.who.int/news-room/fact-sheets/detail/antibiotic-resistance

Antimicrobial resistance. (2021, November 17). [Non profit]. World Health Organization (WHO). https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

Antimicrobial resistance in the EU/EEA (EARS-Net)—Annual Epidemiological Report 2019. (2020). European Centre for Disease Prevention and Control. https://www.ecdc.europa.eu/sites/default/files/documents/surveillance-antimicrobial-resistance-Europe-2019.pdf

Antunes, N., & Fisher, J. (2014). Acquired Class D β-Lactamases. *Antibiotics*, *3*(3), 398–434. https://doi.org/10.3390/antibiotics3030398

Aucken, H., Berlau, J., Malnick, H., & Pitt, T. (1999). Distribution of Acinetobacter Species on Skin of Healthy Humans. *European Journal of Clinical Microbiology & Infectious Diseases*, *18*(3), 179–183. https://doi.org/10.1007/s100960050254

Bauer, A. W., Kirby, W. M., Sherris, J. C., & Turck, M. (1966). Antibiotic susceptibility testing by a standardized single disk method. *American Journal of Clinical Pathology*, *45*(4), 493–496.

Baumann, P. (1968). Isolation of Acinetobacter from soil and water. *Journal of Bacteriology*, *96*(1), 39–42. https://doi.org/10.1128/jb.96.1.39-42.1968

Baumann, P., Doudoroff, M., & Stanier, R. Y. (1968). A study of the Moraxella group. II. Oxidative-negative species (genus Acinetobacter). *Journal of Bacteriology*, *95*(5), 1520–1541. https://doi.org/10.1128/jb.95.5.1520-1541.1968

Bayot, M. L., & Bragg, B. N. (2022). Antimicrobial Susceptibility Testing. In *StatPearls*. StatPearls Publishing. http://www.ncbi.nlm.nih.gov/books/NBK539714/

Beijerinck, M. (1911). Pigmenten als oxydatieproducten gevormd door bacterien. *Versl Koninklijke Akad Wetensch Amsterdam*, *19*, 1092–1103.

Bergey, D. H., Buchanan, R. E., & Gibbons, N. E. (1975). *Bergey's Manual of Determinative Bacteriology* (8th ed.). Williams & Wilkins Company, Baltimore.

Berlau, J., Aucken, H. M., Houang, E., & Pitt, T. L. (1999). Isolation of Acinetobacter spp including A. baumannii from vegetables: Implications for hospital-acquired infections. *Journal of Hospital Infection*, *42*(3), 201–204. https://doi.org/10.1053/jhin.1999.0602

Beveridge, T. J. (1999). Structures of gram-negative cell walls and their derived membrane vesicles. *Journal of Bacteriology*, *181*(16), 4725–4733. https://doi.org/10.1128/JB.181.16.4725-4733.1999

Blair, J. M. A., Webber, M. A., Baylay, A. J., Ogbolu, D. O., & Piddock, L. J. V. (2015). Molecular mechanisms of antibiotic resistance. *Nature Reviews Microbiology*, *13*(1), 42–51. https://doi.org/10.1038/nrmicro3380

Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: A flexible trimmer for Illumina sequence data. *Bioinformatics*, *30*(15), 2114–2120. https://doi.org/10.1093/bioinformatics/btu170

Boll, J. M., Tucker, A. T., Klein, D. R., Beltran, A. M., Brodbelt, J. S., Davies, B. W., & Trent, M. S. (2015). Reinforcing Lipid A Acylation on the Cell Surface of Acinetobacter baumannii Promotes Cationic Antimicrobial Peptide Resistance and Desiccation Survival. *MBio*, *6*(3). https://doi.org/10.1128/mBio.00478-15

Bouvet, P. J. M., & Grimont, P. A. D. (1986). Taxonomy of the Genus Acinetobacter with the Recognition of Acinetobacter baumannii sp. Nov., Acinetobacter haemolyticus sp. Nov., Acinetobacter johnsonii sp. Nov., and Acinetobacter junii sp. Nov. And Emended Descriptions of Acinetobacter calcoaceticus and Acinetobacter lwoffii. *International Journal of Systematic Bacteriology*, *36*(2), 228–240. https://doi.org/10.1099/00207713-36-2-228

Brisou, J., & Prevot, A. R. (1954). [Studies on bacterial taxonomy. X. The revision of species under Acromobacter group]. *Annales De l'Institut Pasteur*, *86*(6), 722–728.

Burmeister, A. R. (2015). Horizontal Gene Transfer. *Evolution, Medicine, and Public Health*, *2015*(1), 193–194. https://doi.org/10.1093/emph/eov018

C Reygaert, W. (2018). An overview of the antimicrobial resistance mechanisms of bacteria. *AIMS Microbiology*, *4*(3), 482–501. https://doi.org/10.3934/microbiol.2018.3.482

Cai, Y., Chai, D., Wang, R., Liang, B., & Bai, N. (2012). Colistin resistance of Acinetobacter baumannii: Clinical reports, mechanisms and antimicrobial strategies. *Journal of Antimicrobial Chemotherapy*, *67*(7), 1607–1615. https://doi.org/10.1093/jac/dks084

Calhoun, J. H., Murray, C. K., & Manring, M. M. (2008). Multidrug-resistant Organisms in Military Wounds from Iraq and Afghanistan. *Clinical Orthopaedics & Related Research*, *466*(6), 1356–1362. https://doi.org/10.1007/s11999-008-0212-9

Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: Architecture and applications. *BMC Bioinformatics*, *10*(1), 421. https://doi.org/10.1186/1471-2105-10-421

Cerqueira, G. M., & Peleg, A. Y. (2011). Insights into Acinetobacter baumannii pathogenicity. *IUBMB Life*, *63*(12), 1055–1060. https://doi.org/10.1002/iub.533

Chapartegui-González, I., Lázaro-Díez, M., Redondo-Salvo, S., Ocejo-Vinyals, J. G., Navas-Méndez, J., & Ramos-Vivas, J. (2019). Whole-Genome Sequence of Acinetobacter baumannii HUMV-3743, Isolated from a Human Wound Exudate. *Microbiology Resource Announcements*, *8*(19), e01640-18. https://doi.org/10.1128/MRA.01640-18

Chatterjee, S., Mondal, A., Mitra, S., & Basu, S. (2017). Acinetobacter baumannii transfers the blaNDM-1 gene via outer membrane vesicles. *Journal of Antimicrobial Chemotherapy*, *72*(8), 2201–2207. https://doi.org/10.1093/jac/dkx131

Chaudhary, M., & Payasi, A. (2013). Incidence, prevalence and control of multidrug resistant (MDR) carbapenemase producing Acinetobacter baumanii in Indian intensive care units. *Journal of Pharmacy Research*, *7*(2), 175–180. https://doi.org/10.1016/j.jopr.2013.03.002

Chen, Y., Zhou, Z., Jiang, Y., & Yu, Y. (2011). Emergence of NDM-1-producing Acinetobacter baumannii in China. *Journal of Antimicrobial Chemotherapy*, *66*(6), 1255–1259. https://doi.org/10.1093/jac/dkr082

Choi, C. H., Hyun, S. H., Lee, J. Y., Lee, J. S., Lee, Y. S., Kim, S. A., Chae, J.-P., Yoo, S. M., & Lee, J. C. (2007). Acinetobacter baumannii outer membrane protein A targets the nucleus and induces cytotoxicity. *Cellular Microbiology*, *0*(0), 070907125921001-??? https://doi.org/10.1111/j.1462-5822.2007.01041.x

Choi, C. H., Lee, E. Y., Lee, Y. C., Park, T. I., Kim, H. J., Hyun, S. H., Kim, S. A., Lee, S.-K., & Lee, J. C. (2005). Outer membrane protein 38 of Acinetobacter baumannii localizes to the mitochondria and induces apoptosis of epithelial cells. *Cellular Microbiology*, *7*(8), 1127–1138. https://doi.org/10.1111/j.1462-5822.2005.00538.x

Choi, C. H., Lee, J. S., Lee, Y. C., Park, T. I., & Lee, J. C. (2008). Acinetobacter baumannii invades epithelial cells and outer membrane protein A mediates interactions with epithelial cells. *BMC Microbiology*, *8*(1), 216. https://doi.org/10.1186/1471-2180-8-216

Choi, J. A., Kim, C.-M., Jang, S.-J., Cho, S.-S., Jang, C. H., Ko, Y.-J., Kang, S.-H., & Park, G. (2020). Role of Efflux Pump Gene *adeIJK* to Multidrug Resistance in *Acinetobacter baumannii* Clinical Isolates. *Annals of Clinical Microbiology*, *23*(1), 45. https://doi.org/10.5145/ACM.2020.23.1.45

Choudhuri, S., & Kotewicz, M. (2014). *Bioinformatics for beginners: Genes, genomes, molecular evolution, databases, and analytical tools*. Elsevier/AP.

Chu, Y. W., Leung, C. M., Houang, E. T., Ng, K. C., Leung, C. B., Leung, H. Y., & Cheng, A. F. (1999). Skin carriage of acinetobacters in Hong Kong. *Journal of Clinical Microbiology*, *37*(9), 2962–2967. https://doi.org/10.1128/JCM.37.9.2962-2967.1999

Chuang, Y.-C., Sheng, W.-H., Li, S.-Y., Lin, Y.-C., Wang, J.-T., Chen, Y.-C., & Chang, S.-C. (2011). Influence of Genospecies of Acinetobacter baumannii Complex on Clinical Outcomes of Patients with Acinetobacter Bacteremia. *Clinical Infectious Diseases*, *52*(3), 352–360. https://doi.org/10.1093/cid/ciq154

Chung, D. R., Song, J.-H., Kim, S. H., Thamlikitkul, V., Huang, S.-G., Wang, H., So, T. M.-K., Yasin, R. M. D., Hsueh, P.-R., Carlos, C. C., Hsu, L. Y., Buntaran, L., Lalitha, M. K., Kim, M. J., Choi, J. Y., Kim, S. I., Ko, K. S., Kang, C.-I., Peck, K. R., & Asian Network for Surveillance of Resistant Pathogens Study Group. (2011). High prevalence of multidrug-resistant nonfermenters in hospital-acquired pneumonia in Asia. *American Journal of Respiratory and Critical Care Medicine*, *184*(12), 1409–1417. https://doi.org/10.1164/rccm.201102-0349OC

Cisneros, J. M., Reyes, M. J., Pachon, J., Becerril, B., Caballero, F. J., Garcia Garmendia, J. L., Ortiz, C., & Cobacho, A. R. (1996). Bacteremia Due to Acinetobacter baumannii: Epidemiology, Clinical Findings, and Prognostic Features. *Clinical Infectious Diseases*, *22*(6), 1026–1032. https://doi.org/10.1093/clinids/22.6.1026

Clemmer, K. M., Bonomo, R. A., & Rather, P. N. (2011). Genetic analysis of surface motility in Acinetobacter baumannii. *Microbiology*, *157*(9), 2534–2544. https://doi.org/10.1099/mic.0.049791-0

Cockerill, F. R. (1999). Genetic Methods for Assessing Antimicrobial Resistance. *Antimicrobial Agents and Chemotherapy*, *43*(2), 199–212. https://doi.org/10.1128/AAC.43.2.199

Conde-Pérez, K., Vázquez-Ucha, J. C., Álvarez-Fraga, L., Ageitos, L., Rumbo-Feal, S., Martínez-Guitián, M., Trigo-Tasende, N., Rodríguez, J., Bou, G., Jiménez, C., Beceiro, A., & Poza, M. (2021). In-Depth Analysis of the Role of the Acinetobactin Cluster in the Virulence of Acinetobacter baumannii. *Frontiers in Microbiology*, *12*, 752070. https://doi.org/10.3389/fmicb.2021.752070

Corvec, S., Poirel, L., Naas, T., Drugeon, H., & Nordmann, P. (2007). Genetics and expression of the carbapenem-hydrolyzing oxacillinase gene blaOXA-23 in Acinetobacter baumannii. *Antimicrobial Agents and Chemotherapy*, *51*(4), 1530–1533. https://doi.org/10.1128/AAC.01132-06

Coyne, S., Courvalin, P., & Périchon, B. (2011). Efflux-Mediated Antibiotic Resistance in *Acinetobacter* spp. *Antimicrobial Agents and Chemotherapy*, *55*(3), 947–953. https://doi.org/10.1128/AAC.01388-10

Custovic, A., Smajlovic, J., Tihic, N., Hadzic, S., Ahmetagic, S., & Hadzagic, H. (2014). Epidemiological monitoring of nosocomial infections caused by acinetobacter baumannii. *Medical Archives (Sarajevo, Bosnia and Herzegovina)*, *68*(6), 402–406. https://doi.org/10.5455/medarh.2014.68.402-406

Damier-Piolle, L., Magnet, S., Brémont, S., Lambert, T., & Courvalin, P. (2008). AdeIJK, a Resistance-Nodulation-Cell Division Pump Effluxing Multiple Antibiotics in *Acinetobacter baumannii*. *Antimicrobial Agents and Chemotherapy*, *52*(2), 557–562. https://doi.org/10.1128/AAC.00732-07

Davis, J. S., McMillan, M., Swaminathan, A., Kelly, J. A., Piera, K. E., Baird, R. W., Currie, B. J., & Anstey, N. M. (2014). A 16-Year Prospective Study of Community-Onset Bacteremic Acinetobacter Pneumonia. *Chest*, *146*(4), 1038–1045. https://doi.org/10.1378/chest.13-3065

de Melo, A. N. F., Monte, D. F. M., de Souza Pedrosa, G. T., Balkey, M., Jin, Q., Brown, E., Allard, M., de Oliveira, T. C. R. M., Cao, G., Magnani, M., & Macarisin, D. (2021). Genomic investigation of antimicrobial resistance determinants and virulence factors in Salmonella enterica serovars isolated from contaminated food and human stool samples in Brazil. *International Journal of Food Microbiology*, *343*, 109091. https://doi.org/10.1016/j.ijfoodmicro.2021.109091

de Vries, J., & Wackernagel, W. (2002). Integration of foreign DNA during natural transformation of *Acinetobacter* sp. By homology-facilitated illegitimate recombination. *Proceedings of the National Academy of Sciences*, *99*(4), 2094–2099. https://doi.org/10.1073/pnas.042263399

Dexter, C., Murray, G. L., Paulsen, I. T., & Peleg, A. Y. (2015). Community-acquired *Acinetobacter baumannii*: Clinical characteristics, epidemiology and pathogenesis. *Expert Review of Anti-Infective Therapy*, *13*(5), 567–573. https://doi.org/10.1586/14787210.2015.1025055

Dijkshoorn, L., Nemec, A., & Seifert, H. (2007). An increasing threat in hospitals: Multidrug-resistant Acinetobacter baumannii. *Nature Reviews Microbiology*, *5*(12), 939–951. https://doi.org/10.1038/nrmicro1789

Dijkshoorn, L., van Aken, E., Shunburne, L., van der Reijden, T. J. K., Bernards, A. T., Nemec, A., & Towner, K. J. (2005). Prevalence of Acinetobacter baumannii and other Acinetobacter spp. In faecal samples from non-hospitalised individuals. *Clinical Microbiology and Infection*, *11*(4), 329–332. https://doi.org/10.1111/j.1469-0691.2005.01093.x

Dortet, L., Girlich, D., Virlouvet, A.-L., Poirel, L., Nordmann, P., Iorga, B. I., & Naas, T. (2017). Characterization of BRP $_{\text{MBL}}$, the Bleomycin Resistance Protein Associated with the Carbapenemase NDM. *Antimicrobial Agents and Chemotherapy*, *61*(3), e02413-16. https://doi.org/10.1128/AAC.02413-16

Dortet, L., Nordmann, P., & Poirel, L. (2012). Association of the Emerging Carbapenemase NDM-1 with a Bleomycin Resistance Protein in Enterobacteriaceae and Acinetobacter baumannii. *Antimicrobial Agents and Chemotherapy*, *56*(4), 1693–1697. https://doi.org/10.1128/AAC.05583-11

Eber, M. R., Shardell, M., Schweizer, M. L., Laxminarayan, R., & Perencevich, E. N. (2011). Seasonal and temperature-associated increases in gram-negative bacterial bloodstream infections among hospitalized patients. *PloS One*, *6*(9), e25298. https://doi.org/10.1371/journal.pone.0025298

Eijkelkamp, B. A., Hassan, K. A., Paulsen, I. T., & Brown, M. H. (2011). Investigation of the human pathogen Acinetobacter baumannii under iron limiting conditions. *BMC Genomics*, *12*(1), 126. https://doi.org/10.1186/1471-2164-12-126

Ekblom, R., & Wolf, J. B. W. (2014). A field guide to whole-genome sequencing, assembly and annotation. *Evolutionary Applications*, *7*(9), 1026–1042. https://doi.org/10.1111/eva.12178

Espinal, P., Fugazza, G., López, Y., Kasma, M., Lerman, Y., Malhotra-Kumar, S., Goossens, H., Carmeli, Y., & Vila, J. (2011). Dissemination of an NDM-2-Producing Acinetobacter baumannii Clone in an Israeli Rehabilitation Center. *Antimicrobial Agents and Chemotherapy*, *55*(11), 5396–5398. https://doi.org/10.1128/AAC.00679-11

Espinal, P., Martí, S., & Vila, J. (2012). Effect of biofilm formation on the survival of Acinetobacter baumannii on dry surfaces. *Journal of Hospital Infection*, *80*(1), 56–60. https://doi.org/10.1016/j.jhin.2011.08.013

Farrow, J. M., Pesci, E. C., & Slade, D. J. (2021). Genome Sequences for Two Acinetobacter baumannii Strains Obtained Using the Unicycler Hybrid Assembly Pipeline. *Microbiology Resource Announcements*, *10*(10), e00017-21. https://doi.org/10.1128/MRA.00017-21

Fiester, S. E., Arivett, B. A., Schmidt, R. E., Beckett, A. C., Ticak, T., Carrier, M. V., Ghosh, R., Ohneck, E. J., Metz, M. L., Sellin Jeffries, M. K., & Actis, L. A. (2016). Iron-Regulated Phospholipase C Activity Contributes to the Cytolytic Activity and Virulence of Acinetobacter baumannii. *PLOS ONE*, *11*(11), e0167068. https://doi.org/10.1371/journal.pone.0167068

Fournier, P. E., Richet, H., & Weinstein, R. A. (2006). The Epidemiology and Control of Acinetobacter baumannii in Health Care Facilities. *Clinical Infectious Diseases*, *42*(5), 692–699. https://doi.org/10.1086/500202

Gaddy, J. A., Tomaras, A. P., & Actis, L. A. (2009). The *Acinetobacter baumannii* 19606 OmpA Protein Plays a Role in Biofilm Formation on Abiotic Surfaces and in the Interaction of This Pathogen with Eukaryotic Cells. *Infection and Immunity*, *77*(8), 3150–3160. https://doi.org/10.1128/IAI.00096-09

Galata, V., Fehlmann, T., Backes, C., & Keller, A. (2019). PLSDB: A resource of complete bacterial plasmids. *Nucleic Acids Research*, *47*(D1), D195–D202. https://doi.org/10.1093/nar/gky1050

Galhano, B. S. P., Ferrari, R. G., Panzenhagen, P., de Jesus, A. C. S., & Conte-Junior, C. A. (2021). Antimicrobial Resistance Gene Detection Methods for Bacteria in Animal-Based Foods: A Brief Review of Highlights and Advantages. *Microorganisms*, *9*(5), 923. https://doi.org/10.3390/microorganisms9050923

García-Garmendia, J., Ortiz-Leyba, C., Garnacho-Montero, J., Jiménez-Jiménez, F., Pérez-Paredes, C., Barrero-Almodóvar, A. E., & Gili-Miner, M. (2001). Risk Factors for *Acinetobacter baumannii* Nosocomial Bacteremia in Critically Ill Patients: A Cohort Study. *Clinical Infectious Diseases*, *33*(7), 939–946. https://doi.org/10.1086/322584

Ghaly, T. M., Paulsen, I. T., Sajjad, A., Tetu, S. G., & Gillings, M. R. (2020). A Novel Family of Acinetobacter Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. *Frontiers in Microbiology*, *11*, 605952. https://doi.org/10.3389/fmicb.2020.605952

Gootz, T. D., & Marra, A. (2008). *Acinetobacter baumannii:* an emerging multidrug-resistant threat. *Expert Review of Anti-Infective Therapy*, *6*(3), 309–325. https://doi.org/10.1586/14787210.6.3.309

Gottig, S., Gruber, T. M., Higgins, P. G., Wachsmuth, M., Seifert, H., & Kempf, V. A. J. (2014). Detection of pan drug-resistant Acinetobacter baumannii in Germany. *Journal of Antimicrobial Chemotherapy*, *69*(9), 2578–2579. https://doi.org/10.1093/jac/dku170

Griffiths, A. J. F. (2012, July 5). *DNA sequencing*. Encyclopedia Britannica. https://www.britannica.com/science/DNA-sequencing

Gurevich, A., Saveliev, V., Vyahhi, N., & Tesler, G. (2013). QUAST: Quality assessment tool for genome assemblies. *Bioinformatics*, *29*(8), 1072–1075. https://doi.org/10.1093/bioinformatics/btt086

Hall-Stoodley, L., Costerton, J. W., & Stoodley, P. (2004). Bacterial biofilms: From the Natural environment to infectious diseases. *Nature Reviews Microbiology*, *2*(2), 95–108. https://doi.org/10.1038/nrmicro821

Hans, R., Bisht, D., Agarwal, R., & Irfan, M. (2015). Phenotypic detection of MBL, Ampc beta-lactamase and carbapenemases in multi drug resistant isolates of *Acinetobacter baumannii*. *International Journal of Medical Research & Health Sciences*, *4*(2), 311. https://doi.org/10.5958/2319-5886.2015.00058.2

Harding, C. M., Hennon, S. W., & Feldman, M. F. (2018). Uncovering the mechanisms of Acinetobacter baumannii virulence. *Nature Reviews Microbiology*, *16*(2), 91–102. https://doi.org/10.1038/nrmicro.2017.148

Harding, C. M., Nasr, M. A., Kinsella, R. L., Scott, N. E., Foster, L. J., Weber, B. S., Fiester, S. E., Actis, L. A., Tracy, E. N., Munson, R. S., & Feldman, M. F. (2015). Acinetobacter</i> strains carry two functional oligosaccharyltransferases, one devoted exclusively to type IV pilin, and the other one dedicated to *O* -glycosylation of multiple proteins: Acinetobacter strains carry two functional oligosaccharyltransferases. *Molecular Microbiology*, *96*(5), 1023–1041. https://doi.org/10.1111/mmi.12986

He, Y., Zhang, Z., Peng, X., Wu, F., & Wang, J. (2013). De novo assembly methods for next generation sequencing data. *Tsinghua Science and Technology*, *18*(5), 500–514. https://doi.org/10.1109/TST.2013.6616523

Hendriksen, R. S., Bortolaia, V., Tate, H., Tyson, G. H., Aarestrup, F. M., & McDermott, P. F. (2019). Using Genomics to Track Global Antimicrobial Resistance. *Frontiers in Public Health*, *7*, 242. https://doi.org/10.3389/fpubh.2019.00242

Hernan, R. C., Karina, B., Gabriela, G., Marcela, N., Carlos, V., & Angela, F. (2009). Selection of colistin-resistant Acinetobacter baumannii isolates in postneurosurgical meningitis in an intensive care unit with high presence of heteroresistance to colistin. *Diagnostic Microbiology and Infectious Disease*, *65*(2), 188–191. https://doi.org/10.1016/j.diagmicrobio.2009.05.019

Houang, E. T. S., Chu, Y. W., Leung, C. M., Chu, K. Y., Berlau, J., Ng, K. C., & Cheng, A. F. B. (2001). Epidemiology and Infection Control Implications of *Acinetobacter* spp. In Hong Kong. *Journal of Clinical Microbiology*, *39*(1), 228–234. https://doi.org/10.1128/JCM.39.1.228-234.2001

Hsu, L.-Y., Apisarnthanarak, A., Khan, E., Suwantarat, N., Ghafur, A., & Tambyah, P. A. (2017). Carbapenem-Resistant Acinetobacter baumannii and Enterobacteriaceae in South and Southeast Asia. *Clinical Microbiology Reviews*, *30*(1), 1–22. https://doi.org/10.1128/CMR.00042-16

Iwashkiw, J. A., Seper, A., Weber, B. S., Scott, N. E., Vinogradov, E., Stratilo, C., Reiz, B., Cordwell, S. J., Whittal, R., Schild, S., & Feldman, M. F. (2012). Identification of a General O-linked Protein Glycosylation System in Acinetobacter baumannii and Its Role in Virulence and Biofilm Formation. *PLoS Pathogens*, *8*(6), e1002758. https://doi.org/10.1371/journal.ppat.1002758

Jacobs, A. C., Hood, I., Boyd, K. L., Olson, P. D., Morrison, J. M., Carson, S., Sayood, K., Iwen, P. C., Skaar, E. P., & Dunman, P. M. (2010). Inactivation of Phospholipase D

Diminishes *Acinetobacter baumannii* Pathogenesis. *Infection and Immunity*, *78*(5), 1952–1962. https://doi.org/10.1128/IAI.00889-09

Jawad, A., Seifert, H., Snelling, A. M., Heritage, J., & Hawkey, P. M. (1998). Survival of Acinetobacter baumannii on dry surfaces: Comparison of outbreak and sporadic isolates. *Journal of Clinical Microbiology*, *36*(7), 1938–1941. https://doi.org/10.1128/JCM.36.7.1938-1941.1998

Jin, J. S., Kwon, S.-O., Moon, D. C., Gurung, M., Lee, J. H., Kim, S. I., & Lee, J. C. (2011). Acinetobacter baumannii Secretes Cytotoxic Outer Membrane Protein A via Outer Membrane Vesicles. *PLoS ONE*, *6*(2), e17027. https://doi.org/10.1371/journal.pone.0017027

Jorgensen, J. H., & Ferraro, M. J. (2009). Antimicrobial Susceptibility Testing: A Review of General Principles and Contemporary Practices. *Clinical Infectious Diseases*, *49*(11), 1749–1755. https://doi.org/10.1086/647952

Kaase, M., Nordmann, P., Wichelhaus, T. A., Gatermann, S. G., Bonnin, R. A., & Poirel, L. (2011). NDM-2 carbapenemase in Acinetobacter baumannii from Egypt. *Journal of Antimicrobial Chemotherapy*, *66*(6), 1260–1262. https://doi.org/10.1093/jac/dkr135

Kalyanaraman, A., Hammond, K., Nieplocha †, J., Krishnan, M., Palmer, B., Tipparaju, V., Harrison, R., Chavarría-Miranda, D., Makino, J., Bader, D., Cong, G., Hendrickson, B., Shalf, J., Donofrio, D., Rowen, C., Oliker, L., Wehner, M., & Gustafson, J. L. (2011). Genome Assembly. In D. Padua (Ed.), *Encyclopedia of Parallel Computing* (pp. 755–768). Springer US. https://doi.org/10.1007/978-0-387-09766-4_402

Karthikeyan, K., Thirunarayan, M. A., & Krishnan, P. (2010). Coexistence of blaOXA-23 with blaNDM-1 and armA in clinical isolates of Acinetobacter baumannii from India. *Journal of Antimicrobial Chemotherapy*, *65*(10), 2253–2254. https://doi.org/10.1093/jac/dkq273

Kchouk, M., Gibrat, J. F., & Elloumi, M. (2017). Generations of Sequencing Technologies: From First to Next Generation. *Biology and Medicine*, *09*(03). https://doi.org/10.4172/0974-8369.1000395

Kengkla, K., Kongpakwattana, K., Saokaew, S., Apisarnthanarak, A., & Chaiyakunapruk, N. (2018). Comparative efficacy and safety of treatment options for MDR and XDR Acinetobacter baumannii infections: A systematic review and network meta-analysis. *Journal of Antimicrobial Chemotherapy*, *73*(1), 22–32. https://doi.org/10.1093/jac/dkx368

Khezri, A., Avershina, E., & Ahmad, R. (2021). Hybrid Assembly Provides Improved Resolution of Plasmids, Antimicrobial Resistance Genes, and Virulence Factors in Escherichia coli and Klebsiella pneumoniae Clinical Isolates. *Microorganisms*, *9*(12), 2560. https://doi.org/10.3390/microorganisms9122560

Kim, S. W., Choi, C. H., Moon, D. C., Jin, J. S., Lee, J. H., Shin, J.-H., Kim, J. M., Lee, Y. C., Seol, S. Y., Cho, D. T., & Lee, J. C. (2009). Serum resistance of *Acinetobacter baumannii* through the binding of factor H to outer membrane proteins. *FEMS Microbiology Letters*, *301*(2), 224–231. https://doi.org/10.1111/j.1574-6968.2009.01820.x

Kwon, S.-O., Gho, Y. S., Lee, J. C., & Kim, S. I. (2009). Proteome analysis of outer membrane vesicles from a clinical *Acinetobacter baumannii* isolate. *FEMS Microbiology Letters*, *297*(2), 150–156. https://doi.org/10.1111/j.1574-6968.2009.01669.x

Kyriakidis, I., Vasileiou, E., Pana, Z. D., & Tragiannidis, A. (2021). Acinetobacter baumannii Antibiotic Resistance Mechanisms. *Pathogens*, *10*(3), 373. https://doi.org/10.3390/pathogens10030373

Larsen, M. V., Cosentino, S., Rasmussen, S., Friis, C., Hasman, H., Marvig, R. L., Jelsbak, L., Sicheritz-Pontén, T., Ussery, D. W., Aarestrup, F. M., & Lund, O. (2012). Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. *Journal of Clinical Microbiology*, *50*(4), 1355–1361. https://doi.org/10.1128/JCM.06094-11

Laxminarayan, R., & Chaudhury, R. R. (2016). Antibiotic Resistance in India: Drivers and Opportunities for Action. *PLOS Medicine*, *13*(3), e1001974. https://doi.org/10.1371/journal.pmed.1001974

Lee, C.-R., Lee, J. H., Park, M., Park, K. S., Bae, I. K., Kim, Y. B., Cha, C.-J., Jeong, B. C., & Lee, S. H. (2017). Biology of Acinetobacter baumannii: Pathogenesis, Antibiotic

Resistance Mechanisms, and Prospective Treatment Options. *Frontiers in Cellular and Infection Microbiology*, *7*. https://doi.org/10.3389/fcimb.2017.00055

Leopold, S. R., Goering, R. V., Witten, A., Harmsen, D., & Mellmann, A. (2014). Bacterial Whole-Genome Sequencing Revisited: Portable, Scalable, and Standardized Analysis for Typing and Detection of Virulence and Antibiotic Resistance Genes. *Journal of Clinical Microbiology*, *52*(7), 2365–2370. https://doi.org/10.1128/JCM.00262-14

Leung, W.-S., Chu, C.-M., Tsang, K.-Y., Lo, F.-H., Lo, K.-F., & Ho, P.-L. (2006). Fulminant Community-Acquired Acinetobacter baumannii Pneumonia as a Distinct Clinical Syndrome. *Chest*, *129*(1), 102–109. https://doi.org/10.1378/chest.129.1.102

Leus, I. V., Weeks, J. W., Bonifay, V., Smith, L., Richardson, S., & Zgurskaya, H. I. (2018). Substrate Specificities and Efflux Efficiencies of RND Efflux Pumps of Acinetobacter baumannii. *Journal of Bacteriology*, *200*(13). https://doi.org/10.1128/JB.00049-18

Limansky, A. S., Mussi, M. A., & Viale, A. M. (2002). Loss of a 29-Kilodalton Outer Membrane Protein in *Acinetobacter baumannii* Is Associated with Imipenem Resistance. *Journal of Clinical Microbiology*, *40*(12), 4776–4778. https://doi.org/10.1128/JCM.40.12.4776-4778.2002

Liu, B., Zheng, D., Jin, Q., Chen, L., & Yang, J. (2019). VFDB 2019: A comparative pathogenomic platform with an interactive web interface. *Nucleic Acids Research*, *47*(D1), D687–D692. https://doi.org/10.1093/nar/gky1080

Liu, C., Chang, Y., Xu, Y., Luo, Y., Wu, L., Mei, Z., Li, S., Wang, R., & Jia, X. (2018). Distribution of virulence-associated genes and antimicrobial susceptibility in clinical Acinetobacter baumannii isolates. *Oncotarget*, *9*(31), 21663–21673. PubMed. https://doi.org/10.18632/oncotarget.24651

Liu, J., Shu, Y., Zhu, F., Feng, B., Zhang, Z., Liu, L., & Wang, G. (2021). Comparative efficacy and safety of combination therapy with high-dose sulbactam or colistin with additional antibacterial agents for multiple drug-resistant and extensively drug-resistant Acinetobacter baumannii infections: A systematic review and network meta-analysis. *Journal of Global Antimicrobial Resistance*, *24*, 136–147. https://doi.org/10.1016/j.jgar.2020.08.021

Loehfelm, T. W., Luke, N. R., & Campagnari, A. A. (2008). Identification and Characterization of an *Acinetobacter baumannii* Biofilm-Associated Protein. *Journal of Bacteriology*, *190*(3), 1036–1044. https://doi.org/10.1128/JB.01416-07

López-Rojas, R., McConnell, M. J., Jiménez-Mejías, M. E., Domínguez-Herrera, J., Fernández-Cuenca, F., & Pachón, J. (2013). Colistin Resistance in a Clinical Acinetobacter baumannii Strain Appearing after Colistin Treatment: Effect on Virulence and Bacterial Fitness. *Antimicrobial Agents and Chemotherapy*, *57*(9), 4587–4589. https://doi.org/10.1128/AAC.00543-13

Magiorakos, A.-P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., Harbarth, S., Hindler, J. F., Kahlmeter, G., Olsson-Liljequist, B., Paterson, D. L., Rice, L. B., Stelling, J., Struelens, M. J., Vatopoulos, A., Weber, J. T., & Monnet, D. L. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, *18*(3), 268–281. https://doi.org/10.1111/j.1469-0691.2011.03570.x

Maragakis, L. L., & Perl, T. M. (2008). Acinetobacter baumannii: Epidemiology, Antimicrobial Resistance, and Treatment Options. *Clinical Infectious Diseases*, *46*(8), 1254–1263. https://doi.org/10.1086/529198

Massova, I., & Mobashery, S. (1998). Kinship and diversification of bacterial penicillin-binding proteins and beta-lactamases. *Antimicrobial Agents and Chemotherapy*, *42*(1), 1–17. https://doi.org/10.1128/AAC.42.1.1

Maxam, A. M., & Gilbert, W. (1977). A new method for sequencing DNA. *Proceedings of the National Academy of Sciences*, *74*(2), 560–564. https://doi.org/10.1073/pnas.74.2.560

Monegro, A. F., Muppidi, V., & Regunath, H. (2022). Hospital Acquired Infections. In *StatPearls*. StatPearls Publishing. http://www.ncbi.nlm.nih.gov/books/NBK441857/

Morris, F. C., Dexter, C., Kostoulias, X., Uddin, M. I., & Peleg, A. Y. (2019). The Mechanisms of Disease Caused by Acinetobacter baumannii. *Frontiers in Microbiology*, *10*, 1601. https://doi.org/10.3389/fmicb.2019.01601

Mulani, M. S., Kamble, E. E., Kumkar, S. N., Tawre, M. S., & Pardesi, K. R. (2019). Emerging Strategies to Combat ESKAPE Pathogens in the Era of Antimicrobial Resistance: A Review. *Frontiers in Microbiology*, *10*, 539. https://doi.org/10.3389/fmicb.2019.00539

Munoz-Price, L. S., & Weinstein, R. A. (2008). Acinetobacter Infection. *New England Journal of Medicine*, *358*(12), 1271–1281. https://doi.org/10.1056/NEJMra070741

Mussi, M. A., Limansky, A. S., & Viale, A. M. (2005). Acquisition of Resistance to Carbapenems in Multidrug-Resistant Clinical Strains of *Acinetobacter baumannii*: Natural Insertional Inactivation of a Gene Encoding a Member of a Novel Family of β-Barrel Outer Membrane Proteins. *Antimicrobial Agents and Chemotherapy*, *49*(4), 1432–1440. https://doi.org/10.1128/AAC.49.4.1432-1440.2005

Navidinia, M. (2016). The clinical importance of emerging ESKAPE pathogens in nosocomial infections. *Archives of Advances in Biosciences*, *7*(3), 43–57. https://doi.org/10.22037/jps.v7i3.12584

Nawfal Dagher, T., Al-Bayssari, C., Chabou, S., Antar, N., Diene, S. M., Azar, E., & Rolain, J.-M. (2019). Investigation of multidrug-resistant ST2 Acinetobacter baumannii isolated from Saint George hospital in Lebanon. *BMC Microbiology*, *19*(1), 29. https://doi.org/10.1186/s12866-019-1401-2

Ng, P. C., & Kirkness, E. F. (2010). Whole Genome Sequencing. In M. R. Barnes & G. Breen (Eds.), *Genetic Variation* (Vol. 628, pp. 215–226). Humana Press. https://doi.org/10.1007/978-1-60327-367-1_12

O’Hara, J. A., Ambe, L. A., Casella, L. G., Townsend, B. M., Pelletier, M. R., Ernst, R. K., Shanks, R. M. Q., & Doi, Y. (2013). Activities of Vancomycin-Containing Regimens against Colistin-Resistant Acinetobacter baumannii Clinical Strains. *Antimicrobial Agents and Chemotherapy*, *57*(5), 2103–2108. https://doi.org/10.1128/AAC.02501-12

OmicsBox—Bioinformatics made easy (2.0.29). (2019). [Computer software]. BioBam Bioinformatics. https://www.biobam.com/omicsbox/

Ong, C. W. M., Lye, D. C. B., Khoo, K. L., Chua, G. S. W., Yeoh, S. F., Leo, Y. S., Tambyah, P. A., & Chua, A. C. (2009). Severe community-acquired *Acinetobacter baumannii* pneumonia: An emerging highly lethal infectious disease in the Asia-Pacific. *Respirology*, *14*(8), 1200–1205. https://doi.org/10.1111/j.1440-1843.2009.01630.x

Peleg, A. Y., Seifert, H., & Paterson, D. L. (2008). *Acinetobacter baumannii*: Emergence of a Successful Pathogen. *Clinical Microbiology Reviews*, *21*(3), 538–582. https://doi.org/10.1128/CMR.00058-07

Petersen, K., Riddle, M. S., Danko, J. R., Blazes, D. L., Hayden, R., Tasker, S. A., & Dunne, J. R. (2007). Trauma-related Infections in Battlefield Casualties From Iraq. *Annals of Surgery*, *245*(5), 803–811. https://doi.org/10.1097/01.sla.0000251707.32332.c1

Pevsner, J. (2015). *Bioinformatics and functional genomics* (Third edition). John Wiley and Sons, Inc.

