



MASSIVE
BIOINFORMATICS

BACTERIAL GENOME ANALYSIS REPORT

by Massive Bioinformatics

Sample: barcode08

Klebsiella pneumoniae

Version: 1.0.0 | 2026-04-13

Table of Contents

Wet Laboratory Methods	2
Bioinformatics Analysis	3
Read Quality Control	6
Assembly Quality Metrics	8
Species-Specific Typing	9
Plasmid Analysis	10
Antimicrobial Resistance	11
Resistance Determinants	13
Stress & Biocide Resistance	15
Virulence Factors	16
Genome Annotation	20
Mobile Genetic Elements	21
Defense Systems & CRISPR-Cas Arrays	23
Biosynthetic Gene Clusters	24
Prophage Regions	28
Software & Database References	30

Wet Laboratory Methods

DNA Quantification: Genomic double-stranded DNA (dsDNA) concentration of each isolated bacterial sample was quantified using the Qubit™ dsDNA HS Assay Kit on a Qubit™ 4 Fluorometer, following the manufacturer's instructions.

End-Prep Reaction: Library preparation was performed following the "Ligation sequencing gDNA – Native Barcoding Kit 96 V14 (SQK-NBD114.96)" protocol. For each sample, 400 ng of DNA was transferred to a 0.2 mL PCR tube and brought to a final volume of 11 µL with nuclease-free water. End-prep reagents were then added: 1 µL Diluted DCS, 0.875 µL NEBNext FFPE DNA Repair Buffer, 0.5 µL NEBNext FFPE DNA Repair Mix, 0.875 µL Ultra II End-prep Reaction Buffer, and 0.75 µL Ultra II End-prep Enzyme Mix. The reaction was incubated in a thermal cycler at 20°C for 5 minutes followed by 65°C for 5 minutes.

Native Barcode Ligation: Following end-prep, native barcode ligation was performed by combining 0.75 µL of the end-prepped DNA with 2 µL nuclease-free water, 1.25 µL Native Barcode (NB01–96), and 5 µL Blunt/TA Ligase Master Mix. The mixture was briefly vortexed and incubated at room temperature for 20 minutes. Reactions were terminated using EDTA. Barcoded samples were pooled and purified using 0.4x AMPure XP (AXP) beads. The bead mixture was incubated at 37°C for 10 minutes, placed on a magnetic stand, and the supernatant was removed. Two washes with 125 µL Short Fragment Buffer (SFB) were performed before eluting DNA with 37 µL nuclease-free water.

Adapter Ligation: Adapter ligation was performed by combining 35 µL pooled barcoded DNA with 5 µL Native Adapter (NA), 50 µL 2x Rapid Buffer, and 10 µL T4 DNA ligase (Rapid). The mixture was incubated at 30°C for 10 minutes. A final AXP bead purification was performed: 40 µL AXP beads were added, incubated at 37°C for 10 minutes, washed with 125 µL SFB, and the adapted library was eluted in 25 µL Elution Buffer (EB). The final library concentration was measured by fluorometric quantification.

Sequencing: The sequencing library was prepared by combining 1170 µL Flow Cell Flush (FCF) with 30 µL Flow Cell Tether (FCT) as the priming mixture. The flow cell (R10.4.1 chemistry) was primed by drawing 200 µL air from the inlet port and adding 500 µL priming mixture. After a 5-minute incubation, 100 fmol of the adapted library was combined with 100 µL Sequencing Buffer (SB) and 68 µL Loading Beads (LIB), and 200 µL was loaded onto the flow cell via the inlet port. Sequencing was performed on a PromethION 2 Solo or GridION (Oxford Nanopore Technologies) and controlled using the MinKNOW software. Base-calling and demultiplexing were performed using Dorado with the super-accuracy model.

Bioinformatics Analysis

Read Quality Control: Raw Oxford Nanopore sequencing reads were subjected to quality control and adapter trimming using Fastplong. Adapter sequences at both the 5' and 3' ends of reads were automatically detected and removed. Reads with a mean quality score below Q10 or a length shorter than 400 bp were discarded, and homopolymer (polyX) tails exceeding 15 bp were trimmed to reduce systematic basecalling artifacts. These filtering criteria were applied to ensure that only high-quality, informative reads were retained for downstream assembly and analysis.

Contamination Screening: Taxonomic profiling of the quality-filtered reads was performed using Kraken2 with the `/home/workstation/Desktop/databases/wf-bacterial-dbs/kraken` reference database to screen for potential inter-species contamination. Reads classified as belonging to non-target taxa were flagged for review, providing a quality checkpoint prior to genome assembly.

Genome Assembly: De novo genome assembly was performed using the Autocycler consensus assembly framework. Filtered reads were subsampled into independent read sets, each of which was assembled using 2 long-read assemblers (Flye, Raven). The resulting assemblies were clustered, trimmed, and combined into a single high-quality consensus assembly that leverages the strengths of each individual assembler while minimizing assembly artifacts. The consensus assembly was subsequently polished using Medaka with the `r1041_e82_400bps_hac_v5.2.0` neural network model to correct systematic basecalling errors and improve per-base accuracy.

Assembly Quality Assessment: Assembly quality was evaluated using CheckM2, which employs machine learning models to estimate genome completeness and contamination from single-copy marker gene analysis. Gene content completeness was further assessed using BUSCO against both generic (`bacteria_odb12`) and lineage-specific marker sets to evaluate the presence, duplication, and fragmentation of conserved orthologs. Chromosomal contigs were identified and reoriented to the `dnaA` gene using DNAAPLER to ensure a standardized genome representation.

Taxonomic Classification: Taxonomic classification was performed using GTDB-Tk v2 against the Genome Taxonomy Database (GTDB release R220), which employs average nucleotide identity (ANI) screening, relative evolutionary divergence (RED), and phylogenetic placement to assign taxonomy. Plasmid sequences were identified and separated from chromosomal contigs using MOB-suite, which classifies replicons based on relaxase typing, mate-pair formation typing, and replication initiator protein analysis.

Molecular Typing: Molecular epidemiological typing was performed at multiple resolution levels. Multi-locus sequence typing (MLST) was conducted using `mlst` against curated allele profiles from the PubMLST database, assigning sequence types (STs) based on exact allelic matches at seven housekeeping gene loci. Core genome MLST (cgMLST) was performed using MiST with allele schemas automatically retrieved from `cgMLST.org` or PubMLST, providing high-resolution strain discrimination suitable for outbreak investigations and transmission tracking.

Species-Specific Typing: Species-specific typing and characterization tools were automatically selected based on the identified taxonomy. The following tools were applied: Kleborate v3 for comprehensive *Klebsiella* species identification, virulence scoring (yersiniabactin, colibactin, aerobactin, salmochelin siderophores), resistance determinant profiling, and capsule (K) and O-antigen (O) locus typing.

Antimicrobial Resistance: In silico prediction of antimicrobial resistance (AMR) determinants was performed using a dual-tool approach to maximize sensitivity and specificity. AMRFinderPlus was used to identify acquired resistance genes, stress response genes, and resistance-associated point mutations against the NCBI AMR Reference Gene Catalog using a combination of BLASTx and HMM-based detection methods. Independently, ResFinder was employed to detect acquired resistance genes (minimum coverage 60%, minimum identity 80%), with PointFinder for species-specific chromosomal point mutation detection and DisinFinder for biocide and disinfectant resistance gene identification. Drug-level phenotype predictions were derived from the ResFinder phenotype table. Results from both tools were harmonized by normalizing gene names, deduplicating overlapping detections with source tracking, consolidating repeated point mutations, and annotating genomic locations (chromosome or plasmid) using MOB-suite contig classification.

