## **Assembly Statistics**

Tool Used: MEGAHIT

# contigs	Largest contig	Total length	GC (%)	N50
74	251,689	1,820,756	38.98	96,040

### **CheckM Statistics**

Tool Used: CheckM

Bin	Completeness	Contamination	Strain heterogeneity
SRR34410864	100.00	0.00	0.00

## **Taxonomic Identification**

Tool Used: Mash

Query	Distance	P-value
Streptococcus pyogenes	0.0116	<0.001
Streptococcus dysgalactiae	0.0779	<0.001
Streptococcus canis	0.1369	<0.001
Streptococcus agalactiae	0.1744	<0.001

## **MLST Sequence Typing**

Tool Used: PubMLST

Scheme	ST-type	gki	gtr	murl	mutS	recP	xpt	yqiL
spyogenes	46	9	8	1	1	1	3	4

### **Plasmid Results**

Tool Used: ABRicate

No plasmid results	

### **AMR Results**

Tool Used: ABRicate

SEQUENCE	START	END	STRAND	GENE	%COVERAGE	%IDENTITY	DATABASE	RESISTANCE
k141_43	29928	31098	-	mefE	96.53	82.32	CARD	macrolide

SEQUENCE	START	END	STRAND	GENE	%COVERAGE	%IDENTITY	DATABASE	RESISTANCE
								lincosamide;macrolid
k141_87	192310	193529	-	ImrP	99.92	98.69	CARD	e;streptogramin;tetra
								cycline

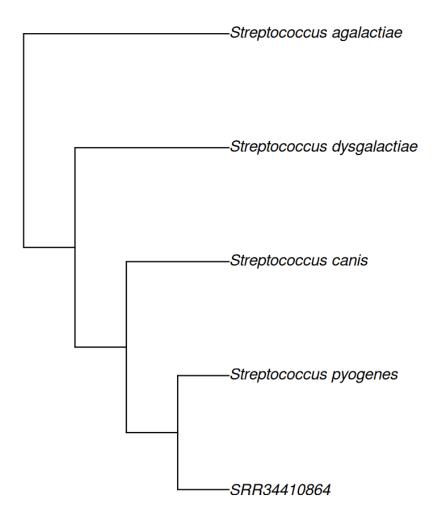
## **VF** Results

Tool Used: ABRicate

SEQUENCE	START	END	STRAND	GENE	%COVERAGE	%IDENTITY	DATABASE	PRODUCT
k141_16	71648	73363	+	slo	100.0	98.78	vfdb	streptolysin O precursor
k141_3	5610	6392	+	ssa	100.0	99.87	vfdb	streptococcal superantigen SSA - phage
k141_73	118423	119211	-	spel	100.0	99.75	vfdb	streptococcal exotoxin L precursor
k141_73	119493	120206	-	spem	100.0	99.86	vfdb	streptococcal exotoxin M precursor
k141_83	7228	7932	+	speg	100.0	99.57	vfdb	streptococcal exotoxin G precursor
k141_87	64345	65667	+	ska	99.92	84.74	vfdb	streptokinase A precursor
k141_87	82528	83229	+	smeZ	100.0	95.3	vfdb	streptococcal mitogenic exotoxin Z
k141_87	91855	92775	-	lmb	100.0	98.91	vfdb	laminin-binding surface protein
k141_87	94305	97853	-	scpA	100.0	98.39	vfdb	C5a peptidase precursor
k141_87	120834	122030	-	speB	100.0	99.75	vfdb	pyrogenic exotoxin B
k141_87	124054	124869	-	mf/spd	100.0	99.51	vfdb	deoxyribonuclease
k141_91	5572	6591	+	ideS/mac	100.0	99.22	vfdb	immunoglobulin G-degrading enzyme
k141_99	63659	65311	-	fbp54	100.0	98.49	vfdb	fibronectin-bing protein FbaA

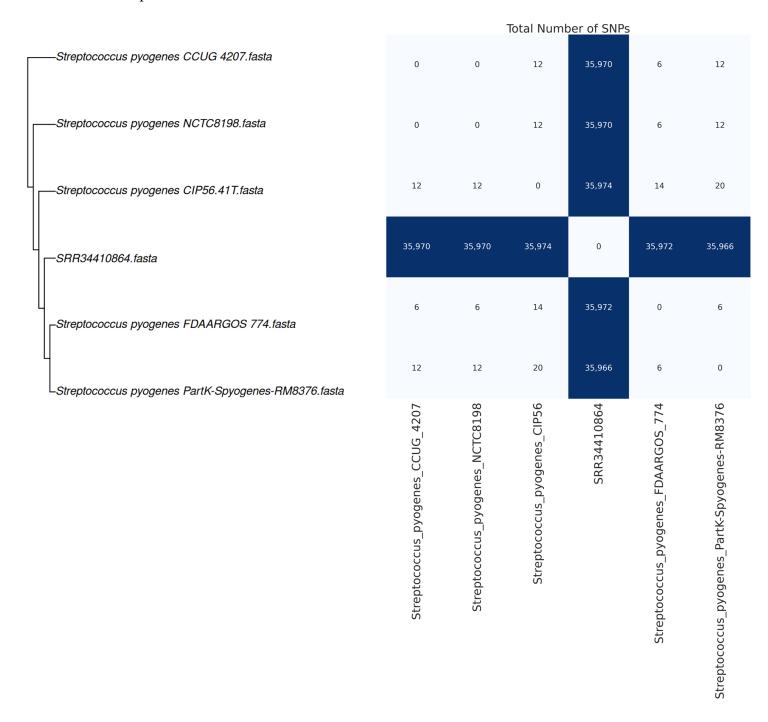
# 16S Phylogeny

Tool Used: MAFFT - FastTree



## **SNP** Analysis

Tool Used: Parsnp



Genome	Core Gene Fraction
Streptococcus_pyogenes_FDAARGOS_774	85.5%
Streptococcus_pyogenes_CCUG_4207	85.5%
Streptococcus_pyogenes_CIP56	87.5%
Streptococcus_pyogenes_NCTC8198	85.5%
SRR34410864	89.1%
Streptococcus_pyogenes_PartK-Spyogenes-RM8376	85.5%