Pevzner, P. A., Tang, H., & Waterman, M. S. (2001). An Eulerian path approach to DNA fragment assembly. *Proceedings of the National Academy of Sciences*, *98*(17), 9748–9753. https://doi.org/10.1073/pnas.171285098

Piepenbrink, K. H., Lillehoj, E., Harding, C. M., Labonte, J. W., Zuo, X., Rapp, C. A., Munson, R. S., Goldblum, S. E., Feldman, M. F., Gray, J. J., & Sundberg, E. J. (2016). Structural Diversity in the Type IV Pili of Multidrug-resistant Acinetobacter. *Journal of Biological Chemistry*, *291*(44), 22924–22935. https://doi.org/10.1074/jbc.M116.751099

Pop, M. (2009). Genome assembly reborn: Recent computational challenges. *Briefings in Bioinformatics*, *10*(4), 354–366. https://doi.org/10.1093/bib/bbp026

Prjibelski, A., Antipov, D., Meleshko, D., Lapidus, A., & Korobeynikov, A. (2020). Using SPAdes De Novo Assembler. *Current Protocols in Bioinformatics*, *70*(1). https://doi.org/10.1002/cpbi.102

Quainoo, S., Coolen, J. P. M., van Hijum, S. A. F. T., Huynen, M. A., Melchers, W. J. G., van Schaik, W., & Wertheim, H. F. L. (2017). Whole-Genome Sequencing of Bacterial Pathogens: The Future of Nosocomial Outbreak Analysis. *Clinical Microbiology Reviews*, *30*(4), 1015–1063. https://doi.org/10.1128/CMR.00016-17

Ramirez, M. S., Don, M., Merkier, A. K., Bistué, A. J. S., Zorreguieta, A., Centrón, D., & Tolmasky, M. E. (2010). Naturally Competent *Acinetobacter baumannii* Clinical Isolate as a Convenient Model for Genetic Studies. *Journal of Clinical Microbiology*, *48*(4), 1488–1490. https://doi.org/10.1128/JCM.01264-09

Rice, L. B. (2008). Federal Funding for the Study of Antimicrobial Resistance in Nosocomial Pathogens: No ESKAPE. *The Journal of Infectious Diseases*, *197*(8), 1079–1081. https://doi.org/10.1086/533452

Rodríguez, C. H., Nastro, M., & Famiglietti, A. (2018). Carbapenemases in Acinetobacter baumannii. Review of their dissemination in Latin America. *Revista Argentina de Microbiología*, *50*(3), 327–333. https://doi.org/10.1016/j.ram.2017.10.006

Rossau, R., Van Landschoot, A., Gillis, M., & De Ley, J. (1991). Taxonomy of Moraxellaceae fam. Nov., a New Bacterial Family To Accommodate the Genera Moraxella, Acinetobacter, and Psychrobacter and Related Organisms. *International Journal of Systematic Bacteriology*, *41*(2), 310–319. https://doi.org/10.1099/00207713-41-2-310

Rumbo, C., Tomás, M., Fernández Moreira, E., Soares, N. C., Carvajal, M., Santillana, E., Beceiro, A., Romero, A., & Bou, G. (2014). The Acinetobacter baumannii Omp33-36 Porin Is a Virulence Factor That Induces Apoptosis and Modulates Autophagy in Human Cells. *Infection and Immunity*, *82*(11), 4666–4680. https://doi.org/10.1128/IAI.02034-14

Russo, T. A., Luke, N. R., Beanan, J. M., Olson, R., Sauberan, S. L., MacDonald, U., Schultz, L. W., Umland, T. C., & Campagnari, A. A. (2010). The K1 capsular polysaccharide of Acinetobacter baumannii strain 307-0294 is a major virulence factor. *Infection and Immunity*, *78*(9), 3993–4000. https://doi.org/10.1128/IAI.00366-10

Salgado-Camargo, A. D., Castro-Jaimes, S., Gutierrez-Rios, R.-M., Lozano, L. F., Altamirano-Pacheco, L., Silva-Sanchez, J., Pérez-Oseguera, Á., Volkow, P., Castillo-Ramírez, S., & Cevallos, M. A. (2020). Structure and Evolution of Acinetobacter baumannii Plasmids. *Frontiers in Microbiology*, *11*, 1283. https://doi.org/10.3389/fmicb.2020.01283

Salto, I. P., Torres Tejerizo, G., Wibberg, D., Pühler, A., Schlüter, A., & Pistorio, M. (2018). Comparative genomic analysis of Acinetobacter spp. Plasmids originating from clinical settings and environmental habitats. *Scientific Reports*, *8*(1), 7783. https://doi.org/10.1038/s41598-018-26180-3

Sanger, F., Nicklen, S., & Coulson, A. R. (1977). DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences*, *74*(12), 5463–5467. https://doi.org/10.1073/pnas.74.12.5463

Scott, P., Deye, G., Srinivasan, A., Murray, C., Moran, K., Hulten, E., Fishbain, J., Craft, D., Riddell, S., Lindler, L., Mancuso, J., Milstrey, E., Bautista, C. T., Patel, J., Ewell, A., Hamilton, T., Gaddy, C., Tenney, M., Christopher, G., … Petruccelli, B. (2007). An Outbreak of Multidrug-Resistant Acinetobacter baumannii-calcoaceticus Complex Infection in the US Military Health Care System Associated with Military Operations in Iraq. *Clinical Infectious Diseases*, *44*(12), 1577–1584. https://doi.org/10.1086/518170

Sebeny, P. J., Riddle, M. S., & Petersen, K. (2008). *Acinetobacter baumannii* Skin and Soft-Tissue Infection Associated with War Trauma. *Clinical Infectious Diseases*, *47*(4), 444–449. https://doi.org/10.1086/590568

Seemann, T. (2014). Prokka: Rapid prokaryotic genome annotation. *Bioinformatics*, *30*(14), 2068–2069. https://doi.org/10.1093/bioinformatics/btu153

Segerman, B. (2020). The Most Frequently Used Sequencing Technologies and Assembly Methods in Different Time Segments of the Bacterial Surveillance and RefSeq Genome Databases. *Frontiers in Cellular and Infection Microbiology*, *10*, 527102. https://doi.org/10.3389/fcimb.2020.527102

Seifert, H., Dijkshoorn, L., Gerner-Smidt, P., Pelzer, N., Tjernberg, I., & Vaneechoutte, M. (1997). Distribution of Acinetobacter species on human skin: Comparison of phenotypic and genotypic identification methods. *Journal of Clinical Microbiology*, *35*(11), 2819–2825. https://doi.org/10.1128/jcm.35.11.2819-2825.1997

Seifert, H., Strate, A., & Pulverer, G. (1995). Nosocomial Bacteremia due to Acinetobacter baumannii: Clinical Features, Epidemiology, and Predictors of Mortality: *Medicine*, *74*(6), 340–349. https://doi.org/10.1097/00005792-199511000-00004

Sheldon, J. R., & Skaar, E. P. (2020). Acinetobacter baumannii can use multiple siderophores for iron acquisition, but only acinetobactin is required for virulence. *PLOS Pathogens*, *16*(10), e1008995. https://doi.org/10.1371/journal.ppat.1008995

Simão, F. A., Waterhouse, R. M., Ioannidis, P., Kriventseva, E. V., & Zdobnov, E. M. (2015). BUSCO: Assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics*, *31*(19), 3210–3212. https://doi.org/10.1093/bioinformatics/btv351

Simpson, J. T., Wong, K., Jackman, S. D., Schein, J. E., Jones, S. J. M., & Birol, I. (2009). ABySS: A parallel assembler for short read sequence data. *Genome Research*, *19*(6), 1117–1123. https://doi.org/10.1101/gr.089532.108

Smani, Y., Fàbrega, A., Roca, I., Sánchez-Encinales, V., Vila, J., & Pachón, J. (2014). Role of OmpA in the Multidrug Resistance Phenotype of Acinetobacter baumannii. *Antimicrobial Agents and Chemotherapy*, *58*(3), 1806–1808. https://doi.org/10.1128/AAC.02101-13

Smillie, C., Garcillán-Barcia, M. P., Francia, M. V., Rocha, E. P. C., & de la Cruz, F. (2010). Mobility of Plasmids. *Microbiology and Molecular Biology Reviews*, *74*(3), 434–452. https://doi.org/10.1128/MMBR.00020-10

Stahl, J., Bergmann, H., Göttig, S., Ebersberger, I., & Averhoff, B. (2015). Acinetobacter baumannii Virulence Is Mediated by the Concerted Action of Three Phospholipases D. *PLOS ONE*, *10*(9), e0138360. https://doi.org/10.1371/journal.pone.0138360

Sugawara, E., & Nikaido, H. (2012). OmpA Is the Principal Nonspecific Slow Porin of Acinetobacter baumannii. *Journal of Bacteriology*, *194*(15), 4089–4096. https://doi.org/10.1128/JB.00435-12

Tacconelli, E., Carrara, E., Savoldi, A., Harbarth, S., Mendelson, M., Monnet, D. L., Pulcini, C., Kahlmeter, G., Kluytmans, J., Carmeli, Y., Ouellette, M., Outterson, K., Patel, J., Cavaleri, M., Cox, E. M., Houchens, C. R., Grayson, M. L., Hansen, P., Singh, N., … WHO Pathogens Priority List Working Group. (2018). Discovery, research, and development of new antibiotics: The WHO priority list of antibiotic-resistant bacteria and tuberculosis. *The Lancet. Infectious Diseases*, *18*(3), 318–327. https://doi.org/10.1016/S1473-3099(17)30753-3

Tooke, C. L., Hinchliffe, P., Bragginton, E. C., Colenso, C. K., Hirvonen, V. H. A., Takebayashi, Y., & Spencer, J. (2019). β-Lactamases and β-Lactamase Inhibitors in the 21st Century. *Journal of Molecular Biology*, *431*(18), 3472–3500. https://doi.org/10.1016/j.jmb.2019.04.002

Uppalapati, S. R., Sett, A., & Pathania, R. (2020). The Outer Membrane Proteins OmpA, CarO, and OprD of Acinetobacter baumannii Confer a Two-Pronged Defense in Facilitating Its Success as a Potent Human Pathogen. *Frontiers in Microbiology*, *11*, 589234. https://doi.org/10.3389/fmicb.2020.589234

Van Looveren, M., & Goossens, H. (2004). Antimicrobial resistance of Acinetobacter spp. In Europe. *Clinical Microbiology and Infection*, *10*(8), 684–704. https://doi.org/10.1111/j.1469-0691.2004.00942.x

Vila, J., Martí, S., & Sánchez-Céspedes, J. (2007). Porins, efflux pumps and multidrug resistance in Acinetobacter baumannii. *Journal of Antimicrobial Chemotherapy*, *59*(6), 1210–1215. https://doi.org/10.1093/jac/dkl509

Wajid, B., & Serpedin, E. (2016). Do it yourself guide to genome assembly. *Briefings in Functional Genomics*, *15*(1), 1–9. https://doi.org/10.1093/bfgp/elu042

Wandersman, C., & Delepelaire, P. (2004). Bacterial Iron Sources: From Siderophores to Hemophores. *Annual Review of Microbiology*, *58*(1), 611–647. https://doi.org/10.1146/annurev.micro.58.030603.123811

Wang, J.-T., McDonald, L. C., Chang, S.-C., & Ho, M. (2002). Community-Acquired *Acinetobacter baumannii* Bacteremia in Adult Patients in Taiwan. *Journal of Clinical Microbiology*, *40*(4), 1526–1529. https://doi.org/10.1128/JCM.40.4.1526-1529.2002

Wendt, C., Dietze, B., Dietz, E., & Rüden, H. (1997). Survival of Acinetobacter baumannii on dry surfaces. *Journal of Clinical Microbiology*, *35*(6), 1394–1397. https://doi.org/10.1128/jcm.35.6.1394-1397.1997

Whole Genome Sequencing (WGS). (2019, May 14). Centers for Disease Control and Prevention. https://www.cdc.gov/pulsenet/pathogens/wgs.html

Wick, R. R., Judd, L. M., Gorrie, C. L., & Holt, K. E. (2017). Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. *PLOS Computational Biology*, *13*(6), e1005595. https://doi.org/10.1371/journal.pcbi.1005595

Wick, R. R., Schultz, M. B., Zobel, J., & Holt, K. E. (2015). Bandage: Interactive visualization of *de novo* genome assemblies: Fig. 1. *Bioinformatics*, *31*(20), 3350–3352. https://doi.org/10.1093/bioinformatics/btv383

Wongsuk, T., Boonsilp, S., Homkaew, A., Thananon, K., & Oonanant, W. (2022). Whole genome sequence of pan drug-resistant clinical isolate of Acinetobacter baumannii ST1890. *PLOS ONE*, *17*(3), e0264374. https://doi.org/10.1371/journal.pone.0264374

Wood, D. E., Lu, J., & Langmead, B. (2019). Improved metagenomic analysis with Kraken 2. *Genome Biology*, *20*(1), 257. https://doi.org/10.1186/s13059-019-1891-0

Wood, D. E., & Salzberg, S. L. (2014). Kraken: Ultrafast metagenomic sequence classification using exact alignments. *Genome Biology*, *15*(3), R46. https://doi.org/10.1186/gb-2014-15-3-r46

Xiong, J. (2006). *Essential Bioinformatics.* Cambridge University Press. https://doi.org/10.1017/CBO9780511806087

Yong, D., Toleman, M. A., Giske, C. G., Cho, H. S., Sundman, K., Lee, K., & Walsh, T. R. (2009). Characterization of a New Metallo-β-Lactamase Gene, *bla* $_{\text{NDM-1}}$, and a Novel Erythromycin Esterase Gene Carried on a Unique Genetic Structure in *Klebsiella pneumoniae* Sequence Type 14 from India. *Antimicrobial Agents and Chemotherapy*, *53*(12), 5046–5054. https://doi.org/10.1128/AAC.00774-09

Yoon, E.-J., Nait Chabane, Y., Goussard, S., Snesrud, E., Courvalin, P., Dé, E., & Grillot-Courvalin, C. (2015). Contribution of Resistance-Nodulation-Cell Division Efflux Systems to Antibiotic Resistance and Biofilm Formation in Acinetobacter baumannii. *MBio*, *6*(2), e00309-15. https://doi.org/10.1128/mBio.00309-15

Yun, H. C., Murray, C. K., Roop, S. A., Hospenthal, D. R., Gourdine, E., & Dooley, D. P. (2006). Bacteria Recovered from Patients Admitted to a Deployed U.S. Military Hospital in Baghdad, Iraq. *Military Medicine*, *171*(9), 821–825. https://doi.org/10.7205/MILMED.171.9.821

Zhao, Y., Hu, K., Zhang, J., Guo, Y., Fan, X., Wang, Y., Mensah, S. D., & Zhang, X. (2019). Outbreak of carbapenem-resistant Acinetobacter baumannii carrying the carbapenemase OXA-23 in ICU of the eastern Heilongjiang Province, China. *BMC Infectious Diseases*, *19*(1), 452. https://doi.org/10.1186/s12879-019-4073-5

Zhu, L., Chen, X., & Hou, P. (2019). Mutation of CarO participates in drug resistance in imipenem-resistant *Acinetobacter baumannii*. *Journal of Clinical Laboratory Analysis*, *33*(8). https://doi.org/10.1002/jcla.22976

Appendices

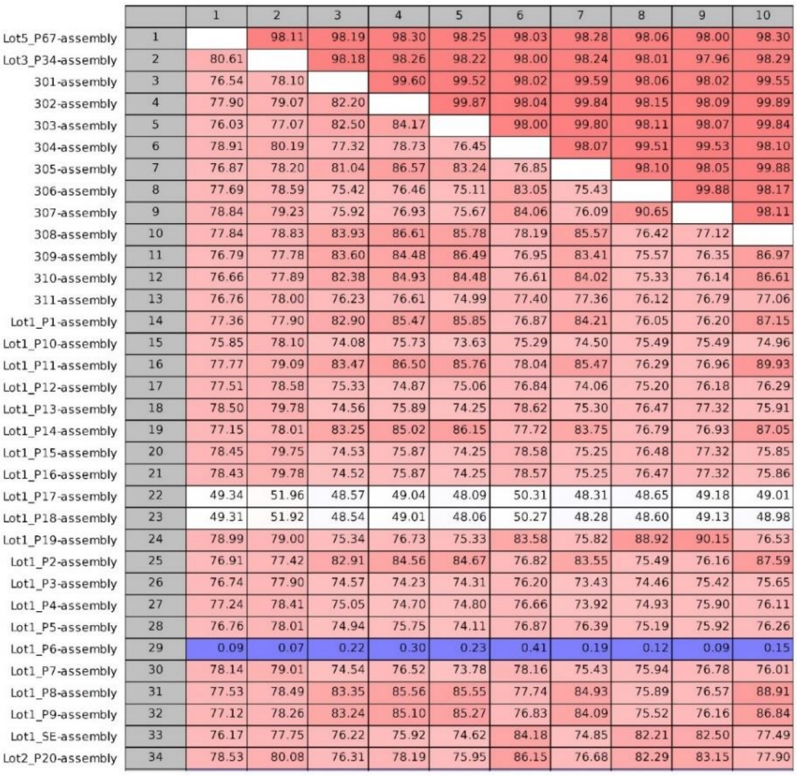
Appendix A: Statistics of illumina sequencing datasets before and after trimming using Trimmomatic

	Isolates	File size before trimming (MB)	Average number of base pairs (bp)		Average number of reads		Mean coverage	
			Before trimming	After trimming	Before trimming	After trimming	Before trimming	After trimming
Norwegian isolates	301_S1_L001	360.8	163182033	93339546	542133	528523	41.05	23.48
	302_S4_L001	614.7	278038516	187182846	923716	899726	69.95	47.09
	303_S7_L001	216.9	98094696	48891667	325896	314201	24.68	12.30
	304_S10_L001	284.2	128548371	62350193	427071	410773	32.34	15.69
	305_S13_L001	389.9	176383893	97336384	585993	567258	44.38	24.49
	306_S16_L001	525.4	237652142	134357070	789542	768498	59.79	33.80
	307_S19_L001	454.5	205580592	105310514	682992	663686	51.72	26.50
	308_S22_L001	683.1	308989142	192128061	1026542	999096	77.74	48.34
	309_S2_L001	748.4	338541924	238968427	1124724	1095191	85.17	60.12
	310_S5_L001	580.9	262782933	172877329	873033	845702	66.11	43.49
	311_S8_L001	361.2	163370459	86011114	542759	524944	41.10	21.64
Indian isolates	Lot1_P1	1500	608937247	587353607	4032697	3916178	153.20	147.77
	Lot1_P2	1300	551187146	531579977	3650246	3548372	138.67	133.74
	Lot1_P3	1400	580803229	560199776	3846379	3739059	146.12	140.94
	Lot1_P4	1600	660670753	637085981	4375303	4246124	166.22	160.28
	Lot1_P5	1500	614402239	586612545	4068889	3928354	154.58	147.59
	Lot1_P6	1300	536716061	516563714	3554411	3452676	135.03	129.96
	Lot1_P7	1400	570012014	551128096	3774914	3674605	143.41	138.66
	Lot1_P8	1200	520486732	500872789	3446932	3345029	130.95	126.01
	Lot1_P9	1500	607219320	589922566	4021320	3929208	152.77	148.42
	Lot1_P10	1500	629826436	607548542	4171036	4055820	158.46	152.85
	Lot1_P11	1400	574647110	554561498	3805610	3700136	144.58	139.52
	Lot1_P12	1300	532675301	513810874	3527651	3432949	134.02	129.27
	Lot1_P13	1400	581485900	561386386	3850900	3749746	146.30	141.24
	Lot1_P14	1300	541068636	519661754	3583236	3472884	136.13	130.74
	Lot1_P15	1500	618316914	594383765	4094814	3972393	155.56	149.54
	Lot1_P16	1400	572395549	550771291	3790699	3680744	144.01	138.57
	Lot1_P17	1400	583916396	561389672	3866996	3753156	146.91	141.24
	Lot1_P18	1400	586934735	566255150	3886985	3781586	147.67	142.46
	Lot1_P19	1500	624904893	602567053	4138443	4022394	157.22	151.60
	Lot1_SE	1500	646490494	636143893	4281394	4237954	162.65	160.05
	Lot2_P20	1300	550276767	531645297	3644217	3539955	138.44	133.76
	Lot2_P21	1600	658191937	639749975	4358887	4254122	165.59	160.95
	Lot2_P22	1500	646490494	625048591	4281394	4165885	162.65	157.26
	Lot2_P23	1400	596118857	576337074	3947807	3840157	149.98	145.00
	Lot2_P24	1500	610159894	592437868	4040794	3941720	153.51	149.05
	Lot2_P25	1600	684164390	662786831	4530890	4412823	172.13	166.75
	Lot2_P26	1300	552052074	534931830	3655974	3560746	138.89	134.58
	Lot2_P27	1700	704581100	682576495	4666100	4544063	177.27	171.73
	Lot2_P28	1700	691255501	669524572	4577851	4455943	173.91	168.45
	Lot3_P29	992.4	413726410	379792435	2739910	2598253	104.09	95.55
	Lot3_P30	1100	467937826	426768567	3098926	2928360	117.73	107.37
	Lot3_P31	1100	438693807	402098368	2905257	2753531	110.37	101.16
	Lot3_P32	1100	473450232	438116369	3135432	2990030	119.12	110.23

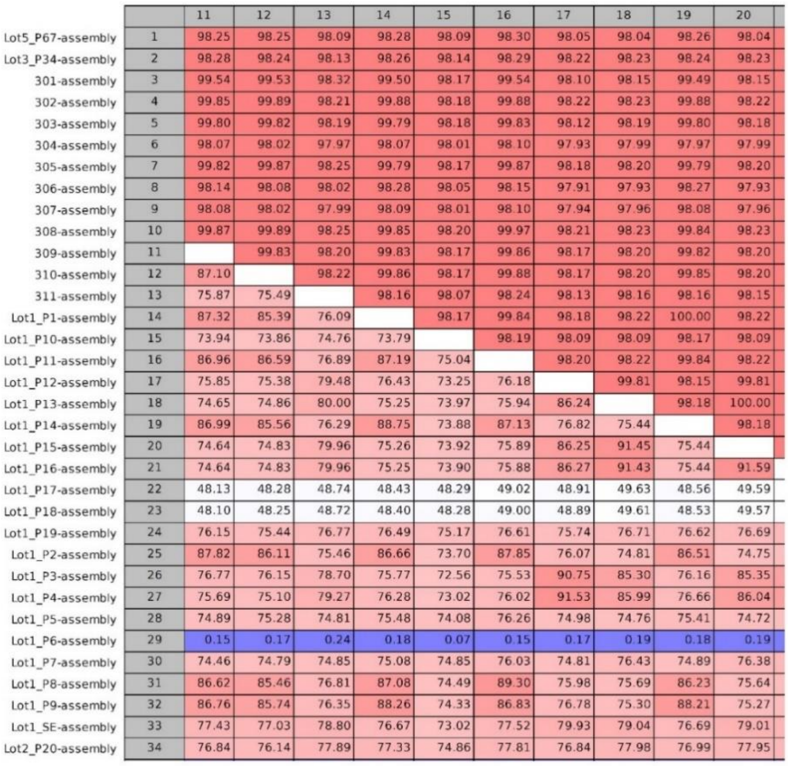
Lot3_P33	1700	698778170	639719084	4627670	4390048	175.81	160.95
Lot3_P34	1300	529297582	504296628	3505282	3389556	133.17	126.88
Lot3_P35	920.8	384931767	364350650	2549217	2454400	96.84	91.67
Lot3_P36	1000	424007245	401781303	2807995	2704924	106.68	101.08
Lot3_P37	1100	471445103	447357278	3122153	3008083	118.61	112.55
Lot3_P38	1400	575385500	530250581	3810500	3624287	144.76	133.41
Lot3_P39	984.6	411615581	388817158	2725931	2619916	103.56	97.82
Lot3_P40	825	344883245	328068261	2283995	2202995	86.77	82.54
Lot3_P41	1500	630464864	592083537	4175264	4017238	158.62	148.96
Lot3_P42	1100	437753681	397421232	2899031	2731752	110.13	99.99
Lot3_P43	1200	513241903	467955721	3398953	3211500	129.13	117.73
Lot3_P44	1100	450673543	415761560	2984593	2842274	113.38	104.60
Lot3_P45	1300	547051860	505758642	3622860	3450992	137.63	127.24
Lot3_P46	1100	465251385	429468239	3081135	2931994	117.05	108.05
Lot3_SE	1200	520211006	495093153	3445106	3383940	130.88	124.56
Lot4_P47	1500	643257600	549886795	4288384	3800930	161.84	138.35
Lot4_P48	1300	527459700	455693524	3516398	3145361	132.70	114.65
Lot4_P49	1500	613635600	524088342	4090904	3617712	154.38	131.86
Lot4_P50	1600	659131200	571101891	4394208	3934864	165.83	143.68
Lot4_P51	1400	584382750	502318174	3895885	3465266	147.02	126.38
Lot4_P52	1400	569275200	483802163	3795168	3340548	143.22	121.72
Lot4_P53	3400	1403504400	1234341652	9356696	8469088	353.11	310.55
Lot4_P54	1300	546701400	468897447	3644676	3235399	137.54	117.97
Lot4_P55	3300	1376299800	1220150516	9175332	8364566	346.26	306.98
Lot4_P56	1500	616973550	533708786	4113157	3681125	155.22	134.28
Lot4_P57	997.8	415015350	363110301	2766769	2502516	104.41	91.35
Lot4_P58	1700	687542700	602369718	4583618	4148620	172.98	151.55
Lot4_P59	1400	567027450	495810408	3780183	3416520	142.66	124.74
Lot4_P60	1500	608437350	528399599	4056249	3640739	153.08	132.94
Lot4_P61	1400	583428150	508057286	3889521	3503685	146.78	127.82
Lot5_P62	1700	714245250	643336485	4761635	4459246	179.70	161.86
Lot5_P63	1400	583468950	526971426	3889793	3640851	146.79	132.58
Lot5_P64	1400	595846950	524262119	3972313	3613431	149.91	131.90
Lot5_P65	1400	580478400	517493592	3869856	3573862	146.04	130.20
Lot5_P66	1200	516598050	462166003	3443987	3194397	129.97	116.28
Lot5_P67	1700	722733900	624377419	4818226	4312493	181.83	157.09
Lot5_P68	1000	422325300	364845994	2815502	2530388	106.25	91.79
Lot5_P69	1800	753402150	676378742	5022681	4663621	189.55	170.17
Lot5_P70	1500	628602600	548212168	4190684	3787598	158.15	137.92
Lot5_P71	1600	677082600	592695031	4513884	4087199	170.35	149.12
Lot5_P72	1600	668351250	592813057	4455675	4084706	168.15	149.15
Lot5_P73	1500	609793800	549062391	4065292	3790423	153.42	138.14
Lot5_P74	1400	598689300	522698720	3991262	3622302	150.62	131.51
Lot5_P75	1300	546107550	488671625	3640717	3368713	137.39	122.94
Lot5_P76	1300	545223450	477293962	3634823	3296616	137.17	120.08
Lot5_P77	1700	716671500	633997911	4777810	4358602	180.31	159.51
Lot5_P78	1500	624721050	559181963	4164807	3854455	157.17	140.68
Lot5_P79	1400	599482200	527554979	3996548	3641136	150.82	132.73
Lot5_P80	1300	523779750	472625329	3491865	3267602	131.78	118.91
Lot5_P81	1600	660623400	593492838	4404156	4109217	166.21	149.32
Lot5_P82	1400	601982250	516047691	4013215	3570944	151.45	129.83
Lot5_P83	1100	450201450	393294778	3001343	2715243	113.27	98.95
Mean	1313.96	549362884	496539169	3567913	3354338	138.21	125

Appendix B: Matrix of ANI and AP based on WGA of all the 96 isolates

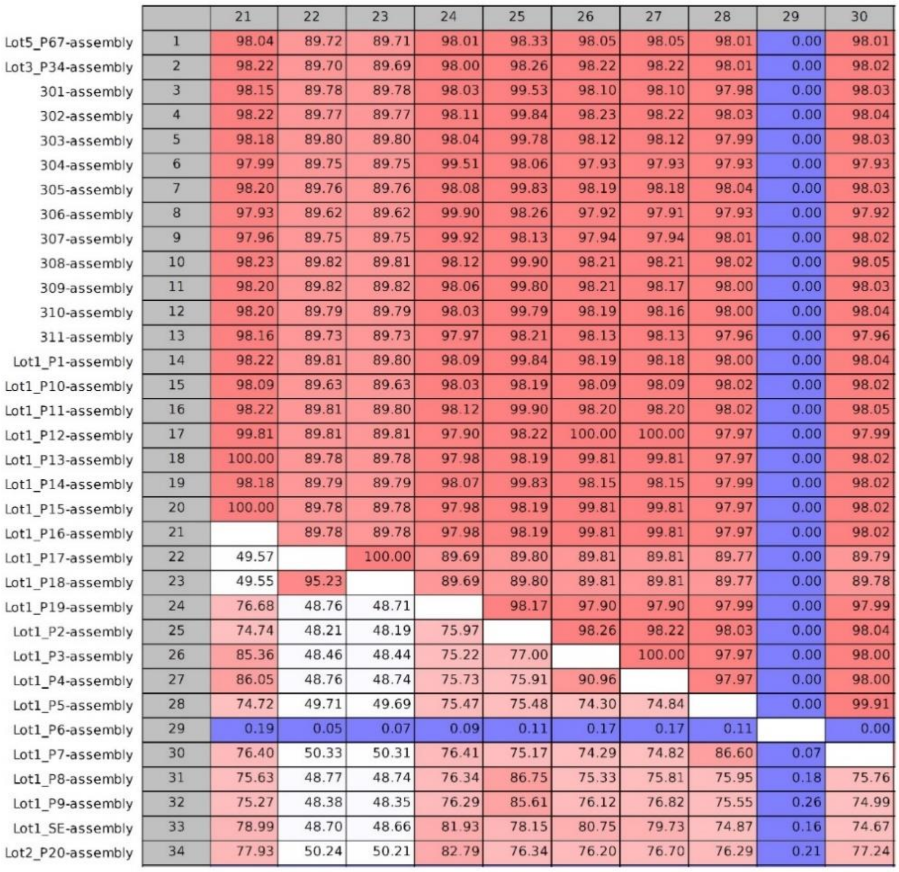
ANI (%) and AP (%) of each genome sequence comparison are shown in the upper and lower diagonals of the matrix respectively.



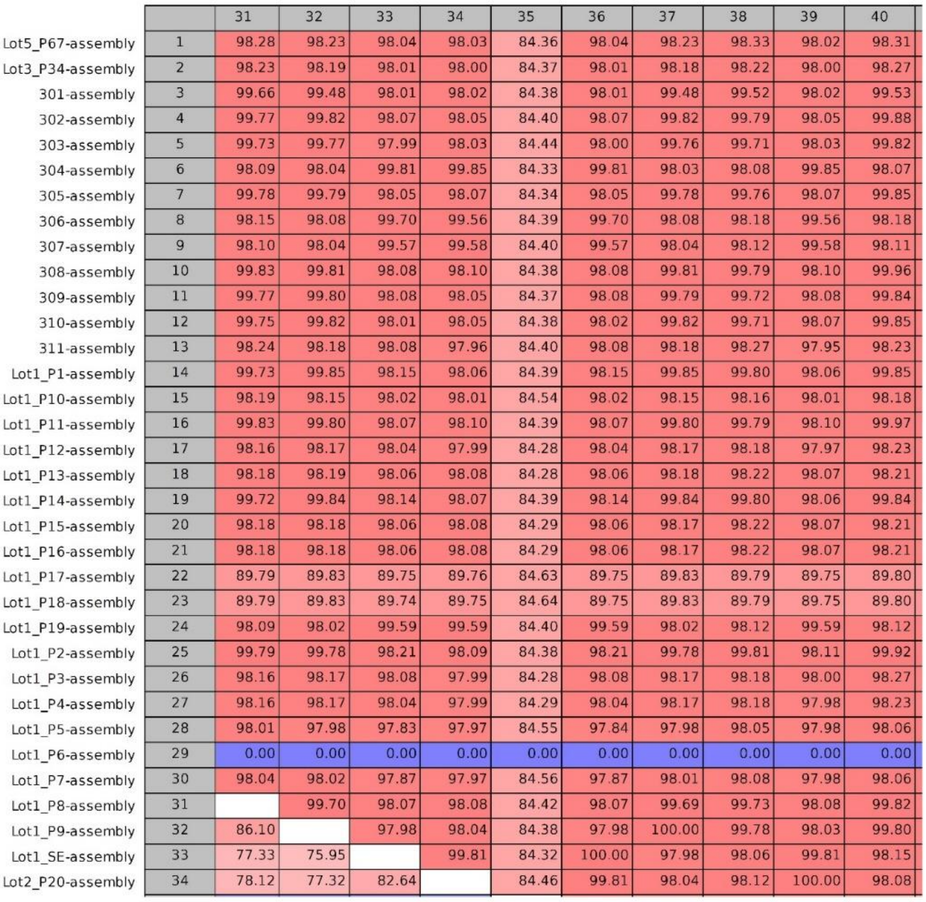
		1	2	3	4	5	6	7	8	9	10
Lot5_P67-assembly	1		98.11	98.19	98.30	98.25	98.03	98.28	98.06	98.00	98.30
Lot3_P34-assembly	2	80.61		98.18	98.26	98.22	98.00	98.24	98.01	97.96	98.29
301-assembly	3	76.54	78.10		99.60	99.52	98.02	99.59	98.06	98.02	99.55
302-assembly	4	77.90	79.07	82.20		99.87	98.04	99.84	98.15	98.09	99.89
303-assembly	5	76.03	77.07	82.50	84.17		98.00	99.80	98.11	98.07	99.84
304-assembly	6	78.91	80.19	77.32	78.73	76.45		98.07	99.51	99.53	98.10
305-assembly	7	76.87	78.20	81.04	86.57	83.24	76.85		98.10	98.05	99.88
306-assembly	8	77.69	78.59	75.42	76.46	75.11	83.05	75.43		99.88	98.17
307-assembly	9	78.84	79.23	75.92	76.93	75.67	84.06	76.09	90.65		98.11
308-assembly	10	77.84	78.83	83.93	86.61	85.78	78.19	85.57	76.42	77.12	
309-assembly	11	76.79	77.78	83.60	84.48	86.49	76.95	83.41	75.57	76.35	86.97
310-assembly	12	76.66	77.89	82.38	84.93	84.48	76.61	84.02	75.33	76.14	86.61
311-assembly	13	76.76	78.00	76.23	76.61	74.99	77.40	77.36	76.12	76.79	77.06
Lot1_P1-assembly	14	77.36	77.90	82.90	85.47	85.85	76.87	84.21	76.05	76.20	87.15
Lot1_P10-assembly	15	75.85	78.10	74.08	75.73	73.63	75.29	74.50	75.49	75.49	74.96
Lot1_P11-assembly	16	77.77	79.09	83.47	86.50	85.76	78.04	85.47	76.29	76.96	89.93
Lot1_P12-assembly	17	77.51	78.58	75.33	74.87	75.06	76.84	74.06	75.20	76.18	76.29
Lot1_P13-assembly	18	78.50	79.78	74.56	75.89	74.25	78.62	75.30	76.47	77.32	75.91
Lot1_P14-assembly	19	77.15	78.01	83.25	85.02	86.15	77.72	83.75	76.79	76.93	87.05
Lot1_P15-assembly	20	78.45	79.75	74.53	75.87	74.25	78.58	75.25	76.48	77.32	75.85
Lot1_P16-assembly	21	78.43	79.78	74.52	75.87	74.25	78.57	75.25	76.47	77.32	75.86
Lot1_P17-assembly	22	49.34	51.96	48.57	49.04	48.09	50.31	48.31	48.65	49.18	49.01
Lot1_P18-assembly	23	49.31	51.92	48.54	49.01	48.06	50.27	48.28	48.60	49.13	48.98
Lot1_P19-assembly	24	78.99	79.00	75.34	76.73	75.33	83.58	75.82	88.92	90.15	76.53
Lot1_P2-assembly	25	76.91	77.42	82.91	84.56	84.67	76.82	83.55	75.49	76.16	87.59
Lot1_P3-assembly	26	76.74	77.90	74.57	74.23	74.31	76.20	73.43	74.46	75.42	75.65
Lot1_P4-assembly	27	77.24	78.41	75.05	74.70	74.80	76.66	73.92	74.93	75.90	76.11
Lot1_P5-assembly	28	76.76	78.01	74.94	75.75	74.11	76.87	76.39	75.19	75.92	76.26
Lot1_P6-assembly	29	0.09	0.07	0.22	0.30	0.23	0.41	0.19	0.12	0.09	0.15
Lot1_P7-assembly	30	78.14	79.01	74.54	76.52	73.78	78.16	75.43	75.94	76.78	76.01
Lot1_P8-assembly	31	77.53	78.49	83.35	85.56	85.55	77.74	84.93	75.89	76.57	88.91
Lot1_P9-assembly	32	77.12	78.26	83.24	85.10	85.27	76.83	84.09	75.52	76.16	86.84
Lot1_SE-assembly	33	76.17	77.75	76.22	75.92	74.62	84.18	74.85	82.21	82.50	77.49
Lot2_P20-assembly	34	78.53	80.08	76.31	78.19	75.95	86.15	76.68	82.29	83.15	77.90



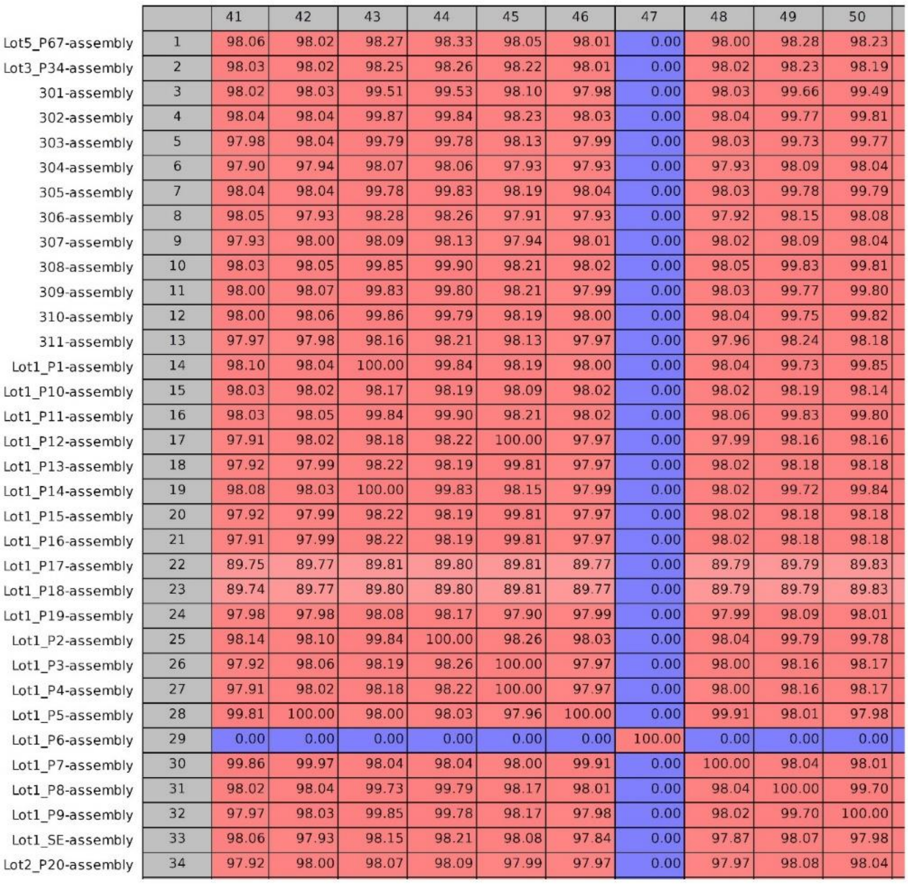
		11	12	13	14	15	16	17	18	19	20
Lot5_P67-assembly	1	98.25	98.25	98.09	98.28	98.09	98.30	98.05	98.04	98.26	98.04
Lot3_P34-assembly	2	98.28	98.24	98.13	98.26	98.14	98.29	98.22	98.23	98.24	98.23
301-assembly	3	99.54	99.53	98.32	99.50	98.17	99.54	98.10	98.15	99.49	98.15
302-assembly	4	99.85	99.89	98.21	99.88	98.18	99.88	98.22	98.23	99.88	98.22
303-assembly	5	99.80	99.82	98.19	99.79	98.18	99.83	98.12	98.19	99.80	98.18
304-assembly	6	98.07	98.02	97.97	98.07	98.01	98.10	97.93	97.99	97.97	97.99
305-assembly	7	99.82	99.87	98.25	99.79	98.17	99.87	98.18	98.20	99.79	98.20
306-assembly	8	98.14	98.08	98.02	98.28	98.05	98.15	97.91	97.93	98.27	97.93
307-assembly	9	98.08	98.02	97.99	98.09	98.01	98.10	97.94	97.96	98.08	97.96
308-assembly	10	99.87	99.89	98.25	99.85	98.20	99.97	98.21	98.23	99.84	98.23
309-assembly	11		99.83	98.20	99.83	98.17	99.86	98.17	98.20	99.82	98.20
310-assembly	12	87.10		98.22	99.86	98.17	99.88	98.17	98.20	99.85	98.20
311-assembly	13	75.87	75.49		98.16	98.07	98.24	98.13	98.16	98.16	98.15
Lot1_P1-assembly	14	87.32	85.39	76.09		98.17	99.84	98.18	98.22	100.00	98.22
Lot1_P10-assembly	15	73.94	73.86	74.76	73.79		98.19	98.09	98.09	98.17	98.09
Lot1_P11-assembly	16	86.96	86.59	76.89	87.19	75.04		98.20	98.22	99.84	98.22
Lot1_P12-assembly	17	75.85	75.38	79.48	76.43	73.25	76.18		99.81	98.15	99.81
Lot1_P13-assembly	18	74.65	74.86	80.00	75.25	73.97	75.94	86.24		98.18	100.00
Lot1_P14-assembly	19	86.99	85.56	76.29	88.75	73.88	87.13	76.82	75.44		98.18
Lot1_P15-assembly	20	74.64	74.83	79.96	75.26	73.92	75.89	86.25	91.45	75.44	
Lot1_P16-assembly	21	74.64	74.83	79.96	75.25	73.90	75.88	86.27	91.43	75.44	91.59
Lot1_P17-assembly	22	48.13	48.28	48.74	48.43	48.29	49.02	48.91	49.63	48.56	49.59
Lot1_P18-assembly	23	48.10	48.25	48.72	48.40	48.28	49.00	48.89	49.61	48.53	49.57
Lot1_P19-assembly	24	76.15	75.44	76.77	76.49	75.17	76.61	75.74	76.71	76.62	76.69
Lot1_P2-assembly	25	87.82	86.11	75.46	86.66	73.70	87.85	76.07	74.81	86.51	74.75
Lot1_P3-assembly	26	76.77	76.15	78.70	75.77	72.56	75.53	90.75	85.30	76.16	85.35
Lot1_P4-assembly	27	75.69	75.10	79.27	76.28	73.02	76.02	91.53	85.99	76.66	86.04
Lot1_P5-assembly	28	74.89	75.28	74.81	75.48	74.08	76.26	74.98	74.76	75.41	74.72
Lot1_P6-assembly	29	0.15	0.17	0.24	0.18	0.07	0.15	0.17	0.19	0.18	0.19
Lot1_P7-assembly	30	74.46	74.79	74.85	75.08	74.85	76.03	74.81	76.43	74.89	76.38
Lot1_P8-assembly	31	86.62	85.46	76.81	87.08	74.49	89.30	75.98	75.69	86.23	75.64
Lot1_P9-assembly	32	86.76	85.74	76.35	88.26	74.33	86.83	76.78	75.30	88.21	75.27
Lot1_SE-assembly	33	77.43	77.03	78.80	76.67	73.02	77.52	79.93	79.04	76.69	79.01
Lot2_P20-assembly	34	76.84	76.14	77.89	77.33	74.86	77.81	76.84	77.98	76.99	77.95



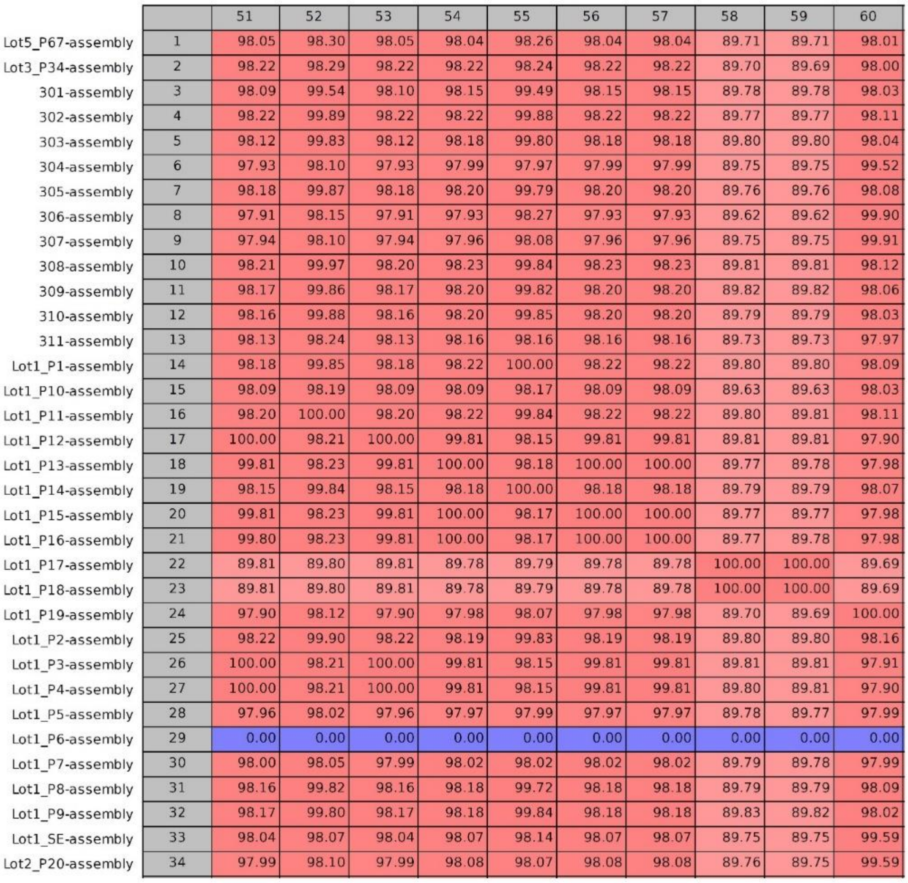
		21	22	23	24	25	26	27	28	29	30
Lot5_P67-assembly	1	98.04	89.72	89.71	98.01	98.33	98.05	98.05	98.01	0.00	98.01
Lot3_P34-assembly	2	98.22	89.70	89.69	98.00	98.26	98.22	98.22	98.01	0.00	98.02
301-assembly	3	98.15	89.78	89.78	98.03	99.53	98.10	98.10	97.98	0.00	98.03
302-assembly	4	98.22	89.77	89.77	98.11	99.84	98.23	98.22	98.03	0.00	98.04
303-assembly	5	98.18	89.80	89.80	98.04	99.78	98.12	98.12	97.99	0.00	98.03
304-assembly	6	97.99	89.75	89.75	99.51	98.06	97.93	97.93	97.93	0.00	97.93
305-assembly	7	98.20	89.76	89.76	98.08	99.83	98.19	98.18	98.04	0.00	98.03
306-assembly	8	97.93	89.62	89.62	99.90	98.26	97.92	97.91	97.93	0.00	97.92
307-assembly	9	97.96	89.75	89.75	99.92	98.13	97.94	97.94	98.01	0.00	98.02
308-assembly	10	98.23	89.82	89.81	98.12	99.90	98.21	98.21	98.02	0.00	98.05
309-assembly	11	98.20	89.82	89.82	98.06	99.80	98.21	98.17	98.00	0.00	98.03
310-assembly	12	98.20	89.79	89.79	98.03	99.79	98.19	98.16	98.00	0.00	98.04
311-assembly	13	98.16	89.73	89.73	97.97	98.21	98.13	98.13	97.96	0.00	97.96
Lot1_P1-assembly	14	98.22	89.81	89.80	98.09	99.84	98.19	98.18	98.00	0.00	98.04
Lot1_P10-assembly	15	98.09	89.63	89.63	98.03	98.19	98.09	98.09	98.02	0.00	98.02
Lot1_P11-assembly	16	98.22	89.81	89.80	98.12	99.90	98.20	98.20	98.02	0.00	98.05
Lot1_P12-assembly	17	99.81	89.81	89.81	97.90	98.22	100.00	100.00	97.97	0.00	97.99
Lot1_P13-assembly	18	100.00	89.78	89.78	97.98	98.19	99.81	99.81	97.97	0.00	98.02
Lot1_P14-assembly	19	98.18	89.79	89.79	98.07	99.83	98.15	98.15	97.99	0.00	98.02
Lot1_P15-assembly	20	100.00	89.78	89.78	97.98	98.19	99.81	99.81	97.97	0.00	98.02
Lot1_P16-assembly	21		89.78	89.78	97.98	98.19	99.81	99.81	97.97	0.00	98.02
Lot1_P17-assembly	22	49.57		100.00	89.69	89.80	89.81	89.81	89.77	0.00	89.79
Lot1_P18-assembly	23	49.55	95.23		89.69	89.80	89.81	89.81	89.77	0.00	89.78
Lot1_P19-assembly	24	76.68	48.76	48.71		98.17	97.90	97.90	97.99	0.00	97.99
Lot1_P2-assembly	25	74.74	48.21	48.19	75.97		98.26	98.22	98.03	0.00	98.04
Lot1_P3-assembly	26	85.36	48.46	48.44	75.22	77.00		100.00	97.97	0.00	98.00
Lot1_P4-assembly	27	86.05	48.76	48.74	75.73	75.91	90.96		97.97	0.00	98.00
Lot1_P5-assembly	28	74.72	49.71	49.69	75.47	75.48	74.30	74.84		0.00	99.91
Lot1_P6-assembly	29	0.19	0.05	0.07	0.09	0.11	0.17	0.17	0.11		0.00
Lot1_P7-assembly	30	76.40	50.33	50.31	76.41	75.17	74.29	74.82	86.60	0.07	
Lot1_P8-assembly	31	75.63	48.77	48.74	76.34	86.75	75.33	75.81	75.95	0.18	75.76
Lot1_P9-assembly	32	75.27	48.38	48.35	76.29	85.61	76.12	76.82	75.55	0.26	74.99
Lot1_SE-assembly	33	78.99	48.70	48.66	81.93	78.15	80.75	79.73	74.87	0.16	74.67
Lot2_P20-assembly	34	77.93	50.24	50.21	82.79	76.34	76.20	76.70	76.29	0.21	77.24