Genome Annotation: Structural and functional genome annotation was performed using Bakta, a rapid and standardized annotation tool optimized for bacterial genomes. Bakta employs a comprehensive database integrating UniProt, AMRFinderPlus, NCBI COG, Pfam, and RFAM references for coding sequence (CDS) prediction, tRNA/rRNA/tmRNA/ncRNA identification, and functional classification. Annotation was performed on all contigs including both chromosomal and plasmid sequences.

Virulence Factors: Virulence factor screening was performed using ABRicate against the Virulence Factor Database (VFDB), applying minimum nucleotide identity (80%) and minimum coverage (80%) thresholds. Identified virulence genes were categorized into functional classes including adhesion, toxins, secretion systems, iron uptake, immune evasion, invasion, and regulation based on keyword matching against VFDB product annotations. Virulence genes detected by AMRFinderPlus (VIRULENCE type) were additionally integrated and deduplicated.

Mobile Genetic Elements: Mobile genetic elements were systematically identified to assess the mobilome. Insertion sequences (IS elements) were detected using ISEScan, which identifies IS elements based on profile HMM searches for transposases and inverted terminal repeat (ITR) boundary detection. Integron detection was performed using IntegronFinder, which identifies integrase genes and associated gene cassette arrays. IS elements from both chromosomal and plasmid contigs were reported with family classification and genomic coordinates.

Defense Systems & CRISPR: Bacterial defense systems were identified using DefenseFinder, which employs MacSyFinder-based HMM profiles to detect a comprehensive set of anti-phage defense mechanisms including restriction-modification (RM), abortive infection (Abi), BREX, DISARM, and other characterized and putative defense systems. CRISPR-Cas adaptive immunity systems were typed using CRISPRCasTyper, which identifies CRISPR arrays based on repeat-spacer architecture and classifies associated Cas operons into subtypes using profile HMM searches against curated Cas protein databases.

Biosynthetic Gene Clusters: Biosynthetic gene cluster (BGC) mining was performed using antiSMASH v8, which identifies and annotates secondary metabolite biosynthetic loci including nonribosomal peptide synthetases (NRPS), polyketide synthases (PKS), ribosomally synthesized and post-translationally modified peptides (RiPPs), terpenes, and other natural product classes. Detected clusters were categorized by biosynthesis type and annotated with core biosynthetic gene functions, tailoring enzymes, and NRPS/PKS domain architecture. Terpene product predictions were derived from prenyl transferase domain analysis.

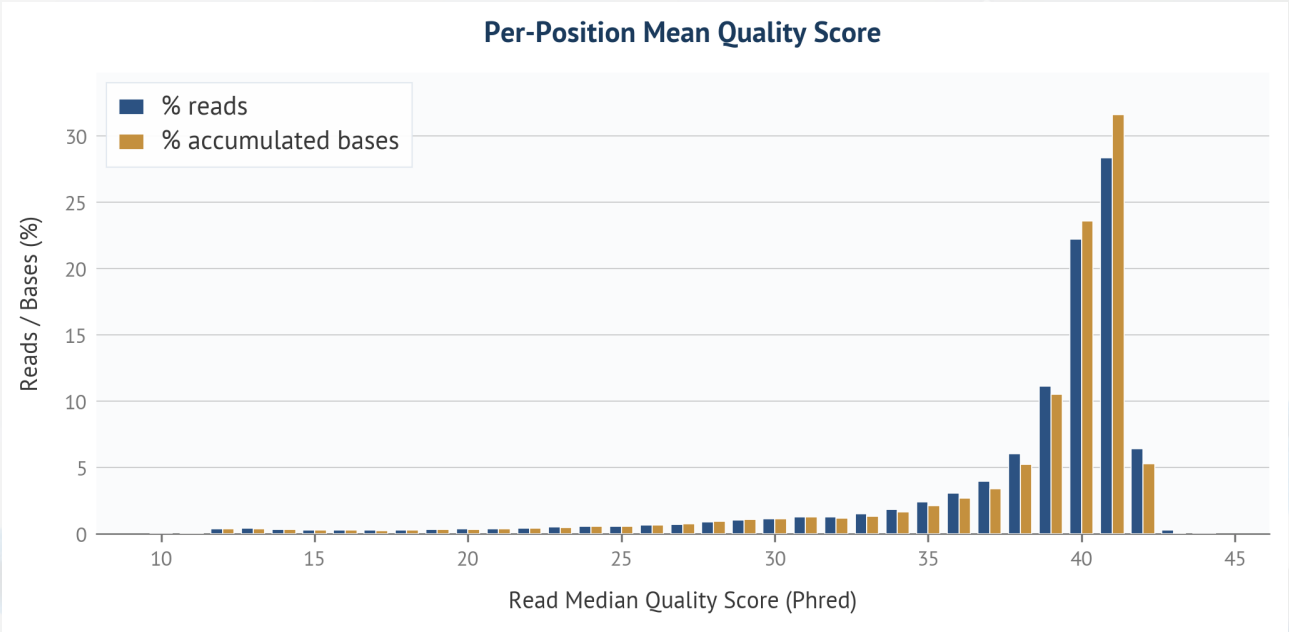
Prophage Analysis: Prophage detection and characterization followed a four-stage cascade. Prophage regions were initially identified using geNomad, which employs neural network-based classification of viral sequences with marker gene enrichment scoring. Detected prophage regions were subjected to quality assessment using CheckV, which estimates completeness based on alignment to a comprehensive database of complete viral genomes and applies quality tiers (high-quality, medium-quality, low-quality) with configurable minimum thresholds. Prophages passing quality filters were annotated using Pharokka, which performs gene calling and functional annotation against the PHROG (Prokaryotic Virus Remote Homologous Groups) database, with additional screening for phage-encoded antimicrobial resistance genes (CARD database) and virulence factors (VFDB). Finally, phage lifecycle prediction (temperate versus virulent) and putative bacterial host assignment were performed using PhaBOX2, which integrates deep learning-based taxonomy (PhaGCN), lifestyle classification (PhaTYP), and host prediction (CHERRY) through CRISPR spacer matching and average amino acid identity (AAI) comparison.

Read Quality Control

Read Filtering

91,193 Total Reads (Raw)	85,689 Total Reads (Filtered)	94.0% Reads Retained
9,919 bp Mean Read Length	86.7% Q20 Rate	75.1% Q30 Rate

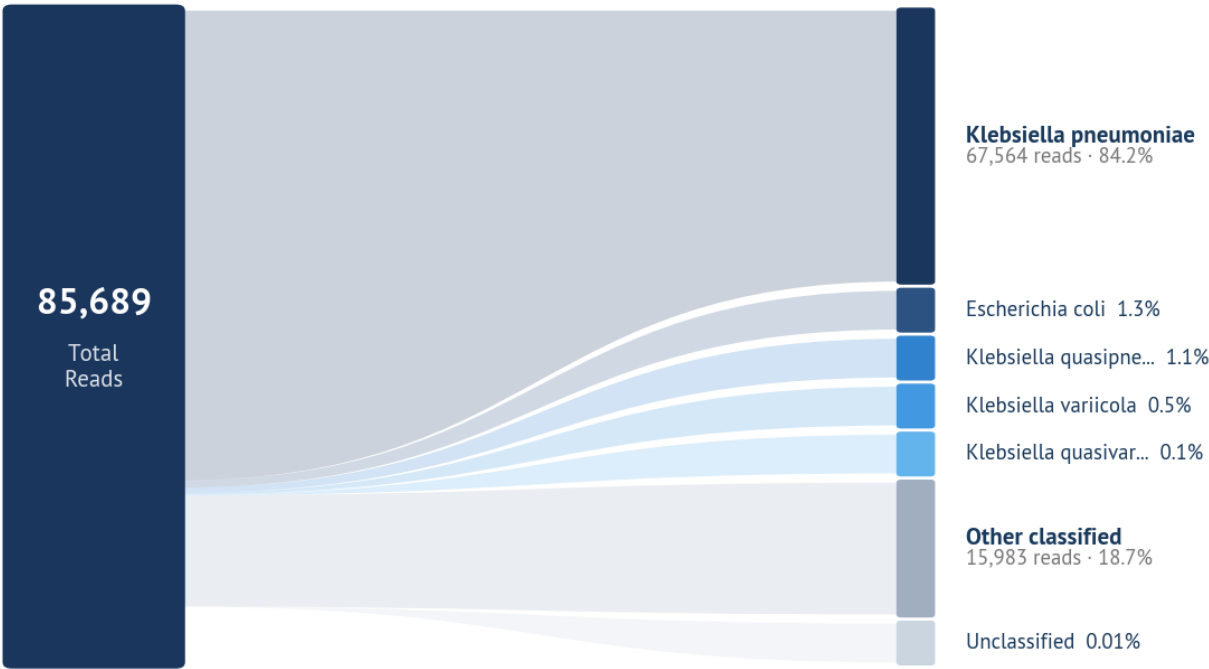
Reason	Reads	%
Passed	85,689	94.0%
Low Quality	340	0.4%
Too Short	5,251	5.8%
Adapter Trimmed	90,738	99.5%
PolyX Trimmed	99	0.1%



