

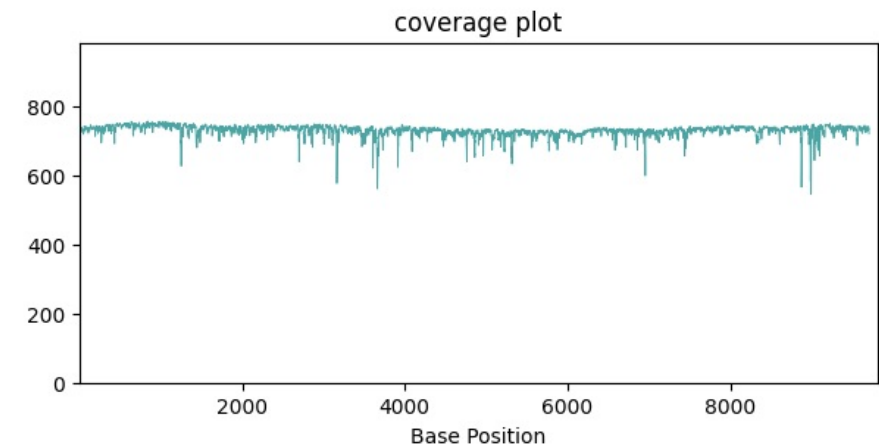
Name	Reads	Bases
Total DNA	945	7426639
Host Genomic DNA	9 (0.95%)	75713 (1.02%)

Assembly Status: form 1 contig

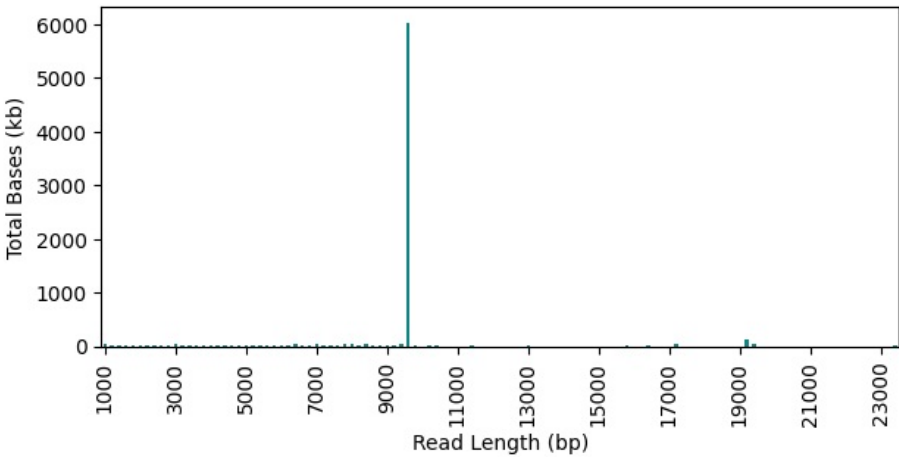
Contig	Length (bp)	Reads Mapped	Bases Mapped	Multimer	Coverage	Is Circular
004_pZX021-4_contig	9709	858 (90.79%)	7231102 (97.37%)	1.85%	730x	True

004_pZX021-4_contig Coverage Map

low confidence positions are marked with orange "x"



Read Length Distribution



Files Included:

- fasta file (per contig)
- annotated genbank file (per contig)
- ab1 chromatogram file(s) (per contig)
- detailed per-base csv file (per contig)
- low-confidence positions csv file (per contig)
- raw reads fastq file (per order)
- order summary csv file (per order)
- virtual gel image (per order)

Good Data Indicators:

- coverage greater than 200x
- read length peaks at expected plasmid size
- all reads form only 1 contig
- more than 90% of bases map to the contig sequence