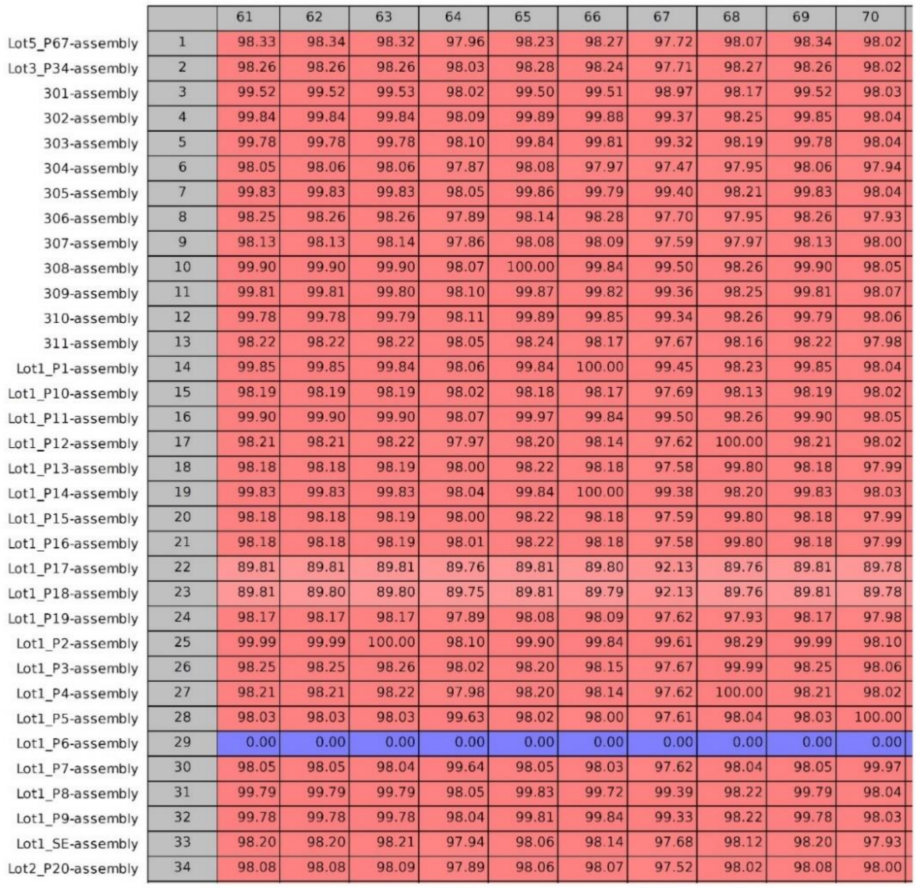
		31	32	33	34	35	36	37	38	39	40
Lot5_P67-assembly	1	98.28	98.23	98.04	98.03	84.36	98.04	98.23	98.33	98.02	98.31
Lot3_P34-assembly	2	98.23	98.19	98.01	98.00	84.37	98.01	98.18	98.22	98.00	98.27
301-assembly	3	99.66	99.48	98.01	98.02	84.38	98.01	99.48	99.52	98.02	99.53
302-assembly	4	99.77	99.82	98.07	98.05	84.40	98.07	99.82	99.79	98.05	99.88
303-assembly	5	99.73	99.77	97.99	98.03	84.44	98.00	99.76	99.71	98.03	99.82
304-assembly	6	98.09	98.04	99.81	99.85	84.33	99.81	98.03	98.08	99.85	98.07
305-assembly	7	99.78	99.79	98.05	98.07	84.34	98.05	99.78	99.76	98.07	99.85
306-assembly	8	98.15	98.08	99.70	99.56	84.39	99.70	98.08	98.18	99.56	98.18
307-assembly	9	98.10	98.04	99.57	99.58	84.40	99.57	98.04	98.12	99.58	98.11
308-assembly	10	99.83	99.81	98.08	98.10	84.38	98.08	99.81	99.79	98.10	99.96
309-assembly	11	99.77	99.80	98.08	98.05	84.37	98.08	99.79	99.72	98.08	99.84
310-assembly	12	99.75	99.82	98.01	98.05	84.38	98.02	99.82	99.71	98.07	99.85
311-assembly	13	98.24	98.18	98.08	97.96	84.40	98.08	98.18	98.27	97.95	98.23
Lot1_P1-assembly	14	99.73	99.85	98.15	98.06	84.39	98.15	99.85	99.80	98.06	99.85
Lot1_P10-assembly	15	98.19	98.15	98.02	98.01	84.54	98.02	98.15	98.16	98.01	98.18
Lot1_P11-assembly	16	99.83	99.80	98.07	98.10	84.39	98.07	99.80	99.79	98.10	99.97
Lot1_P12-assembly	17	98.16	98.17	98.04	97.99	84.28	98.04	98.17	98.18	97.97	98.23
Lot1_P13-assembly	18	98.18	98.19	98.06	98.08	84.28	98.06	98.18	98.22	98.07	98.21
Lot1_P14-assembly	19	99.72	99.84	98.14	98.07	84.39	98.14	99.84	99.80	98.06	99.84
Lot1_P15-assembly	20	98.18	98.18	98.06	98.08	84.29	98.06	98.17	98.22	98.07	98.21
Lot1_P16-assembly	21	98.18	98.18	98.06	98.08	84.29	98.06	98.17	98.22	98.07	98.21
Lot1_P17-assembly	22	89.79	89.83	89.75	89.76	84.63	89.75	89.83	89.79	89.75	89.80
Lot1_P18-assembly	23	89.79	89.83	89.74	89.75	84.64	89.75	89.83	89.79	89.75	89.80
Lot1_P19-assembly	24	98.09	98.02	99.59	99.59	84.40	99.59	98.02	98.12	99.59	98.12
Lot1_P2-assembly	25	99.79	99.78	98.21	98.09	84.38	98.21	99.78	99.81	98.11	99.92
Lot1_P3-assembly	26	98.16	98.17	98.08	97.99	84.28	98.08	98.17	98.18	98.00	98.27
Lot1_P4-assembly	27	98.16	98.17	98.04	97.99	84.29	98.04	98.17	98.18	97.98	98.23
Lot1_P5-assembly	28	98.01	97.98	97.83	97.97	84.55	97.84	97.98	98.05	97.98	98.06
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.04	98.02	97.87	97.97	84.56	97.87	98.01	98.08	97.98	98.06
Lot1_P8-assembly	31		99.70	98.07	98.08	84.42	98.07	99.69	99.73	98.08	99.82
Lot1_P9-assembly	32	86.10		97.98	98.04	84.38	97.98	100.00	99.78	98.03	99.80
Lot1_SE-assembly	33	77.33	75.95		99.81	84.32	100.00	97.98	98.06	99.81	98.15
Lot2_P20-assembly	34	78.12	77.32	82.64		84.46	99.81	98.04	98.12	100.00	98.08



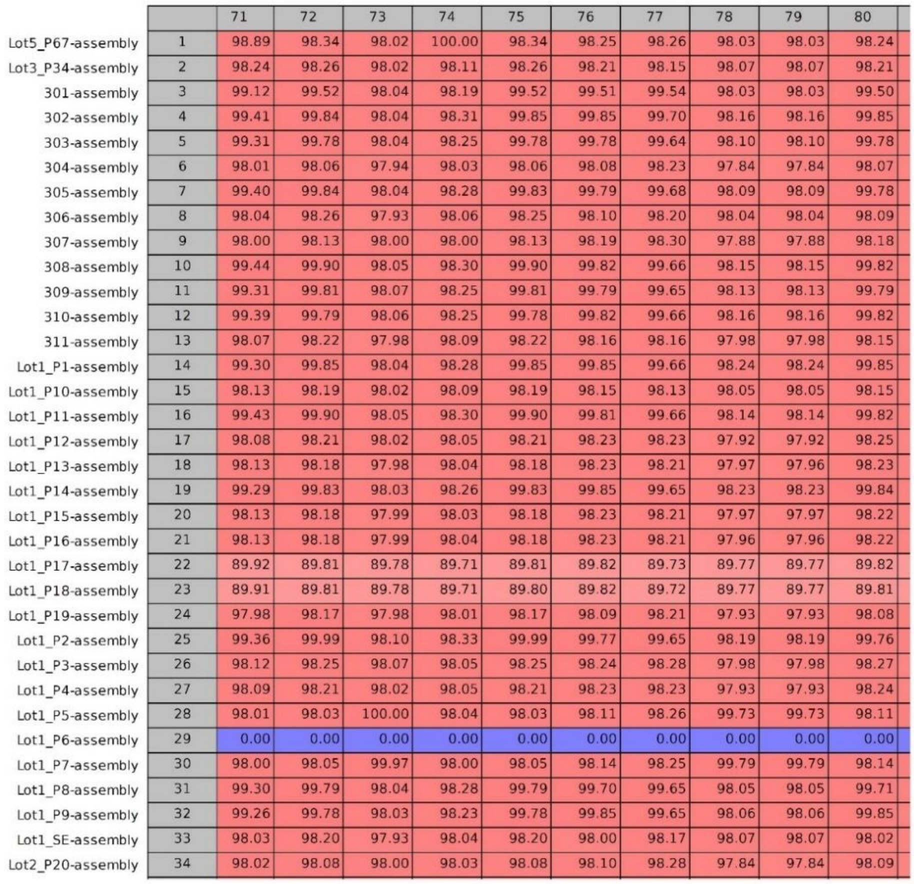
		41	42	43	44	45	46	47	48	49	50
Lot5_P67-assembly	1	98.06	98.02	98.27	98.33	98.05	98.01	0.00	98.00	98.28	98.23
Lot3_P34-assembly	2	98.03	98.02	98.25	98.26	98.22	98.01	0.00	98.02	98.23	98.19
301-assembly	3	98.02	98.03	99.51	99.53	98.10	97.98	0.00	98.03	99.66	99.49
302-assembly	4	98.04	98.04	99.87	99.84	98.23	98.03	0.00	98.04	99.77	99.81
303-assembly	5	97.98	98.04	99.79	99.78	98.13	97.99	0.00	98.03	99.73	99.77
304-assembly	6	97.90	97.94	98.07	98.06	97.93	97.93	0.00	97.93	98.09	98.04
305-assembly	7	98.04	98.04	99.78	99.83	98.19	98.04	0.00	98.03	99.78	99.79
306-assembly	8	98.05	97.93	98.28	98.26	97.91	97.93	0.00	97.92	98.15	98.08
307-assembly	9	97.93	98.00	98.09	98.13	97.94	98.01	0.00	98.02	98.09	98.04
308-assembly	10	98.03	98.05	99.85	99.90	98.21	98.02	0.00	98.05	99.83	99.81
309-assembly	11	98.00	98.07	99.83	99.80	98.21	97.99	0.00	98.03	99.77	99.80
310-assembly	12	98.00	98.06	99.86	99.79	98.19	98.00	0.00	98.04	99.75	99.82
311-assembly	13	97.97	97.98	98.16	98.21	98.13	97.97	0.00	97.96	98.24	98.18
Lot1_P1-assembly	14	98.10	98.04	100.00	99.84	98.19	98.00	0.00	98.04	99.73	99.85
Lot1_P10-assembly	15	98.03	98.02	98.17	98.19	98.09	98.02	0.00	98.02	98.19	98.14
Lot1_P11-assembly	16	98.03	98.05	99.84	99.90	98.21	98.02	0.00	98.06	99.83	99.80
Lot1_P12-assembly	17	97.91	98.02	98.18	98.22	100.00	97.97	0.00	97.99	98.16	98.16
Lot1_P13-assembly	18	97.92	97.99	98.22	98.19	99.81	97.97	0.00	98.02	98.18	98.18
Lot1_P14-assembly	19	98.08	98.03	100.00	99.83	98.15	97.99	0.00	98.02	99.72	99.84
Lot1_P15-assembly	20	97.92	97.99	98.22	98.19	99.81	97.97	0.00	98.02	98.18	98.18
Lot1_P16-assembly	21	97.91	97.99	98.22	98.19	99.81	97.97	0.00	98.02	98.18	98.18
Lot1_P17-assembly	22	89.75	89.77	89.81	89.80	89.81	89.77	0.00	89.79	89.79	89.83
Lot1_P18-assembly	23	89.74	89.77	89.80	89.80	89.81	89.77	0.00	89.79	89.79	89.83
Lot1_P19-assembly	24	97.98	97.98	98.08	98.17	97.90	97.99	0.00	97.99	98.09	98.01
Lot1_P2-assembly	25	98.14	98.10	99.84	100.00	98.26	98.03	0.00	98.04	99.79	99.78
Lot1_P3-assembly	26	97.92	98.06	98.19	98.26	100.00	97.97	0.00	98.00	98.16	98.17
Lot1_P4-assembly	27	97.91	98.02	98.18	98.22	100.00	97.97	0.00	98.00	98.16	98.17
Lot1_P5-assembly	28	99.81	100.00	98.00	98.03	97.96	100.00	0.00	99.91	98.01	97.98
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
Lot1_P7-assembly	30	99.86	99.97	98.04	98.04	98.00	99.91	0.00	100.00	98.04	98.01
Lot1_P8-assembly	31	98.02	98.04	99.73	99.79	98.17	98.01	0.00	98.04	100.00	99.70
Lot1_P9-assembly	32	97.97	98.03	99.85	99.78	98.17	97.98	0.00	98.02	99.70	100.00
Lot1_SE-assembly	33	98.06	97.93	98.15	98.21	98.08	97.84	0.00	97.87	98.07	97.98
Lot2_P20-assembly	34	97.92	98.00	98.07	98.09	97.99	97.97	0.00	97.97	98.08	98.04



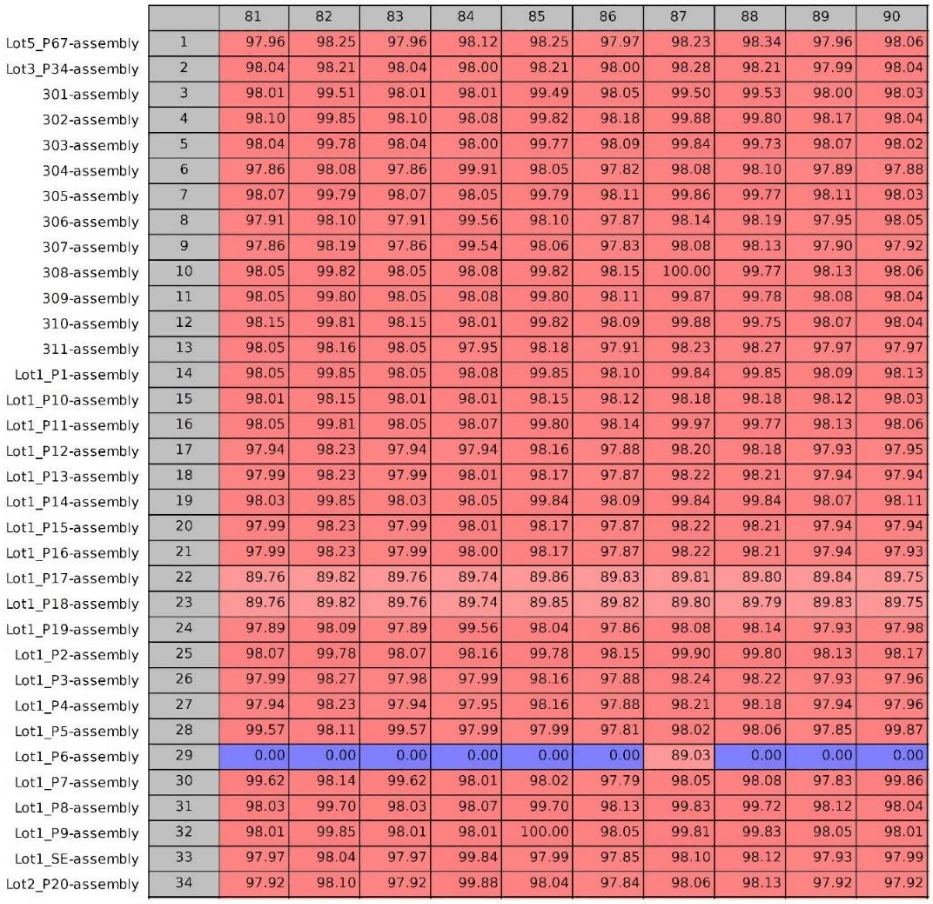
		51	52	53	54	55	56	57	58	59	60
Lot5_P67-assembly	1	98.05	98.30	98.05	98.04	98.26	98.04	98.04	89.71	89.71	98.01
Lot3_P34-assembly	2	98.22	98.29	98.22	98.22	98.24	98.22	98.22	89.70	89.69	98.00
301-assembly	3	98.09	99.54	98.10	98.15	99.49	98.15	98.15	89.78	89.78	98.03
302-assembly	4	98.22	99.89	98.22	98.22	99.88	98.22	98.22	89.77	89.77	98.11
303-assembly	5	98.12	99.83	98.12	98.18	99.80	98.18	98.18	89.80	89.80	98.04
304-assembly	6	97.93	98.10	97.93	97.99	97.97	97.99	97.99	89.75	89.75	99.52
305-assembly	7	98.18	99.87	98.18	98.20	99.79	98.20	98.20	89.76	89.76	98.08
306-assembly	8	97.91	98.15	97.91	97.93	98.27	97.93	97.93	89.62	89.62	99.90
307-assembly	9	97.94	98.10	97.94	97.96	98.08	97.96	97.96	89.75	89.75	99.91
308-assembly	10	98.21	99.97	98.20	98.23	99.84	98.23	98.23	89.81	89.81	98.12
309-assembly	11	98.17	99.86	98.17	98.20	99.82	98.20	98.20	89.82	89.82	98.06
310-assembly	12	98.16	99.88	98.16	98.20	99.85	98.20	98.20	89.79	89.79	98.03
311-assembly	13	98.13	98.24	98.13	98.16	98.16	98.16	98.16	89.73	89.73	97.97
Lot1_P1-assembly	14	98.18	99.85	98.18	98.22	100.00	98.22	98.22	89.80	89.80	98.09
Lot1_P10-assembly	15	98.09	98.19	98.09	98.09	98.17	98.09	98.09	89.63	89.63	98.03
Lot1_P11-assembly	16	98.20	100.00	98.20	98.22	99.84	98.22	98.22	89.80	89.81	98.11
Lot1_P12-assembly	17	100.00	98.21	100.00	99.81	98.15	99.81	99.81	89.81	89.81	97.90
Lot1_P13-assembly	18	99.81	98.23	99.81	100.00	98.18	100.00	100.00	89.77	89.78	97.98
Lot1_P14-assembly	19	98.15	99.84	98.15	98.18	100.00	98.18	98.18	89.79	89.79	98.07
Lot1_P15-assembly	20	99.81	98.23	99.81	100.00	98.17	100.00	100.00	89.77	89.77	97.98
Lot1_P16-assembly	21	99.80	98.23	99.81	100.00	98.17	100.00	100.00	89.77	89.78	97.98
Lot1_P17-assembly	22	89.81	89.80	89.81	89.78	89.79	89.78	89.78	100.00	100.00	89.69
Lot1_P18-assembly	23	89.81	89.80	89.81	89.78	89.79	89.78	89.78	100.00	100.00	89.69
Lot1_P19-assembly	24	97.90	98.12	97.90	97.98	98.07	97.98	97.98	89.70	89.69	100.00
Lot1_P2-assembly	25	98.22	99.90	98.22	98.19	99.83	98.19	98.19	89.80	89.80	98.16
Lot1_P3-assembly	26	100.00	98.21	100.00	99.81	98.15	99.81	99.81	89.81	89.81	97.91
Lot1_P4-assembly	27	100.00	98.21	100.00	99.81	98.15	99.81	99.81	89.80	89.81	97.90
Lot1_P5-assembly	28	97.96	98.02	97.96	97.97	97.99	97.97	97.97	89.78	89.77	97.99
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.00	98.05	97.99	98.02	98.02	98.02	98.02	89.79	89.78	97.99
Lot1_P8-assembly	31	98.16	99.82	98.16	98.18	99.72	98.18	98.18	89.79	89.79	98.09
Lot1_P9-assembly	32	98.17	99.80	98.17	98.18	99.84	98.18	98.18	89.83	89.82	98.02
Lot1_SE-assembly	33	98.04	98.07	98.04	98.07	98.14	98.07	98.07	89.75	89.75	99.59
Lot2_P20-assembly	34	97.99	98.10	97.99	98.08	98.07	98.08	98.08	89.76	89.75	99.59



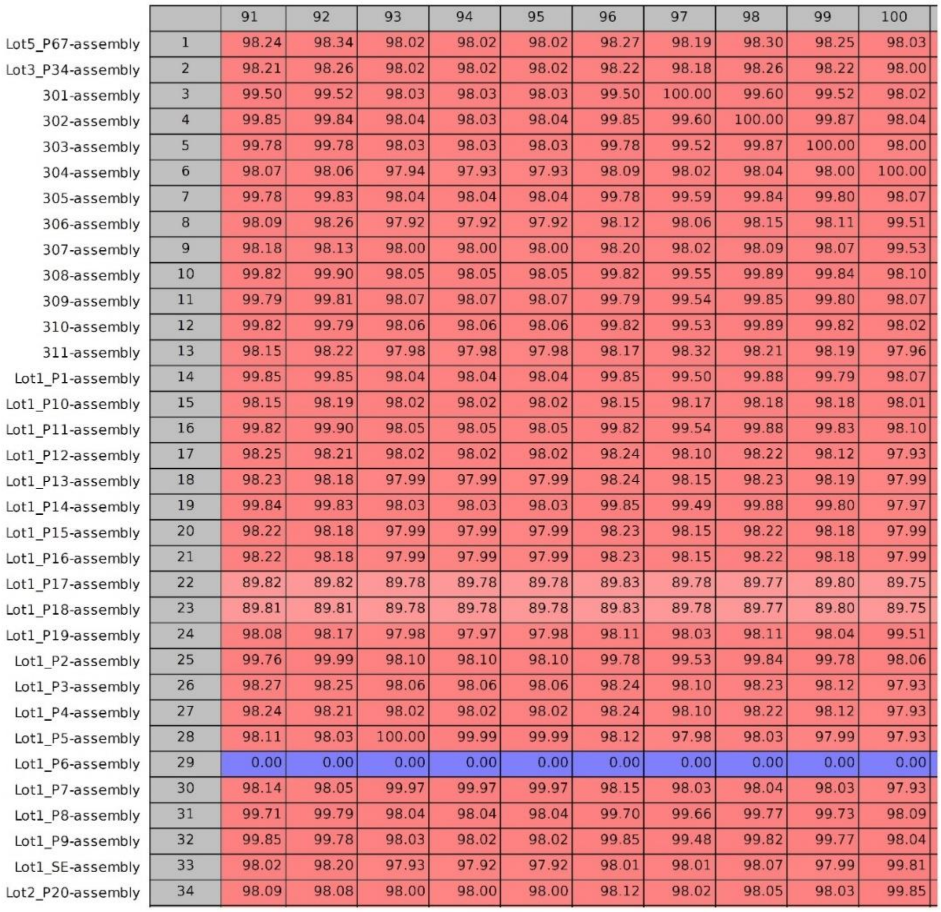
		61	62	63	64	65	66	67	68	69	70
Lot5_P67-assembly	1	98.33	98.34	98.32	97.96	98.23	98.27	97.72	98.07	98.34	98.02
Lot3_P34-assembly	2	98.26	98.26	98.26	98.03	98.28	98.24	97.71	98.27	98.26	98.02
301-assembly	3	99.52	99.52	99.53	98.02	99.50	99.51	98.97	98.17	99.52	98.03
302-assembly	4	99.84	99.84	99.84	98.09	99.89	99.88	99.37	98.25	99.85	98.04
303-assembly	5	99.78	99.78	99.78	98.10	99.84	99.81	99.32	98.19	99.78	98.04
304-assembly	6	98.05	98.06	98.06	97.87	98.08	97.97	97.47	97.95	98.06	97.94
305-assembly	7	99.83	99.83	99.83	98.05	99.86	99.79	99.40	98.21	99.83	98.04
306-assembly	8	98.25	98.26	98.26	97.89	98.14	98.28	97.70	97.95	98.26	97.93
307-assembly	9	98.13	98.13	98.14	97.86	98.08	98.09	97.59	97.97	98.13	98.00
308-assembly	10	99.90	99.90	99.90	98.07	100.00	99.84	99.50	98.26	99.90	98.05
309-assembly	11	99.81	99.81	99.80	98.10	99.87	99.82	99.36	98.25	99.81	98.07
310-assembly	12	99.78	99.78	99.79	98.11	99.89	99.85	99.34	98.26	99.79	98.06
311-assembly	13	98.22	98.22	98.22	98.05	98.24	98.17	97.67	98.16	98.22	97.98
Lot1_P1-assembly	14	99.85	99.85	99.84	98.06	99.84	100.00	99.45	98.23	99.85	98.04
Lot1_P10-assembly	15	98.19	98.19	98.19	98.02	98.18	98.17	97.69	98.13	98.19	98.02
Lot1_P11-assembly	16	99.90	99.90	99.90	98.07	99.97	99.84	99.50	98.26	99.90	98.05
Lot1_P12-assembly	17	98.21	98.21	98.22	97.97	98.20	98.14	97.62	100.00	98.21	98.02
Lot1_P13-assembly	18	98.18	98.18	98.19	98.00	98.22	98.18	97.58	99.80	98.18	97.99
Lot1_P14-assembly	19	99.83	99.83	99.83	98.04	99.84	100.00	99.38	98.20	99.83	98.03
Lot1_P15-assembly	20	98.18	98.18	98.19	98.00	98.22	98.18	97.59	99.80	98.18	97.99
Lot1_P16-assembly	21	98.18	98.18	98.19	98.01	98.22	98.18	97.58	99.80	98.18	97.99
Lot1_P17-assembly	22	89.81	89.81	89.81	89.76	89.81	89.80	92.13	89.76	89.81	89.78
Lot1_P18-assembly	23	89.81	89.80	89.80	89.75	89.81	89.79	92.13	89.76	89.81	89.78
Lot1_P19-assembly	24	98.17	98.17	98.17	97.89	98.08	98.09	97.62	97.93	98.17	97.98
Lot1_P2-assembly	25	99.99	99.99	100.00	98.10	99.90	99.84	99.61	98.29	99.99	98.10
Lot1_P3-assembly	26	98.25	98.25	98.26	98.02	98.20	98.15	97.67	99.99	98.25	98.06
Lot1_P4-assembly	27	98.21	98.21	98.22	97.98	98.20	98.14	97.62	100.00	98.21	98.02
Lot1_P5-assembly	28	98.03	98.03	98.03	99.63	98.02	98.00	97.61	98.04	98.03	100.00
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.05	98.05	98.04	99.64	98.05	98.03	97.62	98.04	98.05	99.97
Lot1_P8-assembly	31	99.79	99.79	99.79	98.05	99.83	99.72	99.39	98.22	99.79	98.04
Lot1_P9-assembly	32	99.78	99.78	99.78	98.04	99.81	99.84	99.33	98.22	99.78	98.03
Lot1_SE-assembly	33	98.20	98.20	98.21	97.94	98.06	98.14	97.68	98.12	98.20	97.93
Lot2_P20-assembly	34	98.08	98.08	98.09	97.89	98.06	98.07	97.52	98.02	98.08	98.00



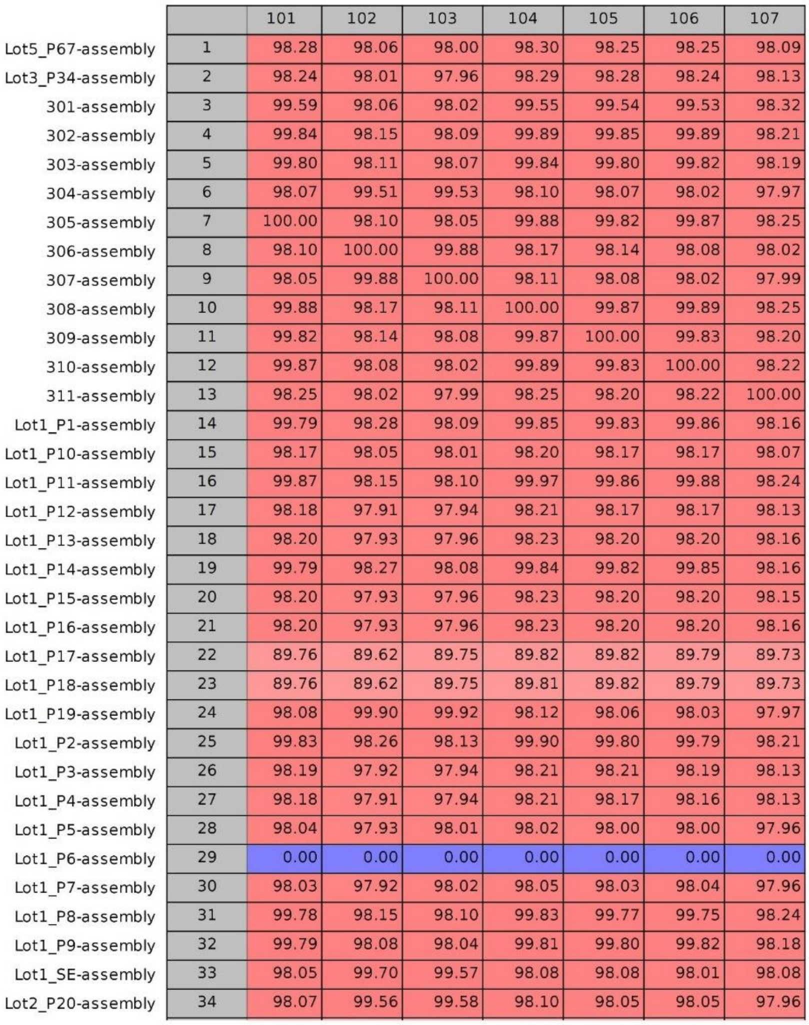
		71	72	73	74	75	76	77	78	79	80
Lot5_P67-assembly	1	98.89	98.34	98.02	100.00	98.34	98.25	98.26	98.03	98.03	98.24
Lot3_P34-assembly	2	98.24	98.26	98.02	98.11	98.26	98.21	98.15	98.07	98.07	98.21
301-assembly	3	99.12	99.52	98.04	98.19	99.52	99.51	99.54	98.03	98.03	99.50
302-assembly	4	99.41	99.84	98.04	98.31	99.85	99.85	99.70	98.16	98.16	99.85
303-assembly	5	99.31	99.78	98.04	98.25	99.78	99.78	99.64	98.10	98.10	99.78
304-assembly	6	98.01	98.06	97.94	98.03	98.06	98.08	98.23	97.84	97.84	98.07
305-assembly	7	99.40	99.84	98.04	98.28	99.83	99.79	99.68	98.09	98.09	99.78
306-assembly	8	98.04	98.26	97.93	98.06	98.25	98.10	98.20	98.04	98.04	98.09
307-assembly	9	98.00	98.13	98.00	98.00	98.13	98.19	98.30	97.88	97.88	98.18
308-assembly	10	99.44	99.90	98.05	98.30	99.90	99.82	99.66	98.15	98.15	99.82
309-assembly	11	99.31	99.81	98.07	98.25	99.81	99.79	99.65	98.13	98.13	99.79
310-assembly	12	99.39	99.79	98.06	98.25	99.78	99.82	99.66	98.16	98.16	99.82
311-assembly	13	98.07	98.22	97.98	98.09	98.22	98.16	98.16	97.98	97.98	98.15
Lot1_P1-assembly	14	99.30	99.85	98.04	98.28	99.85	99.85	99.66	98.24	98.24	99.85
Lot1_P10-assembly	15	98.13	98.19	98.02	98.09	98.19	98.15	98.13	98.05	98.05	98.15
Lot1_P11-assembly	16	99.43	99.90	98.05	98.30	99.90	99.81	99.66	98.14	98.14	99.82
Lot1_P12-assembly	17	98.08	98.21	98.02	98.05	98.21	98.23	98.23	97.92	97.92	98.25
Lot1_P13-assembly	18	98.13	98.18	97.98	98.04	98.18	98.23	98.21	97.97	97.96	98.23
Lot1_P14-assembly	19	99.29	99.83	98.03	98.26	99.83	99.85	99.65	98.23	98.23	99.84
Lot1_P15-assembly	20	98.13	98.18	97.99	98.03	98.18	98.23	98.21	97.97	97.97	98.22
Lot1_P16-assembly	21	98.13	98.18	97.99	98.04	98.18	98.23	98.21	97.96	97.96	98.22
Lot1_P17-assembly	22	89.92	89.81	89.78	89.71	89.81	89.82	89.73	89.77	89.77	89.82
Lot1_P18-assembly	23	89.91	89.81	89.78	89.71	89.80	89.82	89.72	89.77	89.77	89.81
Lot1_P19-assembly	24	97.98	98.17	97.98	98.01	98.17	98.09	98.21	97.93	97.93	98.08
Lot1_P2-assembly	25	99.36	99.99	98.10	98.33	99.99	99.77	99.65	98.19	98.19	99.76
Lot1_P3-assembly	26	98.12	98.25	98.07	98.05	98.25	98.24	98.28	97.98	97.98	98.27
Lot1_P4-assembly	27	98.09	98.21	98.02	98.05	98.21	98.23	98.23	97.93	97.93	98.24
Lot1_P5-assembly	28	98.01	98.03	100.00	98.04	98.03	98.11	98.26	99.73	99.73	98.11
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.00	98.05	99.97	98.00	98.05	98.14	98.25	99.79	99.79	98.14
Lot1_P8-assembly	31	99.30	99.79	98.04	98.28	99.79	99.70	99.65	98.05	98.05	99.71
Lot1_P9-assembly	32	99.26	99.78	98.03	98.23	99.78	99.85	99.65	98.06	98.06	99.85
Lot1_SE-assembly	33	98.03	98.20	97.93	98.04	98.20	98.00	98.17	98.07	98.07	98.02
Lot2_P20-assembly	34	98.02	98.08	98.00	98.03	98.08	98.10	98.28	97.84	97.84	98.09



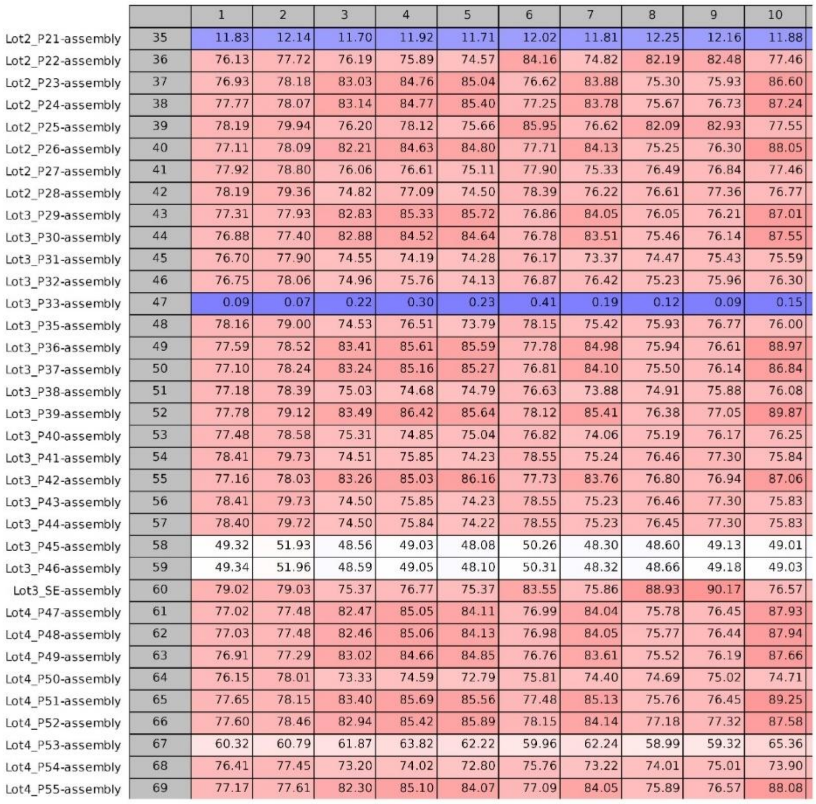
		81	82	83	84	85	86	87	88	89	90
Lot5_P67-assembly	1	97.96	98.25	97.96	98.12	98.25	97.97	98.23	98.34	97.96	98.06
Lot3_P34-assembly	2	98.04	98.21	98.04	98.00	98.21	98.00	98.28	98.21	97.99	98.04
301-assembly	3	98.01	99.51	98.01	98.01	99.49	98.05	99.50	99.53	98.00	98.03
302-assembly	4	98.10	99.85	98.10	98.08	99.82	98.18	99.88	99.80	98.17	98.04
303-assembly	5	98.04	99.78	98.04	98.00	99.77	98.09	99.84	99.73	98.07	98.02
304-assembly	6	97.86	98.08	97.86	99.91	98.05	97.82	98.08	98.10	97.89	97.88
305-assembly	7	98.07	99.79	98.07	98.05	99.79	98.11	99.86	99.77	98.11	98.03
306-assembly	8	97.91	98.10	97.91	99.56	98.10	97.87	98.14	98.19	97.95	98.05
307-assembly	9	97.86	98.19	97.86	99.54	98.06	97.83	98.08	98.13	97.90	97.92
308-assembly	10	98.05	99.82	98.05	98.08	99.82	98.15	100.00	99.77	98.13	98.06
309-assembly	11	98.05	99.80	98.05	98.08	99.80	98.11	99.87	99.78	98.08	98.04
310-assembly	12	98.15	99.81	98.15	98.01	99.82	98.09	99.88	99.75	98.07	98.04
311-assembly	13	98.05	98.16	98.05	97.95	98.18	97.91	98.23	98.27	97.97	97.97
Lot1_P1-assembly	14	98.05	99.85	98.05	98.08	99.85	98.10	99.84	99.85	98.09	98.13
Lot1_P10-assembly	15	98.01	98.15	98.01	98.01	98.15	98.12	98.18	98.18	98.12	98.03
Lot1_P11-assembly	16	98.05	99.81	98.05	98.07	99.80	98.14	99.97	99.77	98.13	98.06
Lot1_P12-assembly	17	97.94	98.23	97.94	97.94	98.16	97.88	98.20	98.18	97.93	97.95
Lot1_P13-assembly	18	97.99	98.23	97.99	98.01	98.17	97.87	98.22	98.21	97.94	97.94
Lot1_P14-assembly	19	98.03	99.85	98.03	98.05	99.84	98.09	99.84	99.84	98.07	98.11
Lot1_P15-assembly	20	97.99	98.23	97.99	98.01	98.17	97.87	98.22	98.21	97.94	97.94
Lot1_P16-assembly	21	97.99	98.23	97.99	98.00	98.17	97.87	98.22	98.21	97.94	97.93
Lot1_P17-assembly	22	89.76	89.82	89.76	89.74	89.86	89.83	89.81	89.80	89.84	89.75
Lot1_P18-assembly	23	89.76	89.82	89.76	89.74	89.85	89.82	89.80	89.79	89.83	89.75
Lot1_P19-assembly	24	97.89	98.09	97.89	99.56	98.04	97.86	98.08	98.14	97.93	97.98
Lot1_P2-assembly	25	98.07	99.78	98.07	98.16	99.78	98.15	99.90	99.80	98.13	98.17
Lot1_P3-assembly	26	97.99	98.27	97.98	97.99	98.16	97.88	98.24	98.22	97.93	97.96
Lot1_P4-assembly	27	97.94	98.23	97.94	97.95	98.16	97.88	98.21	98.18	97.94	97.96
Lot1_P5-assembly	28	99.57	98.11	99.57	97.99	97.99	97.81	98.02	98.06	97.85	99.87
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	89.03	0.00	0.00	0.00
Lot1_P7-assembly	30	99.62	98.14	99.62	98.01	98.02	97.79	98.05	98.08	97.83	99.86
Lot1_P8-assembly	31	98.03	99.70	98.03	98.07	99.70	98.13	99.83	99.72	98.12	98.04
Lot1_P9-assembly	32	98.01	99.85	98.01	98.01	100.00	98.05	99.81	99.83	98.05	98.01
Lot1_SE-assembly	33	97.97	98.04	97.97	99.84	97.99	97.85	98.10	98.12	97.93	97.99
Lot2_P20-assembly	34	97.92	98.10	97.92	99.88	98.04	97.84	98.06	98.13	97.92	97.92