Contamination Screen

85,689 Total Reads	100.0% Classified	0.0% Unclassified
------------------------------	-----------------------------	-----------------------------

Read Classification



Species	Reads	%
Klebsiella pneumoniae	67,564	84.17%
Escherichia coli	1,020	1.28%
Klebsiella quasipneumoniae	756	1.05%
Klebsiella variicola	246	0.48%
Klebsiella quasivariicola	112	0.13%
Acinetobacter baumannii	115	0.13%
Klebsiella africana	88	0.10%
Klebsiella aerogenes	63	0.07%
Salmonella enterica	19	0.06%
Klebsiella michiganensis	38	0.04%

Assembly Quality Metrics

HIGH QUALITY ASSEMBLY

PASS

Assembly Statistics

Genome Size	5.47 Mb	Total Contigs	2
N50	5.39 Mb	Max Contig	5.39 Mb
GC Content	57.0%	Coding Density	87.5%
Total CDS	5,017	Hypothetical	113

Quality Assessment

COMPLETENESS (CHECKM2)

PASS

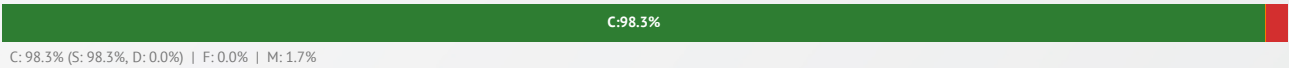
100.0%

CONTAMINATION (CHECKM2)

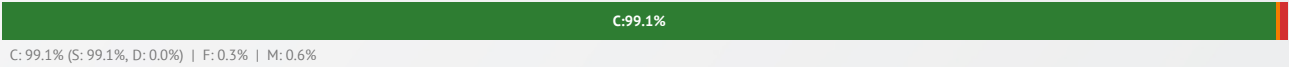
PASS

0.09%

BUSCO Generic (bacteria_odb12) – 116 markers



BUSCO Specific (enterobacteriaceae_odb12) – 874 markers



Taxonomic Classification

DOMAIN Bacteria	PHYLUM Pseudomonadota	ORDER Enterobacterales
FAMILY Enterobacteriaceae	GENUS Klebsiella	SPECIES Klebsiella pneumoniae
ANI 98.97%	ALIGNMENT FRACTION 86.1%	REFERENCE (GTDBTK) GCF_000742135.1

Molecular Typing

MLST | klebsiella

PERFECT

ST101

gapA 2	infB 6	mdh 1	pgi 5	phoE 4	rpoB 1	tonB 6
-----------	-----------	----------	----------	-----------	-----------	-----------

cgMLST

2330 / 2358 (98.8% Exact Matches)

Exact 2330	Novel 8	Absent 10	Indel 5	Multi 0	Other 5
---------------	------------	--------------	------------	------------	------------

Species-Specific Typing

Kleborate v3 | Species & Typing

STRONG

Klebsiella pneumoniae

ST
ST101

K Type
K17

O Type
O2a

wzi
wzi137

VIRULENCE DETERMINANTS

SCORE 1

Yersiniabactin
ybt 9; ICEKp3

Colibactin
Negative

Aerobactin
Negative

Salmonelisin
Negative

RESISTANCE DETERMINANTS

SCORE 1

SHV Mutations
None

Omp Mutations
OmpK36.p.134_135insGlyAsp;OmpK35.p.Ile61fs

Flq Mutations
GyrA.p.Ser83Tyr;GyrA.p.Asp87Asn;ParC.p.Ser80Ile

ESBL
CTX-M-15

Carbapenem
None

Colistin
None

Cipro MIC
2 mg/L [2-4]

CAPSULE & LPS TYPING

K Locus
KL17

K Identity
100.00%

K Confidence
Typeable

O Locus
OL2.1

O Identity
98.91%

Bla (chr)
SHV-1*

CIPROFLOXACIN SUSCEPTIBILITY PREDICTION

RESISTANT

Prediction
nonwildtype R

MIC
2 mg/L [2-4]

Profile
>1 QRDR, 0 PMQR, *aac(6)-Ib-cr

Gene	Mutation	Type	Drug Class	Identity	Coverage
CTX-M-15	-	Gene presence	third-generation cephalosporin	100.00%	100.00%
SHV-1	-	Gene presence	penicillin beta-lactam	99.88%	100.00%
OmpK36	p.134_135insGlyAsp	Protein variant	-	94.72%	100.00%
OmpK35	p.Ile61fs	Inactivating mutation	-	99.54%	17.27%
GyrA	p.Ser83Tyr	Protein variant	fluoroquinolone antibiotic	99.44%	100.00%
GyrA	p.Asp87Asn	Protein variant	fluoroquinolone antibiotic	99.44%	100.00%
ParC	p.Ser80Ile	Protein variant	fluoroquinolone antibiotic	99.72%	100.00%

Plasmid Analysis

1 Plasmid Replicons Detected

AB187

IncFIA,IncR,rep_cluster_1418

MOBILIZABLE

Size 77.6 kb	GC Content 52.3%	Relaxase -
MPF Type -	Host Range Enterobacteriaceae (family)	Nearest Reference Klebsiella pneumoniae

Antimicrobial Resistance

Predicted Resistant

Beta-lactam AMR+ PF RF Amoxicillin ** Ampicillin ** Cefepime ** Cefotaxime ** Ceftazidime ** Piperacillin ** Aztreonam ** Ticarcillin ** ...	RESISTANT
Fluoroquinolone AMR+ PF Fluoroquinolone ** Ciprofloxacin ** Quinolone	RESISTANT
Fosfomycin AMR+ RF Fosfomycin **	RESISTANT
Phenicol AMR+ RF Chloramphenicol	RESISTANT
Aminoglycoside/Quinolone AMR+ Amikacin Kanamycin Quinolone Tobramycin	RESISTANT
Rifamycin AMR+ RF Rifamycin Rifampicin	RESISTANT
Sulfonamide AMR+ RF Sulfonamide Sulfamethoxazole	RESISTANT
Aminoglycoside RF Tobramycin Dibekacin Amikacin Sisomicin Netilmicin Fluoroquinolone Ciprofloxacin	RESISTANT

