FASTQ file(s)

Jellyfish (estimate genome size)

FASTQ file(s)

FASTQC

FASTQ file(s)

Input files

Output file/s

Programs ran

FASTQ Sequence File(s)

Trimmomatic

Summary.txt, Report.html, Data.txt, Fastqc.fo, .png (9 files)

Mer\_counts.jf, Histo\_output.histo, count\_output.jf

FASTQ file(s)

CANU

Contigs.fasta

Assembled FASTA file