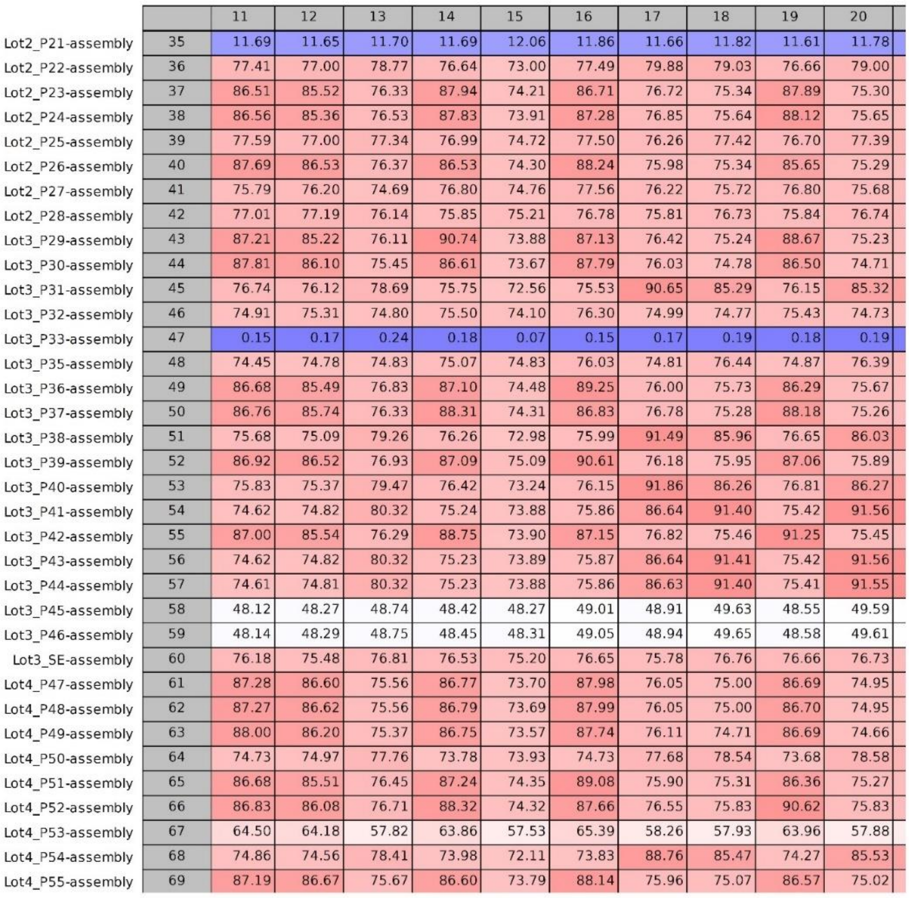
		91	92	93	94	95	96	97	98	99	100
Lot5_P67-assembly	1	98.24	98.34	98.02	98.02	98.02	98.27	98.19	98.30	98.25	98.03
Lot3_P34-assembly	2	98.21	98.26	98.02	98.02	98.02	98.22	98.18	98.26	98.22	98.00
301-assembly	3	99.50	99.52	98.03	98.03	98.03	99.50	100.00	99.60	99.52	98.02
302-assembly	4	99.85	99.84	98.04	98.03	98.04	99.85	99.60	100.00	99.87	98.04
303-assembly	5	99.78	99.78	98.03	98.03	98.03	99.78	99.52	99.87	100.00	98.00
304-assembly	6	98.07	98.06	97.94	97.93	97.93	98.09	98.02	98.04	98.00	100.00
305-assembly	7	99.78	99.83	98.04	98.04	98.04	99.78	99.59	99.84	99.80	98.07
306-assembly	8	98.09	98.26	97.92	97.92	97.92	98.12	98.06	98.15	98.11	99.51
307-assembly	9	98.18	98.13	98.00	98.00	98.00	98.20	98.02	98.09	98.07	99.53
308-assembly	10	99.82	99.90	98.05	98.05	98.05	99.82	99.55	99.89	99.84	98.10
309-assembly	11	99.79	99.81	98.07	98.07	98.07	99.79	99.54	99.85	99.80	98.07
310-assembly	12	99.82	99.79	98.06	98.06	98.06	99.82	99.53	99.89	99.82	98.02
311-assembly	13	98.15	98.22	97.98	97.98	97.98	98.17	98.32	98.21	98.19	97.96
Lot1_P1-assembly	14	99.85	99.85	98.04	98.04	98.04	99.85	99.50	99.88	99.79	98.07
Lot1_P10-assembly	15	98.15	98.19	98.02	98.02	98.02	98.15	98.17	98.18	98.18	98.01
Lot1_P11-assembly	16	99.82	99.90	98.05	98.05	98.05	99.82	99.54	99.88	99.83	98.10
Lot1_P12-assembly	17	98.25	98.21	98.02	98.02	98.02	98.24	98.10	98.22	98.12	97.93
Lot1_P13-assembly	18	98.23	98.18	97.99	97.99	97.99	98.24	98.15	98.23	98.19	97.99
Lot1_P14-assembly	19	99.84	99.83	98.03	98.03	98.03	99.85	99.49	99.88	99.80	97.97
Lot1_P15-assembly	20	98.22	98.18	97.99	97.99	97.99	98.23	98.15	98.22	98.18	97.99
Lot1_P16-assembly	21	98.22	98.18	97.99	97.99	97.99	98.23	98.15	98.22	98.18	97.99
Lot1_P17-assembly	22	89.82	89.82	89.78	89.78	89.78	89.83	89.78	89.77	89.80	89.75
Lot1_P18-assembly	23	89.81	89.81	89.78	89.78	89.78	89.83	89.78	89.77	89.80	89.75
Lot1_P19-assembly	24	98.08	98.17	97.98	97.97	97.98	98.11	98.03	98.11	98.04	99.51
Lot1_P2-assembly	25	99.76	99.99	98.10	98.10	98.10	99.78	99.53	99.84	99.78	98.06
Lot1_P3-assembly	26	98.27	98.25	98.06	98.06	98.06	98.24	98.10	98.23	98.12	97.93
Lot1_P4-assembly	27	98.24	98.21	98.02	98.02	98.02	98.24	98.10	98.22	98.12	97.93
Lot1_P5-assembly	28	98.11	98.03	100.00	99.99	99.99	98.12	97.98	98.03	97.99	97.93
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.14	98.05	99.97	99.97	99.97	98.15	98.03	98.04	98.03	97.93
Lot1_P8-assembly	31	99.71	99.79	98.04	98.04	98.04	99.70	99.66	99.77	99.73	98.09
Lot1_P9-assembly	32	99.85	99.78	98.03	98.02	98.02	99.85	99.48	99.82	99.77	98.04
Lot1_SE-assembly	33	98.02	98.20	97.93	97.92	97.92	98.01	98.01	98.07	97.99	99.81
Lot2_P20-assembly	34	98.09	98.08	98.00	98.00	98.00	98.12	98.02	98.05	98.03	99.85



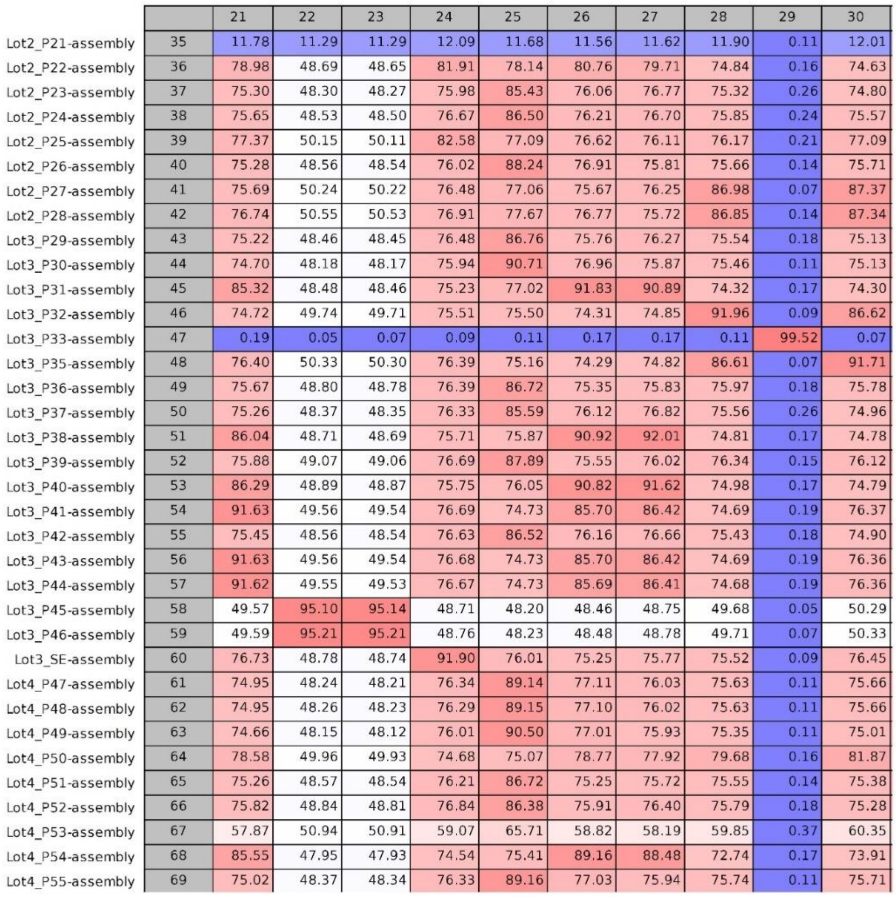
		101	102	103	104	105	106	107
Lot5_P67-assembly	1	98.28	98.06	98.00	98.30	98.25	98.25	98.09
Lot3_P34-assembly	2	98.24	98.01	97.96	98.29	98.28	98.24	98.13
301-assembly	3	99.59	98.06	98.02	99.55	99.54	99.53	98.32
302-assembly	4	99.84	98.15	98.09	99.89	99.85	99.89	98.21
303-assembly	5	99.80	98.11	98.07	99.84	99.80	99.82	98.19
304-assembly	6	98.07	99.51	99.53	98.10	98.07	98.02	97.97
305-assembly	7	100.00	98.10	98.05	99.88	99.82	99.87	98.25
306-assembly	8	98.10	100.00	99.88	98.17	98.14	98.08	98.02
307-assembly	9	98.05	99.88	100.00	98.11	98.08	98.02	97.99
308-assembly	10	99.88	98.17	98.11	100.00	99.87	99.89	98.25
309-assembly	11	99.82	98.14	98.08	99.87	100.00	99.83	98.20
310-assembly	12	99.87	98.08	98.02	99.89	99.83	100.00	98.22
311-assembly	13	98.25	98.02	97.99	98.25	98.20	98.22	100.00
Lot1_P1-assembly	14	99.79	98.28	98.09	99.85	99.83	99.86	98.16
Lot1_P10-assembly	15	98.17	98.05	98.01	98.20	98.17	98.17	98.07
Lot1_P11-assembly	16	99.87	98.15	98.10	99.97	99.86	99.88	98.24
Lot1_P12-assembly	17	98.18	97.91	97.94	98.21	98.17	98.17	98.13
Lot1_P13-assembly	18	98.20	97.93	97.96	98.23	98.20	98.20	98.16
Lot1_P14-assembly	19	99.79	98.27	98.08	99.84	99.82	99.85	98.16
Lot1_P15-assembly	20	98.20	97.93	97.96	98.23	98.20	98.20	98.15
Lot1_P16-assembly	21	98.20	97.93	97.96	98.23	98.20	98.20	98.16
Lot1_P17-assembly	22	89.76	89.62	89.75	89.82	89.82	89.79	89.73
Lot1_P18-assembly	23	89.76	89.62	89.75	89.81	89.82	89.79	89.73
Lot1_P19-assembly	24	98.08	99.90	99.92	98.12	98.06	98.03	97.97
Lot1_P2-assembly	25	99.83	98.26	98.13	99.90	99.80	99.79	98.21
Lot1_P3-assembly	26	98.19	97.92	97.94	98.21	98.21	98.19	98.13
Lot1_P4-assembly	27	98.18	97.91	97.94	98.21	98.17	98.16	98.13
Lot1_P5-assembly	28	98.04	97.93	98.01	98.02	98.00	98.00	97.96
Lot1_P6-assembly	29	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot1_P7-assembly	30	98.03	97.92	98.02	98.05	98.03	98.04	97.96
Lot1_P8-assembly	31	99.78	98.15	98.10	99.83	99.77	99.75	98.24
Lot1_P9-assembly	32	99.79	98.08	98.04	99.81	99.80	99.82	98.18
Lot1_SE-assembly	33	98.05	99.70	99.57	98.08	98.08	98.01	98.08
Lot2_P20-assembly	34	98.07	99.56	99.58	98.10	98.05	98.05	97.96



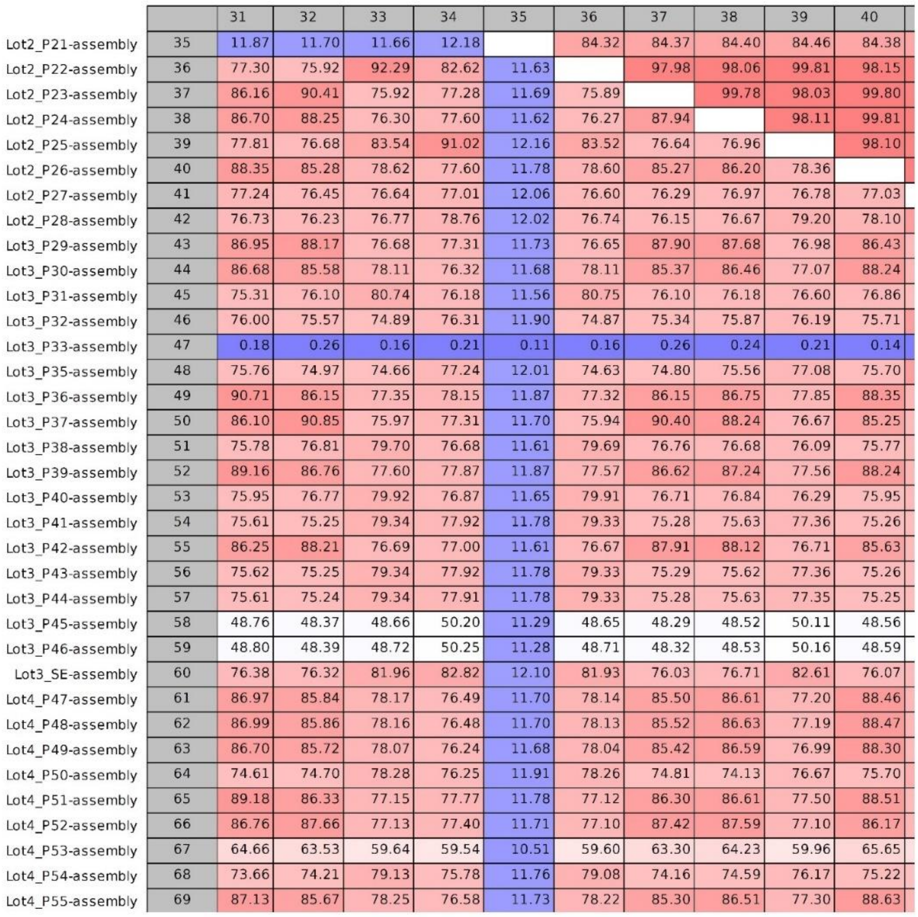
		1	2	3	4	5	6	7	8	9	10
Lot2_P21-assembly	35	11.83	12.14	11.70	11.92	11.71	12.02	11.81	12.25	12.16	11.88
Lot2_P22-assembly	36	76.13	77.72	76.19	75.89	74.57	84.16	74.82	82.19	82.48	77.46
Lot2_P23-assembly	37	76.93	78.18	83.03	84.76	85.04	76.62	83.88	75.30	75.93	86.60
Lot2_P24-assembly	38	77.77	78.07	83.14	84.77	85.40	77.25	83.78	75.67	76.73	87.24
Lot2_P25-assembly	39	78.19	79.94	76.20	78.12	75.66	85.95	76.62	82.09	82.93	77.55
Lot2_P26-assembly	40	77.11	78.09	82.21	84.63	84.80	77.71	84.13	75.25	76.30	88.05
Lot2_P27-assembly	41	77.92	78.80	76.06	76.61	75.11	77.90	75.33	76.49	76.84	77.46
Lot2_P28-assembly	42	78.19	79.36	74.82	77.09	74.50	78.39	76.22	76.61	77.36	76.77
Lot3_P29-assembly	43	77.31	77.93	82.83	85.33	85.72	76.86	84.05	76.05	76.21	87.01
Lot3_P30-assembly	44	76.88	77.40	82.88	84.52	84.64	76.78	83.51	75.46	76.14	87.55
Lot3_P31-assembly	45	76.70	77.90	74.55	74.19	74.28	76.17	73.37	74.47	75.43	75.59
Lot3_P32-assembly	46	76.75	78.06	74.96	75.76	74.13	76.87	76.42	75.23	75.96	76.30
Lot3_P33-assembly	47	0.09	0.07	0.22	0.30	0.23	0.41	0.19	0.12	0.09	0.15
Lot3_P35-assembly	48	78.16	79.00	74.53	76.51	73.79	78.15	75.42	75.93	76.77	76.00
Lot3_P36-assembly	49	77.59	78.52	83.41	85.61	85.59	77.78	84.98	75.94	76.61	88.97
Lot3_P37-assembly	50	77.10	78.24	83.24	85.16	85.27	76.81	84.10	75.50	76.14	86.84
Lot3_P38-assembly	51	77.18	78.39	75.03	74.68	74.79	76.63	73.88	74.91	75.88	76.08
Lot3_P39-assembly	52	77.78	79.12	83.49	86.42	85.64	78.12	85.41	76.38	77.05	89.87
Lot3_P40-assembly	53	77.48	78.58	75.31	74.85	75.04	76.82	74.06	75.19	76.17	76.25
Lot3_P41-assembly	54	78.41	79.73	74.51	75.85	74.23	78.55	75.24	76.46	77.30	75.84
Lot3_P42-assembly	55	77.16	78.03	83.26	85.03	86.16	77.73	83.76	76.80	76.94	87.06
Lot3_P43-assembly	56	78.41	79.73	74.50	75.85	74.23	78.55	75.23	76.46	77.30	75.83
Lot3_P44-assembly	57	78.40	79.72	74.50	75.84	74.22	78.55	75.23	76.45	77.30	75.83
Lot3_P45-assembly	58	49.32	51.93	48.56	49.03	48.08	50.26	48.30	48.60	49.13	49.01
Lot3_P46-assembly	59	49.34	51.96	48.59	49.05	48.10	50.31	48.32	48.66	49.18	49.03
Lot3_SE-assembly	60	79.02	79.03	75.37	76.77	75.37	83.55	75.86	88.93	90.17	76.57
Lot4_P47-assembly	61	77.02	77.48	82.47	85.05	84.11	76.99	84.04	75.78	76.45	87.93
Lot4_P48-assembly	62	77.03	77.48	82.46	85.06	84.13	76.98	84.05	75.77	76.44	87.94
Lot4_P49-assembly	63	76.91	77.29	83.02	84.66	84.85	76.76	83.61	75.52	76.19	87.66
Lot4_P50-assembly	64	76.15	78.01	73.33	74.59	72.79	75.81	74.40	74.69	75.02	74.71
Lot4_P51-assembly	65	77.65	78.15	83.40	85.69	85.56	77.48	85.13	75.76	76.45	89.25
Lot4_P52-assembly	66	77.60	78.46	82.94	85.42	85.89	78.15	84.14	77.18	77.32	87.58
Lot4_P53-assembly	67	60.32	60.79	61.87	63.82	62.22	59.96	62.24	58.99	59.32	65.36
Lot4_P54-assembly	68	76.41	77.45	73.20	74.02	72.80	75.76	73.22	74.01	75.01	73.90
Lot4_P55-assembly	69	77.17	77.61	82.30	85.10	84.07	77.09	84.05	75.89	76.57	88.08



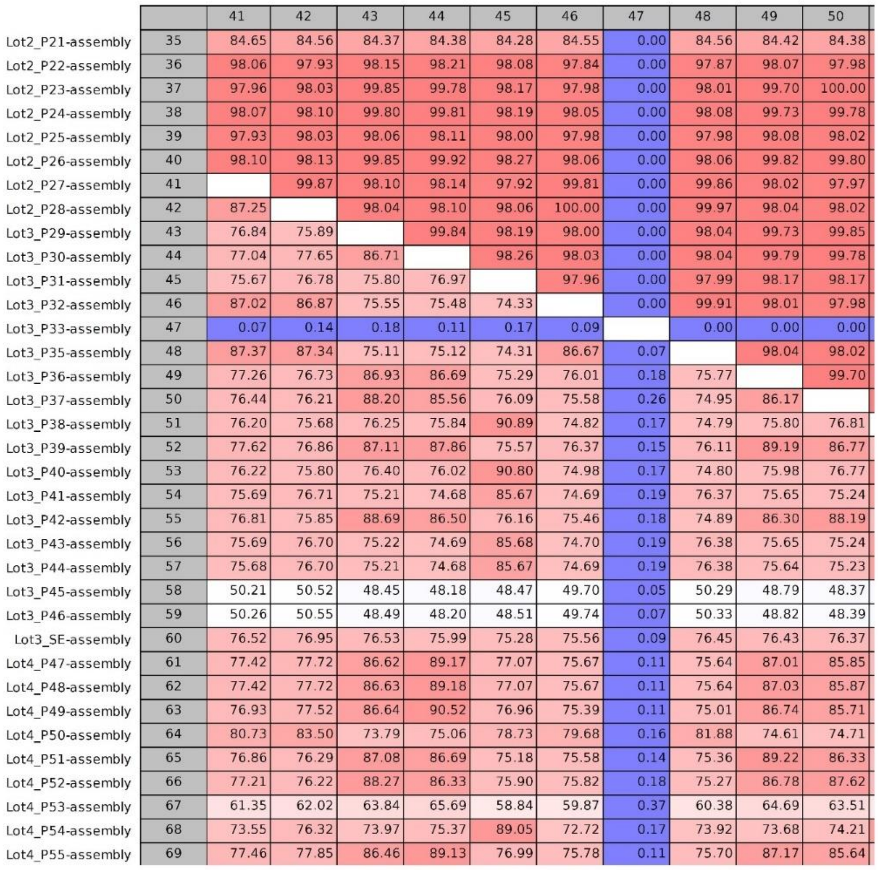
		11	12	13	14	15	16	17	18	19	20
Lot2_P21-assembly	35	11.69	11.65	11.70	11.69	12.06	11.86	11.66	11.82	11.61	11.78
Lot2_P22-assembly	36	77.41	77.00	78.77	76.64	73.00	77.49	79.88	79.03	76.66	79.00
Lot2_P23-assembly	37	86.51	85.52	76.33	87.94	74.21	86.71	76.72	75.34	87.89	75.30
Lot2_P24-assembly	38	86.56	85.36	76.53	87.83	73.91	87.28	76.85	75.64	88.12	75.65
Lot2_P25-assembly	39	77.59	77.00	77.34	76.99	74.72	77.50	76.26	77.42	76.70	77.39
Lot2_P26-assembly	40	87.69	86.53	76.37	86.53	74.30	88.24	75.98	75.34	85.65	75.29
Lot2_P27-assembly	41	75.79	76.20	74.69	76.80	74.76	77.56	76.22	75.72	76.80	75.68
Lot2_P28-assembly	42	77.01	77.19	76.14	75.85	75.21	76.78	75.81	76.73	75.84	76.74
Lot3_P29-assembly	43	87.21	85.22	76.11	90.74	73.88	87.13	76.42	75.24	88.67	75.23
Lot3_P30-assembly	44	87.81	86.10	75.45	86.61	73.67	87.79	76.03	74.78	86.50	74.71
Lot3_P31-assembly	45	76.74	76.12	78.69	75.75	72.56	75.53	90.65	85.29	76.15	85.32
Lot3_P32-assembly	46	74.91	75.31	74.80	75.50	74.10	76.30	74.99	74.77	75.43	74.73
Lot3_P33-assembly	47	0.15	0.17	0.24	0.18	0.07	0.15	0.17	0.19	0.18	0.19
Lot3_P35-assembly	48	74.45	74.78	74.83	75.07	74.83	76.03	74.81	76.44	74.87	76.39
Lot3_P36-assembly	49	86.68	85.49	76.83	87.10	74.48	89.25	76.00	75.73	86.29	75.67
Lot3_P37-assembly	50	86.76	85.74	76.33	88.31	74.31	86.83	76.78	75.28	88.18	75.26
Lot3_P38-assembly	51	75.68	75.09	79.26	76.26	72.98	75.99	91.49	85.96	76.65	86.03
Lot3_P39-assembly	52	86.92	86.52	76.93	87.09	75.09	90.61	76.18	75.95	87.06	75.89
Lot3_P40-assembly	53	75.83	75.37	79.47	76.42	73.24	76.15	91.86	86.26	76.81	86.27
Lot3_P41-assembly	54	74.62	74.82	80.32	75.24	73.88	75.86	86.64	91.40	75.42	91.56
Lot3_P42-assembly	55	87.00	85.54	76.29	88.75	73.90	87.15	76.82	75.46	91.25	75.45
Lot3_P43-assembly	56	74.62	74.82	80.32	75.23	73.89	75.87	86.64	91.41	75.42	91.56
Lot3_P44-assembly	57	74.61	74.81	80.32	75.23	73.88	75.86	86.63	91.40	75.41	91.55
Lot3_P45-assembly	58	48.12	48.27	48.74	48.42	48.27	49.01	48.91	49.63	48.55	49.59
Lot3_P46-assembly	59	48.14	48.29	48.75	48.45	48.31	49.05	48.94	49.65	48.58	49.61
Lot3_SE-assembly	60	76.18	75.48	76.81	76.53	75.20	76.65	75.78	76.76	76.66	76.73
Lot4_P47-assembly	61	87.28	86.60	75.56	86.77	73.70	87.98	76.05	75.00	86.69	74.95
Lot4_P48-assembly	62	87.27	86.62	75.56	86.79	73.69	87.99	76.05	75.00	86.70	74.95
Lot4_P49-assembly	63	88.00	86.20	75.37	86.75	73.57	87.74	76.11	74.71	86.69	74.66
Lot4_P50-assembly	64	74.73	74.97	77.76	73.78	73.93	74.73	77.68	78.54	73.68	78.58
Lot4_P51-assembly	65	86.68	85.51	76.45	87.24	74.35	89.08	75.90	75.31	86.36	75.27
Lot4_P52-assembly	66	86.83	86.08	76.71	88.32	74.32	87.66	76.55	75.83	90.62	75.83
Lot4_P53-assembly	67	64.50	64.18	57.82	63.86	57.53	65.39	58.26	57.93	63.96	57.88
Lot4_P54-assembly	68	74.86	74.56	78.41	73.98	72.11	73.83	88.76	85.47	74.27	85.53
Lot4_P55-assembly	69	87.19	86.67	75.67	86.60	73.79	88.14	75.96	75.07	86.57	75.02



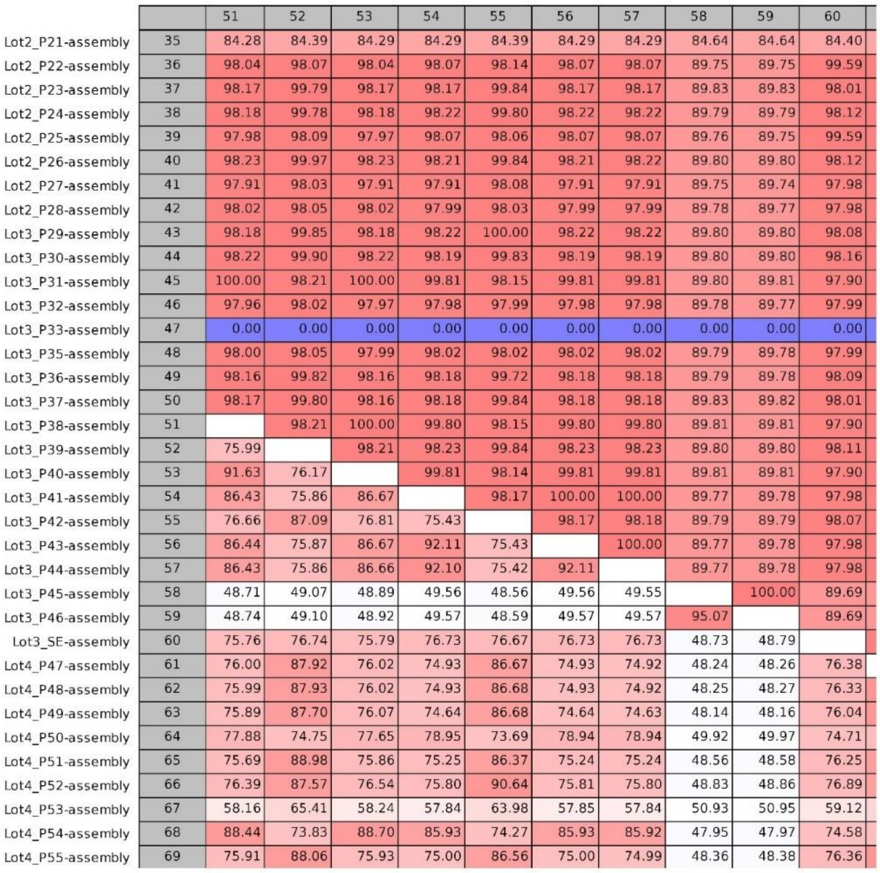
		21	22	23	24	25	26	27	28	29	30
Lot2_P21-assembly	35	11.78	11.29	11.29	12.09	11.68	11.56	11.62	11.90	0.11	12.01
Lot2_P22-assembly	36	78.98	48.69	48.65	81.91	78.14	80.76	79.71	74.84	0.16	74.63
Lot2_P23-assembly	37	75.30	48.30	48.27	75.98	85.43	76.06	76.77	75.32	0.26	74.80
Lot2_P24-assembly	38	75.65	48.53	48.50	76.67	86.50	76.21	76.70	75.85	0.24	75.57
Lot2_P25-assembly	39	77.37	50.15	50.11	82.58	77.09	76.62	76.11	76.17	0.21	77.09
Lot2_P26-assembly	40	75.28	48.56	48.54	76.02	88.24	76.91	75.81	75.66	0.14	75.71
Lot2_P27-assembly	41	75.69	50.24	50.22	76.48	77.06	75.67	76.25	86.98	0.07	87.37
Lot2_P28-assembly	42	76.74	50.55	50.53	76.91	77.67	76.77	75.72	86.85	0.14	87.34
Lot3_P29-assembly	43	75.22	48.46	48.45	76.48	86.76	75.76	76.27	75.54	0.18	75.13
Lot3_P30-assembly	44	74.70	48.18	48.17	75.94	90.71	76.96	75.87	75.46	0.11	75.13
Lot3_P31-assembly	45	85.32	48.48	48.46	75.23	77.02	91.83	90.89	74.32	0.17	74.30
Lot3_P32-assembly	46	74.72	49.74	49.71	75.51	75.50	74.31	74.85	91.96	0.09	86.62
Lot3_P33-assembly	47	0.19	0.05	0.07	0.09	0.11	0.17	0.17	0.11	99.52	0.07
Lot3_P35-assembly	48	76.40	50.33	50.30	76.39	75.16	74.29	74.82	86.61	0.07	91.71
Lot3_P36-assembly	49	75.67	48.80	48.78	76.39	86.72	75.35	75.83	75.97	0.18	75.78
Lot3_P37-assembly	50	75.26	48.37	48.35	76.33	85.59	76.12	76.82	75.56	0.26	74.96
Lot3_P38-assembly	51	86.04	48.71	48.69	75.71	75.87	90.92	92.01	74.81	0.17	74.78
Lot3_P39-assembly	52	75.88	49.07	49.06	76.69	87.89	75.55	76.02	76.34	0.15	76.12
Lot3_P40-assembly	53	86.29	48.89	48.87	75.75	76.05	90.82	91.62	74.98	0.17	74.79
Lot3_P41-assembly	54	91.63	49.56	49.54	76.69	74.73	85.70	86.42	74.69	0.19	76.37
Lot3_P42-assembly	55	75.45	48.56	48.54	76.63	86.52	76.16	76.66	75.43	0.18	74.90
Lot3_P43-assembly	56	91.63	49.56	49.54	76.68	74.73	85.70	86.42	74.69	0.19	76.36
Lot3_P44-assembly	57	91.62	49.55	49.53	76.67	74.73	85.69	86.41	74.68	0.19	76.36
Lot3_P45-assembly	58	49.57	95.10	95.14	48.71	48.20	48.46	48.75	49.68	0.05	50.29
Lot3_P46-assembly	59	49.59	95.21	95.21	48.76	48.23	48.48	48.78	49.71	0.07	50.33
Lot3_SE-assembly	60	76.73	48.78	48.74	91.90	76.01	75.25	75.77	75.52	0.09	76.45
Lot4_P47-assembly	61	74.95	48.24	48.21	76.34	89.14	77.11	76.03	75.63	0.11	75.66
Lot4_P48-assembly	62	74.95	48.26	48.23	76.29	89.15	77.10	76.02	75.63	0.11	75.66
Lot4_P49-assembly	63	74.66	48.15	48.12	76.01	90.50	77.01	75.93	75.35	0.11	75.01
Lot4_P50-assembly	64	78.58	49.96	49.93	74.68	75.07	78.77	77.92	79.68	0.16	81.87
Lot4_P51-assembly	65	75.26	48.57	48.54	76.21	86.72	75.25	75.72	75.55	0.14	75.38
Lot4_P52-assembly	66	75.82	48.84	48.81	76.84	86.38	75.91	76.40	75.79	0.18	75.28
Lot4_P53-assembly	67	57.87	50.94	50.91	59.07	65.71	58.82	58.19	59.85	0.37	60.35
Lot4_P54-assembly	68	85.55	47.95	47.93	74.54	75.41	89.16	88.48	72.74	0.17	73.91
Lot4_P55-assembly	69	75.02	48.37	48.34	76.33	89.16	77.03	75.94	75.74	0.11	75.71



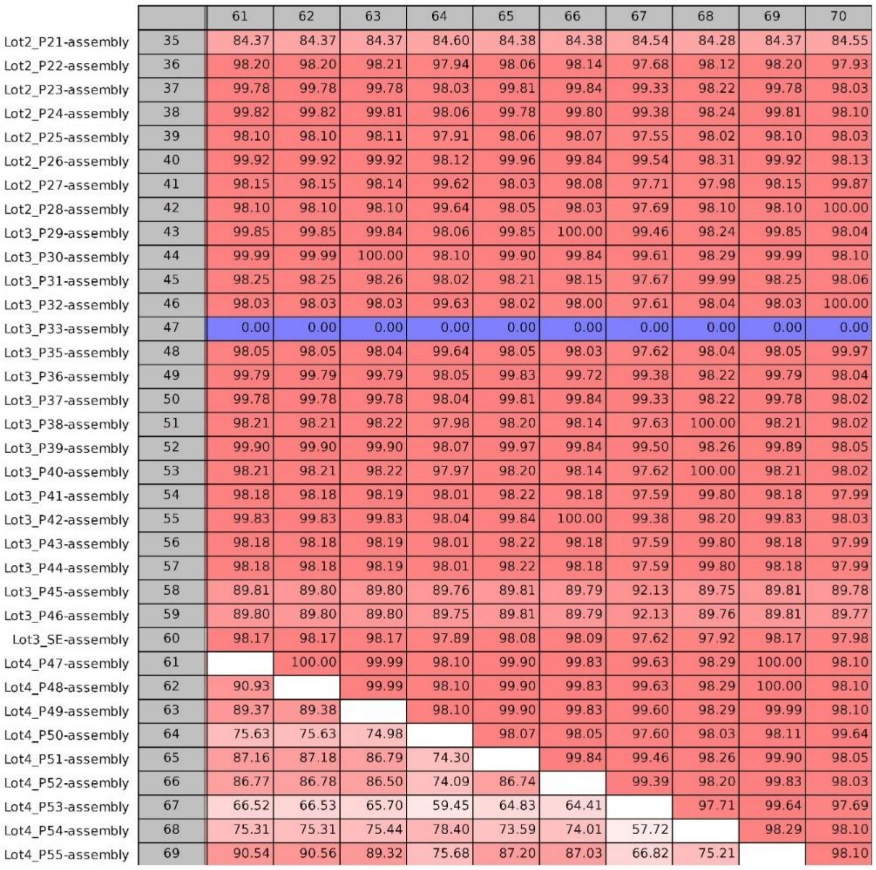
		31	32	33	34	35	36	37	38	39	40
Lot2_P21-assembly	35	11.87	11.70	11.66	12.18		84.32	84.37	84.40	84.46	84.38
Lot2_P22-assembly	36	77.30	75.92	92.29	82.62	11.63		97.98	98.06	99.81	98.15
Lot2_P23-assembly	37	86.16	90.41	75.92	77.28	11.69	75.89		99.78	98.03	99.80
Lot2_P24-assembly	38	86.70	88.25	76.30	77.60	11.62	76.27	87.94		98.11	99.81
Lot2_P25-assembly	39	77.81	76.68	83.54	91.02	12.16	83.52	76.64	76.96		98.10
Lot2_P26-assembly	40	88.35	85.28	78.62	77.60	11.78	78.60	85.27	86.20	78.36	
Lot2_P27-assembly	41	77.24	76.45	76.64	77.01	12.06	76.60	76.29	76.97	76.78	77.03
Lot2_P28-assembly	42	76.73	76.23	76.77	78.76	12.02	76.74	76.15	76.67	79.20	78.10
Lot3_P29-assembly	43	86.95	88.17	76.68	77.31	11.73	76.65	87.90	87.68	76.98	86.43
Lot3_P30-assembly	44	86.68	85.58	78.11	76.32	11.68	78.11	85.37	86.46	77.07	88.24
Lot3_P31-assembly	45	75.31	76.10	80.74	76.18	11.56	80.75	76.10	76.18	76.60	76.86
Lot3_P32-assembly	46	76.00	75.57	74.89	76.31	11.90	74.87	75.34	75.87	76.19	75.71
Lot3_P33-assembly	47	0.18	0.26	0.16	0.21	0.11	0.16	0.26	0.24	0.21	0.14
Lot3_P35-assembly	48	75.76	74.97	74.66	77.24	12.01	74.63	74.80	75.56	77.08	75.70
Lot3_P36-assembly	49	90.71	86.15	77.35	78.15	11.87	77.32	86.15	86.75	77.85	88.35
Lot3_P37-assembly	50	86.10	90.85	75.97	77.31	11.70	75.94	90.40	88.24	76.67	85.25
Lot3_P38-assembly	51	75.78	76.81	79.70	76.68	11.61	79.69	76.76	76.68	76.09	75.77
Lot3_P39-assembly	52	89.16	86.76	77.60	77.87	11.87	77.57	86.62	87.24	77.56	88.24
Lot3_P40-assembly	53	75.95	76.77	79.92	76.87	11.65	79.91	76.71	76.84	76.29	75.95
Lot3_P41-assembly	54	75.61	75.25	79.34	77.92	11.78	79.33	75.28	75.63	77.36	75.26
Lot3_P42-assembly	55	86.25	88.21	76.69	77.00	11.61	76.67	87.91	88.12	76.71	85.63
Lot3_P43-assembly	56	75.62	75.25	79.34	77.92	11.78	79.33	75.29	75.62	77.36	75.26
Lot3_P44-assembly	57	75.61	75.24	79.34	77.91	11.78	79.33	75.28	75.63	77.35	75.25
Lot3_P45-assembly	58	48.76	48.37	48.66	50.20	11.29	48.65	48.29	48.52	50.11	48.56
Lot3_P46-assembly	59	48.80	48.39	48.72	50.25	11.28	48.71	48.32	48.53	50.16	48.59
Lot3_SE-assembly	60	76.38	76.32	81.96	82.82	12.10	81.93	76.03	76.71	82.61	76.07
Lot4_P47-assembly	61	86.97	85.84	78.17	76.49	11.70	78.14	85.50	86.61	77.20	88.46
Lot4_P48-assembly	62	86.99	85.86	78.16	76.48	11.70	78.13	85.52	86.63	77.19	88.47
Lot4_P49-assembly	63	86.70	85.72	78.07	76.24	11.68	78.04	85.42	86.59	76.99	88.30
Lot4_P50-assembly	64	74.61	74.70	78.28	76.25	11.91	78.26	74.81	74.13	76.67	75.70
Lot4_P51-assembly	65	89.18	86.33	77.15	77.77	11.78	77.12	86.30	86.61	77.50	88.51
Lot4_P52-assembly	66	86.76	87.66	77.13	77.40	11.71	77.10	87.42	87.59	77.10	86.17
Lot4_P53-assembly	67	64.66	63.53	59.64	59.54	10.51	59.60	63.30	64.23	59.96	65.65
Lot4_P54-assembly	68	73.66	74.21	79.13	75.78	11.76	79.08	74.16	74.59	76.17	75.22
Lot4_P55-assembly	69	87.13	85.67	78.25	76.58	11.73	78.22	85.30	86.51	77.30	88.63



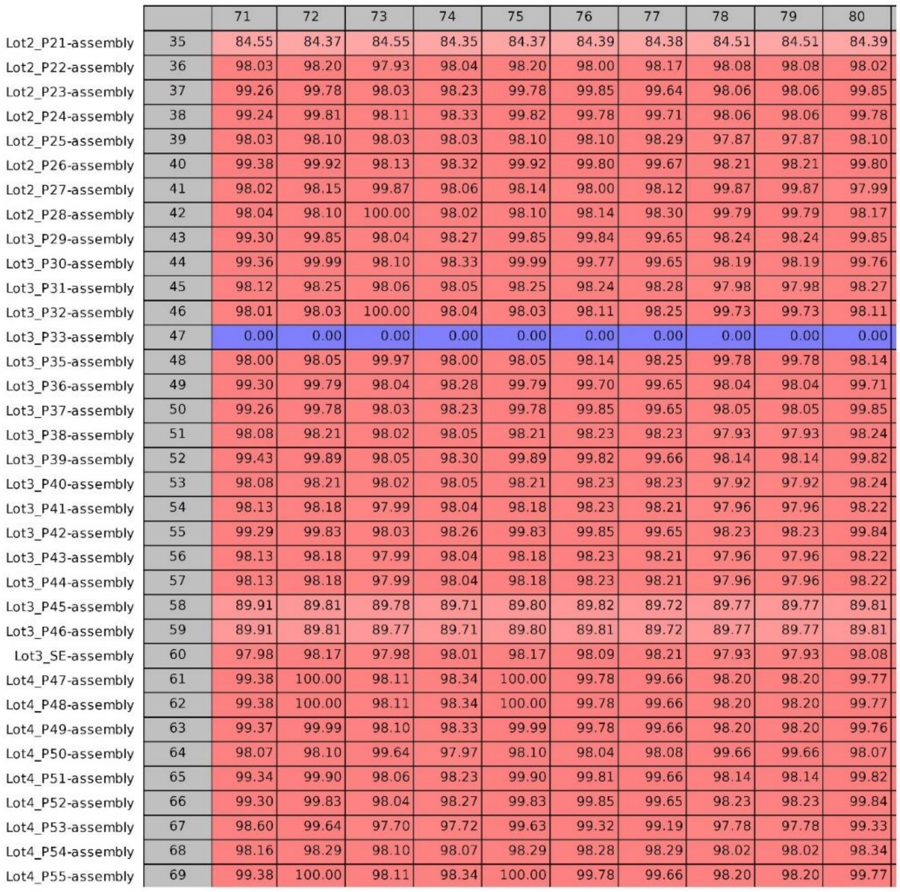
		41	42	43	44	45	46	47	48	49	50
Lot2_P21-assembly	35	84.65	84.56	84.37	84.38	84.28	84.55	0.00	84.56	84.42	84.38
Lot2_P22-assembly	36	98.06	97.93	98.15	98.21	98.08	97.84	0.00	97.87	98.07	97.98
Lot2_P23-assembly	37	97.96	98.03	99.85	99.78	98.17	97.98	0.00	98.01	99.70	100.00
Lot2_P24-assembly	38	98.07	98.10	99.80	99.81	98.19	98.05	0.00	98.08	99.73	99.78
Lot2_P25-assembly	39	97.93	98.03	98.06	98.11	98.00	97.98	0.00	97.98	98.08	98.02
Lot2_P26-assembly	40	98.10	98.13	99.85	99.92	98.27	98.06	0.00	98.06	99.82	99.80
Lot2_P27-assembly	41		99.87	98.10	98.14	97.92	99.81	0.00	99.86	98.02	97.97
Lot2_P28-assembly	42	87.25		98.04	98.10	98.06	100.00	0.00	99.97	98.04	98.02
Lot3_P29-assembly	43	76.84	75.89		99.84	98.19	98.00	0.00	98.04	99.73	99.85
Lot3_P30-assembly	44	77.04	77.65	86.71		98.26	98.03	0.00	98.04	99.79	99.78
Lot3_P31-assembly	45	75.67	76.78	75.80	76.97		97.96	0.00	97.99	98.17	98.17
Lot3_P32-assembly	46	87.02	86.87	75.55	75.48	74.33		0.00	99.91	98.01	97.98
Lot3_P33-assembly	47	0.07	0.14	0.18	0.11	0.17	0.09		0.00	0.00	0.00
Lot3_P35-assembly	48	87.37	87.34	75.11	75.12	74.31	86.67	0.07		98.04	98.02
Lot3_P36-assembly	49	77.26	76.73	86.93	86.69	75.29	76.01	0.18	75.77		99.70
Lot3_P37-assembly	50	76.44	76.21	88.20	85.56	76.09	75.58	0.26	74.95	86.17	
Lot3_P38-assembly	51	76.20	75.68	76.25	75.84	90.89	74.82	0.17	74.79	75.80	76.81
Lot3_P39-assembly	52	77.62	76.86	87.11	87.86	75.57	76.37	0.15	76.11	89.19	86.77
Lot3_P40-assembly	53	76.22	75.80	76.40	76.02	90.80	74.98	0.17	74.80	75.98	76.77
Lot3_P41-assembly	54	75.69	76.71	75.21	74.68	85.67	74.69	0.19	76.37	75.65	75.24
Lot3_P42-assembly	55	76.81	75.85	88.69	86.50	76.16	75.46	0.18	74.89	86.30	88.19
Lot3_P43-assembly	56	75.69	76.70	75.22	74.69	85.68	74.70	0.19	76.38	75.65	75.24
Lot3_P44-assembly	57	75.68	76.70	75.21	74.68	85.67	74.69	0.19	76.38	75.64	75.23
Lot3_P45-assembly	58	50.21	50.52	48.45	48.18	48.47	49.70	0.05	50.29	48.79	48.37
Lot3_P46-assembly	59	50.26	50.55	48.49	48.20	48.51	49.74	0.07	50.33	48.82	48.39
Lot3_SE-assembly	60	76.52	76.95	76.53	75.99	75.28	75.56	0.09	76.45	76.43	76.37
Lot4_P47-assembly	61	77.42	77.72	86.62	89.17	77.07	75.67	0.11	75.64	87.01	85.85
Lot4_P48-assembly	62	77.42	77.72	86.63	89.18	77.07	75.67	0.11	75.64	87.03	85.87
Lot4_P49-assembly	63	76.93	77.52	86.64	90.52	76.96	75.39	0.11	75.01	86.74	85.71
Lot4_P50-assembly	64	80.73	83.50	73.79	75.06	78.73	79.68	0.16	81.88	74.61	74.71
Lot4_P51-assembly	65	76.86	76.29	87.08	86.69	75.18	75.58	0.14	75.36	89.22	86.33
Lot4_P52-assembly	66	77.21	76.22	88.27	86.33	75.90	75.82	0.18	75.27	86.78	87.62
Lot4_P53-assembly	67	61.35	62.02	63.84	65.69	58.84	59.87	0.37	60.38	64.69	63.51
Lot4_P54-assembly	68	73.55	76.32	73.97	75.37	89.05	72.72	0.17	73.92	73.68	74.21
Lot4_P55-assembly	69	77.46	77.85	86.46	89.13	76.99	75.78	0.11	75.70	87.17	85.64