** = high confidence (100% identity match) * = partial match

Predicted Susceptible

Aldehyde	SUSCEPTIBLE	Aminocyclitol	SUSCEPTIBLE
Amphenicol	SUSCEPTIBLE	Folate Pathway Antagonist	SUSCEPTIBLE
Glycopeptide	SUSCEPTIBLE	Ionophores	SUSCEPTIBLE
Lincosamide	SUSCEPTIBLE	Macrolide	SUSCEPTIBLE
Nitroimidazole	SUSCEPTIBLE	Oxazolidinone	SUSCEPTIBLE
Peroxide	SUSCEPTIBLE	Pleuromutilin	SUSCEPTIBLE
Polymyxin	SUSCEPTIBLE	Pseudomonic Acid	SUSCEPTIBLE
Quaternary Ammonium Compound	SUSCEPTIBLE	Steroid Antibacterial	SUSCEPTIBLE
Streptogramin A	SUSCEPTIBLE	Streptogramin B	SUSCEPTIBLE
Tetracycline	SUSCEPTIBLE		

Resistance Determinants

Beta-lactam							RESISTANT
Amoxicillin, Ampicillin, Cefepime, Cefotaxime, Ceftazidime, Piperacillin, Aztreonam, Ticarcillin, Ceftriaxone, Cephalosporins, Carbapenem, Cephalosporin, Beta-Lactam, Amoxicillin+Clavulanic Acid, Ampicillin+Clavulanic Acid, Piperacillin+Tazobactam, Cephalothin							
Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
blaCTX-M-15	Cephalosporin, Amoxicillin, Ampicillin, Aztreonam Cefepime, Cefotaxime, Ceftazidime, Ceftriaxone Piperacillin, Ticarcillin	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+, RF
blaSHV-1	Beta-Lactam, Amoxicillin, Ampicillin, Aztreonam Cefepime, Cefotaxime, Ceftazidime, Ceftriaxone Piperacillin, Ticarcillin	Acquired	Chromosome	100.0%	100.0%	Acquired	AMR+, RF
blaOXA-1	Cephalosporin, Amoxicillin Amoxicillin+Clavulanic Acid, Ampicillin Ampicillin+Clavulanic Acid, Cefepime, Piperacillin Piperacillin+Tazobactam	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+, RF
blaTEM-1	Beta-Lactam	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+
blaTEM-1A	Amoxicillin, Ampicillin, Cephalothin, Piperacillin Ticarcillin	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	RF
ompK36	Carbapenem	D135DGD	Chromosome	-	-	Mutation	AMR+
ompK35	Carbapenem	G62AfsTer1	Chromosome	-	-	Mutation	AMR+
ompK36	Cephalosporins, Carbapenem	10 point variants	Chromosome	-	-	Mutation	PF
ompK37	Carbapenem	2 point variants	Chromosome	-	-	Mutation	PF

Fluoroquinolone							RESISTANT
Fluoroquinolone, Ciprofloxacin, Quinolone							
Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
parC	Quinolone	S80I	Chromosome	-	-	Mutation	AMR+, PF
gyrA	Quinolone	D87N	Chromosome	-	-	Mutation	AMR+, PF
gyrA	Quinolone	S83Y	Chromosome	-	-	Mutation	AMR+
acrR	Fluoroquinolone	7 point variants	Chromosome	-	-	Mutation	PF

Fosfomycin							RESISTANT
Fosfomycin							
Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
fosA	Fosfomycin	Acquired	Chromosome	98.6%	100.0%	Acquired	AMR+, RF

Phenicol							RESISTANT
Chloramphenicol							
Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
catB3	Chloramphenicol	Acquired	Plasmid AB187	100.0%	70.0%	Acquired	AMR+, RF

Aminoglycoside/Quinolone

Amikacin, Kanamycin, Quinolone, Tobramycin

RESISTANT

Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
aac(6')-Ib-cr5	Amikacin, Kanamycin, Quinolone, Tobramycin	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+

Rifamycin

Rifamycin, Rifampicin

RESISTANT

Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
arr-3	Rifamycin, Rifampicin	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+, RF

Sulfonamide

Sulfonamide, Sulfamethoxazole

RESISTANT

Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
sul1	Sulfonamide, Sulfamethoxazole	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	AMR+, RF

Aminoglycoside

Tobramycin, Dibekacin, Amikacin, Sisomicin, Netilmicin, Fluoroquinolone, Ciprofloxacin

RESISTANT

Resistance Gene	Drug	Change	Location	Identity (%)	Coverage (%)	Type	Source
aac(6')-Ib-cr	Tobramycin, Dibekacin, Amikacin, Sisomicin Netilmicin, Fluoroquinolone, Ciprofloxacin	Acquired	Plasmid AB187	100.0%	100.0%	Acquired	RF

Stress & Biocide Resistance

METAL

7 genes

BIOCIDE

1 genes

Metal Resistance

7 GENES

Resistance Gene	Description	Substance	Location	Identity (%)	Coverage (%)	Source
fieF	CDF family cation-efflux transporter Fie	Unknown	Chromosome	100.0%	100.0%	AMR+
merC	organomercurial transporter MerC	Organomercury	Plasmid AB187	100.0%	100.0%	AMR+
merR	mercury resistance transcriptional regul	Mercury	Plasmid AB187	93.0%	98.6%	AMR+
merT	mercuric transport protein MerT	Mercury	Plasmid AB187	98.3%	99.1%	AMR+
merA	mercury(II) reductase	Mercury	Plasmid AB187	93.2%	100.0%	AMR+
merD	mercury resistance co-regulator MerD	Mercury	Plasmid AB187	90.1%	100.0%	AMR+
merE	broad-spectrum mercury transporter MerE	Mercury	Plasmid AB187	96.2%	100.0%	AMR+

Biocide / Disinfectant Resistance

1 GENES

Resistance Gene	Description	Substance	Location	Identity (%)	Coverage (%)	Source
qacEdelta1	quatarnary ammonium compound efflux SMR	Quaternary Ammonium	Plasmid AB187	100.0%	100.0%	AMR+

Virulence Factors

ADH 24 IRON 22 SEC 17 OTH 11 IMM 8 REG 2					
Adhesion					24 GENES
Gene	Product	Location	Identity (%)	Coverage (%)	Source
mrkH	(mrkH) transcriptional activator [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	100.0%	100.0%	VF
mrkB	(mrkB) fimbrial chaperone protein mrkB precursor [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.9%	100.0%	VF
fimA	(fimA) type 1 major fimbrial subunit precursor [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.8%	100.0%	VF
mrkD	(mrkD) fimbrial adhesin protein precursor MrkD [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.8%	100.0%	VF
fimC	(fimC) periplasmic chaperone [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.7%	100.0%	VF
mrkF	(mrkF) type 3 fimbrial minor pilin subunit MrkF [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.7%	100.0%	VF
mrkC	(mrkC) fimbrial biogenesis outer membrane usher protein mrkC precursor [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.7%	100.0%	VF
mrkA	(mrkA) type 3 fimbrial major pilin subunit MrkA [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.7%	100.0%	VF
fimI	(fimI) type 1 pilus biosynthesis fimbrial protein [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.6%	100.0%	VF
fimG	(fimG) type 1 fimbrial minor component [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.6%	100.0%	VF
mrkJ	(mrkJ) phosphodiesterase [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.4%	100.0%	VF
fimD	(fimD) outer membrane usher protein [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.4%	100.0%	VF
fimK	(fimK) transcriptional regulator [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.4%	100.0%	VF
fimE	(fimE) tyrosine recombinase [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.3%	100.0%	VF
mrkI	(mrkI) LuxR family regulatory protein [Type 3 fimbriae (VF0567) - Biofilm (VFC0271)]	Chromosome	99.3%	100.0%	VF
fimH	(fimH) type 1 fimbrial adhesin precursor [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.2%	100.0%	VF
fimB	(fimB) tyrosine recombinase [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	99.2%	100.0%	VF
fimF	(fimF) type 1 fimbrial minor component [Type 1 fimbriae (VF0566) - Adherence (VFC0001)]	Chromosome	98.9%	100.0%	VF
yagZ/ecpA	(yagZ/ecpA) E. coli common pilus structural subunit EcpA [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	90.1%	99.3%	VF
yagW/ecpD	(yagW/ecpD) polymerized tip adhesin of ECP fibers [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	88.8%	100.0%	VF
yagY/ecpB	(yagY/ecpB) E. coli common pilus chaperone EcpB [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	87.9%	100.0%	VF
yagX/ecpC	(yagX/ecpC) E. coli common pilus usher EcpC [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	87.3%	100.0%	VF
yagV/ecpE	(yagV/ecpE) E. coli common pilus chaperone EcpE [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	84.4%	100.0%	VF
ompA	(ompA) outer membrane protein A [OmpA (VF0236) - Invasion (VFC0083)]	Chromosome	83.7%	100.0%	VF

