

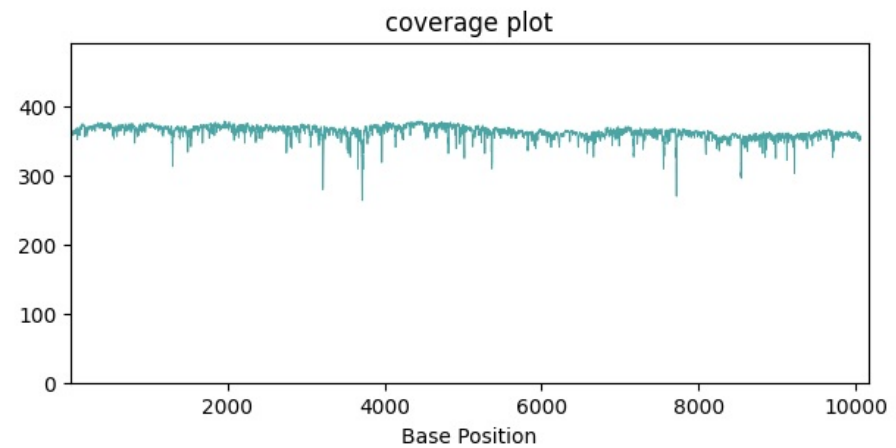
Name	Reads	Bases
Total DNA	513	3856840
Host Genomic DNA	8 (1.56%)	47016 (1.22%)

Assembly Status: form 1 contig

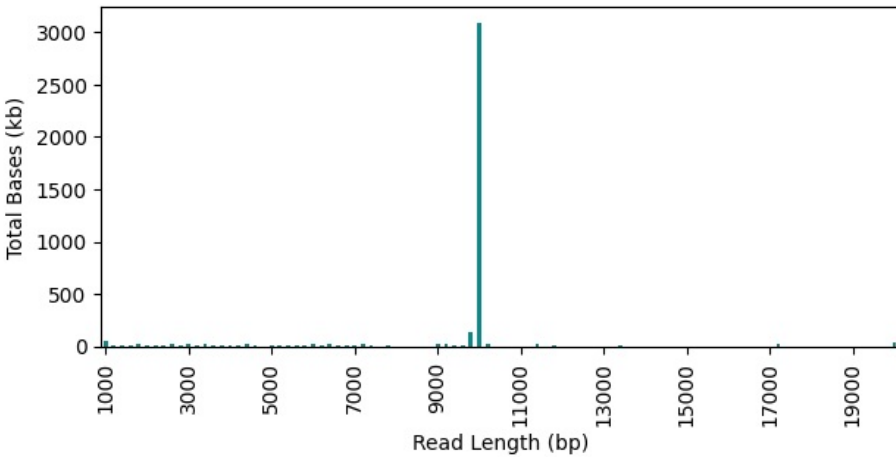
Contig	Length (bp)	Reads Mapped	Bases Mapped	Multimer	Coverage	Is Circular
002_pZX020-4_contig	10061	433 (84.41%)	3720601 (96.47%)	0.60%	363x	True

002\_pZX020-4\_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