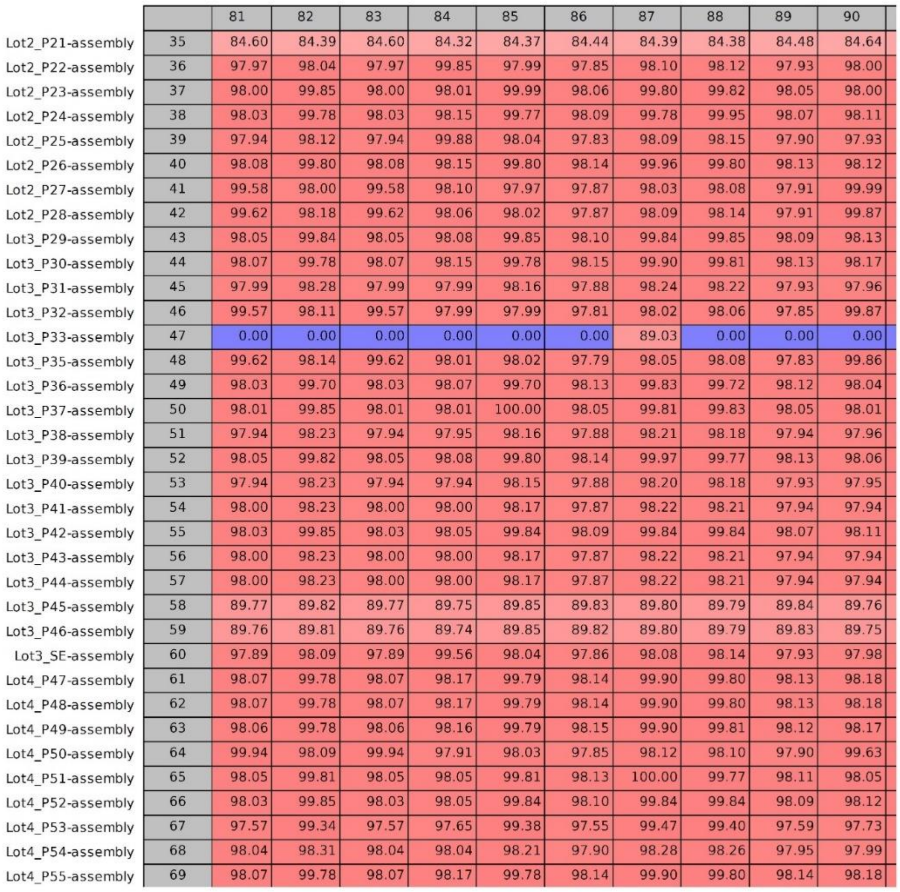
		51	52	53	54	55	56	57	58	59	60
Lot2_P21-assembly	35	84.28	84.39	84.29	84.29	84.39	84.29	84.29	84.64	84.64	84.40
Lot2_P22-assembly	36	98.04	98.07	98.04	98.07	98.14	98.07	98.07	89.75	89.75	99.59
Lot2_P23-assembly	37	98.17	99.79	98.17	98.17	99.84	98.17	98.17	89.83	89.83	98.01
Lot2_P24-assembly	38	98.18	99.78	98.18	98.22	99.80	98.22	98.22	89.79	89.79	98.12
Lot2_P25-assembly	39	97.98	98.09	97.97	98.07	98.06	98.07	98.07	89.76	89.75	99.59
Lot2_P26-assembly	40	98.23	99.97	98.23	98.21	99.84	98.21	98.22	89.80	89.80	98.12
Lot2_P27-assembly	41	97.91	98.03	97.91	97.91	98.08	97.91	97.91	89.75	89.74	97.98
Lot2_P28-assembly	42	98.02	98.05	98.02	97.99	98.03	97.99	97.99	89.78	89.77	97.98
Lot3_P29-assembly	43	98.18	99.85	98.18	98.22	100.00	98.22	98.22	89.80	89.80	98.08
Lot3_P30-assembly	44	98.22	99.90	98.22	98.19	99.83	98.19	98.19	89.80	89.80	98.16
Lot3_P31-assembly	45	100.00	98.21	100.00	99.81	98.15	99.81	99.81	89.80	89.81	97.90
Lot3_P32-assembly	46	97.96	98.02	97.97	97.98	97.99	97.98	97.98	89.78	89.77	97.99
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot3_P35-assembly	48	98.00	98.05	97.99	98.02	98.02	98.02	98.02	89.79	89.78	97.99
Lot3_P36-assembly	49	98.16	99.82	98.16	98.18	99.72	98.18	98.18	89.79	89.78	98.09
Lot3_P37-assembly	50	98.17	99.80	98.16	98.18	99.84	98.18	98.18	89.83	89.82	98.01
Lot3_P38-assembly	51		98.21	100.00	99.80	98.15	99.80	99.80	89.81	89.81	97.90
Lot3_P39-assembly	52	75.99		98.21	98.23	99.84	98.23	98.23	89.80	89.80	98.11
Lot3_P40-assembly	53	91.63	76.17		99.81	98.14	99.81	99.81	89.81	89.81	97.90
Lot3_P41-assembly	54	86.43	75.86	86.67		98.17	100.00	100.00	89.77	89.78	97.98
Lot3_P42-assembly	55	76.66	87.09	76.81	75.43		98.17	98.18	89.79	89.79	98.07
Lot3_P43-assembly	56	86.44	75.87	86.67	92.11	75.43		100.00	89.77	89.78	97.98
Lot3_P44-assembly	57	86.43	75.86	86.66	92.10	75.42	92.11		89.77	89.78	97.98
Lot3_P45-assembly	58	48.71	49.07	48.89	49.56	48.56	49.56	49.55		100.00	89.69
Lot3_P46-assembly	59	48.74	49.10	48.92	49.57	48.59	49.57	49.57	95.07		89.69
Lot3_SE-assembly	60	75.76	76.74	75.79	76.73	76.67	76.73	76.73	48.73	48.79	
Lot4_P47-assembly	61	76.00	87.92	76.02	74.93	86.67	74.93	74.92	48.24	48.26	76.38
Lot4_P48-assembly	62	75.99	87.93	76.02	74.93	86.68	74.93	74.92	48.25	48.27	76.33
Lot4_P49-assembly	63	75.89	87.70	76.07	74.64	86.68	74.64	74.63	48.14	48.16	76.04
Lot4_P50-assembly	64	77.88	74.75	77.65	78.95	73.69	78.94	78.94	49.92	49.97	74.71
Lot4_P51-assembly	65	75.69	88.98	75.86	75.25	86.37	75.24	75.24	48.56	48.58	76.25
Lot4_P52-assembly	66	76.39	87.57	76.54	75.80	90.64	75.81	75.80	48.83	48.86	76.89
Lot4_P53-assembly	67	58.16	65.41	58.24	57.84	63.98	57.85	57.84	50.93	50.95	59.12
Lot4_P54-assembly	68	88.44	73.83	88.70	85.93	74.27	85.93	85.92	47.95	47.97	74.58
Lot4_P55-assembly	69	75.91	88.06	75.93	75.00	86.56	75.00	74.99	48.36	48.38	76.36



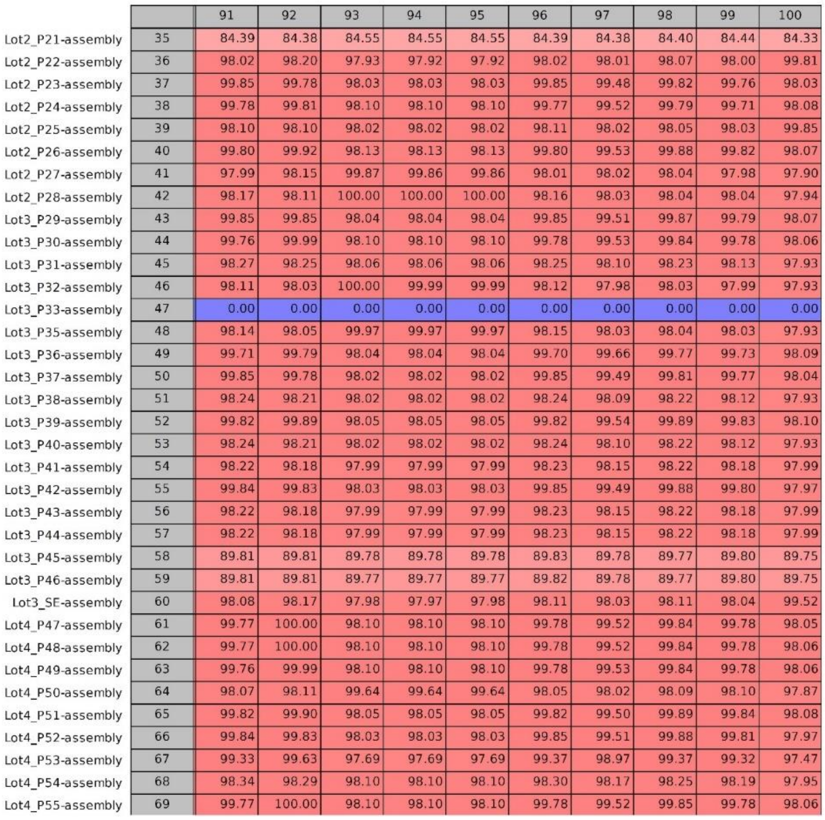
		61	62	63	64	65	66	67	68	69	70
Lot2_P21-assembly	35	84.37	84.37	84.37	84.60	84.38	84.38	84.54	84.28	84.37	84.55
Lot2_P22-assembly	36	98.20	98.20	98.21	97.94	98.06	98.14	97.68	98.12	98.20	97.93
Lot2_P23-assembly	37	99.78	99.78	99.78	98.03	99.81	99.84	99.33	98.22	99.78	98.03
Lot2_P24-assembly	38	99.82	99.82	99.81	98.06	99.78	99.80	99.38	98.24	99.81	98.10
Lot2_P25-assembly	39	98.10	98.10	98.11	97.91	98.06	98.07	97.55	98.02	98.10	98.03
Lot2_P26-assembly	40	99.92	99.92	99.92	98.12	99.96	99.84	99.54	98.31	99.92	98.13
Lot2_P27-assembly	41	98.15	98.15	98.14	99.62	98.03	98.08	97.71	97.98	98.15	99.87
Lot2_P28-assembly	42	98.10	98.10	98.10	99.64	98.05	98.03	97.69	98.10	98.10	100.00
Lot3_P29-assembly	43	99.85	99.85	99.84	98.06	99.85	100.00	99.46	98.24	99.85	98.04
Lot3_P30-assembly	44	99.99	99.99	100.00	98.10	99.90	99.84	99.61	98.29	99.99	98.10
Lot3_P31-assembly	45	98.25	98.25	98.26	98.02	98.21	98.15	97.67	99.99	98.25	98.06
Lot3_P32-assembly	46	98.03	98.03	98.03	99.63	98.02	98.00	97.61	98.04	98.03	100.00
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot3_P35-assembly	48	98.05	98.05	98.04	99.64	98.05	98.03	97.62	98.04	98.05	99.97
Lot3_P36-assembly	49	99.79	99.79	99.79	98.05	99.83	99.72	99.38	98.22	99.79	98.04
Lot3_P37-assembly	50	99.78	99.78	99.78	98.04	99.81	99.84	99.33	98.22	99.78	98.02
Lot3_P38-assembly	51	98.21	98.21	98.22	97.98	98.20	98.14	97.63	100.00	98.21	98.02
Lot3_P39-assembly	52	99.90	99.90	99.90	98.07	99.97	99.84	99.50	98.26	99.89	98.05
Lot3_P40-assembly	53	98.21	98.21	98.22	97.97	98.20	98.14	97.62	100.00	98.21	98.02
Lot3_P41-assembly	54	98.18	98.18	98.19	98.01	98.22	98.18	97.59	99.80	98.18	97.99
Lot3_P42-assembly	55	99.83	99.83	99.83	98.04	99.84	100.00	99.38	98.20	99.83	98.03
Lot3_P43-assembly	56	98.18	98.18	98.19	98.01	98.22	98.18	97.59	99.80	98.18	97.99
Lot3_P44-assembly	57	98.18	98.18	98.19	98.01	98.22	98.18	97.59	99.80	98.18	97.99
Lot3_P45-assembly	58	89.81	89.80	89.80	89.76	89.81	89.79	92.13	89.75	89.81	89.78
Lot3_P46-assembly	59	89.80	89.80	89.80	89.75	89.81	89.79	92.13	89.76	89.81	89.77
Lot3_SE-assembly	60	98.17	98.17	98.17	97.89	98.08	98.09	97.62	97.92	98.17	97.98
Lot4_P47-assembly	61		100.00	99.99	98.10	99.90	99.83	99.63	98.29	100.00	98.10
Lot4_P48-assembly	62	90.93		99.99	98.10	99.90	99.83	99.63	98.29	100.00	98.10
Lot4_P49-assembly	63	89.37	89.38		98.10	99.90	99.83	99.60	98.29	99.99	98.10
Lot4_P50-assembly	64	75.63	75.63	74.98		98.07	98.05	97.60	98.03	98.11	99.64
Lot4_P51-assembly	65	87.16	87.18	86.79	74.30		99.84	99.46	98.26	99.90	98.05
Lot4_P52-assembly	66	86.77	86.78	86.50	74.09	86.74		99.39	98.20	99.83	98.03
Lot4_P53-assembly	67	66.52	66.53	65.70	59.45	64.83	64.41		97.71	99.64	97.69
Lot4_P54-assembly	68	75.31	75.31	75.44	78.40	73.59	74.01	57.72		98.29	98.10
Lot4_P55-assembly	69	90.54	90.56	89.32	75.68	87.20	87.03	66.82	75.21		98.10



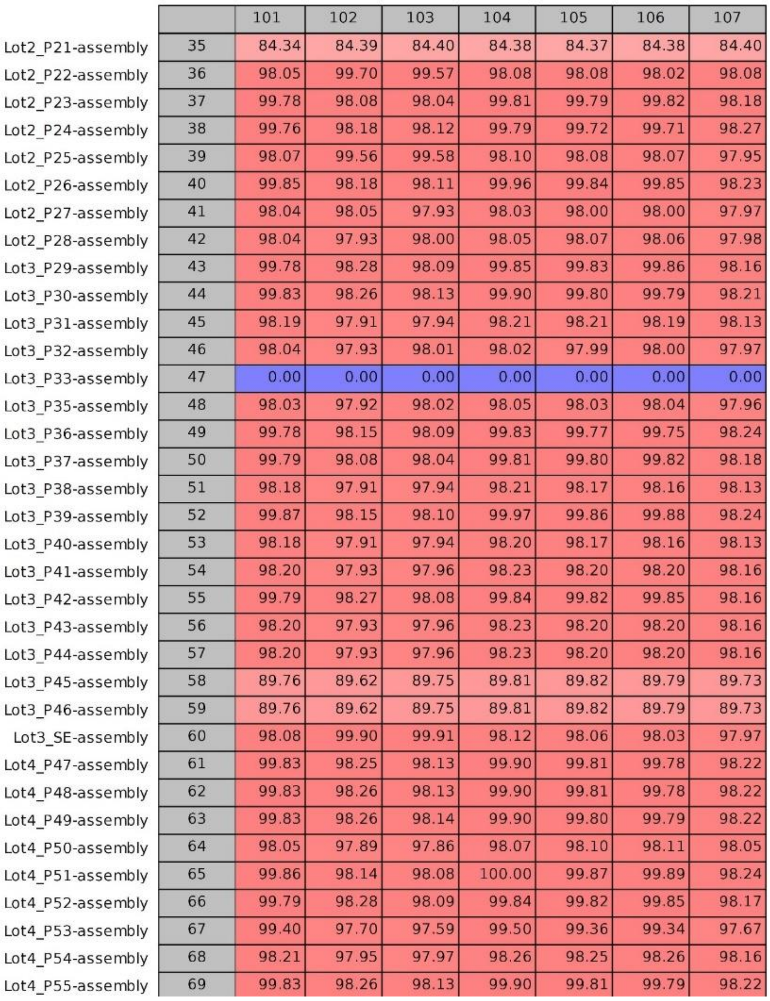
		71	72	73	74	75	76	77	78	79	80
Lot2_P21-assembly	35	84.55	84.37	84.55	84.35	84.37	84.39	84.38	84.51	84.51	84.39
Lot2_P22-assembly	36	98.03	98.20	97.93	98.04	98.20	98.00	98.17	98.08	98.08	98.02
Lot2_P23-assembly	37	99.26	99.78	98.03	98.23	99.78	99.85	99.64	98.06	98.06	99.85
Lot2_P24-assembly	38	99.24	99.81	98.11	98.33	99.82	99.78	99.71	98.06	98.06	99.78
Lot2_P25-assembly	39	98.03	98.10	98.03	98.03	98.10	98.10	98.29	97.87	97.87	98.10
Lot2_P26-assembly	40	99.38	99.92	98.13	98.32	99.92	99.80	99.67	98.21	98.21	99.80
Lot2_P27-assembly	41	98.02	98.15	99.87	98.06	98.14	98.00	98.12	99.87	99.87	97.99
Lot2_P28-assembly	42	98.04	98.10	100.00	98.02	98.10	98.14	98.30	99.79	99.79	98.17
Lot3_P29-assembly	43	99.30	99.85	98.04	98.27	99.85	99.84	99.65	98.24	98.24	99.85
Lot3_P30-assembly	44	99.36	99.99	98.10	98.33	99.99	99.77	99.65	98.19	98.19	99.76
Lot3_P31-assembly	45	98.12	98.25	98.06	98.05	98.25	98.24	98.28	97.98	97.98	98.27
Lot3_P32-assembly	46	98.01	98.03	100.00	98.04	98.03	98.11	98.25	99.73	99.73	98.11
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot3_P35-assembly	48	98.00	98.05	99.97	98.00	98.05	98.14	98.25	99.78	99.78	98.14
Lot3_P36-assembly	49	99.30	99.79	98.04	98.28	99.79	99.70	99.65	98.04	98.04	99.71
Lot3_P37-assembly	50	99.26	99.78	98.03	98.23	99.78	99.85	99.65	98.05	98.05	99.85
Lot3_P38-assembly	51	98.08	98.21	98.02	98.05	98.21	98.23	98.23	97.93	97.93	98.24
Lot3_P39-assembly	52	99.43	99.89	98.05	98.30	99.89	99.82	99.66	98.14	98.14	99.82
Lot3_P40-assembly	53	98.08	98.21	98.02	98.05	98.21	98.23	98.23	97.92	97.92	98.24
Lot3_P41-assembly	54	98.13	98.18	97.99	98.04	98.18	98.23	98.21	97.96	97.96	98.22
Lot3_P42-assembly	55	99.29	99.83	98.03	98.26	99.83	99.85	99.65	98.23	98.23	99.84
Lot3_P43-assembly	56	98.13	98.18	97.99	98.04	98.18	98.23	98.21	97.96	97.96	98.22
Lot3_P44-assembly	57	98.13	98.18	97.99	98.04	98.18	98.23	98.21	97.96	97.96	98.22
Lot3_P45-assembly	58	89.91	89.81	89.78	89.71	89.80	89.82	89.72	89.77	89.77	89.81
Lot3_P46-assembly	59	89.91	89.81	89.77	89.71	89.80	89.81	89.72	89.77	89.77	89.81
Lot3_SE-assembly	60	97.98	98.17	97.98	98.01	98.17	98.09	98.21	97.93	97.93	98.08
Lot4_P47-assembly	61	99.38	100.00	98.11	98.34	100.00	99.78	99.66	98.20	98.20	99.77
Lot4_P48-assembly	62	99.38	100.00	98.11	98.34	100.00	99.78	99.66	98.20	98.20	99.77
Lot4_P49-assembly	63	99.37	99.99	98.10	98.33	99.99	99.78	99.66	98.20	98.20	99.76
Lot4_P50-assembly	64	98.07	98.10	99.64	97.97	98.10	98.04	98.08	99.66	99.66	98.07
Lot4_P51-assembly	65	99.34	99.90	98.06	98.23	99.90	99.81	99.66	98.14	98.14	99.82
Lot4_P52-assembly	66	99.30	99.83	98.04	98.27	99.83	99.85	99.65	98.23	98.23	99.84
Lot4_P53-assembly	67	98.60	99.64	97.70	97.72	99.63	99.32	99.19	97.78	97.78	99.33
Lot4_P54-assembly	68	98.16	98.29	98.10	98.07	98.29	98.28	98.29	98.02	98.02	98.34
Lot4_P55-assembly	69	99.38	100.00	98.11	98.34	100.00	99.78	99.66	98.20	98.20	99.77



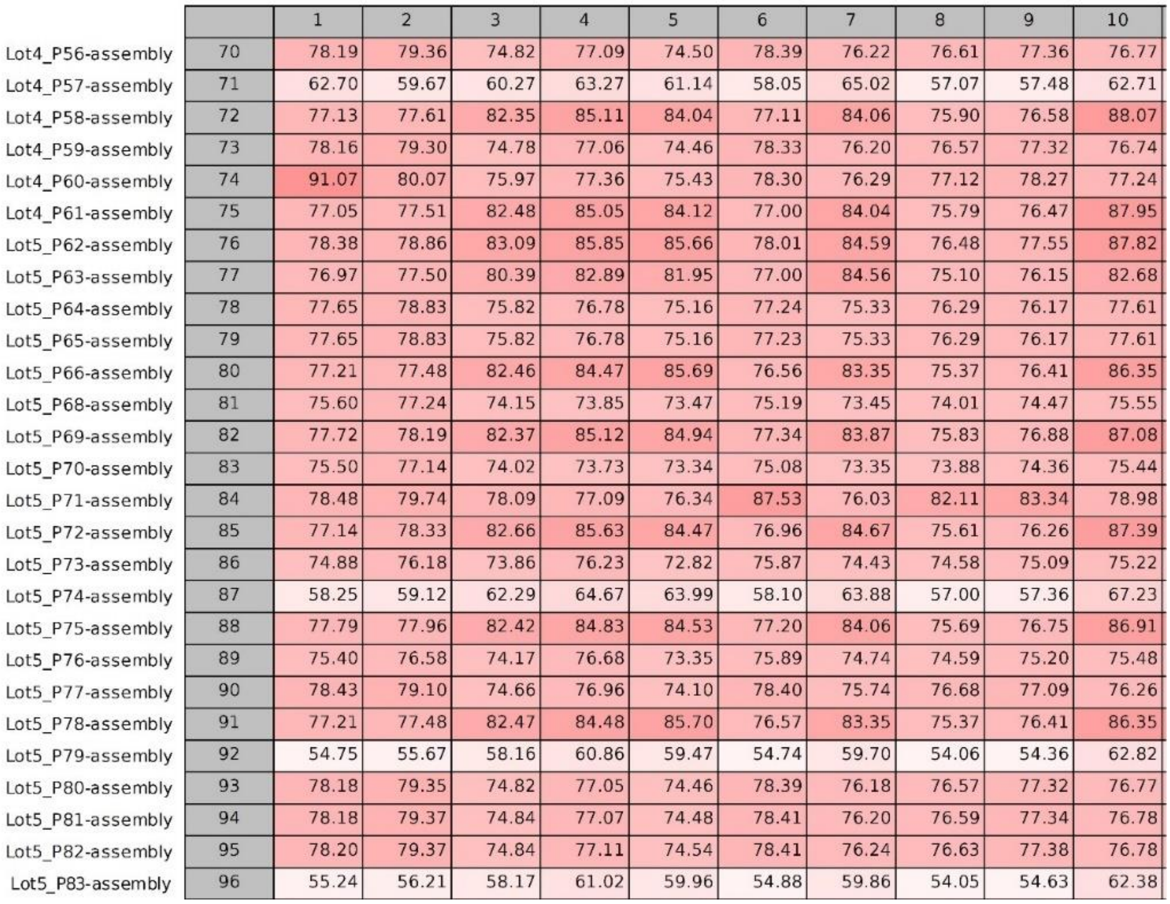
		81	82	83	84	85	86	87	88	89	90
Lot2_P21-assembly	35	84.60	84.39	84.60	84.32	84.37	84.44	84.39	84.38	84.48	84.64
Lot2_P22-assembly	36	97.97	98.04	97.97	99.85	97.99	97.85	98.10	98.12	97.93	98.00
Lot2_P23-assembly	37	98.00	99.85	98.00	98.01	99.99	98.06	99.80	99.82	98.05	98.00
Lot2_P24-assembly	38	98.03	99.78	98.03	98.15	99.77	98.09	99.78	99.95	98.07	98.11
Lot2_P25-assembly	39	97.94	98.12	97.94	99.88	98.04	97.83	98.09	98.15	97.90	97.93
Lot2_P26-assembly	40	98.08	99.80	98.08	98.15	99.80	98.14	99.96	99.80	98.13	98.12
Lot2_P27-assembly	41	99.58	98.00	99.58	98.10	97.97	97.87	98.03	98.08	97.91	99.99
Lot2_P28-assembly	42	99.62	98.18	99.62	98.06	98.02	97.87	98.09	98.14	97.91	99.87
Lot3_P29-assembly	43	98.05	99.84	98.05	98.08	99.85	98.10	99.84	99.85	98.09	98.13
Lot3_P30-assembly	44	98.07	99.78	98.07	98.15	99.78	98.15	99.90	99.81	98.13	98.17
Lot3_P31-assembly	45	97.99	98.28	97.99	97.99	98.16	97.88	98.24	98.22	97.93	97.96
Lot3_P32-assembly	46	99.57	98.11	99.57	97.99	97.99	97.81	98.02	98.06	97.85	99.87
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	89.03	0.00	0.00	0.00
Lot3_P35-assembly	48	99.62	98.14	99.62	98.01	98.02	97.79	98.05	98.08	97.83	99.86
Lot3_P36-assembly	49	98.03	99.70	98.03	98.07	99.70	98.13	99.83	99.72	98.12	98.04
Lot3_P37-assembly	50	98.01	99.85	98.01	98.01	100.00	98.05	99.81	99.83	98.05	98.01
Lot3_P38-assembly	51	97.94	98.23	97.94	97.95	98.16	97.88	98.21	98.18	97.94	97.96
Lot3_P39-assembly	52	98.05	99.82	98.05	98.08	99.80	98.14	99.97	99.77	98.13	98.06
Lot3_P40-assembly	53	97.94	98.23	97.94	97.94	98.15	97.88	98.20	98.18	97.93	97.95
Lot3_P41-assembly	54	98.00	98.23	98.00	98.00	98.17	97.87	98.22	98.21	97.94	97.94
Lot3_P42-assembly	55	98.03	99.85	98.03	98.05	99.84	98.09	99.84	99.84	98.07	98.11
Lot3_P43-assembly	56	98.00	98.23	98.00	98.00	98.17	97.87	98.22	98.21	97.94	97.94
Lot3_P44-assembly	57	98.00	98.23	98.00	98.00	98.17	97.87	98.22	98.21	97.94	97.94
Lot3_P45-assembly	58	89.77	89.82	89.77	89.75	89.85	89.83	89.80	89.79	89.84	89.76
Lot3_P46-assembly	59	89.76	89.81	89.76	89.74	89.85	89.82	89.80	89.79	89.83	89.75
Lot3_SE-assembly	60	97.89	98.09	97.89	99.56	98.04	97.86	98.08	98.14	97.93	97.98
Lot4_P47-assembly	61	98.07	99.78	98.07	98.17	99.79	98.14	99.90	99.80	98.13	98.18
Lot4_P48-assembly	62	98.07	99.78	98.07	98.17	99.79	98.14	99.90	99.80	98.13	98.18
Lot4_P49-assembly	63	98.06	99.78	98.06	98.16	99.79	98.15	99.90	99.81	98.12	98.17
Lot4_P50-assembly	64	99.94	98.09	99.94	97.91	98.03	97.85	98.12	98.10	97.90	99.63
Lot4_P51-assembly	65	98.05	99.81	98.05	98.05	99.81	98.13	100.00	99.77	98.11	98.05
Lot4_P52-assembly	66	98.03	99.85	98.03	98.05	99.84	98.10	99.84	99.84	98.09	98.12
Lot4_P53-assembly	67	97.57	99.34	97.57	97.65	99.38	97.55	99.47	99.40	97.59	97.73
Lot4_P54-assembly	68	98.04	98.31	98.04	98.04	98.21	97.90	98.28	98.26	97.95	97.99
Lot4_P55-assembly	69	98.07	99.78	98.07	98.17	99.78	98.14	99.90	99.80	98.14	98.18



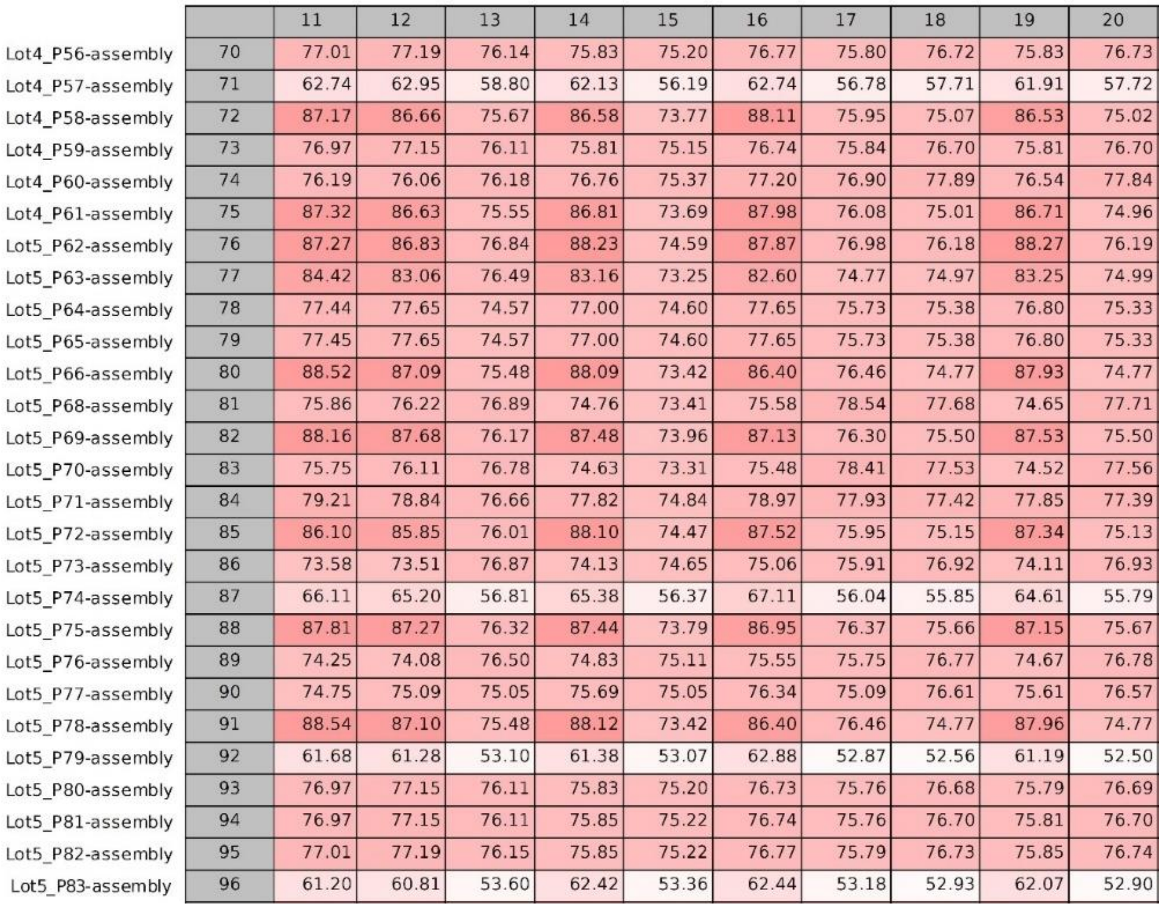
		91	92	93	94	95	96	97	98	99	100
Lot2_P21-assembly	35	84.39	84.38	84.55	84.55	84.55	84.39	84.38	84.40	84.44	84.33
Lot2_P22-assembly	36	98.02	98.20	97.93	97.92	97.92	98.02	98.01	98.07	98.00	99.81
Lot2_P23-assembly	37	99.85	99.78	98.03	98.03	98.03	99.85	99.48	99.82	99.76	98.03
Lot2_P24-assembly	38	99.78	99.81	98.10	98.10	98.10	99.77	99.52	99.79	99.71	98.08
Lot2_P25-assembly	39	98.10	98.10	98.02	98.02	98.02	98.11	98.02	98.05	98.03	99.85
Lot2_P26-assembly	40	99.80	99.92	98.13	98.13	98.13	99.80	99.53	99.88	99.82	98.07
Lot2_P27-assembly	41	97.99	98.15	99.87	99.86	99.86	98.01	98.02	98.04	97.98	97.90
Lot2_P28-assembly	42	98.17	98.11	100.00	100.00	100.00	98.16	98.03	98.04	98.04	97.94
Lot3_P29-assembly	43	99.85	99.85	98.04	98.04	98.04	99.85	99.51	99.87	99.79	98.07
Lot3_P30-assembly	44	99.76	99.99	98.10	98.10	98.10	99.78	99.53	99.84	99.78	98.06
Lot3_P31-assembly	45	98.27	98.25	98.06	98.06	98.06	98.25	98.10	98.23	98.13	97.93
Lot3_P32-assembly	46	98.11	98.03	100.00	99.99	99.99	98.12	97.98	98.03	97.99	97.93
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot3_P35-assembly	48	98.14	98.05	99.97	99.97	99.97	98.15	98.03	98.04	98.03	97.93
Lot3_P36-assembly	49	99.71	99.79	98.04	98.04	98.04	99.70	99.66	99.77	99.73	98.09
Lot3_P37-assembly	50	99.85	99.78	98.02	98.02	98.02	99.85	99.49	99.81	99.77	98.04
Lot3_P38-assembly	51	98.24	98.21	98.02	98.02	98.02	98.24	98.09	98.22	98.12	97.93
Lot3_P39-assembly	52	99.82	99.89	98.05	98.05	98.05	99.82	99.54	99.89	99.83	98.10
Lot3_P40-assembly	53	98.24	98.21	98.02	98.02	98.02	98.24	98.10	98.22	98.12	97.93
Lot3_P41-assembly	54	98.22	98.18	97.99	97.99	97.99	98.23	98.15	98.22	98.18	97.99
Lot3_P42-assembly	55	99.84	99.83	98.03	98.03	98.03	99.85	99.49	99.88	99.80	97.97
Lot3_P43-assembly	56	98.22	98.18	97.99	97.99	97.99	98.23	98.15	98.22	98.18	97.99
Lot3_P44-assembly	57	98.22	98.18	97.99	97.99	97.99	98.23	98.15	98.22	98.18	97.99
Lot3_P45-assembly	58	89.81	89.81	89.78	89.78	89.78	89.83	89.78	89.77	89.80	89.75
Lot3_P46-assembly	59	89.81	89.81	89.77	89.77	89.77	89.82	89.78	89.77	89.80	89.75
Lot3_SE-assembly	60	98.08	98.17	97.98	97.97	97.98	98.11	98.03	98.11	98.04	99.52
Lot4_P47-assembly	61	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.84	99.78	98.05
Lot4_P48-assembly	62	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.84	99.78	98.06
Lot4_P49-assembly	63	99.76	99.99	98.10	98.10	98.10	99.78	99.53	99.84	99.78	98.06
Lot4_P50-assembly	64	98.07	98.11	99.64	99.64	99.64	98.05	98.02	98.09	98.10	97.87
Lot4_P51-assembly	65	99.82	99.90	98.05	98.05	98.05	99.82	99.50	99.89	99.84	98.08
Lot4_P52-assembly	66	99.84	99.83	98.03	98.03	98.03	99.85	99.51	99.88	99.81	97.97
Lot4_P53-assembly	67	99.33	99.63	97.69	97.69	97.69	99.37	98.97	99.37	99.32	97.47
Lot4_P54-assembly	68	98.34	98.29	98.10	98.10	98.10	98.30	98.17	98.25	98.19	97.95
Lot4_P55-assembly	69	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.85	99.78	98.06



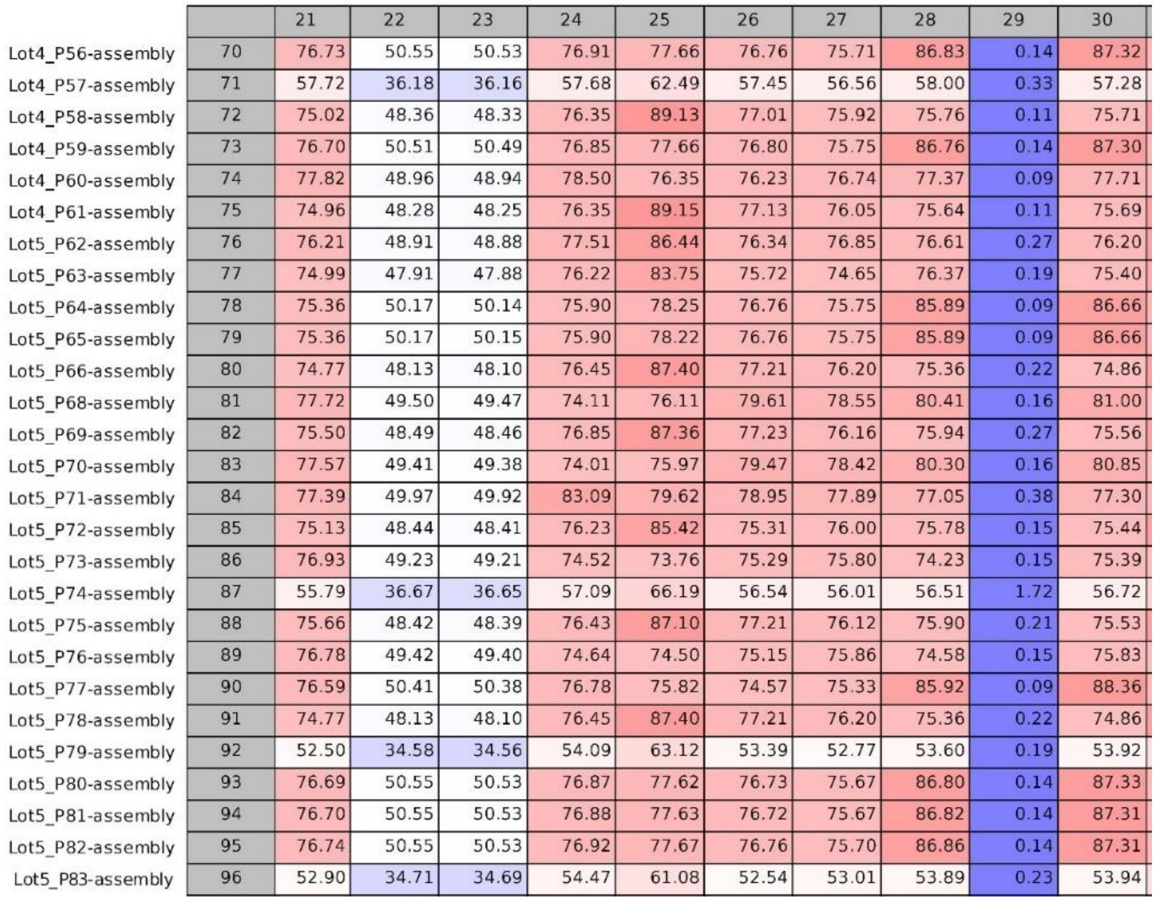
		101	102	103	104	105	106	107
Lot2_P21-assembly	35	84.34	84.39	84.40	84.38	84.37	84.38	84.40
Lot2_P22-assembly	36	98.05	99.70	99.57	98.08	98.08	98.02	98.08
Lot2_P23-assembly	37	99.78	98.08	98.04	99.81	99.79	99.82	98.18
Lot2_P24-assembly	38	99.76	98.18	98.12	99.79	99.72	99.71	98.27
Lot2_P25-assembly	39	98.07	99.56	99.58	98.10	98.08	98.07	97.95
Lot2_P26-assembly	40	99.85	98.18	98.11	99.96	99.84	99.85	98.23
Lot2_P27-assembly	41	98.04	98.05	97.93	98.03	98.00	98.00	97.97
Lot2_P28-assembly	42	98.04	97.93	98.00	98.05	98.07	98.06	97.98
Lot3_P29-assembly	43	99.78	98.28	98.09	99.85	99.83	99.86	98.16
Lot3_P30-assembly	44	99.83	98.26	98.13	99.90	99.80	99.79	98.21
Lot3_P31-assembly	45	98.19	97.91	97.94	98.21	98.21	98.19	98.13
Lot3_P32-assembly	46	98.04	97.93	98.01	98.02	97.99	98.00	97.97
Lot3_P33-assembly	47	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lot3_P35-assembly	48	98.03	97.92	98.02	98.05	98.03	98.04	97.96
Lot3_P36-assembly	49	99.78	98.15	98.09	99.83	99.77	99.75	98.24
Lot3_P37-assembly	50	99.79	98.08	98.04	99.81	99.80	99.82	98.18
Lot3_P38-assembly	51	98.18	97.91	97.94	98.21	98.17	98.16	98.13
Lot3_P39-assembly	52	99.87	98.15	98.10	99.97	99.86	99.88	98.24
Lot3_P40-assembly	53	98.18	97.91	97.94	98.20	98.17	98.16	98.13
Lot3_P41-assembly	54	98.20	97.93	97.96	98.23	98.20	98.20	98.16
Lot3_P42-assembly	55	99.79	98.27	98.08	99.84	99.82	99.85	98.16
Lot3_P43-assembly	56	98.20	97.93	97.96	98.23	98.20	98.20	98.16
Lot3_P44-assembly	57	98.20	97.93	97.96	98.23	98.20	98.20	98.16
Lot3_P45-assembly	58	89.76	89.62	89.75	89.81	89.82	89.79	89.73
Lot3_P46-assembly	59	89.76	89.62	89.75	89.81	89.82	89.79	89.73
Lot3_SE-assembly	60	98.08	99.90	99.91	98.12	98.06	98.03	97.97
Lot4_P47-assembly	61	99.83	98.25	98.13	99.90	99.81	99.78	98.22
Lot4_P48-assembly	62	99.83	98.26	98.13	99.90	99.81	99.78	98.22
Lot4_P49-assembly	63	99.83	98.26	98.14	99.90	99.80	99.79	98.22
Lot4_P50-assembly	64	98.05	97.89	97.86	98.07	98.10	98.11	98.05
Lot4_P51-assembly	65	99.86	98.14	98.08	100.00	99.87	99.89	98.24
Lot4_P52-assembly	66	99.79	98.28	98.09	99.84	99.82	99.85	98.17
Lot4_P53-assembly	67	99.40	97.70	97.59	99.50	99.36	99.34	97.67
Lot4_P54-assembly	68	98.21	97.95	97.97	98.26	98.25	98.26	98.16
Lot4_P55-assembly	69	99.83	98.26	98.13	99.90	99.81	99.79	98.22