BACTERIAL GENOME ANALYSIS REPORT

Iron Uptake

22 GENES

Gene	Product	Location	Identity (%)	Coverage (%)	Source
ybtU	(ybtU) yersiniabactin biosynthetic protein YbtU [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	100.0%	100.0%	VF
ybtE	(ybtE) yersiniabactin siderophore biosynthetic protein [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
ybtQ	(ybtQ) yersiniabactin ABC transporter ATP-binding/permease protein YbtQ [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF, AMR+
ybtX	(ybtX) putative signal transducer [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
ybtS	(ybtS) salicylate synthase Irp9 [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
fyuA/psn	(fyuA/psn) pesticin/yersiniabactin receptor protein [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
ybtA	(ybtA) transcriptional regulator YbtA [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
irp1	(irp1) yersiniabactin biosynthetic protein Irp1 [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.9%	100.0%	VF
ybtP	(ybtP) yersiniabactin ABC transporter ATP-binding/permease protein YbtP [Ybt (VF0564) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.8%	100.0%	VF, AMR+
irp2	(irp2) yersiniabactin biosynthetic protein Irp2 [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.8%	100.0%	VF
entS	(entS) enterobactin exporter EntS [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.8%	100.0%	VF
fepC	(fepC) iron-enterobactin transporter ATP-binding protein [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.8%	100.0%	VF
fepD	(fepD) iron-enterobactin transporter membrane protein [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.7%	100.0%	VF
fepB	(fepB) iron-enterobactin transporter periplasmic binding protein [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.6%	100.0%	VF
fes	(fes) enterobactin/ferric enterobactin esterase [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.4%	100.0%	VF
iroE	(iroE) siderophore esterase IroE [Sal (VF0563) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.4%	100.0%	VF
iutA	(iutA) ferric aerobactin receptor IutA [Aerobactin (VF0565) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.3%	100.0%	VF
ybtT	(ybtT) type II thioesterase YbtT [Yersiniabactin (VF0136) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.2%	100.0%	VF
entF	(entF) enterobactin synthase subunit F [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.0%	100.0%	VF
fepG	(fepG) iron-enterobactin transporter permease [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	98.9%	100.0%	VF
entE	(entE) enterobactin synthase subunit E [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	98.2%	100.0%	VF
fur	(fur) ferric iron uptake transcriptional regulator [Fur (VF0113) - Regulation (VFC0301)]	Chromosome	84.0%	96.5%	VF

Secretion System

17 GENES

Gene	Product	Location	Identity (%)	Coverage (%)	Source
scn/tssJ	(scn/tssJ) type VI secretion system lipoprotein TssJ [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	100.0%	100.0%	VF
vipA/tssB	(vipA/tssB) type VI secretion system contractile sheath small subunit VipA [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	100.0%	100.0%	VF
tssG	(tssG) type VI secretion system baseplate subunit TssG [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.7%	100.0%	VF
tssF	(tssF) type VI secretion system baseplate subunit TssF [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.5%	100.0%	VF
icmF/tssM	(icmF/tssM) type VI secretion protein TssM [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.5%	99.9%	VF
impA/tssA	(impA/tssA) type VI secretion system protein TssA [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.4%	100.0%	VF
dotU/tssL	(dotU/tssL) type VI secretion system protein DotU/TssL family [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.4%	100.0%	VF
vipA/tssB	(vipA/tssB) type VI secretion system contractile sheath small subunit VipA [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.4%	99.8%	VF
vipB/tssC	(vipB/tssC) type VI secretion system contractile sheath large subunit VipB [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.3%	100.0%	VF
vasE/tssK	(vasE/tssK) type VI secretion system baseplate subunit TssK [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.3%	100.0%	VF
hcp/tssD	(hcp/tssD) type VI secretion system protein Hcp family [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.2%	100.0%	VF
ompA	(ompA) OmpA family protein [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.2%	100.0%	VF
vipB/tssC	(vipB/tssC) type VI secretion system contractile sheath large subunit VipB [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.2%	99.9%	VF
clpV/tssH	(clpV/tssH) type VI secretion system ATPase TssH [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	99.1%	100.0%	VF
vgrG/tssI	(vgrG/tssI) type VI secretion system tip protein VgrG [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	96.4%	83.8%	VF
vgrG/tssI	(vgrG/tssI) type VI secretion system tip protein VgrG [T6SS (VF0569) - Effector delivery system (VFC0086)]	Chromosome	96.2%	82.9%	VF
hcp2	(hcp2) type VI secretion system protein Hcp [T6SS-2 (VF1396) - Effector delivery system (VFC0086)]	Chromosome	88.4%	100.0%	VF

Other

11 GENES

Gene	Product	Location	Identity (%)	Coverage (%)	Source
acrB	(acrB) acriflavine resistance protein B [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)]	Chromosome	99.7%	100.0%	VF
entC	(entC) isochorismate synthase [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	99.5%	100.0%	VF
rfbA	(rfbA) O-antigen export ABC transporter permease RfbA [LPS (VF0561) - Immune modulation (VFC0258)]	Chromosome	99.5%	100.0%	VF
rfbB	(rfbB) O-antigen export ABC transporter ATP-binding protein RfbB [LPS (VF0561) - Immune modulation (VFC0258)]	Chromosome	99.5%	100.0%	VF
KP1_RS17230	(KP1_RS17230) glycosyltransferase [LPS (VF0561) - Immune modulation (VFC0258)]	Chromosome	99.4%	100.0%	VF
KP1_RS17240	(KP1_RS17240) DUF4422 domain-containing protein [LPS (VF0561) - Immune modulation (VFC0258)]	Chromosome	99.4%	100.0%	VF
entB	(entB) 23-dihydro-23-dihydroxybenzoate synthetase isochorismatase [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	98.5%	100.0%	VF
KP1_RS17225	(KP1_RS17225) glycosyltransferase family 4 protein [LPS (VF0561) - Immune modulation (VFC0258)]	Chromosome	98.0%	99.4%	VF
fepA	(fepA) outer membrane receptor FepA [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	97.0%	100.0%	VF
entA	(entA) 23-dihydroxybenzoate-23-dehydrogenase [Ent (VF0562) - Nutritional/Metabolic factor (VFC0272)]	Chromosome	96.5%	100.0%	VF
rpoS	(rpoS) RNA polymerase sigma factor RpoS [RpoS (VF0112) - Regulation (VFC0301)]	Chromosome	86.8%	99.8%	VF

