ResFinder 2.1:
- selected threshold – 95%
- selected minimum length - 60%
- selected type of reads – Illumina paired end reads


VirulenceFinder 1.5:
- selected species - E. coli
- selected threshold for %ID – 98%
- selected minimum length - 60%
- selected type of reads – Illumina paired end reads


MLST 1.8 (MultiLocus Sequence Typing):
- selected MLST configuration - E. coli#1
- selected type of reads – Illumina paired end reads

PlasmidFinder 1.3
- selected database - Plasmid – Enterobacteriaceae
- selected threshold for %ID – 98%
- selected type of reads – Illumina paired end reads


CSI Phylogeny 1.1:
- Uploaded reference genome – VI-2011-01-1292
- Selected min depth at SNP positions – 10x
- Selected min relative depth at SNP positions – 10x
- Selected minimum distance between SNPs (prune) – 10bp
- Selected min SNP quality – 30
- Selected min read mapping quality – 25
- Selected min. Z-score – 1.96
- Used FastTree