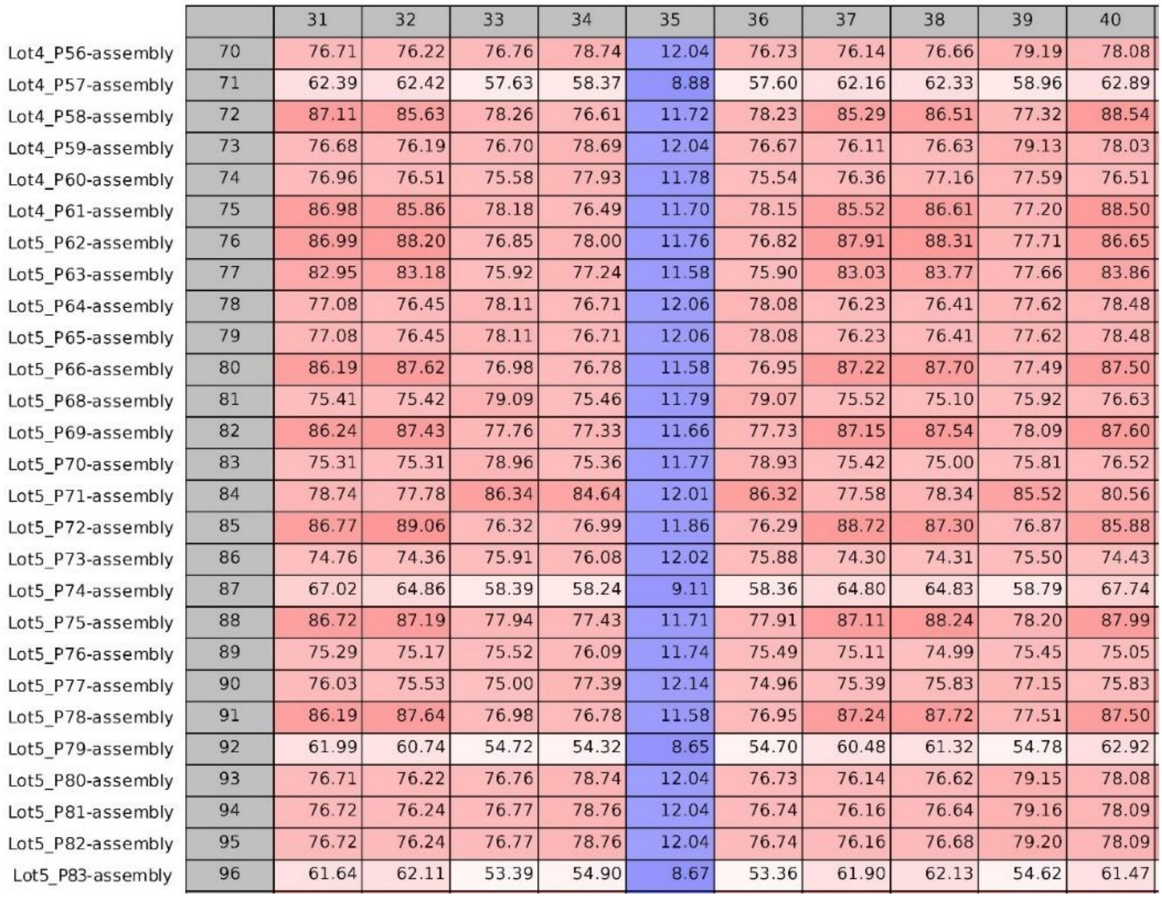
		1	2	3	4	5	6	7	8	9	10
Lot4_P56-assembly	70	78.19	79.36	74.82	77.09	74.50	78.39	76.22	76.61	77.36	76.77
Lot4_P57-assembly	71	62.70	59.67	60.27	63.27	61.14	58.05	65.02	57.07	57.48	62.71
Lot4_P58-assembly	72	77.13	77.61	82.35	85.11	84.04	77.11	84.06	75.90	76.58	88.07
Lot4_P59-assembly	73	78.16	79.30	74.78	77.06	74.46	78.33	76.20	76.57	77.32	76.74
Lot4_P60-assembly	74	91.07	80.07	75.97	77.36	75.43	78.30	76.29	77.12	78.27	77.24
Lot4_P61-assembly	75	77.05	77.51	82.48	85.05	84.12	77.00	84.04	75.79	76.47	87.95
Lot5_P62-assembly	76	78.38	78.86	83.09	85.85	85.66	78.01	84.59	76.48	77.55	87.82
Lot5_P63-assembly	77	76.97	77.50	80.39	82.89	81.95	77.00	84.56	75.10	76.15	82.68
Lot5_P64-assembly	78	77.65	78.83	75.82	76.78	75.16	77.24	75.33	76.29	76.17	77.61
Lot5_P65-assembly	79	77.65	78.83	75.82	76.78	75.16	77.23	75.33	76.29	76.17	77.61
Lot5_P66-assembly	80	77.21	77.48	82.46	84.47	85.69	76.56	83.35	75.37	76.41	86.35
Lot5_P68-assembly	81	75.60	77.24	74.15	73.85	73.47	75.19	73.45	74.01	74.47	75.55
Lot5_P69-assembly	82	77.72	78.19	82.37	85.12	84.94	77.34	83.87	75.83	76.88	87.08
Lot5_P70-assembly	83	75.50	77.14	74.02	73.73	73.34	75.08	73.35	73.88	74.36	75.44
Lot5_P71-assembly	84	78.48	79.74	78.09	77.09	76.34	87.53	76.03	82.11	83.34	78.98
Lot5_P72-assembly	85	77.14	78.33	82.66	85.63	84.47	76.96	84.67	75.61	76.26	87.39
Lot5_P73-assembly	86	74.88	76.18	73.86	76.23	72.82	75.87	74.43	74.58	75.09	75.22
Lot5_P74-assembly	87	58.25	59.12	62.29	64.67	63.99	58.10	63.88	57.00	57.36	67.23
Lot5_P75-assembly	88	77.79	77.96	82.42	84.83	84.53	77.20	84.06	75.69	76.75	86.91
Lot5_P76-assembly	89	75.40	76.58	74.17	76.68	73.35	75.89	74.74	74.59	75.20	75.48
Lot5_P77-assembly	90	78.43	79.10	74.66	76.96	74.10	78.40	75.74	76.68	77.09	76.26
Lot5_P78-assembly	91	77.21	77.48	82.47	84.48	85.70	76.57	83.35	75.37	76.41	86.35
Lot5_P79-assembly	92	54.75	55.67	58.16	60.86	59.47	54.74	59.70	54.06	54.36	62.82
Lot5_P80-assembly	93	78.18	79.35	74.82	77.05	74.46	78.39	76.18	76.57	77.32	76.77
Lot5_P81-assembly	94	78.18	79.37	74.84	77.07	74.48	78.41	76.20	76.59	77.34	76.78
Lot5_P82-assembly	95	78.20	79.37	74.84	77.11	74.54	78.41	76.24	76.63	77.38	76.78
Lot5_P83-assembly	96	55.24	56.21	58.17	61.02	59.96	54.88	59.86	54.05	54.63	62.38



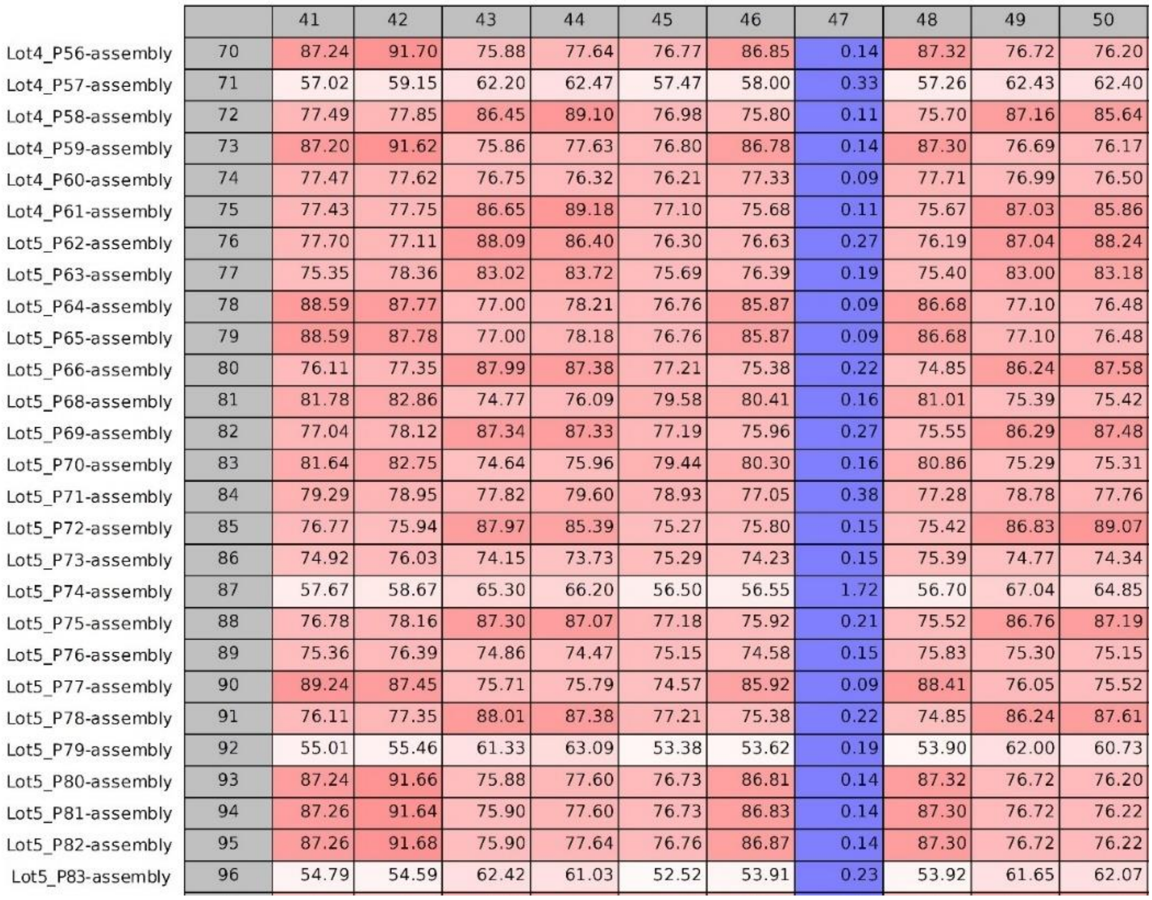
		11	12	13	14	15	16	17	18	19	20
Lot4_P56-assembly	70	77.01	77.19	76.14	75.83	75.20	76.77	75.80	76.72	75.83	76.73
Lot4_P57-assembly	71	62.74	62.95	58.80	62.13	56.19	62.74	56.78	57.71	61.91	57.72
Lot4_P58-assembly	72	87.17	86.66	75.67	86.58	73.77	88.11	75.95	75.07	86.53	75.02
Lot4_P59-assembly	73	76.97	77.15	76.11	75.81	75.15	76.74	75.84	76.70	75.81	76.70
Lot4_P60-assembly	74	76.19	76.06	76.18	76.76	75.37	77.20	76.90	77.89	76.54	77.84
Lot4_P61-assembly	75	87.32	86.63	75.55	86.81	73.69	87.98	76.08	75.01	86.71	74.96
Lot5_P62-assembly	76	87.27	86.83	76.84	88.23	74.59	87.87	76.98	76.18	88.27	76.19
Lot5_P63-assembly	77	84.42	83.06	76.49	83.16	73.25	82.60	74.77	74.97	83.25	74.99
Lot5_P64-assembly	78	77.44	77.65	74.57	77.00	74.60	77.65	75.73	75.38	76.80	75.33
Lot5_P65-assembly	79	77.45	77.65	74.57	77.00	74.60	77.65	75.73	75.38	76.80	75.33
Lot5_P66-assembly	80	88.52	87.09	75.48	88.09	73.42	86.40	76.46	74.77	87.93	74.77
Lot5_P68-assembly	81	75.86	76.22	76.89	74.76	73.41	75.58	78.54	77.68	74.65	77.71
Lot5_P69-assembly	82	88.16	87.68	76.17	87.48	73.96	87.13	76.30	75.50	87.53	75.50
Lot5_P70-assembly	83	75.75	76.11	76.78	74.63	73.31	75.48	78.41	77.53	74.52	77.56
Lot5_P71-assembly	84	79.21	78.84	76.66	77.82	74.84	78.97	77.93	77.42	77.85	77.39
Lot5_P72-assembly	85	86.10	85.85	76.01	88.10	74.47	87.52	75.95	75.15	87.34	75.13
Lot5_P73-assembly	86	73.58	73.51	76.87	74.13	74.65	75.06	75.91	76.92	74.11	76.93
Lot5_P74-assembly	87	66.11	65.20	56.81	65.38	56.37	67.11	56.04	55.85	64.61	55.79
Lot5_P75-assembly	88	87.81	87.27	76.32	87.44	73.79	86.95	76.37	75.66	87.15	75.67
Lot5_P76-assembly	89	74.25	74.08	76.50	74.83	75.11	75.55	75.75	76.77	74.67	76.78
Lot5_P77-assembly	90	74.75	75.09	75.05	75.69	75.05	76.34	75.09	76.61	75.61	76.57
Lot5_P78-assembly	91	88.54	87.10	75.48	88.12	73.42	86.40	76.46	74.77	87.96	74.77
Lot5_P79-assembly	92	61.68	61.28	53.10	61.38	53.07	62.88	52.87	52.56	61.19	52.50
Lot5_P80-assembly	93	76.97	77.15	76.11	75.83	75.20	76.73	75.76	76.68	75.79	76.69
Lot5_P81-assembly	94	76.97	77.15	76.11	75.85	75.22	76.74	75.76	76.70	75.81	76.70
Lot5_P82-assembly	95	77.01	77.19	76.15	75.85	75.22	76.77	75.79	76.73	75.85	76.74
Lot5_P83-assembly	96	61.20	60.81	53.60	62.42	53.36	62.44	53.18	52.93	62.07	52.90



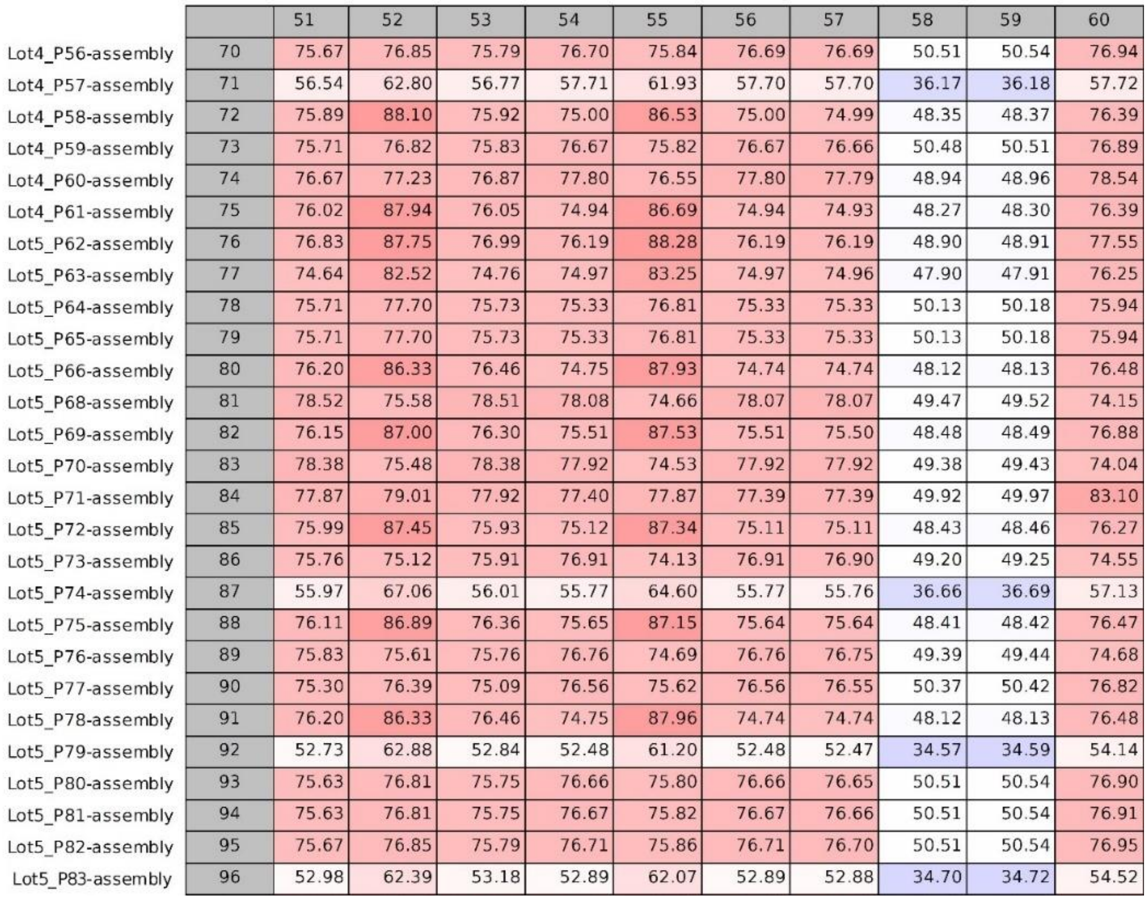
		21	22	23	24	25	26	27	28	29	30
Lot4_P56-assembly	70	76.73	50.55	50.53	76.91	77.66	76.76	75.71	86.83	0.14	87.32
Lot4_P57-assembly	71	57.72	36.18	36.16	57.68	62.49	57.45	56.56	58.00	0.33	57.28
Lot4_P58-assembly	72	75.02	48.36	48.33	76.35	89.13	77.01	75.92	75.76	0.11	75.71
Lot4_P59-assembly	73	76.70	50.51	50.49	76.85	77.66	76.80	75.75	86.76	0.14	87.30
Lot4_P60-assembly	74	77.82	48.96	48.94	78.50	76.35	76.23	76.74	77.37	0.09	77.71
Lot4_P61-assembly	75	74.96	48.28	48.25	76.35	89.15	77.13	76.05	75.64	0.11	75.69
Lot5_P62-assembly	76	76.21	48.91	48.88	77.51	86.44	76.34	76.85	76.61	0.27	76.20
Lot5_P63-assembly	77	74.99	47.91	47.88	76.22	83.75	75.72	74.65	76.37	0.19	75.40
Lot5_P64-assembly	78	75.36	50.17	50.14	75.90	78.25	76.76	75.75	85.89	0.09	86.66
Lot5_P65-assembly	79	75.36	50.17	50.15	75.90	78.22	76.76	75.75	85.89	0.09	86.66
Lot5_P66-assembly	80	74.77	48.13	48.10	76.45	87.40	77.21	76.20	75.36	0.22	74.86
Lot5_P68-assembly	81	77.72	49.50	49.47	74.11	76.11	79.61	78.55	80.41	0.16	81.00
Lot5_P69-assembly	82	75.50	48.49	48.46	76.85	87.36	77.23	76.16	75.94	0.27	75.56
Lot5_P70-assembly	83	77.57	49.41	49.38	74.01	75.97	79.47	78.42	80.30	0.16	80.85
Lot5_P71-assembly	84	77.39	49.97	49.92	83.09	79.62	78.95	77.89	77.05	0.38	77.30
Lot5_P72-assembly	85	75.13	48.44	48.41	76.23	85.42	75.31	76.00	75.78	0.15	75.44
Lot5_P73-assembly	86	76.93	49.23	49.21	74.52	73.76	75.29	75.80	74.23	0.15	75.39
Lot5_P74-assembly	87	55.79	36.67	36.65	57.09	66.19	56.54	56.01	56.51	1.72	56.72
Lot5_P75-assembly	88	75.66	48.42	48.39	76.43	87.10	77.21	76.12	75.90	0.21	75.53
Lot5_P76-assembly	89	76.78	49.42	49.40	74.64	74.50	75.15	75.86	74.58	0.15	75.83
Lot5_P77-assembly	90	76.59	50.41	50.38	76.78	75.82	74.57	75.33	85.92	0.09	88.36
Lot5_P78-assembly	91	74.77	48.13	48.10	76.45	87.40	77.21	76.20	75.36	0.22	74.86
Lot5_P79-assembly	92	52.50	34.58	34.56	54.09	63.12	53.39	52.77	53.60	0.19	53.92
Lot5_P80-assembly	93	76.69	50.55	50.53	76.87	77.62	76.73	75.67	86.80	0.14	87.33
Lot5_P81-assembly	94	76.70	50.55	50.53	76.88	77.63	76.72	75.67	86.82	0.14	87.31
Lot5_P82-assembly	95	76.74	50.55	50.53	76.92	77.67	76.76	75.70	86.86	0.14	87.31
Lot5_P83-assembly	96	52.90	34.71	34.69	54.47	61.08	52.54	53.01	53.89	0.23	53.94



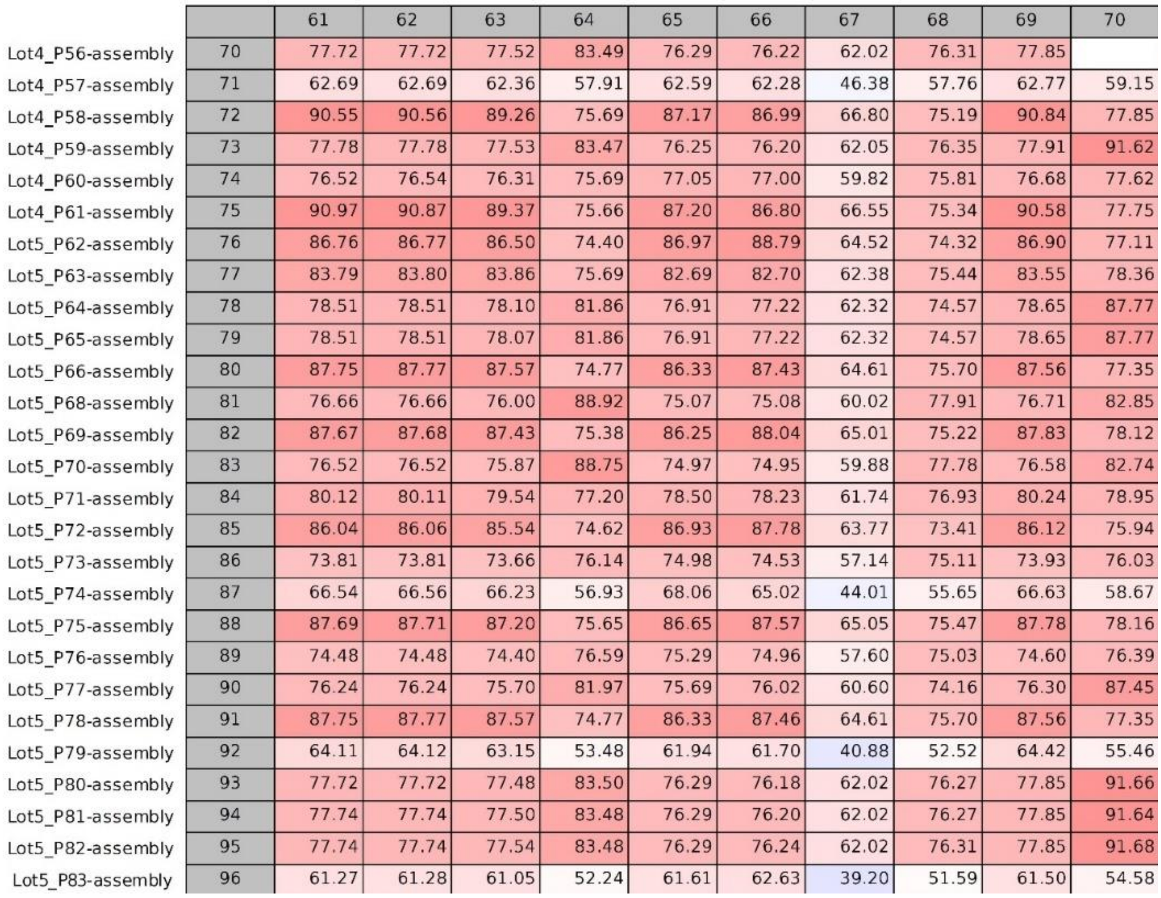
		31	32	33	34	35	36	37	38	39	40
Lot4_P56-assembly	70	76.71	76.22	76.76	78.74	12.04	76.73	76.14	76.66	79.19	78.08
Lot4_P57-assembly	71	62.39	62.42	57.63	58.37	8.88	57.60	62.16	62.33	58.96	62.89
Lot4_P58-assembly	72	87.11	85.63	78.26	76.61	11.72	78.23	85.29	86.51	77.32	88.54
Lot4_P59-assembly	73	76.68	76.19	76.70	78.69	12.04	76.67	76.11	76.63	79.13	78.03
Lot4_P60-assembly	74	76.96	76.51	75.58	77.93	11.78	75.54	76.36	77.16	77.59	76.51
Lot4_P61-assembly	75	86.98	85.86	78.18	76.49	11.70	78.15	85.52	86.61	77.20	88.50
Lot5_P62-assembly	76	86.99	88.20	76.85	78.00	11.76	76.82	87.91	88.31	77.71	86.65
Lot5_P63-assembly	77	82.95	83.18	75.92	77.24	11.58	75.90	83.03	83.77	77.66	83.86
Lot5_P64-assembly	78	77.08	76.45	78.11	76.71	12.06	78.08	76.23	76.41	77.62	78.48
Lot5_P65-assembly	79	77.08	76.45	78.11	76.71	12.06	78.08	76.23	76.41	77.62	78.48
Lot5_P66-assembly	80	86.19	87.62	76.98	76.78	11.58	76.95	87.22	87.70	77.49	87.50
Lot5_P68-assembly	81	75.41	75.42	79.09	75.46	11.79	79.07	75.52	75.10	75.92	76.63
Lot5_P69-assembly	82	86.24	87.43	77.76	77.33	11.66	77.73	87.15	87.54	78.09	87.60
Lot5_P70-assembly	83	75.31	75.31	78.96	75.36	11.77	78.93	75.42	75.00	75.81	76.52
Lot5_P71-assembly	84	78.74	77.78	86.34	84.64	12.01	86.32	77.58	78.34	85.52	80.56
Lot5_P72-assembly	85	86.77	89.06	76.32	76.99	11.86	76.29	88.72	87.30	76.87	85.88
Lot5_P73-assembly	86	74.76	74.36	75.91	76.08	12.02	75.88	74.30	74.31	75.50	74.43
Lot5_P74-assembly	87	67.02	64.86	58.39	58.24	9.11	58.36	64.80	64.83	58.79	67.74
Lot5_P75-assembly	88	86.72	87.19	77.94	77.43	11.71	77.91	87.11	88.24	78.20	87.99
Lot5_P76-assembly	89	75.29	75.17	75.52	76.09	11.74	75.49	75.11	74.99	75.45	75.05
Lot5_P77-assembly	90	76.03	75.53	75.00	77.39	12.14	74.96	75.39	75.83	77.15	75.83
Lot5_P78-assembly	91	86.19	87.64	76.98	76.78	11.58	76.95	87.24	87.72	77.51	87.50
Lot5_P79-assembly	92	61.99	60.74	54.72	54.32	8.65	54.70	60.48	61.32	54.78	62.92
Lot5_P80-assembly	93	76.71	76.22	76.76	78.74	12.04	76.73	76.14	76.62	79.15	78.08
Lot5_P81-assembly	94	76.72	76.24	76.77	78.76	12.04	76.74	76.16	76.64	79.16	78.09
Lot5_P82-assembly	95	76.72	76.24	76.77	78.76	12.04	76.74	76.16	76.68	79.20	78.09
Lot5_P83-assembly	96	61.64	62.11	53.39	54.90	8.67	53.36	61.90	62.13	54.62	61.47



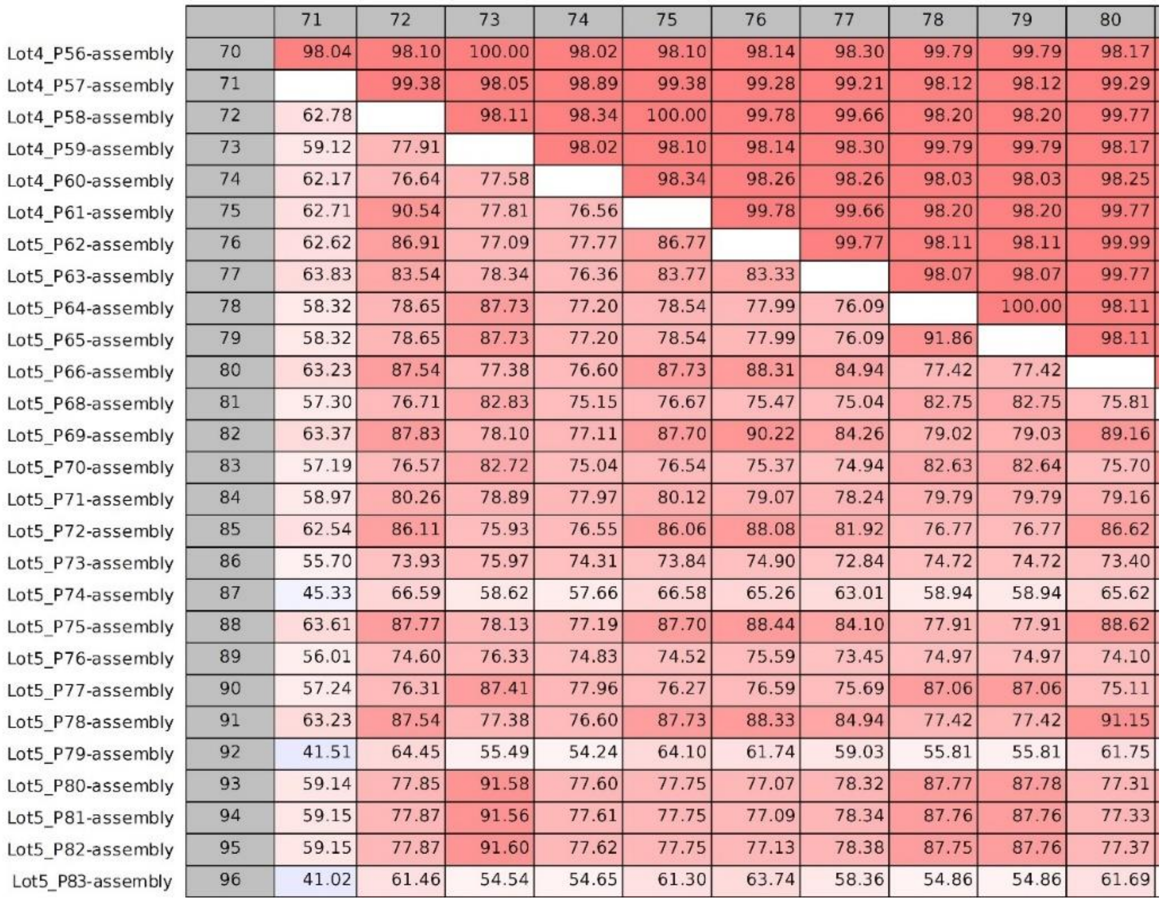
		41	42	43	44	45	46	47	48	49	50
Lot4_P56-assembly	70	87.24	91.70	75.88	77.64	76.77	86.85	0.14	87.32	76.72	76.20
Lot4_P57-assembly	71	57.02	59.15	62.20	62.47	57.47	58.00	0.33	57.26	62.43	62.40
Lot4_P58-assembly	72	77.49	77.85	86.45	89.10	76.98	75.80	0.11	75.70	87.16	85.64
Lot4_P59-assembly	73	87.20	91.62	75.86	77.63	76.80	86.78	0.14	87.30	76.69	76.17
Lot4_P60-assembly	74	77.47	77.62	76.75	76.32	76.21	77.33	0.09	77.71	76.99	76.50
Lot4_P61-assembly	75	77.43	77.75	86.65	89.18	77.10	75.68	0.11	75.67	87.03	85.86
Lot5_P62-assembly	76	77.70	77.11	88.09	86.40	76.30	76.63	0.27	76.19	87.04	88.24
Lot5_P63-assembly	77	75.35	78.36	83.02	83.72	75.69	76.39	0.19	75.40	83.00	83.18
Lot5_P64-assembly	78	88.59	87.77	77.00	78.21	76.76	85.87	0.09	86.68	77.10	76.48
Lot5_P65-assembly	79	88.59	87.78	77.00	78.18	76.76	85.87	0.09	86.68	77.10	76.48
Lot5_P66-assembly	80	76.11	77.35	87.99	87.38	77.21	75.38	0.22	74.85	86.24	87.58
Lot5_P68-assembly	81	81.78	82.86	74.77	76.09	79.58	80.41	0.16	81.01	75.39	75.42
Lot5_P69-assembly	82	77.04	78.12	87.34	87.33	77.19	75.96	0.27	75.55	86.29	87.48
Lot5_P70-assembly	83	81.64	82.75	74.64	75.96	79.44	80.30	0.16	80.86	75.29	75.31
Lot5_P71-assembly	84	79.29	78.95	77.82	79.60	78.93	77.05	0.38	77.28	78.78	77.76
Lot5_P72-assembly	85	76.77	75.94	87.97	85.39	75.27	75.80	0.15	75.42	86.83	89.07
Lot5_P73-assembly	86	74.92	76.03	74.15	73.73	75.29	74.23	0.15	75.39	74.77	74.34
Lot5_P74-assembly	87	57.67	58.67	65.30	66.20	56.50	56.55	1.72	56.70	67.04	64.85
Lot5_P75-assembly	88	76.78	78.16	87.30	87.07	77.18	75.92	0.21	75.52	86.76	87.19
Lot5_P76-assembly	89	75.36	76.39	74.86	74.47	75.15	74.58	0.15	75.83	75.30	75.15
Lot5_P77-assembly	90	89.24	87.45	75.71	75.79	74.57	85.92	0.09	88.41	76.05	75.52
Lot5_P78-assembly	91	76.11	77.35	88.01	87.38	77.21	75.38	0.22	74.85	86.24	87.61
Lot5_P79-assembly	92	55.01	55.46	61.33	63.09	53.38	53.62	0.19	53.90	62.00	60.73
Lot5_P80-assembly	93	87.24	91.66	75.88	77.60	76.73	86.81	0.14	87.32	76.72	76.20
Lot5_P81-assembly	94	87.26	91.64	75.90	77.60	76.73	86.83	0.14	87.30	76.72	76.22
Lot5_P82-assembly	95	87.26	91.68	75.90	77.64	76.76	86.87	0.14	87.30	76.72	76.22
Lot5_P83-assembly	96	54.79	54.59	62.42	61.03	52.52	53.91	0.23	53.92	61.65	62.07



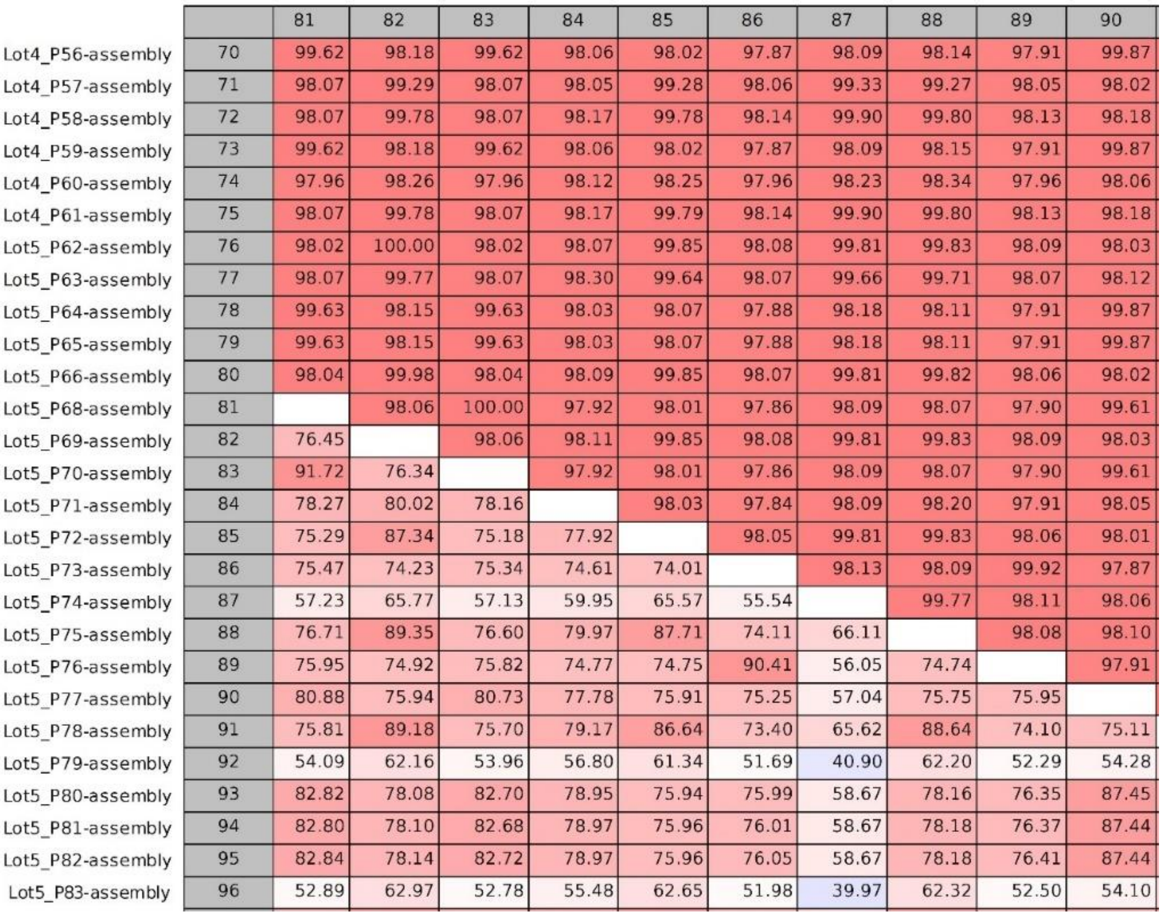
		51	52	53	54	55	56	57	58	59	60
Lot4_P56-assembly	70	75.67	76.85	75.79	76.70	75.84	76.69	76.69	50.51	50.54	76.94
Lot4_P57-assembly	71	56.54	62.80	56.77	57.71	61.93	57.70	57.70	36.17	36.18	57.72
Lot4_P58-assembly	72	75.89	88.10	75.92	75.00	86.53	75.00	74.99	48.35	48.37	76.39
Lot4_P59-assembly	73	75.71	76.82	75.83	76.67	75.82	76.67	76.66	50.48	50.51	76.89
Lot4_P60-assembly	74	76.67	77.23	76.87	77.80	76.55	77.80	77.79	48.94	48.96	78.54
Lot4_P61-assembly	75	76.02	87.94	76.05	74.94	86.69	74.94	74.93	48.27	48.30	76.39
Lot5_P62-assembly	76	76.83	87.75	76.99	76.19	88.28	76.19	76.19	48.90	48.91	77.55
Lot5_P63-assembly	77	74.64	82.52	74.76	74.97	83.25	74.97	74.96	47.90	47.91	76.25
Lot5_P64-assembly	78	75.71	77.70	75.73	75.33	76.81	75.33	75.33	50.13	50.18	75.94
Lot5_P65-assembly	79	75.71	77.70	75.73	75.33	76.81	75.33	75.33	50.13	50.18	75.94
Lot5_P66-assembly	80	76.20	86.33	76.46	74.75	87.93	74.74	74.74	48.12	48.13	76.48
Lot5_P68-assembly	81	78.52	75.58	78.51	78.08	74.66	78.07	78.07	49.47	49.52	74.15
Lot5_P69-assembly	82	76.15	87.00	76.30	75.51	87.53	75.51	75.50	48.48	48.49	76.88
Lot5_P70-assembly	83	78.38	75.48	78.38	77.92	74.53	77.92	77.92	49.38	49.43	74.04
Lot5_P71-assembly	84	77.87	79.01	77.92	77.40	77.87	77.39	77.39	49.92	49.97	83.10
Lot5_P72-assembly	85	75.99	87.45	75.93	75.12	87.34	75.11	75.11	48.43	48.46	76.27
Lot5_P73-assembly	86	75.76	75.12	75.91	76.91	74.13	76.91	76.90	49.20	49.25	74.55
Lot5_P74-assembly	87	55.97	67.06	56.01	55.77	64.60	55.77	55.76	36.66	36.69	57.13
Lot5_P75-assembly	88	76.11	86.89	76.36	75.65	87.15	75.64	75.64	48.41	48.42	76.47
Lot5_P76-assembly	89	75.83	75.61	75.76	76.76	74.69	76.76	76.75	49.39	49.44	74.68
Lot5_P77-assembly	90	75.30	76.39	75.09	76.56	75.62	76.56	76.55	50.37	50.42	76.82
Lot5_P78-assembly	91	76.20	86.33	76.46	74.75	87.96	74.74	74.74	48.12	48.13	76.48
Lot5_P79-assembly	92	52.73	62.88	52.84	52.48	61.20	52.48	52.47	34.57	34.59	54.14
Lot5_P80-assembly	93	75.63	76.81	75.75	76.66	75.80	76.66	76.65	50.51	50.54	76.90
Lot5_P81-assembly	94	75.63	76.81	75.75	76.67	75.82	76.67	76.66	50.51	50.54	76.91
Lot5_P82-assembly	95	75.67	76.85	75.79	76.71	75.86	76.71	76.70	50.51	50.54	76.95
Lot5_P83-assembly	96	52.98	62.39	53.18	52.89	62.07	52.89	52.88	34.70	34.72	54.52



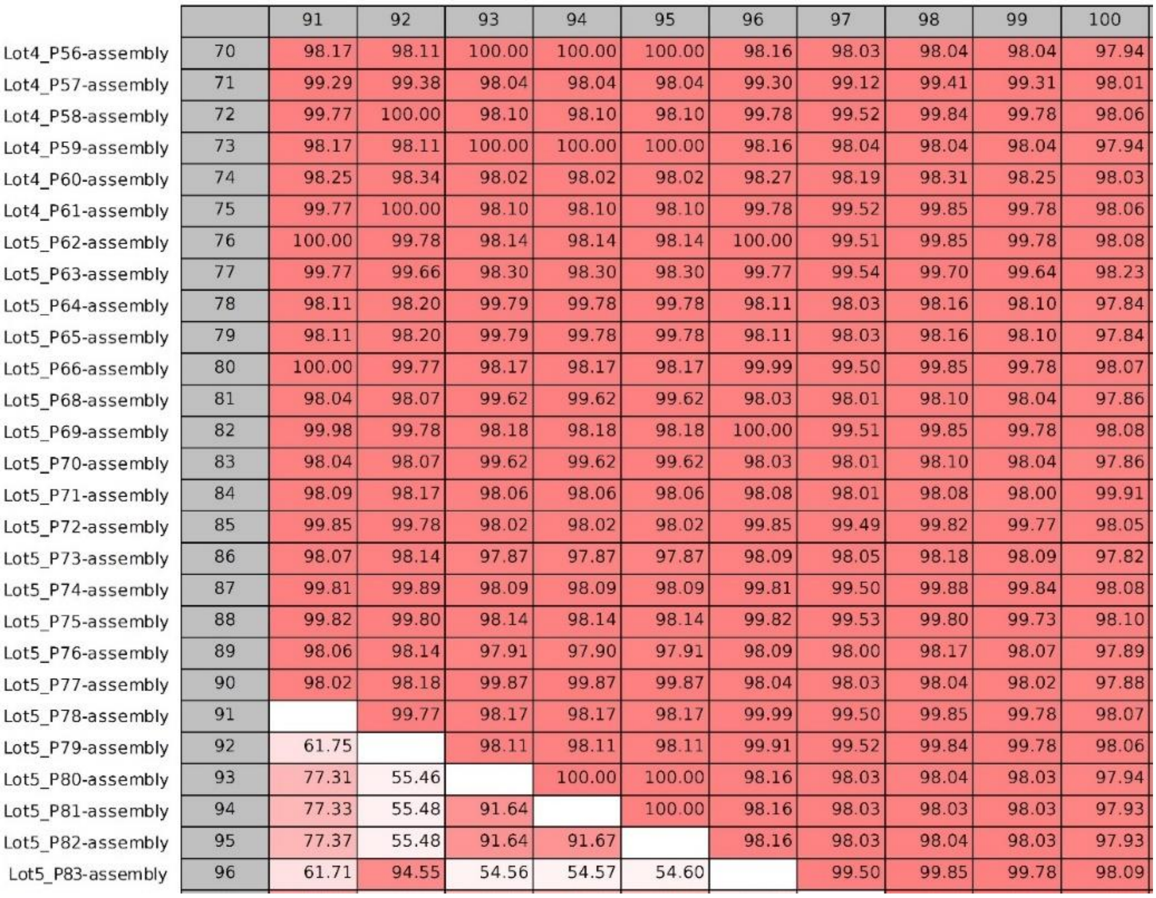
		61	62	63	64	65	66	67	68	69	70
Lot4_P56-assembly	70	77.72	77.72	77.52	83.49	76.29	76.22	62.02	76.31	77.85	
Lot4_P57-assembly	71	62.69	62.69	62.36	57.91	62.59	62.28	46.38	57.76	62.77	59.15
Lot4_P58-assembly	72	90.55	90.56	89.26	75.69	87.17	86.99	66.80	75.19	90.84	77.85
Lot4_P59-assembly	73	77.78	77.78	77.53	83.47	76.25	76.20	62.05	76.35	77.91	91.62
Lot4_P60-assembly	74	76.52	76.54	76.31	75.69	77.05	77.00	59.82	75.81	76.68	77.62
Lot4_P61-assembly	75	90.97	90.87	89.37	75.66	87.20	86.80	66.55	75.34	90.58	77.75
Lot5_P62-assembly	76	86.76	86.77	86.50	74.40	86.97	88.79	64.52	74.32	86.90	77.11
Lot5_P63-assembly	77	83.79	83.80	83.86	75.69	82.69	82.70	62.38	75.44	83.55	78.36
Lot5_P64-assembly	78	78.51	78.51	78.10	81.86	76.91	77.22	62.32	74.57	78.65	87.77
Lot5_P65-assembly	79	78.51	78.51	78.07	81.86	76.91	77.22	62.32	74.57	78.65	87.77
Lot5_P66-assembly	80	87.75	87.77	87.57	74.77	86.33	87.43	64.61	75.70	87.56	77.35
Lot5_P68-assembly	81	76.66	76.66	76.00	88.92	75.07	75.08	60.02	77.91	76.71	82.85
Lot5_P69-assembly	82	87.67	87.68	87.43	75.38	86.25	88.04	65.01	75.22	87.83	78.12
Lot5_P70-assembly	83	76.52	76.52	75.87	88.75	74.97	74.95	59.88	77.78	76.58	82.74
Lot5_P71-assembly	84	80.12	80.11	79.54	77.20	78.50	78.23	61.74	76.93	80.24	78.95
Lot5_P72-assembly	85	86.04	86.06	85.54	74.62	86.93	87.78	63.77	73.41	86.12	75.94
Lot5_P73-assembly	86	73.81	73.81	73.66	76.14	74.98	74.53	57.14	75.11	73.93	76.03
Lot5_P74-assembly	87	66.54	66.56	66.23	56.93	68.06	65.02	44.01	55.65	66.63	58.67
Lot5_P75-assembly	88	87.69	87.71	87.20	75.65	86.65	87.57	65.05	75.47	87.78	78.16
Lot5_P76-assembly	89	74.48	74.48	74.40	76.59	75.29	74.96	57.60	75.03	74.60	76.39
Lot5_P77-assembly	90	76.24	76.24	75.70	81.97	75.69	76.02	60.60	74.16	76.30	87.45
Lot5_P78-assembly	91	87.75	87.77	87.57	74.77	86.33	87.46	64.61	75.70	87.56	77.35
Lot5_P79-assembly	92	64.11	64.12	63.15	53.48	61.94	61.70	40.88	52.52	64.42	55.46
Lot5_P80-assembly	93	77.72	77.72	77.48	83.50	76.29	76.18	62.02	76.27	77.85	91.66
Lot5_P81-assembly	94	77.74	77.74	77.50	83.48	76.29	76.20	62.02	76.27	77.85	91.64
Lot5_P82-assembly	95	77.74	77.74	77.54	83.48	76.29	76.24	62.02	76.31	77.85	91.68
Lot5_P83-assembly	96	61.27	61.28	61.05	52.24	61.61	62.63	39.20	51.59	61.50	54.58