BACTERIAL GENOME ANALYSIS REPORT

Immune Evasion

8 GENES

Gene	Product	Location	Identity (%)	Coverage (%)	Source
rcaA	(rcaA) transcriptional activator for ctr capsule biosynthesis [RcsAB (VF0571) - Regulation (VFC0301)]	Chromosome	100.0%	100.0%	VF
acrA	(acrA) acriflavine resistance protein A [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)]	Chromosome	99.7%	100.0%	VF
galF	(galF) GalU regulator GalF [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	99.3%	100.0%	VF
ugd	(ugd) UDP-glucose 6-dehydrogenase [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	97.1%	100.0%	VF
gndA	(gndA) NADP-dependent phosphogluconate dehydrogenase [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	95.5%	100.0%	VF
KP1_RS17355	(KP1_RS17355) phosphatase PAP2 family protein [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	94.6%	99.8%	VF
KP1_RS17345	(KP1_RS17345) capsule assembly Wzi family protein [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	87.1%	100.0%	VF
KP1_RS17340	(KP1_RS17340) polysaccharide export protein [Capsule (VF0560) - Immune modulation (VFC0258)]	Chromosome	81.6%	97.5%	VF

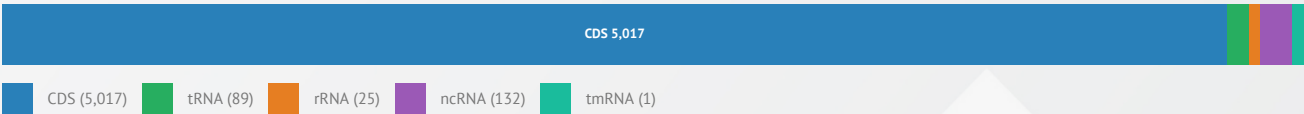
Regulation

2 GENES

Gene	Product	Location	Identity (%)	Coverage (%)	Source
rcaB	(rcaB) transcriptional regulator RcsB [RcsAB (VF0571) - Regulation (VFC0301)]	Chromosome	99.8%	100.0%	VF
ykgK/ecpR	(ykgK/ecpR) regulator protein EcpR [ECP (VF0404) - Adherence (VFC0001)]	Chromosome	86.7%	100.0%	VF

Genome Annotation

Chromosome



Plasmid Annotations

Plasmid	Total CDS	tRNA	rRNA	Hypothetical	ncRNA
AB187	97	0	0	10	2

Total genome: 5,114 CDS (123 hypothetical) | 89 tRNA | 25 rRNA – chromosome + 1 plasmids

Mobile Genetic Elements

53

Insertion Sequences (IS Elements)

0

Integrans

IS Family:

IS6 12

IS5 10

IS3 10

ISNCY 8

IS1 5

IS1380 3

IS21 2

IS630 1

IS256 1

Insertion Sequences (IS Elements)

IS Family	Cluster	Length	Location	Position
IS21	IS21_259	2,933 bp	Chromosome	75 - 3,007
IS3	IS3_461	711 bp	Plasmid AB187	2,943 - 3,653
IS110	IS110_544 IS110 protein:plasmid:1214	3,876 bp	Plasmid AB187	4,006 - 7,881
IS6	IS6_292	820 bp	Plasmid AB187	8,107 - 8,926
IS6	IS6_292	820 bp	Plasmid AB187	11,113 - 11,932
IS5	IS5_222	1,057 bp	Chromosome	13,567 - 14,623
IS1	IS1_316	540 bp	Plasmid AB187	17,496 - 18,035
IS6	IS6_292	820 bp	Plasmid AB187	19,316 - 20,135
IS6	IS6_292	3,075 bp	Plasmid AB187	21,443 - 24,517
IS1	IS1_316	768 bp	Plasmid AB187	26,808 - 27,575
IS6	IS6_292	820 bp	Plasmid AB187	47,507 - 48,326
IS6	IS6_292	820 bp	Plasmid AB187	55,007 - 55,826
IS1	IS1_316	768 bp	Plasmid AB187	56,638 - 57,405
IS1380	IS1380_141	1,690 bp	Plasmid AB187	57,453 - 59,142
IS6	IS6_292	822 bp	Plasmid AB187	61,846 - 62,667
IS6	IS6_292	820 bp	Plasmid AB187	63,515 - 64,334
IS6	IS6_292	1,155 bp	Plasmid AB187	69,537 - 70,691
IS1	IS1_316	267 bp	Plasmid AB187	73,532 - 73,798
IS6	IS6_292	794 bp	Plasmid AB187	74,494 - 75,287
IS3	IS3_506	1,221 bp	Plasmid AB187	75,288 - 76,508
IS6	IS6_292	820 bp	Chromosome	644,918 - 645,737
IS5	IS5_222	1,057 bp	Chromosome	853,600 - 854,656
IS5	IS5_112	1,196 bp	Chromosome	1,120,662 - 1,121,857
ISNCY	ISNCY_229	1,381 bp	Chromosome	1,322,944 - 1,324,324
ISNCY	ISNCY_229	1,096 bp	Chromosome	1,521,194 - 1,522,289
IS1	IS1_316	1,181 bp	Chromosome	1,700,486 - 1,701,666
IS5	IS5_222	1,057 bp	Chromosome	1,730,637 - 1,731,693
IS630	IS630_214	587 bp	Chromosome	1,786,736 - 1,787,322
IS6	IS6_292	1,027 bp	Chromosome	2,023,136 - 2,024,162
IS1380	IS1380_141	1,656 bp	Chromosome	2,025,461 - 2,027,116

IS Family	Cluster	Length	Location	Position
IS1380	IS1380_141	1,656 bp	Chromosome	2,100,361 - 2,102,016
IS3	IS3_168	1,258 bp	Chromosome	2,352,941 - 2,354,198
IS3	IS3_168	1,258 bp	Chromosome	2,386,074 - 2,387,331
IS5	IS5_222	1,057 bp	Chromosome	2,412,888 - 2,413,944
ISNCY	ISNCY_86	2,014 bp	Chromosome	2,682,597 - 2,684,610
IS5	IS5_222	1,057 bp	Chromosome	2,849,691 - 2,850,747
IS3	IS3_271	1,183 bp	Chromosome	3,010,856 - 3,012,038
IS5	IS5_222	1,057 bp	Chromosome	3,383,234 - 3,384,290
IS3	IS3_506	711 bp	Chromosome	3,400,632 - 3,401,342
IS3	IS3_61	1,552 bp	Chromosome	3,627,498 - 3,629,049
IS5	IS5_222	1,057 bp	Chromosome	3,691,227 - 3,692,283
ISNCY	ISNCY_229	1,448 bp	Chromosome	3,887,747 - 3,889,194
ISNCY	ISNCY_229	1,439 bp	Chromosome	4,110,058 - 4,111,496
IS21	IS21_259	1,301 bp	Chromosome	4,638,236 - 4,639,536
ISNCY	ISNCY_229	1,259 bp	Chromosome	4,642,327 - 4,643,585
IS5	IS5_112	1,200 bp	Chromosome	4,647,918 - 4,649,117
ISNCY	ISNCY_229	841 bp	Chromosome	4,681,669 - 4,682,509
IS256	IS256_47	647 bp	Chromosome	4,743,086 - 4,743,732
IS5	IS5_222	1,057 bp	Chromosome	4,746,751 - 4,747,807
IS3	IS3_271	1,166 bp	Chromosome	4,748,293 - 4,749,458
IS3	IS3_204	1,162 bp	Chromosome	4,755,796 - 4,756,957
IS3	IS3_61	1,552 bp	Chromosome	4,961,572 - 4,963,123
ISNCY	ISNCY_229	1,326 bp	Chromosome	5,174,410 - 5,175,735