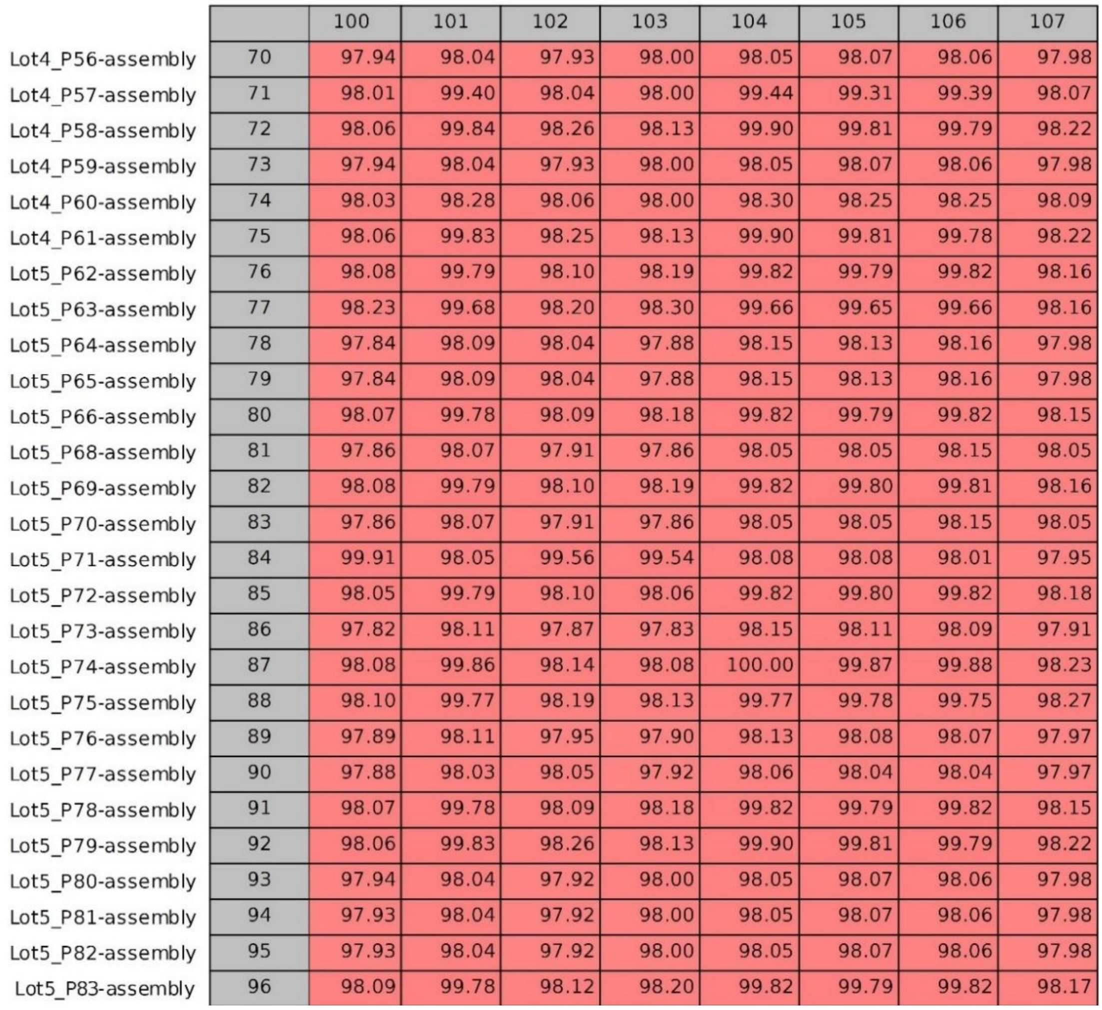
		71	72	73	74	75	76	77	78	79	80
Lot4_P56-assembly	70	98.04	98.10	100.00	98.02	98.10	98.14	98.30	99.79	99.79	98.17
Lot4_P57-assembly	71		99.38	98.05	98.89	99.38	99.28	99.21	98.12	98.12	99.29
Lot4_P58-assembly	72	62.78		98.11	98.34	100.00	99.78	99.66	98.20	98.20	99.77
Lot4_P59-assembly	73	59.12	77.91		98.02	98.10	98.14	98.30	99.79	99.79	98.17
Lot4_P60-assembly	74	62.17	76.64	77.58		98.34	98.26	98.26	98.03	98.03	98.25
Lot4_P61-assembly	75	62.71	90.54	77.81	76.56		99.78	99.66	98.20	98.20	99.77
Lot5_P62-assembly	76	62.62	86.91	77.09	77.77	86.77		99.77	98.11	98.11	99.99
Lot5_P63-assembly	77	63.83	83.54	78.34	76.36	83.77	83.33		98.07	98.07	99.77
Lot5_P64-assembly	78	58.32	78.65	87.73	77.20	78.54	77.99	76.09		100.00	98.11
Lot5_P65-assembly	79	58.32	78.65	87.73	77.20	78.54	77.99	76.09	91.86		98.11
Lot5_P66-assembly	80	63.23	87.54	77.38	76.60	87.73	88.31	84.94	77.42	77.42	
Lot5_P68-assembly	81	57.30	76.71	82.83	75.15	76.67	75.47	75.04	82.75	82.75	75.81
Lot5_P69-assembly	82	63.37	87.83	78.10	77.11	87.70	90.22	84.26	79.02	79.03	89.16
Lot5_P70-assembly	83	57.19	76.57	82.72	75.04	76.54	75.37	74.94	82.63	82.64	75.70
Lot5_P71-assembly	84	58.97	80.26	78.89	77.97	80.12	79.07	78.24	79.79	79.79	79.16
Lot5_P72-assembly	85	62.54	86.11	75.93	76.55	86.06	88.08	81.92	76.77	76.77	86.62
Lot5_P73-assembly	86	55.70	73.93	75.97	74.31	73.84	74.90	72.84	74.72	74.72	73.40
Lot5_P74-assembly	87	45.33	66.59	58.62	57.66	66.58	65.26	63.01	58.94	58.94	65.62
Lot5_P75-assembly	88	63.61	87.77	78.13	77.19	87.70	88.44	84.10	77.91	77.91	88.62
Lot5_P76-assembly	89	56.01	74.60	76.33	74.83	74.52	75.59	73.45	74.97	74.97	74.10
Lot5_P77-assembly	90	57.24	76.31	87.41	77.96	76.27	76.59	75.69	87.06	87.06	75.11
Lot5_P78-assembly	91	63.23	87.54	77.38	76.60	87.73	88.33	84.94	77.42	77.42	91.15
Lot5_P79-assembly	92	41.51	64.45	55.49	54.24	64.10	61.74	59.03	55.81	55.81	61.75
Lot5_P80-assembly	93	59.14	77.85	91.58	77.60	77.75	77.07	78.32	87.77	87.78	77.31
Lot5_P81-assembly	94	59.15	77.87	91.56	77.61	77.75	77.09	78.34	87.76	87.76	77.33
Lot5_P82-assembly	95	59.15	77.87	91.60	77.62	77.75	77.13	78.38	87.75	87.76	77.37
Lot5_P83-assembly	96	41.02	61.46	54.54	54.65	61.30	63.74	58.36	54.86	54.86	61.69



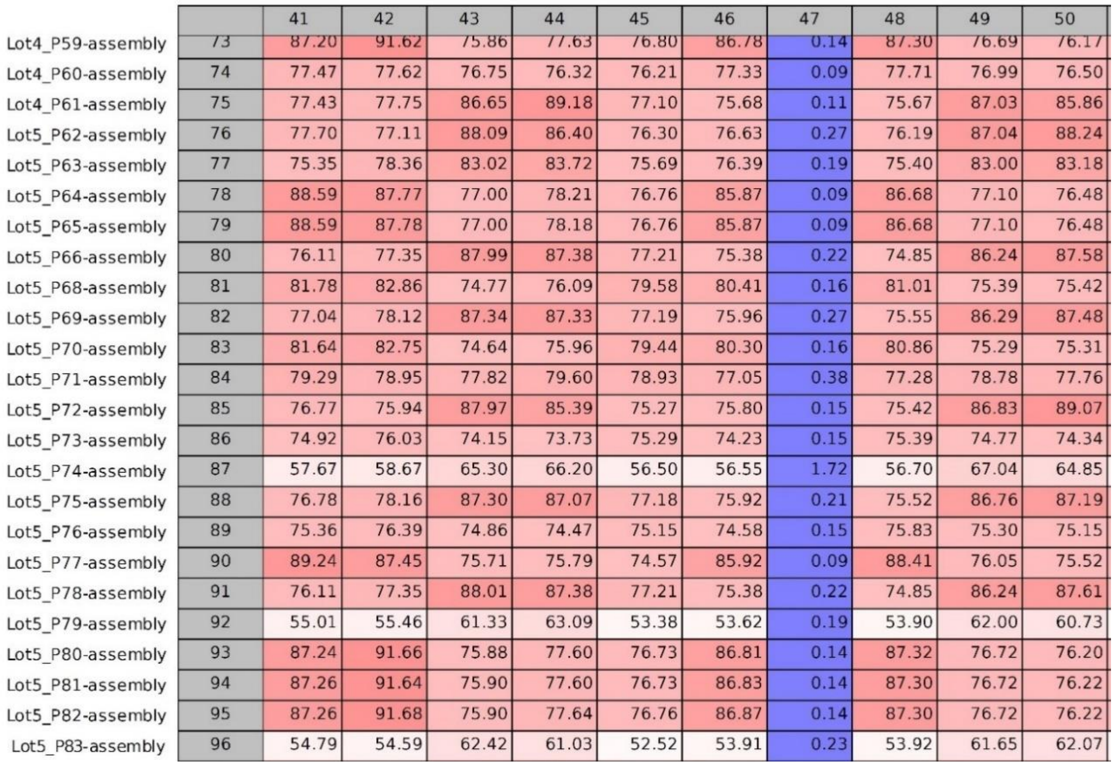
		81	82	83	84	85	86	87	88	89	90
Lot4_P56-assembly	70	99.62	98.18	99.62	98.06	98.02	97.87	98.09	98.14	97.91	99.87
Lot4_P57-assembly	71	98.07	99.29	98.07	98.05	99.28	98.06	99.33	99.27	98.05	98.02
Lot4_P58-assembly	72	98.07	99.78	98.07	98.17	99.78	98.14	99.90	99.80	98.13	98.18
Lot4_P59-assembly	73	99.62	98.18	99.62	98.06	98.02	97.87	98.09	98.15	97.91	99.87
Lot4_P60-assembly	74	97.96	98.26	97.96	98.12	98.25	97.96	98.23	98.34	97.96	98.06
Lot4_P61-assembly	75	98.07	99.78	98.07	98.17	99.79	98.14	99.90	99.80	98.13	98.18
Lot5_P62-assembly	76	98.02	100.00	98.02	98.07	99.85	98.08	99.81	99.83	98.09	98.03
Lot5_P63-assembly	77	98.07	99.77	98.07	98.30	99.64	98.07	99.66	99.71	98.07	98.12
Lot5_P64-assembly	78	99.63	98.15	99.63	98.03	98.07	97.88	98.18	98.11	97.91	99.87
Lot5_P65-assembly	79	99.63	98.15	99.63	98.03	98.07	97.88	98.18	98.11	97.91	99.87
Lot5_P66-assembly	80	98.04	99.98	98.04	98.09	99.85	98.07	99.81	99.82	98.06	98.02
Lot5_P68-assembly	81		98.06	100.00	97.92	98.01	97.86	98.09	98.07	97.90	99.61
Lot5_P69-assembly	82	76.45		98.06	98.11	99.85	98.08	99.81	99.83	98.09	98.03
Lot5_P70-assembly	83	91.72	76.34		97.92	98.01	97.86	98.09	98.07	97.90	99.61
Lot5_P71-assembly	84	78.27	80.02	78.16		98.03	97.84	98.09	98.20	97.91	98.05
Lot5_P72-assembly	85	75.29	87.34	75.18	77.92		98.05	99.81	99.83	98.06	98.01
Lot5_P73-assembly	86	75.47	74.23	75.34	74.61	74.01		98.13	98.09	99.92	97.87
Lot5_P74-assembly	87	57.23	65.77	57.13	59.95	65.57	55.54		99.77	98.11	98.06
Lot5_P75-assembly	88	76.71	89.35	76.60	79.97	87.71	74.11	66.11		98.08	98.10
Lot5_P76-assembly	89	75.95	74.92	75.82	74.77	74.75	90.41	56.05	74.74		97.91
Lot5_P77-assembly	90	80.88	75.94	80.73	77.78	75.91	75.25	57.04	75.75	75.95	
Lot5_P78-assembly	91	75.81	89.18	75.70	79.17	86.64	73.40	65.62	88.64	74.10	75.11
Lot5_P79-assembly	92	54.09	62.16	53.96	56.80	61.34	51.69	40.90	62.20	52.29	54.28
Lot5_P80-assembly	93	82.82	78.08	82.70	78.95	75.94	75.99	58.67	78.16	76.35	87.45
Lot5_P81-assembly	94	82.80	78.10	82.68	78.97	75.96	76.01	58.67	78.18	76.37	87.44
Lot5_P82-assembly	95	82.84	78.14	82.72	78.97	75.96	76.05	58.67	78.18	76.41	87.44
Lot5_P83-assembly	96	52.89	62.97	52.78	55.48	62.65	51.98	39.97	62.32	52.50	54.10



		91	92	93	94	95	96	97	98	99	100
Lot4_P56-assembly	70	98.17	98.11	100.00	100.00	100.00	98.16	98.03	98.04	98.04	97.94
Lot4_P57-assembly	71	99.29	99.38	98.04	98.04	98.04	99.30	99.12	99.41	99.31	98.01
Lot4_P58-assembly	72	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.84	99.78	98.06
Lot4_P59-assembly	73	98.17	98.11	100.00	100.00	100.00	98.16	98.04	98.04	98.04	97.94
Lot4_P60-assembly	74	98.25	98.34	98.02	98.02	98.02	98.27	98.19	98.31	98.25	98.03
Lot4_P61-assembly	75	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.85	99.78	98.06
Lot5_P62-assembly	76	100.00	99.78	98.14	98.14	98.14	100.00	99.51	99.85	99.78	98.08
Lot5_P63-assembly	77	99.77	99.66	98.30	98.30	98.30	99.77	99.54	99.70	99.64	98.23
Lot5_P64-assembly	78	98.11	98.20	99.79	99.78	99.78	98.11	98.03	98.16	98.10	97.84
Lot5_P65-assembly	79	98.11	98.20	99.79	99.78	99.78	98.11	98.03	98.16	98.10	97.84
Lot5_P66-assembly	80	100.00	99.77	98.17	98.17	98.17	99.99	99.50	99.85	99.78	98.07
Lot5_P68-assembly	81	98.04	98.07	99.62	99.62	99.62	98.03	98.01	98.10	98.04	97.86
Lot5_P69-assembly	82	99.98	99.78	98.18	98.18	98.18	100.00	99.51	99.85	99.78	98.08
Lot5_P70-assembly	83	98.04	98.07	99.62	99.62	99.62	98.03	98.01	98.10	98.04	97.86
Lot5_P71-assembly	84	98.09	98.17	98.06	98.06	98.06	98.08	98.01	98.08	98.00	99.91
Lot5_P72-assembly	85	99.85	99.78	98.02	98.02	98.02	99.85	99.49	99.82	99.77	98.05
Lot5_P73-assembly	86	98.07	98.14	97.87	97.87	97.87	98.09	98.05	98.18	98.09	97.82
Lot5_P74-assembly	87	99.81	99.89	98.09	98.09	98.09	99.81	99.50	99.88	99.84	98.08
Lot5_P75-assembly	88	99.82	99.80	98.14	98.14	98.14	99.82	99.53	99.80	99.73	98.10
Lot5_P76-assembly	89	98.06	98.14	97.91	97.90	97.91	98.09	98.00	98.17	98.07	97.89
Lot5_P77-assembly	90	98.02	98.18	99.87	99.87	99.87	98.04	98.03	98.04	98.02	97.88
Lot5_P78-assembly	91		99.77	98.17	98.17	98.17	99.99	99.50	99.85	99.78	98.07
Lot5_P79-assembly	92	61.75		98.11	98.11	98.11	99.91	99.52	99.84	99.78	98.06
Lot5_P80-assembly	93	77.31	55.46		100.00	100.00	98.16	98.03	98.04	98.03	97.94
Lot5_P81-assembly	94	77.33	55.48	91.64		100.00	98.16	98.03	98.03	98.03	97.93
Lot5_P82-assembly	95	77.37	55.48	91.64	91.67		98.16	98.03	98.04	98.03	97.93
Lot5_P83-assembly	96	61.71	94.55	54.56	54.57	54.60		99.50	99.85	99.78	98.09

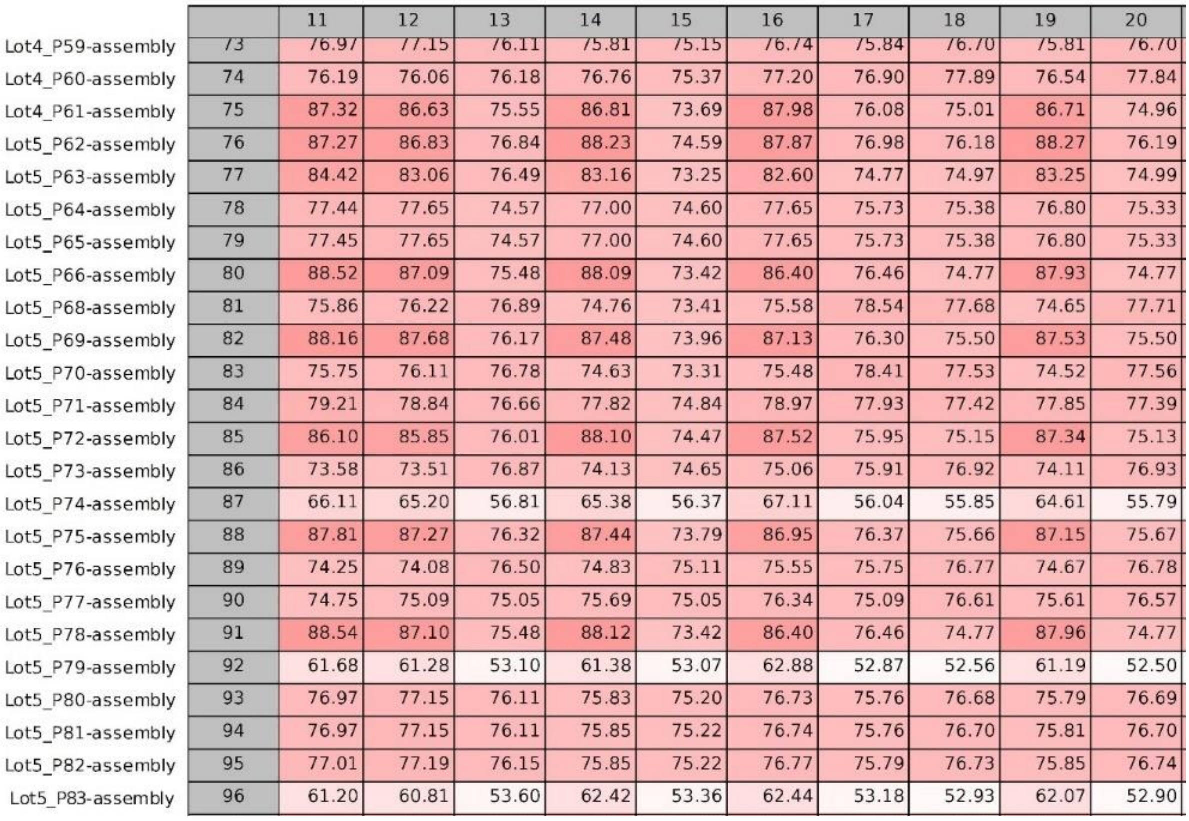


		100	101	102	103	104	105	106	107
Lot4_P56-assembly	70	97.94	98.04	97.93	98.00	98.05	98.07	98.06	97.98
Lot4_P57-assembly	71	98.01	99.40	98.04	98.00	99.44	99.31	99.39	98.07
Lot4_P58-assembly	72	98.06	99.84	98.26	98.13	99.90	99.81	99.79	98.22
Lot4_P59-assembly	73	97.94	98.04	97.93	98.00	98.05	98.07	98.06	97.98
Lot4_P60-assembly	74	98.03	98.28	98.06	98.00	98.30	98.25	98.25	98.09
Lot4_P61-assembly	75	98.06	99.83	98.25	98.13	99.90	99.81	99.78	98.22
Lot5_P62-assembly	76	98.08	99.79	98.10	98.19	99.82	99.79	99.82	98.16
Lot5_P63-assembly	77	98.23	99.68	98.20	98.30	99.66	99.65	99.66	98.16
Lot5_P64-assembly	78	97.84	98.09	98.04	97.88	98.15	98.13	98.16	97.98
Lot5_P65-assembly	79	97.84	98.09	98.04	97.88	98.15	98.13	98.16	97.98
Lot5_P66-assembly	80	98.07	99.78	98.09	98.18	99.82	99.79	99.82	98.15
Lot5_P68-assembly	81	97.86	98.07	97.91	97.86	98.05	98.05	98.15	98.05
Lot5_P69-assembly	82	98.08	99.79	98.10	98.19	99.82	99.80	99.81	98.16
Lot5_P70-assembly	83	97.86	98.07	97.91	97.86	98.05	98.05	98.15	98.05
Lot5_P71-assembly	84	99.91	98.05	99.56	99.54	98.08	98.08	98.01	97.95
Lot5_P72-assembly	85	98.05	99.79	98.10	98.06	99.82	99.80	99.82	98.18
Lot5_P73-assembly	86	97.82	98.11	97.87	97.83	98.15	98.11	98.09	97.91
Lot5_P74-assembly	87	98.08	99.86	98.14	98.08	100.00	99.87	99.88	98.23
Lot5_P75-assembly	88	98.10	99.77	98.19	98.13	99.77	99.78	99.75	98.27
Lot5_P76-assembly	89	97.89	98.11	97.95	97.90	98.13	98.08	98.07	97.97
Lot5_P77-assembly	90	97.88	98.03	98.05	97.92	98.06	98.04	98.04	97.97
Lot5_P78-assembly	91	98.07	99.78	98.09	98.18	99.82	99.79	99.82	98.15
Lot5_P79-assembly	92	98.06	99.83	98.26	98.13	99.90	99.81	99.79	98.22
Lot5_P80-assembly	93	97.94	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P81-assembly	94	97.93	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P82-assembly	95	97.93	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P83-assembly	96	98.09	99.78	98.12	98.20	99.82	99.79	99.82	98.17

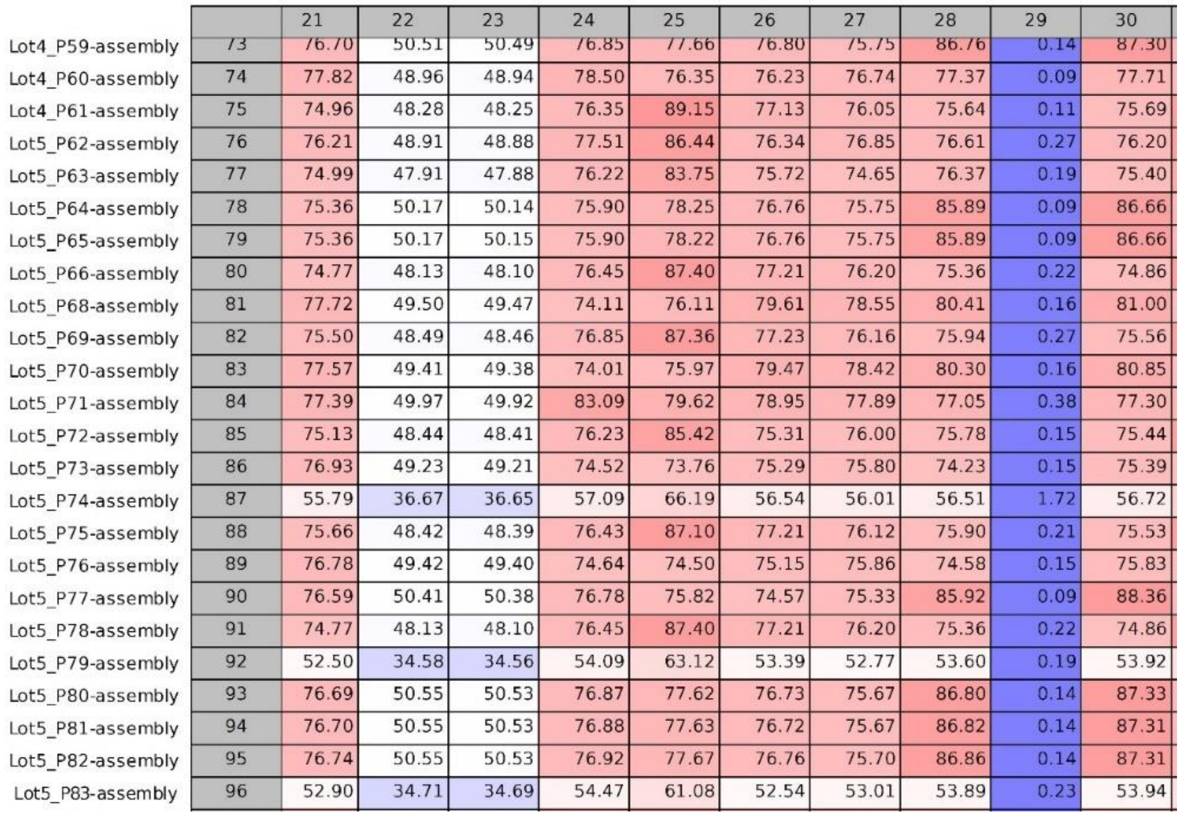


		41	42	43	44	45	46	47	48	49	50
Lot4_P59-assembly	73	87.20	91.62	75.86	77.63	76.80	86.78	0.14	87.30	76.69	76.17
Lot4_P60-assembly	74	77.47	77.62	76.75	76.32	76.21	77.33	0.09	77.71	76.99	76.50
Lot4_P61-assembly	75	77.43	77.75	86.65	89.18	77.10	75.68	0.11	75.67	87.03	85.86
Lot5_P62-assembly	76	77.70	77.11	88.09	86.40	76.30	76.63	0.27	76.19	87.04	88.24
Lot5_P63-assembly	77	75.35	78.36	83.02	83.72	75.69	76.39	0.19	75.40	83.00	83.18
Lot5_P64-assembly	78	88.59	87.77	77.00	78.21	76.76	85.87	0.09	86.68	77.10	76.48
Lot5_P65-assembly	79	88.59	87.78	77.00	78.18	76.76	85.87	0.09	86.68	77.10	76.48
Lot5_P66-assembly	80	76.11	77.35	87.99	87.38	77.21	75.38	0.22	74.85	86.24	87.58
Lot5_P68-assembly	81	81.78	82.86	74.77	76.09	79.58	80.41	0.16	81.01	75.39	75.42
Lot5_P69-assembly	82	77.04	78.12	87.34	87.33	77.19	75.96	0.27	75.55	86.29	87.48
Lot5_P70-assembly	83	81.64	82.75	74.64	75.96	79.44	80.30	0.16	80.86	75.29	75.31
Lot5_P71-assembly	84	79.29	78.95	77.82	79.60	78.93	77.05	0.38	77.28	78.78	77.76
Lot5_P72-assembly	85	76.77	75.94	87.97	85.39	75.27	75.80	0.15	75.42	86.83	89.07
Lot5_P73-assembly	86	74.92	76.03	74.15	73.73	75.29	74.23	0.15	75.39	74.77	74.34
Lot5_P74-assembly	87	57.67	58.67	65.30	66.20	56.50	56.55	1.72	56.70	67.04	64.85
Lot5_P75-assembly	88	76.78	78.16	87.30	87.07	77.18	75.92	0.21	75.52	86.76	87.19
Lot5_P76-assembly	89	75.36	76.39	74.86	74.47	75.15	74.58	0.15	75.83	75.30	75.15
Lot5_P77-assembly	90	89.24	87.45	75.71	75.79	74.57	85.92	0.09	88.41	76.05	75.52
Lot5_P78-assembly	91	76.11	77.35	88.01	87.38	77.21	75.38	0.22	74.85	86.24	87.61
Lot5_P79-assembly	92	55.01	55.46	61.33	63.09	53.38	53.62	0.19	53.90	62.00	60.73
Lot5_P80-assembly	93	87.24	91.66	75.88	77.60	76.73	86.81	0.14	87.32	76.72	76.20
Lot5_P81-assembly	94	87.26	91.64	75.90	77.60	76.73	86.83	0.14	87.30	76.72	76.22
Lot5_P82-assembly	95	87.26	91.68	75.90	77.64	76.76	86.87	0.14	87.30	76.72	76.22
Lot5_P83-assembly	96	54.79	54.59	62.42	61.03	52.52	53.91	0.23	53.92	61.65	62.07

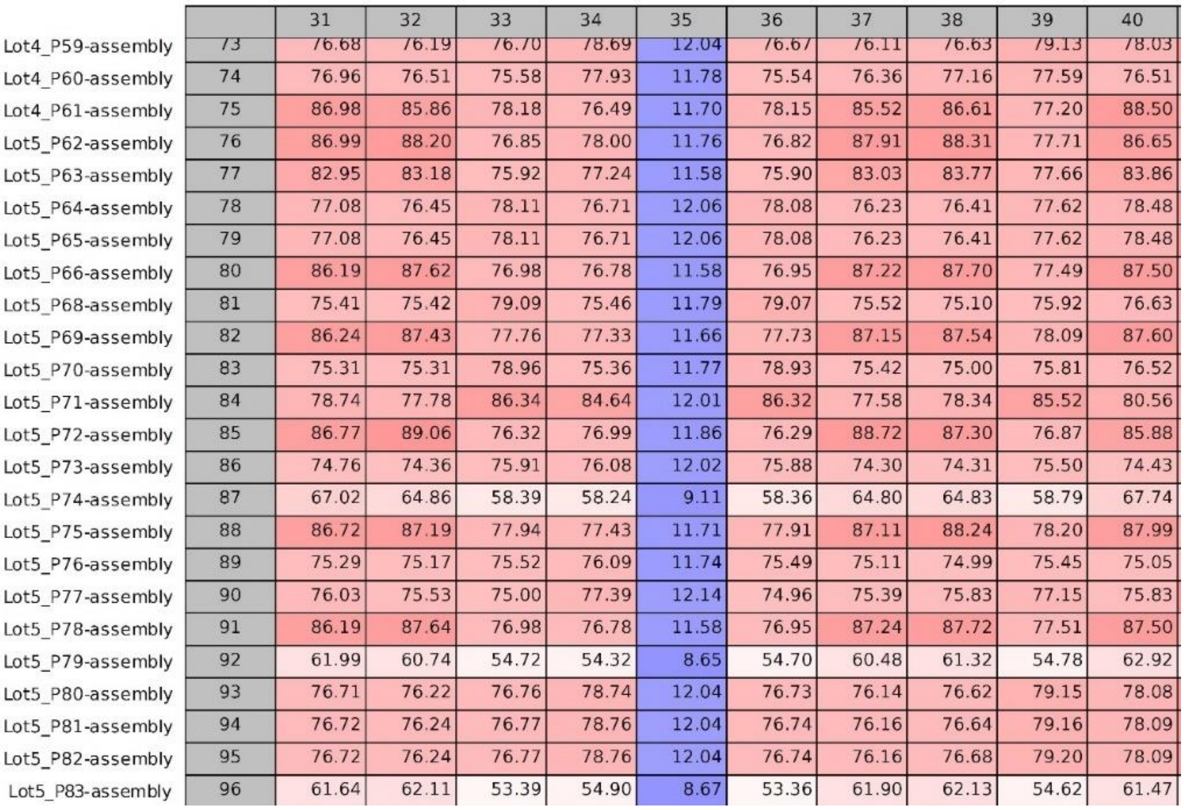
		1	2	3	4	5	6	7	8	9	10
Lot4_P59-assembly	73	78.16	79.30	74.78	77.06	74.46	78.33	76.20	76.57	77.32	76.74
Lot4_P60-assembly	74	91.07	80.07	75.97	77.36	75.43	78.30	76.29	77.12	78.27	77.24
Lot4_P61-assembly	75	77.05	77.51	82.48	85.05	84.12	77.00	84.04	75.79	76.47	87.95
Lot5_P62-assembly	76	78.38	78.86	83.09	85.85	85.66	78.01	84.59	76.48	77.55	87.82
Lot5_P63-assembly	77	76.97	77.50	80.39	82.89	81.95	77.00	84.56	75.10	76.15	82.68
Lot5_P64-assembly	78	77.65	78.83	75.82	76.78	75.16	77.24	75.33	76.29	76.17	77.61
Lot5_P65-assembly	79	77.65	78.83	75.82	76.78	75.16	77.23	75.33	76.29	76.17	77.61
Lot5_P66-assembly	80	77.21	77.48	82.46	84.47	85.69	76.56	83.35	75.37	76.41	86.35
Lot5_P68-assembly	81	75.60	77.24	74.15	73.85	73.47	75.19	73.45	74.01	74.47	75.55
Lot5_P69-assembly	82	77.72	78.19	82.37	85.12	84.94	77.34	83.87	75.83	76.88	87.08
Lot5_P70-assembly	83	75.50	77.14	74.02	73.73	73.34	75.08	73.35	73.88	74.36	75.44
Lot5_P71-assembly	84	78.48	79.74	78.09	77.09	76.34	87.53	76.03	82.11	83.34	78.98
Lot5_P72-assembly	85	77.14	78.33	82.66	85.63	84.47	76.96	84.67	75.61	76.26	87.39
Lot5_P73-assembly	86	74.88	76.18	73.86	76.23	72.82	75.87	74.43	74.58	75.09	75.22
Lot5_P74-assembly	87	58.25	59.12	62.29	64.67	63.99	58.10	63.88	57.00	57.36	67.23
Lot5_P75-assembly	88	77.79	77.96	82.42	84.83	84.53	77.20	84.06	75.69	76.75	86.91
Lot5_P76-assembly	89	75.40	76.58	74.17	76.68	73.35	75.89	74.74	74.59	75.20	75.48
Lot5_P77-assembly	90	78.43	79.10	74.66	76.96	74.10	78.40	75.74	76.68	77.09	76.26
Lot5_P78-assembly	91	77.21	77.48	82.47	84.48	85.70	76.57	83.35	75.37	76.41	86.35
Lot5_P79-assembly	92	54.75	55.67	58.16	60.86	59.47	54.74	59.70	54.06	54.36	62.82
Lot5_P80-assembly	93	78.18	79.35	74.82	77.05	74.46	78.39	76.18	76.57	77.32	76.77
Lot5_P81-assembly	94	78.18	79.37	74.84	77.07	74.48	78.41	76.20	76.59	77.34	76.78
Lot5_P82-assembly	95	78.20	79.37	74.84	77.11	74.54	78.41	76.24	76.63	77.38	76.78
Lot5_P83-assembly	96	55.24	56.21	58.17	61.02	59.96	54.88	59.86	54.05	54.63	62.38



		11	12	13	14	15	16	17	18	19	20
Lot4_P59-assembly	73	76.97	77.15	76.11	75.81	75.15	76.74	75.84	76.70	75.81	76.70
Lot4_P60-assembly	74	76.19	76.06	76.18	76.76	75.37	77.20	76.90	77.89	76.54	77.84
Lot4_P61-assembly	75	87.32	86.63	75.55	86.81	73.69	87.98	76.08	75.01	86.71	74.96
Lot5_P62-assembly	76	87.27	86.83	76.84	88.23	74.59	87.87	76.98	76.18	88.27	76.19
Lot5_P63-assembly	77	84.42	83.06	76.49	83.16	73.25	82.60	74.77	74.97	83.25	74.99
Lot5_P64-assembly	78	77.44	77.65	74.57	77.00	74.60	77.65	75.73	75.38	76.80	75.33
Lot5_P65-assembly	79	77.45	77.65	74.57	77.00	74.60	77.65	75.73	75.38	76.80	75.33
Lot5_P66-assembly	80	88.52	87.09	75.48	88.09	73.42	86.40	76.46	74.77	87.93	74.77
Lot5_P68-assembly	81	75.86	76.22	76.89	74.76	73.41	75.58	78.54	77.68	74.65	77.71
Lot5_P69-assembly	82	88.16	87.68	76.17	87.48	73.96	87.13	76.30	75.50	87.53	75.50
Lot5_P70-assembly	83	75.75	76.11	76.78	74.63	73.31	75.48	78.41	77.53	74.52	77.56
Lot5_P71-assembly	84	79.21	78.84	76.66	77.82	74.84	78.97	77.93	77.42	77.85	77.39
Lot5_P72-assembly	85	86.10	85.85	76.01	88.10	74.47	87.52	75.95	75.15	87.34	75.13
Lot5_P73-assembly	86	73.58	73.51	76.87	74.13	74.65	75.06	75.91	76.92	74.11	76.93
Lot5_P74-assembly	87	66.11	65.20	56.81	65.38	56.37	67.11	56.04	55.85	64.61	55.79
Lot5_P75-assembly	88	87.81	87.27	76.32	87.44	73.79	86.95	76.37	75.66	87.15	75.67
Lot5_P76-assembly	89	74.25	74.08	76.50	74.83	75.11	75.55	75.75	76.77	74.67	76.78
Lot5_P77-assembly	90	74.75	75.09	75.05	75.69	75.05	76.34	75.09	76.61	75.61	76.57
Lot5_P78-assembly	91	88.54	87.10	75.48	88.12	73.42	86.40	76.46	74.77	87.96	74.77
Lot5_P79-assembly	92	61.68	61.28	53.10	61.38	53.07	62.88	52.87	52.56	61.19	52.50
Lot5_P80-assembly	93	76.97	77.15	76.11	75.83	75.20	76.73	75.76	76.68	75.79	76.69
Lot5_P81-assembly	94	76.97	77.15	76.11	75.85	75.22	76.74	75.76	76.70	75.81	76.70
Lot5_P82-assembly	95	77.01	77.19	76.15	75.85	75.22	76.77	75.79	76.73	75.85	76.74
Lot5_P83-assembly	96	61.20	60.81	53.60	62.42	53.36	62.44	53.18	52.93	62.07	52.90

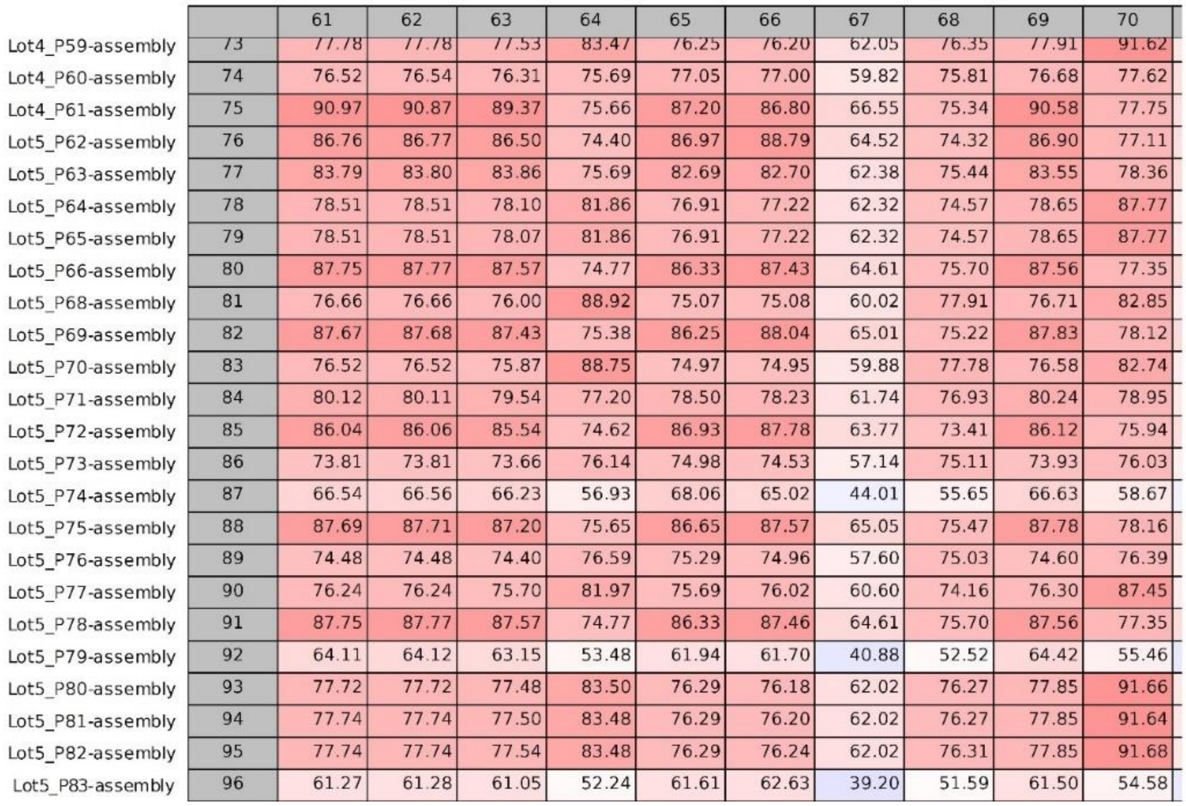


		21	22	23	24	25	26	27	28	29	30
Lot4_P59-assembly	73	76.70	50.51	50.49	76.85	77.66	76.80	75.75	86.76	0.14	87.30
Lot4_P60-assembly	74	77.82	48.96	48.94	78.50	76.35	76.23	76.74	77.37	0.09	77.71
Lot4_P61-assembly	75	74.96	48.28	48.25	76.35	89.15	77.13	76.05	75.64	0.11	75.69
Lot5_P62-assembly	76	76.21	48.91	48.88	77.51	86.44	76.34	76.85	76.61	0.27	76.20
Lot5_P63-assembly	77	74.99	47.91	47.88	76.22	83.75	75.72	74.65	76.37	0.19	75.40
Lot5_P64-assembly	78	75.36	50.17	50.14	75.90	78.25	76.76	75.75	85.89	0.09	86.66
Lot5_P65-assembly	79	75.36	50.17	50.15	75.90	78.22	76.76	75.75	85.89	0.09	86.66
Lot5_P66-assembly	80	74.77	48.13	48.10	76.45	87.40	77.21	76.20	75.36	0.22	74.86
Lot5_P68-assembly	81	77.72	49.50	49.47	74.11	76.11	79.61	78.55	80.41	0.16	81.00
Lot5_P69-assembly	82	75.50	48.49	48.46	76.85	87.36	77.23	76.16	75.94	0.27	75.56
Lot5_P70-assembly	83	77.57	49.41	49.38	74.01	75.97	79.47	78.42	80.30	0.16	80.85
Lot5_P71-assembly	84	77.39	49.97	49.92	83.09	79.62	78.95	77.89	77.05	0.38	77.30
Lot5_P72-assembly	85	75.13	48.44	48.41	76.23	85.42	75.31	76.00	75.78	0.15	75.44
Lot5_P73-assembly	86	76.93	49.23	49.21	74.52	73.76	75.29	75.80	74.23	0.15	75.39
Lot5_P74-assembly	87	55.79	36.67	36.65	57.09	66.19	56.54	56.01	56.51	1.72	56.72
Lot5_P75-assembly	88	75.66	48.42	48.39	76.43	87.10	77.21	76.12	75.90	0.21	75.53
Lot5_P76-assembly	89	76.78	49.42	49.40	74.64	74.50	75.15	75.86	74.58	0.15	75.83
Lot5_P77-assembly	90	76.59	50.41	50.38	76.78	75.82	74.57	75.33	85.92	0.09	88.36
Lot5_P78-assembly	91	74.77	48.13	48.10	76.45	87.40	77.21	76.20	75.36	0.22	74.86
Lot5_P79-assembly	92	52.50	34.58	34.56	54.09	63.12	53.39	52.77	53.60	0.19	53.92
Lot5_P80-assembly	93	76.69	50.55	50.53	76.87	77.62	76.73	75.67	86.80	0.14	87.33
Lot5_P81-assembly	94	76.70	50.55	50.53	76.88	77.63	76.72	75.67	86.82	0.14	87.31
Lot5_P82-assembly	95	76.74	50.55	50.53	76.92	77.67	76.76	75.70	86.86	0.14	87.31
Lot5_P83-assembly	96	52.90	34.71	34.69	54.47	61.08	52.54	53.01	53.89	0.23	53.94