Defense Systems & CRISPR-Cas Arrays

11

Defense Systems

0

CRISPR-Cas Arrays

Defense Systems

System Type	Subtype	Genes
Pycsar	Pycsar	2
Gao_Tmn	Gao_Tmn	1
PD-Lambda-1	PD-Lambda-1	1
PD-T4-3	PD-T4-3	1
MazEF	MazEF	2
Retron	Retron_I_B	2
Lamassu-Fam	Lamassu-Mrr	3
PD-T7-1	PD-T7-1	1
CBASS	CBASS_II	4
RM	RM_Type_IV	1
AbiE	AbiE	2

Biosynthetic Gene Clusters

6

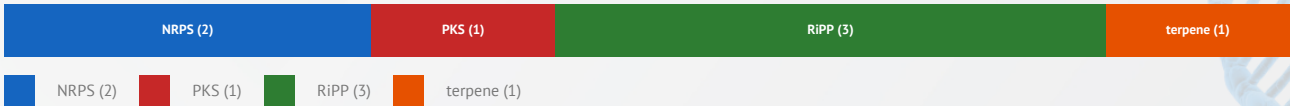
BGCs Detected

197.3 kb

Total BGC Size

7

Product Types



Cluster Details

T1PKS, NRP-metallophore, NRPS

63.2 kb

Chromosome | 1,806,228 - 1,869,428

NRPS

PKS

3 CORE

3 ADDITIONAL

4 TRANSPORT

4 REGULATORY

2 OTHER

16 genes total

Tailoring:

acylase (1)

esterase (1)

isomerase (1)

ligase (2)

Locus	Function	Product	Domains
ILCLDH_01767	TRANSPORT	yersiniabactin receptor FyuA	-
ILCLDH_01768	ADDITIONAL	yersiniabactin biosynthesis salicyl-AMP li...	AMP-binding
ILCLDH_01769	ADDITIONAL	yersiniabactin biosynthesis thioesterase YbtT	Thioesterase, Abhydrolase_6
ILCLDH_01770	ADDITIONAL	yersiniabactin biosynthetic protein YbtU	GFO_IDH_MocA
ILCLDH_01771	CORE	yersiniabactin biosynthetic protein Irp1	PKS_KS, PKS_AT, cMT, PKS_KR, PP-binding
ILCLDH_01772	CORE	yersiniabactin non-ribosomal peptide synth...	PP-binding, Heterocyclization, AMP-binding...
ILCLDH_01773	REGULATORY	yersiniabactin transcriptional regulator YbtA	-
ILCLDH_01774	TRANSPORT	yersiniabactin ABC transporter ATP-binding...	-
ILCLDH_01775	TRANSPORT	yersiniabactin ABC transporter ATP-binding...	-
ILCLDH_01776	TRANSPORT	putative signal transducer	-
ILCLDH_01777	CORE	salicylate synthase Irp9	SalSyn
ILCLDH_01778	OTHER	DUF4102 domain-containing protein	-
ILCLDH_01780	REGULATORY	nitrogen assimilation transcriptional regu...	-
ILCLDH_01781	REGULATORY	HTH-type transcriptional regulator Cbl	-
ILCLDH_01783	REGULATORY	LysR family transcriptional regulator	-
ILCLDH_01788	OTHER	Integrase	-

BACTERIAL GENOME ANALYSIS REPORT

NRP-metallophore, NRPS

54.1 kb

Chromosome | 3,844,883 - 3,899,009

NRPS

3 CORE 15 ADDITIONAL 14 TRANSPORT 2 REGULATORY 2 OTHER

36 genes total

Tailoring: PPTase (1) dehydrogenase (3) esterase (2) hydrolase (1) isomerase (1) kinase (1) ligase (2) phosphatase (1)

Locus	Function	Product	Domains
ILCLDH_03721	ADDITIONAL	Cytosine deaminase	Amidohydro_1
ILCLDH_03722	REGULATORY	LacI family transcriptional regulator	-
ILCLDH_03723	ADDITIONAL	Inositol-1-monophosphatase	-
ILCLDH_03724	TRANSPORT	Major facilitator superfamily (MFS) profil...	-
ILCLDH_03727	ADDITIONAL	S-methyl-5-thioribose kinase	APH
ILCLDH_03729	TRANSPORT	Periplasmic binding protein domain-contain...	-
ILCLDH_03730	TRANSPORT	ABC transporter permease	-
ILCLDH_03731	TRANSPORT	Putative ABC transport system ATPase compo...	-
ILCLDH_03732	ADDITIONAL	oxidoreductase	Fe-ADH
ILCLDH_03733	ADDITIONAL	2,3-dihydro-2,3-dihydroxybenzoate dehydrog...	PKS_KR, adh_short, adh_short_C2
ILCLDH_03736	OTHER	YbdD/YjiX family protein	-
ILCLDH_03737	OTHER	pyruvate/proton symporter CstA	-
ILCLDH_03738	ADDITIONAL	proofreading thioesterase EntH	-
ILCLDH_03739	CORE	2,3-dihydro-2,3-dihydroxybenzoate dehydrog...	PKS_KR, EntA
ILCLDH_03740	ADDITIONAL	enterobactin biosynthesis bifunctional iso...	PP-binding
ILCLDH_03741	ADDITIONAL	enterobactin synthase subunit E	AMP-binding
ILCLDH_03742	CORE	isochorismate synthase	EntC
ILCLDH_03743	TRANSPORT	iron-enterobactin transporter periplasmic ...	-
ILCLDH_03744	TRANSPORT	enterobactin exporter EntS	-
ILCLDH_03745	TRANSPORT	iron-enterobactin transporter membrane pro...	-
ILCLDH_03746	TRANSPORT	iron-enterobactin transporter permease	-
ILCLDH_03747	TRANSPORT	iron-enterobactin transporter ATP-binding ...	-
ILCLDH_03748	CORE	enterobactin synthase subunit F	Condensation_Starter, AMP-binding, PCP, Th...
ILCLDH_03749	ADDITIONAL	Cytoplasmic protein YbdZ	-
ILCLDH_03750	ADDITIONAL	enterobactin/ferric enterobactin esterase	Peptidase_S9
ILCLDH_03751	TRANSPORT	siderophore enterobactin receptor FepA	-
ILCLDH_03752	ADDITIONAL	enterobactin synthase subunit EntD	ACPS
ILCLDH_03753	TRANSPORT	Ribose ABC transporter substrate-binding p...	-
ILCLDH_03755	TRANSPORT	heme ABC exporter ATP-binding protein CcmA	-
ILCLDH_03756	TRANSPORT	Inner-membrane translocator	-
ILCLDH_03759	ADDITIONAL	N-terminal region of transketolase	DXP_synthase_N, TPP_enzyme_C
ILCLDH_03760	ADDITIONAL	Transketolase C-terminal section	-
ILCLDH_03762	ADDITIONAL	ATP:glycerol 3-phosphotransferase	-
ILCLDH_03763	ADDITIONAL	Glutathione S-transferase	GST_N_3
ILCLDH_03764	REGULATORY	Glycine cleavage system transcriptional ac...	-
ILCLDH_03765	TRANSPORT	Small-conductance mechanosensitive channel	-

azole-containing-RiPP

26.3 kb

Chromosome | 3,474,810 - 3,501,080

RIPP

2 CORE 2 ADDITIONAL 1 TRANSPORT 1 OTHER

6 genes total

Tailoring: electron transfer (1)

Locus	Function	Product	Domains
ILCLDH_03375	OTHER	integration host factor subunit beta	-
ILCLDH_03379	ADDITIONAL	3-phosphoserine/phosphohydroxythreonine tr...	Aminotran_5
ILCLDH_03381	CORE	30S ribosomal protein S12 methylthiotransf...	YcaO
ILCLDH_03384	CORE	pyruvate formate lyase 1-activating protein	Fer4_12, PF04055, QueE
ILCLDH_03385	TRANSPORT	MFS transporter	-
ILCLDH_03388	ADDITIONAL	dimethylsulfoxide reductase subunit A	-

redox-cofactor

22.2 kb

Chromosome | 2,583,625 - 2,605,791

RIPP

3 CORE 2 ADDITIONAL 4 REGULATORY 1 OTHER

10 genes total

Tailoring: hydrolase (1)