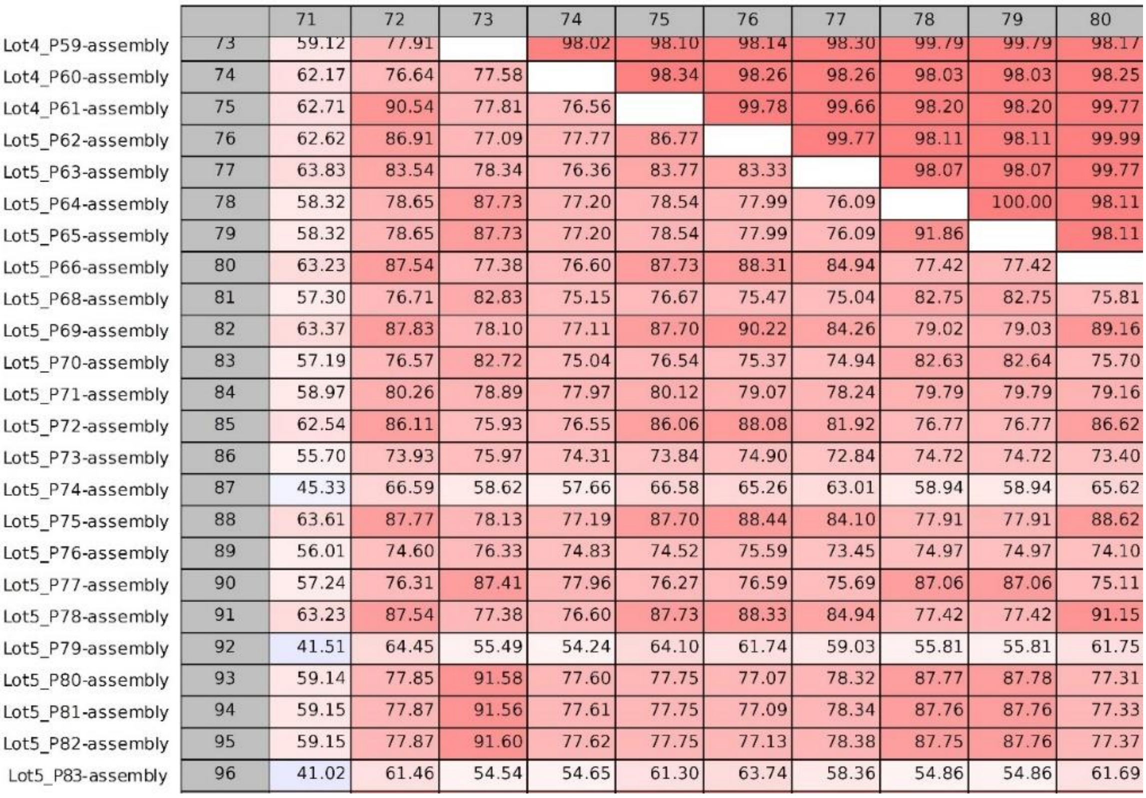


		31	32	33	34	35	36	37	38	39	40
Lot4_P59-assembly	73	76.68	76.19	76.70	78.69	12.04	76.67	76.11	76.63	79.13	78.03
Lot4_P60-assembly	74	76.96	76.51	75.58	77.93	11.78	75.54	76.36	77.16	77.59	76.51
Lot4_P61-assembly	75	86.98	85.86	78.18	76.49	11.70	78.15	85.52	86.61	77.20	88.50
Lot5_P62-assembly	76	86.99	88.20	76.85	78.00	11.76	76.82	87.91	88.31	77.71	86.65
Lot5_P63-assembly	77	82.95	83.18	75.92	77.24	11.58	75.90	83.03	83.77	77.66	83.86
Lot5_P64-assembly	78	77.08	76.45	78.11	76.71	12.06	78.08	76.23	76.41	77.62	78.48
Lot5_P65-assembly	79	77.08	76.45	78.11	76.71	12.06	78.08	76.23	76.41	77.62	78.48
Lot5_P66-assembly	80	86.19	87.62	76.98	76.78	11.58	76.95	87.22	87.70	77.49	87.50
Lot5_P68-assembly	81	75.41	75.42	79.09	75.46	11.79	79.07	75.52	75.10	75.92	76.63
Lot5_P69-assembly	82	86.24	87.43	77.76	77.33	11.66	77.73	87.15	87.54	78.09	87.60
Lot5_P70-assembly	83	75.31	75.31	78.96	75.36	11.77	78.93	75.42	75.00	75.81	76.52
Lot5_P71-assembly	84	78.74	77.78	86.34	84.64	12.01	86.32	77.58	78.34	85.52	80.56
Lot5_P72-assembly	85	86.77	89.06	76.32	76.99	11.86	76.29	88.72	87.30	76.87	85.88
Lot5_P73-assembly	86	74.76	74.36	75.91	76.08	12.02	75.88	74.30	74.31	75.50	74.43
Lot5_P74-assembly	87	67.02	64.86	58.39	58.24	9.11	58.36	64.80	64.83	58.79	67.74
Lot5_P75-assembly	88	86.72	87.19	77.94	77.43	11.71	77.91	87.11	88.24	78.20	87.99
Lot5_P76-assembly	89	75.29	75.17	75.52	76.09	11.74	75.49	75.11	74.99	75.45	75.05
Lot5_P77-assembly	90	76.03	75.53	75.00	77.39	12.14	74.96	75.39	75.83	77.15	75.83
Lot5_P78-assembly	91	86.19	87.64	76.98	76.78	11.58	76.95	87.24	87.72	77.51	87.50
Lot5_P79-assembly	92	61.99	60.74	54.72	54.32	8.65	54.70	60.48	61.32	54.78	62.92
Lot5_P80-assembly	93	76.71	76.22	76.76	78.74	12.04	76.73	76.14	76.62	79.15	78.08
Lot5_P81-assembly	94	76.72	76.24	76.77	78.76	12.04	76.74	76.16	76.64	79.16	78.09
Lot5_P82-assembly	95	76.72	76.24	76.77	78.76	12.04	76.74	76.16	76.68	79.20	78.09
Lot5_P83-assembly	96	61.64	62.11	53.39	54.90	8.67	53.36	61.90	62.13	54.62	61.47

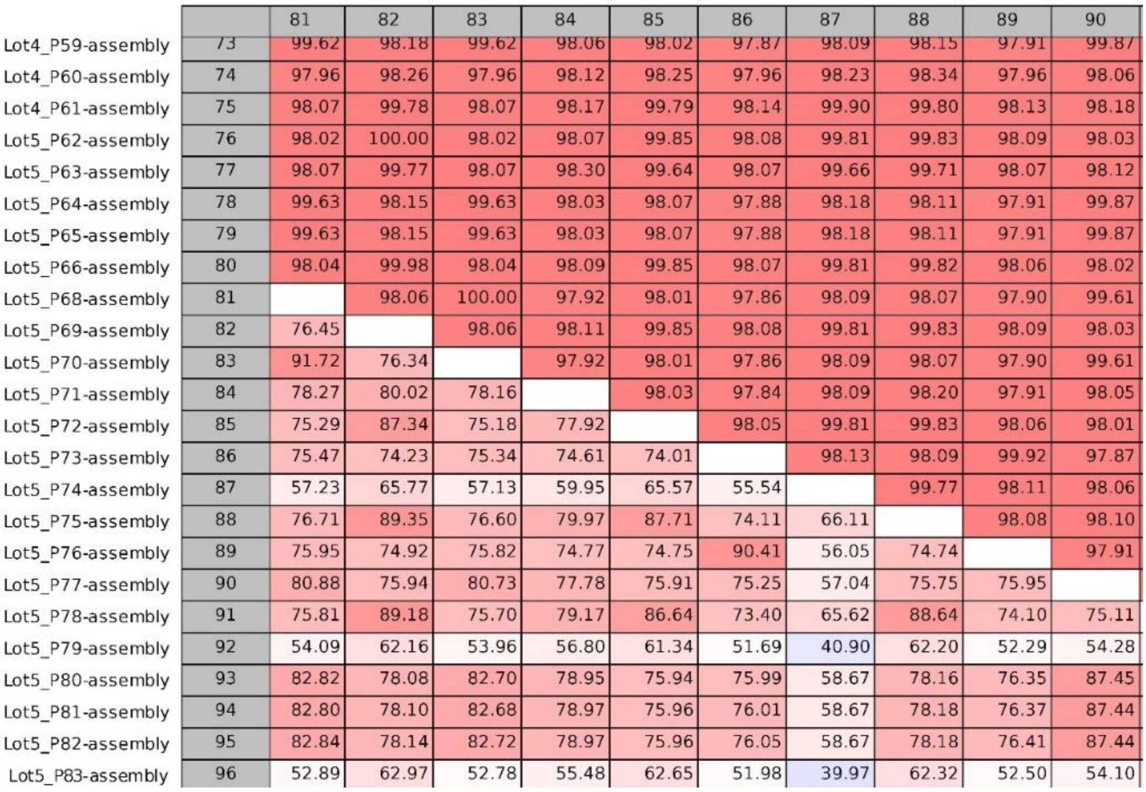
		51	52	53	54	55	56	57	58	59	60
Lot4_P59-assembly	73	75.71	76.82	75.83	76.67	75.82	76.67	76.66	50.48	50.51	76.89
Lot4_P60-assembly	74	76.67	77.23	76.87	77.80	76.55	77.80	77.79	48.94	48.96	78.54
Lot4_P61-assembly	75	76.02	87.94	76.05	74.94	86.69	74.94	74.93	48.27	48.30	76.39
Lot5_P62-assembly	76	76.83	87.75	76.99	76.19	88.28	76.19	76.19	48.90	48.91	77.55
Lot5_P63-assembly	77	74.64	82.52	74.76	74.97	83.25	74.97	74.96	47.90	47.91	76.25
Lot5_P64-assembly	78	75.71	77.70	75.73	75.33	76.81	75.33	75.33	50.13	50.18	75.94
Lot5_P65-assembly	79	75.71	77.70	75.73	75.33	76.81	75.33	75.33	50.13	50.18	75.94
Lot5_P66-assembly	80	76.20	86.33	76.46	74.75	87.93	74.74	74.74	48.12	48.13	76.48
Lot5_P68-assembly	81	78.52	75.58	78.51	78.08	74.66	78.07	78.07	49.47	49.52	74.15
Lot5_P69-assembly	82	76.15	87.00	76.30	75.51	87.53	75.51	75.50	48.48	48.49	76.88
Lot5_P70-assembly	83	78.38	75.48	78.38	77.92	74.53	77.92	77.92	49.38	49.43	74.04
Lot5_P71-assembly	84	77.87	79.01	77.92	77.40	77.87	77.39	77.39	49.92	49.97	83.10
Lot5_P72-assembly	85	75.99	87.45	75.93	75.12	87.34	75.11	75.11	48.43	48.46	76.27
Lot5_P73-assembly	86	75.76	75.12	75.91	76.91	74.13	76.91	76.90	49.20	49.25	74.55
Lot5_P74-assembly	87	55.97	67.06	56.01	55.77	64.60	55.77	55.76	36.66	36.69	57.13
Lot5_P75-assembly	88	76.11	86.89	76.36	75.65	87.15	75.64	75.64	48.41	48.42	76.47
Lot5_P76-assembly	89	75.83	75.61	75.76	76.76	74.69	76.76	76.75	49.39	49.44	74.68
Lot5_P77-assembly	90	75.30	76.39	75.09	76.56	75.62	76.56	76.55	50.37	50.42	76.82
Lot5_P78-assembly	91	76.20	86.33	76.46	74.75	87.96	74.74	74.74	48.12	48.13	76.48
Lot5_P79-assembly	92	52.73	62.88	52.84	52.48	61.20	52.48	52.47	34.57	34.59	54.14
Lot5_P80-assembly	93	75.63	76.81	75.75	76.66	75.80	76.66	76.65	50.51	50.54	76.90
Lot5_P81-assembly	94	75.63	76.81	75.75	76.67	75.82	76.67	76.66	50.51	50.54	76.91
Lot5_P82-assembly	95	75.67	76.85	75.79	76.71	75.86	76.71	76.70	50.51	50.54	76.95
Lot5_P83-assembly	96	52.98	62.39	53.18	52.89	62.07	52.89	52.88	34.70	34.72	54.52



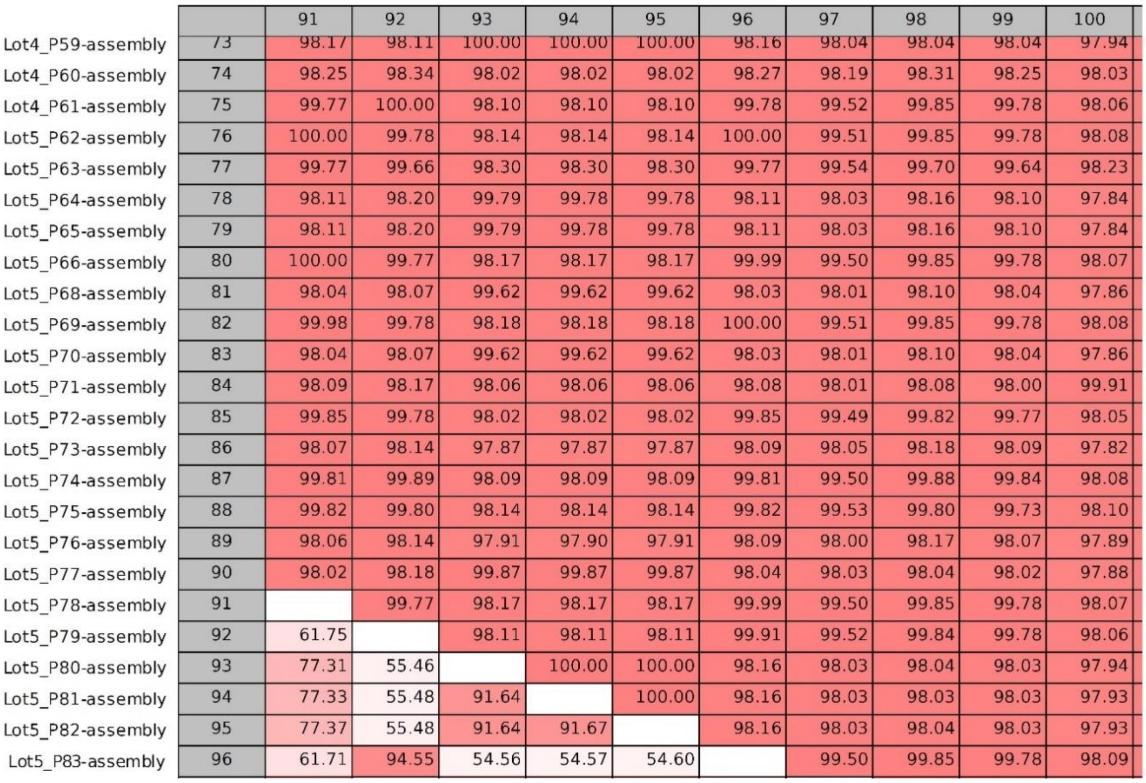
		61	62	63	64	65	66	67	68	69	70
Lot4_P59-assembly	73	77.78	77.78	77.53	83.47	76.25	76.20	62.05	76.35	77.91	91.62
Lot4_P60-assembly	74	76.52	76.54	76.31	75.69	77.05	77.00	59.82	75.81	76.68	77.62
Lot4_P61-assembly	75	90.97	90.87	89.37	75.66	87.20	86.80	66.55	75.34	90.58	77.75
Lot5_P62-assembly	76	86.76	86.77	86.50	74.40	86.97	88.79	64.52	74.32	86.90	77.11
Lot5_P63-assembly	77	83.79	83.80	83.86	75.69	82.69	82.70	62.38	75.44	83.55	78.36
Lot5_P64-assembly	78	78.51	78.51	78.10	81.86	76.91	77.22	62.32	74.57	78.65	87.77
Lot5_P65-assembly	79	78.51	78.51	78.07	81.86	76.91	77.22	62.32	74.57	78.65	87.77
Lot5_P66-assembly	80	87.75	87.77	87.57	74.77	86.33	87.43	64.61	75.70	87.56	77.35
Lot5_P68-assembly	81	76.66	76.66	76.00	88.92	75.07	75.08	60.02	77.91	76.71	82.85
Lot5_P69-assembly	82	87.67	87.68	87.43	75.38	86.25	88.04	65.01	75.22	87.83	78.12
Lot5_P70-assembly	83	76.52	76.52	75.87	88.75	74.97	74.95	59.88	77.78	76.58	82.74
Lot5_P71-assembly	84	80.12	80.11	79.54	77.20	78.50	78.23	61.74	76.93	80.24	78.95
Lot5_P72-assembly	85	86.04	86.06	85.54	74.62	86.93	87.78	63.77	73.41	86.12	75.94
Lot5_P73-assembly	86	73.81	73.81	73.66	76.14	74.98	74.53	57.14	75.11	73.93	76.03
Lot5_P74-assembly	87	66.54	66.56	66.23	56.93	68.06	65.02	44.01	55.65	66.63	58.67
Lot5_P75-assembly	88	87.69	87.71	87.20	75.65	86.65	87.57	65.05	75.47	87.78	78.16
Lot5_P76-assembly	89	74.48	74.48	74.40	76.59	75.29	74.96	57.60	75.03	74.60	76.39
Lot5_P77-assembly	90	76.24	76.24	75.70	81.97	75.69	76.02	60.60	74.16	76.30	87.45
Lot5_P78-assembly	91	87.75	87.77	87.57	74.77	86.33	87.46	64.61	75.70	87.56	77.35
Lot5_P79-assembly	92	64.11	64.12	63.15	53.48	61.94	61.70	40.88	52.52	64.42	55.46
Lot5_P80-assembly	93	77.72	77.72	77.48	83.50	76.29	76.18	62.02	76.27	77.85	91.66
Lot5_P81-assembly	94	77.74	77.74	77.50	83.48	76.29	76.20	62.02	76.27	77.85	91.64
Lot5_P82-assembly	95	77.74	77.74	77.54	83.48	76.29	76.24	62.02	76.31	77.85	91.68
Lot5_P83-assembly	96	61.27	61.28	61.05	52.24	61.61	62.63	39.20	51.59	61.50	54.58



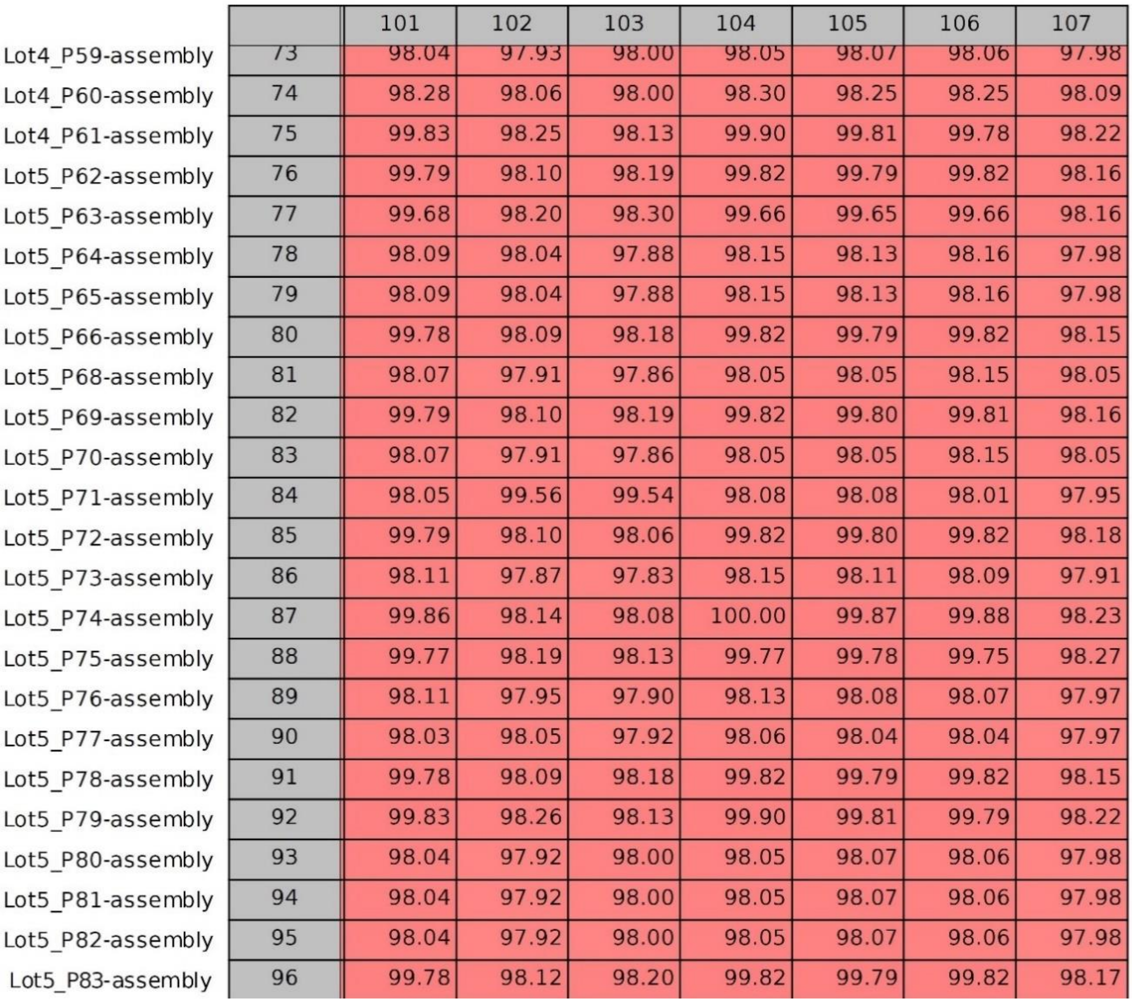
		71	72	73	74	75	76	77	78	79	80
Lot4_P59-assembly	73	59.12	77.91		98.02	98.10	98.14	98.30	99.79	99.79	98.17
Lot4_P60-assembly	74	62.17	76.64	77.58		98.34	98.26	98.26	98.03	98.03	98.25
Lot4_P61-assembly	75	62.71	90.54	77.81	76.56		99.78	99.66	98.20	98.20	99.77
Lot5_P62-assembly	76	62.62	86.91	77.09	77.77	86.77		99.77	98.11	98.11	99.99
Lot5_P63-assembly	77	63.83	83.54	78.34	76.36	83.77	83.33		98.07	98.07	99.77
Lot5_P64-assembly	78	58.32	78.65	87.73	77.20	78.54	77.99	76.09		100.00	98.11
Lot5_P65-assembly	79	58.32	78.65	87.73	77.20	78.54	77.99	76.09	91.86		98.11
Lot5_P66-assembly	80	63.23	87.54	77.38	76.60	87.73	88.31	84.94	77.42	77.42	
Lot5_P68-assembly	81	57.30	76.71	82.83	75.15	76.67	75.47	75.04	82.75	82.75	75.81
Lot5_P69-assembly	82	63.37	87.83	78.10	77.11	87.70	90.22	84.26	79.02	79.03	89.16
Lot5_P70-assembly	83	57.19	76.57	82.72	75.04	76.54	75.37	74.94	82.63	82.64	75.70
Lot5_P71-assembly	84	58.97	80.26	78.89	77.97	80.12	79.07	78.24	79.79	79.79	79.16
Lot5_P72-assembly	85	62.54	86.11	75.93	76.55	86.06	88.08	81.92	76.77	76.77	86.62
Lot5_P73-assembly	86	55.70	73.93	75.97	74.31	73.84	74.90	72.84	74.72	74.72	73.40
Lot5_P74-assembly	87	45.33	66.59	58.62	57.66	66.58	65.26	63.01	58.94	58.94	65.62
Lot5_P75-assembly	88	63.61	87.77	78.13	77.19	87.70	88.44	84.10	77.91	77.91	88.62
Lot5_P76-assembly	89	56.01	74.60	76.33	74.83	74.52	75.59	73.45	74.97	74.97	74.10
Lot5_P77-assembly	90	57.24	76.31	87.41	77.96	76.27	76.59	75.69	87.06	87.06	75.11
Lot5_P78-assembly	91	63.23	87.54	77.38	76.60	87.73	88.33	84.94	77.42	77.42	91.15
Lot5_P79-assembly	92	41.51	64.45	55.49	54.24	64.10	61.74	59.03	55.81	55.81	61.75
Lot5_P80-assembly	93	59.14	77.85	91.58	77.60	77.75	77.07	78.32	87.77	87.78	77.31
Lot5_P81-assembly	94	59.15	77.87	91.56	77.61	77.75	77.09	78.34	87.76	87.76	77.33
Lot5_P82-assembly	95	59.15	77.87	91.60	77.62	77.75	77.13	78.38	87.75	87.76	77.37
Lot5_P83-assembly	96	41.02	61.46	54.54	54.65	61.30	63.74	58.36	54.86	54.86	61.69



		81	82	83	84	85	86	87	88	89	90
Lot4_P59-assembly	73	99.62	98.18	99.62	98.06	98.02	97.87	98.09	98.15	97.91	99.87
Lot4_P60-assembly	74	97.96	98.26	97.96	98.12	98.25	97.96	98.23	98.34	97.96	98.06
Lot4_P61-assembly	75	98.07	99.78	98.07	98.17	99.79	98.14	99.90	99.80	98.13	98.18
Lot5_P62-assembly	76	98.02	100.00	98.02	98.07	99.85	98.08	99.81	99.83	98.09	98.03
Lot5_P63-assembly	77	98.07	99.77	98.07	98.30	99.64	98.07	99.66	99.71	98.07	98.12
Lot5_P64-assembly	78	99.63	98.15	99.63	98.03	98.07	97.88	98.18	98.11	97.91	99.87
Lot5_P65-assembly	79	99.63	98.15	99.63	98.03	98.07	97.88	98.18	98.11	97.91	99.87
Lot5_P66-assembly	80	98.04	99.98	98.04	98.09	99.85	98.07	99.81	99.82	98.06	98.02
Lot5_P68-assembly	81		98.06	100.00	97.92	98.01	97.86	98.09	98.07	97.90	99.61
Lot5_P69-assembly	82	76.45		98.06	98.11	99.85	98.08	99.81	99.83	98.09	98.03
Lot5_P70-assembly	83	91.72	76.34		97.92	98.01	97.86	98.09	98.07	97.90	99.61
Lot5_P71-assembly	84	78.27	80.02	78.16		98.03	97.84	98.09	98.20	97.91	98.05
Lot5_P72-assembly	85	75.29	87.34	75.18	77.92		98.05	99.81	99.83	98.06	98.01
Lot5_P73-assembly	86	75.47	74.23	75.34	74.61	74.01		98.13	98.09	99.92	97.87
Lot5_P74-assembly	87	57.23	65.77	57.13	59.95	65.57	55.54		99.77	98.11	98.06
Lot5_P75-assembly	88	76.71	89.35	76.60	79.97	87.71	74.11	66.11		98.08	98.10
Lot5_P76-assembly	89	75.95	74.92	75.82	74.77	74.75	90.41	56.05	74.74		97.91
Lot5_P77-assembly	90	80.88	75.94	80.73	77.78	75.91	75.25	57.04	75.75	75.95	
Lot5_P78-assembly	91	75.81	89.18	75.70	79.17	86.64	73.40	65.62	88.64	74.10	75.11
Lot5_P79-assembly	92	54.09	62.16	53.96	56.80	61.34	51.69	40.90	62.20	52.29	54.28
Lot5_P80-assembly	93	82.82	78.08	82.70	78.95	75.94	75.99	58.67	78.16	76.35	87.45
Lot5_P81-assembly	94	82.80	78.10	82.68	78.97	75.96	76.01	58.67	78.18	76.37	87.44
Lot5_P82-assembly	95	82.84	78.14	82.72	78.97	75.96	76.05	58.67	78.18	76.41	87.44
Lot5_P83-assembly	96	52.89	62.97	52.78	55.48	62.65	51.98	39.97	62.32	52.50	54.10



		91	92	93	94	95	96	97	98	99	100
Lot4_P59-assembly	73	98.17	98.11	100.00	100.00	100.00	98.16	98.04	98.04	98.04	97.94
Lot4_P60-assembly	74	98.25	98.34	98.02	98.02	98.02	98.27	98.19	98.31	98.25	98.03
Lot4_P61-assembly	75	99.77	100.00	98.10	98.10	98.10	99.78	99.52	99.85	99.78	98.06
Lot5_P62-assembly	76	100.00	99.78	98.14	98.14	98.14	100.00	99.51	99.85	99.78	98.08
Lot5_P63-assembly	77	99.77	99.66	98.30	98.30	98.30	99.77	99.54	99.70	99.64	98.23
Lot5_P64-assembly	78	98.11	98.20	99.79	99.78	99.78	98.11	98.03	98.16	98.10	97.84
Lot5_P65-assembly	79	98.11	98.20	99.79	99.78	99.78	98.11	98.03	98.16	98.10	97.84
Lot5_P66-assembly	80	100.00	99.77	98.17	98.17	98.17	99.99	99.50	99.85	99.78	98.07
Lot5_P68-assembly	81	98.04	98.07	99.62	99.62	99.62	98.03	98.01	98.10	98.04	97.86
Lot5_P69-assembly	82	99.98	99.78	98.18	98.18	98.18	100.00	99.51	99.85	99.78	98.08
Lot5_P70-assembly	83	98.04	98.07	99.62	99.62	99.62	98.03	98.01	98.10	98.04	97.86
Lot5_P71-assembly	84	98.09	98.17	98.06	98.06	98.06	98.08	98.01	98.08	98.00	99.91
Lot5_P72-assembly	85	99.85	99.78	98.02	98.02	98.02	99.85	99.49	99.82	99.77	98.05
Lot5_P73-assembly	86	98.07	98.14	97.87	97.87	97.87	98.09	98.05	98.18	98.09	97.82
Lot5_P74-assembly	87	99.81	99.89	98.09	98.09	98.09	99.81	99.50	99.88	99.84	98.08
Lot5_P75-assembly	88	99.82	99.80	98.14	98.14	98.14	99.82	99.53	99.80	99.73	98.10
Lot5_P76-assembly	89	98.06	98.14	97.91	97.90	97.91	98.09	98.00	98.17	98.07	97.89
Lot5_P77-assembly	90	98.02	98.18	99.87	99.87	99.87	98.04	98.03	98.04	98.02	97.88
Lot5_P78-assembly	91		99.77	98.17	98.17	98.17	99.99	99.50	99.85	99.78	98.07
Lot5_P79-assembly	92	61.75		98.11	98.11	98.11	99.91	99.52	99.84	99.78	98.06
Lot5_P80-assembly	93	77.31	55.46		100.00	100.00	98.16	98.03	98.04	98.03	97.94
Lot5_P81-assembly	94	77.33	55.48	91.64		100.00	98.16	98.03	98.03	98.03	97.93
Lot5_P82-assembly	95	77.37	55.48	91.64	91.67		98.16	98.03	98.04	98.03	97.93
Lot5_P83-assembly	96	61.71	94.55	54.56	54.57	54.60		99.50	99.85	99.78	98.09



		101	102	103	104	105	106	107
Lot4_P59-assembly	73	98.04	97.93	98.00	98.05	98.07	98.06	97.98
Lot4_P60-assembly	74	98.28	98.06	98.00	98.30	98.25	98.25	98.09
Lot4_P61-assembly	75	99.83	98.25	98.13	99.90	99.81	99.78	98.22
Lot5_P62-assembly	76	99.79	98.10	98.19	99.82	99.79	99.82	98.16
Lot5_P63-assembly	77	99.68	98.20	98.30	99.66	99.65	99.66	98.16
Lot5_P64-assembly	78	98.09	98.04	97.88	98.15	98.13	98.16	97.98
Lot5_P65-assembly	79	98.09	98.04	97.88	98.15	98.13	98.16	97.98
Lot5_P66-assembly	80	99.78	98.09	98.18	99.82	99.79	99.82	98.15
Lot5_P68-assembly	81	98.07	97.91	97.86	98.05	98.05	98.15	98.05
Lot5_P69-assembly	82	99.79	98.10	98.19	99.82	99.80	99.81	98.16
Lot5_P70-assembly	83	98.07	97.91	97.86	98.05	98.05	98.15	98.05
Lot5_P71-assembly	84	98.05	99.56	99.54	98.08	98.08	98.01	97.95
Lot5_P72-assembly	85	99.79	98.10	98.06	99.82	99.80	99.82	98.18
Lot5_P73-assembly	86	98.11	97.87	97.83	98.15	98.11	98.09	97.91
Lot5_P74-assembly	87	99.86	98.14	98.08	100.00	99.87	99.88	98.23
Lot5_P75-assembly	88	99.77	98.19	98.13	99.77	99.78	99.75	98.27
Lot5_P76-assembly	89	98.11	97.95	97.90	98.13	98.08	98.07	97.97
Lot5_P77-assembly	90	98.03	98.05	97.92	98.06	98.04	98.04	97.97
Lot5_P78-assembly	91	99.78	98.09	98.18	99.82	99.79	99.82	98.15
Lot5_P79-assembly	92	99.83	98.26	98.13	99.90	99.81	99.79	98.22
Lot5_P80-assembly	93	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P81-assembly	94	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P82-assembly	95	98.04	97.92	98.00	98.05	98.07	98.06	97.98
Lot5_P83-assembly	96	99.78	98.12	98.20	99.82	99.79	99.82	98.17

Appendix C: List of all the identified plasmids

No. of unique plasmids	**Name of the plasmid**	**Accession Number**	**Source organism**	**Occurrence in**		
				Norwegian isolates	**Indian isolates**	**Total**
1	pVB11737_6	NZ_CP050397.1	*A. baumannii*	4	56	60
2	p2AB5075	NZ_CP008708.1	*A. baumannii*	1	10	11
3	pABAUUSACASD_frag2	CP064294.1	*A. baumannii*	0	11	11
4	pAS5-3	NZ_CP061686.1	*A. seifertii*	0	8	8
5	pVB2486_4	NZ_CP050407.1	*A. baumannii*	2	6	8
6	pYQ12450	NZ_KR059864.1	*Klebsiella pneumoniae*	0	8	8
7	pVB11737_4	NZ_CP050395.1	*A. baumannii*	0	7	7
8	p3KSK1	NZ_CP072125.1	*A. baumannii*	0	6	6
9	pVB473_1	NZ_CP050389.1	*A. baumannii*	0	6	6
10	pPM193665_3	NZ_CP050418.1	*A. baumannii*	0	5	5
11	pAC30a	CP007578.1	*A. baumannii*	0	4	4
12	pAS41-4	NZ_CP061638.1	*A. seifertii*	1	3	4
13	pVB11737_5	NZ_CP050396.1	*A. baumannii*	1	2	3
14	pAS51-5	NZ_CP061618.1	*A. seifertii*	0	2	2
15	pD36-1 clone GC1	NZ_CP012953.1	*A. baumannii*	1	1	2
16	pPM193665_4	NZ_CP050419.1	*A. baumannii*	2	0	2
17	pPM193665_5	NZ_CP050420.1	*A. baumannii*	0	2	2
18	pPM194122_2	NZ_CP050427.1	*A. baumannii*	0	2	2
19	pVB11737_3	NZ_CP050394.1	*A. baumannii*	0	2	2
20	Unnamed	NZ_CP027181.1	*A. baumannii*	0	2	2
21	Unnamed	NZ_CP027187.1	*A. baumannii*	0	2	2
22	Unnamed	CP040045.1	*A. baumannii*	0	2	2
23	pA1-1	NZ_CP010782.1	*A. baumannii*	1	0	1
24	pABAY15001_6E	NZ_MK386684.1	*A. baumannii*	0	1	1
25	pAS11-2	NZ_CP061680.1	*A. seifertii*	0	1	1
26	pAS25-2	NZ_CP061668.1	*A. seifertii*	0	1	1
27	pAS31-3	NZ_CP061663.1	*A. seifertii*	0	1	1
28	pAS49-4	NZ_CP061624.1	*A. seifertii*	1	0	1
29	pAS60-2	NZ_CP061594.1	*A. seifertii*	1	0	1
30	pBspH6	NZ_CP055288.1	*Acinetobacter spp.*	0	1	1
31	pHZE23-1-10	NZ_CP044473.1	*A. schindleri*	0	1	1
32	pPM192696_1	NZ_CP050413.1	*A. baumannii*	0	1	1
33	pRAY*-v1	NC_019311.1	*A. baumannii*	0	1	1
34	pWM99c-2	CP031744.1	*A. baumannii*	0	1	1
35	Unnamed	NZ_CP042842.1	*A. baumannii*	0	1	1
36	Unnamed	NZ_CP027608.1	*A. baumannii*	1	0	1
37	Unnamed	NZ_CP033845.1	*Klebsiella oxytoca*	0	1	1
38	Unnamed	NZ_CP040052.1	*A. baumannii*	0	1	1
39	Unnamed	NZ_CP033770.1	*A. baumannii*	0	1	1
40	Unnamed	NZ_CP040049.1	*A. baumannii*	0	1	1
			Total	16	161	177

Appendix D: List of all the identified AMR genes

No. of unique AMR genes	AMR gene	Antibiotic class to which resistance is conferred	Occurrence in		
			Norwegian isolates	**Indian isolates**	**Total**
1	*adeK*	macrolide; fluoroquinolone; lincosamide; carbapenem; cephalosporin; tetracycline; rifamycin; diaminopyrimidine; phenicol; penem	11	76	87
2	*adeI*	macrolide; fluoroquinolone; lincosamide; carbapenem; cephalosporin; tetracycline; rifamycin; diaminopyrimidine; phenicol; penem	11	74	85
3	*AbaQ*	fluoroquinolone	10	70	80
4	*OXA-23*	carbapenem; cephalosporin; penam	9	69	78
5	*adeL*	fluoroquinolone; tetracycline	7	67	74
6	*msrE*	macrolide; lincosamide; streptogramin; tetracycline; oxazolidinone; phenicol; pleuromutilin	8	65	73
7	*mphE*	macrolide	8	64	72
8	*abeS*	macrolide; aminocoumarin	11	59	70
9	*armA*	aminoglycoside	4	60	64
10	*AbaF*	fosfomycin	6	52	58
11	*sul1*	sulfonamide	7	50	57
12	*adeG*	fluoroquinolone; tetracycline	10	39	49
13	*qacEdelta1*	acridine dye; disinfecting agents and intercalating dyes	6	42	48
14	*sul2*	sulfonamide	4	44	48
15	*adeC*	glycylcycline; tetracycline	7	33	40
16	*OXA-66*	carbapenem; cephalosporin; penam	7	33	40
17	*APH(3')-Ia*	aminoglycoside	5	34	39
18	*adeA*	glycylcycline; tetracycline	7	31	38
19	*PER-7*	monobactam; carbapenem; cephalosporin; penam; penem	1	36	37
20	*arr-2*	rifamycin	1	32	33
21	*cmlA5*	phenicol	1	30	31
22	*APH(3')-VIa*	aminoglycoside	1	20	21
23	*ADC-30*	cephalosporin	3	17	20
24	*TEM-1*	monobactam; cephalosporin; penam; penem	5	14	19
25	*ADC-76*	cephalosporin	0	18	18
26	*catB8*	phenicol	2	16	18
27	*ADC-73*	cephalosporin	1	16	17
28	*OXA-144*	carbapenem; cephalosporin; penam	0	14	14

29	*OXA-104*	carbapenem; cephalosporin; penam	0	13	13
30	*aadA*	aminoglycoside	1	10	11
31	*AmvA*	macrolide; acridine dye; disinfecting agents and intercalating dyes	0	10	10
32	*adeF*	fluoroquinolone; tetracycline	3	7	10
33	*adeR*	glycylcycline; tetracycline	3	7	10
34	*BRP(MBL)*	glycopeptide	0	10	10
35	*OXA-69*	carbapenem; cephalosporin; penam	3	7	10
36	*SAT-2*	nucleoside antibiotic	0	8	8
37	*NDM-1*	carbapenem; cephalosporin; cephamycin; penam	0	7	7
38	*OXA-68*	carbapenem; cephalosporin; penam	0	3	3
39	*AAC(6')-Ian*	aminoglycoside	0	2	2
40	*abeM*	fluoroquinolone; acridine dye; triclosan; disinfecting agents and intercalating dyes	0	2	2
41	*ADC-11*	cephalosporin	0	2	2
42	*ADC-158*	cephalosporin	0	2	2
43	*ADC-191*	cephalosporin	0	2	2
44	*catI*	phenicol	1	1	2
45	*dfrB5*	diaminopyrimidine	0	2	2
46	*LpsB*	peptide antibiotic	0	2	2
47	*OXA-129*	carbapenem; cephalosporin; penam	0	2	2
48	*OXA-64*	carbapenem; cephalosporin; penam	0	2	2
49	*OXA-98*	carbapenem; cephalosporin; penam	0	2	2
50	*ADC-115*	cephalosporin	1	0	1
51	*ADC-185*	cephalosporin	1	0	1
52	*OXA-120*	carbapenem; cephalosporin; penam	0	1	1
53	*OXA-20*	carbapenem; cephalosporin; penam	1	0	1
54	*OXA-51*	carbapenem; cephalosporin; penam	1	0	1
55	*OXA-58*	carbapenem; cephalosporin; penam	1	0	1
56	*OXA-72*	carbapenem; cephalosporin; penam	1	0	1
57	*tet(39)*	tetracycline	1	0	1
		Total	171	1279	1450