Locus	Function	Product	Domains
ILCLDH_02531	REGULATORY	HTH-type transcriptional regulator DmlR	-
ILCLDH_02536	ADDITIONAL	pyrroloquinoline quinone biosynthesis prot...	Peptidase_M16
ILCLDH_02537	CORE	pyrroloquinoline quinone biosynthesis prot...	PF04055, Fer4_12, QueE, SPASM
ILCLDH_02538	CORE	pyrroloquinoline quinone biosynthesis pept...	PqqD_RRE, PF05402
ILCLDH_02539	CORE	pyrroloquinoline-quinone synthase PqqC	TIGR02111
ILCLDH_02543	ADDITIONAL	Alpha/beta hydrolase	Abhydrolase_1, PF00561, Abhydrolase_6
ILCLDH_02544	REGULATORY	DNA-binding dual transcriptional regulator...	-
ILCLDH_02545	REGULATORY	Sensor histidine kinase EnvZ	-
ILCLDH_02546	OTHER	Cytochrome c biogenesis protein/redoxin	-
ILCLDH_02547	REGULATORY	HTH lysR-type domain-containing protein	-

terpene-precursor

20.9 kb

Chromosome | 4,180,527 - 4,201,427

TERPENE

1 CORE 4 ADDITIONAL 2 TRANSPORT

7 genes total

Tailoring: oxidoreductase (2) synthase (2) synthetase (1)

Product: FPP | **Substrates:** DMAPP + IPP | **Domain:** PT_FPPS_like

Locus	Function	Product	Domains
ILCLDH_04056	TRANSPORT	4-hydroxybenzoate transporter	-
ILCLDH_04057	ADDITIONAL	1,5-anhydro-D-fructose reductase	GFO_IDH_MocA, GFO_IDH_MocA_C3
ILCLDH_04058	TRANSPORT	Major facilitator superfamily (MFS) profil...	-
ILCLDH_04065	CORE	(2E,6E)-farnesyl diphosphate synthase	PT_FPPS_like
ILCLDH_04066	ADDITIONAL	1-deoxy-D-xylulose-5-phosphate synthase	DXP_synthase_N, TPP_enzyme_C
ILCLDH_04067	ADDITIONAL	Aldo/keto reductase	-
ILCLDH_04072	ADDITIONAL	bifunctional diaminoxyhydroxyphosphoribosyla...	-

RiPP-like

10.6 kb

Chromosome | 5,330,783 - 5,341,407

RIPP

1 CORE 2 ADDITIONAL

3 genes total

Locus	Function	Product	Domains
ILCLDH_05160	CORE	thiol:disulfide interchange protein DsbA	TIGR03651
ILCLDH_05161	ADDITIONAL	serine/threonine protein kinase	APH
ILCLDH_05163	ADDITIONAL	molybdenum cofactor guanylyltransferase MobA	NTP_transf_3

Prophage Regions

7

Prophages Detected

4

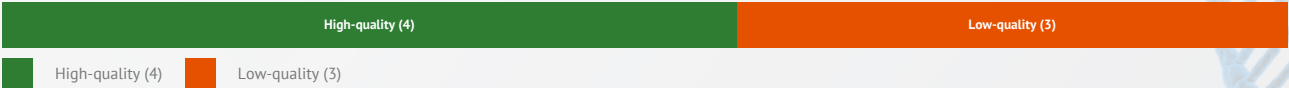
Pass QC

244.7 kb

Total Size

3T / 1V

Temperate / Virulent



Prophage Details

Prophage 1

VIRULENT HIGH PASS

50.0 kb

Caudoviricetes

Position	Virus Score	Completeness
4,022,883 - 4,072,922	0.9998	100.0%
Predicted Host	Host Method	GC Content
Klebsiella aerogenes	CRISPR-based (DB)	53.0%

Head 6

Tail 7

DNA/RNA 9

Reg 7

Unknown 55

Prophage 6

TEMPERATE HIGH PASS

47.8 kb

Caudoviricetes

Position	Virus Score	Completeness
1,849,622 - 1,897,386	0.9993	90.2%
Predicted Host	Host Method	GC Content
Klebsiella aerogenes	CRISPR-based (DB)	51.0%

Head 6

Tail 8

Lysis 4

DNA/RNA 6

Reg 4

Unknown 28

Prophage 2

TEMPERATE HIGH PASS

43.8 kb

Caudoviricetes

Position	Virus Score	Completeness
1,263,204 - 1,306,985	0.9997	99.8%
Predicted Host	Host Method	GC Content
Klebsiella aerogenes	CRISPR-based (DB)	52.0%

Lysis 4

DNA/RNA 4

Unknown 44

Prophage 3 TEMPERATE HIGH PASS 36.0 kb		
<i>Caudoviricetes</i>		
Position 1,919,245 - 1,955,251	Virus Score 0.9996	Completeness 100.0%
Predicted Host Klebsiella pneumoniae	Host Method AAI-based	GC Content 55.0%
Head 4 Tail 12 Lysis 4 Integ 4 Unknown 23		

Prophage 4 LOW FAIL 34.5 kb		
<i>Caudoviricetes</i>		
Position 3,672,755 - 3,707,254	Virus Score 0.9995	Completeness 28.6%
Predicted Host -	Host Method -	GC Content -

Prophage 5 LOW FAIL 17.9 kb		
<i>Caudoviricetes</i>		
Position 127,134 - 145,071	Virus Score 0.9995	Completeness 28.1%
Predicted Host -	Host Method -	GC Content -

Prophage 7 LOW FAIL 14.6 kb		
<i>Caudoviricetes</i>		
Position 4,755,985 - 4,770,630	Virus Score 0.9949	Completeness 44.6%
Predicted Host -	Host Method -	GC Content -

Software & Database References

Read Quality Control

Tool	Version
Fastplong	0.4.1
Kraken2	2.1.3

Assembly & Quality Control

Tool	Version
Autocycler	0.6.0
Flye	2.9.7
Raven	1.8.3
Myloasm	0.2.0
Canu	2.2
Necat	0.0.1
MetaDBG	1.1.2
Hifiasm	0.24.0
Miniasm	0.3
Nextdenovo	2.5.2
Plassembler	1.6.2
Redbean	2.5
Medaka	2.1.1
DNAAPLER	1.3.0
CheckM2	1.1.0
BUSCO	6.0.0
MOB-suite	3.1.9

Taxonomic Classification

Tool	Version
GTDB-Tk	2.6.1
Sourmash	4.9.4

Molecular Typing

Tool	Version
mlst	2.32.2
MiST	1.2.0

Antimicrobial Resistance

Tool	Version
AMRFinderPlus	4.2.7
ResFinder	4.7.2

Genome Annotation

Tool	Version
Bakta	1.12.0

Virulence Factors

Tool	Version
ABRicate	1.2.0

Mobile Genetic Elements

Tool	Version
ISEScan	1.7.3
IntegronFinder	2.0.6

Defense & CRISPR-Cas

Tool	Version
DefenseFinder	2.0.1
CRISPRCasTyper	1.8.0

Biosynthetic Gene Clusters

Tool	Version
antiSMASH	8.0.4

Prophage Analysis

Tool	Version
geNomad	1.11.2
CheckV	1.0.3
Pharokka	1.9.1
PhaBOX2	2.1.13



MASSIVE
BIOINFORMATICS

Contact

massivebioinformatics.com

info@massivebioinformatics.com

+90 216 474 60 01



THANK YOU FOR CHOOSING US!

Website

