Whole Plasmid Sequencing Report: 001_pZX020-1

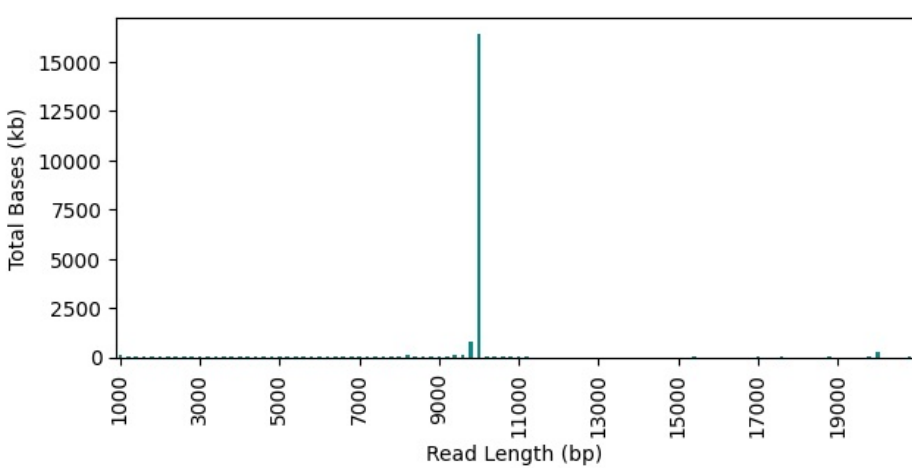| Name	Reads	Bases
Total DNA	2473	20491951
Host Genomic DNA	45 (1.82%)	322349 (1.57%)

Assembly Status: form 1 contig

Contig	Length (bp)	Reads Mapped	Bases Mapped	Multimer	Coverage	Is Circular
001_pZX020-1_contig	10061	2250 (90.98%)	19886496 (97.05%)	0.79%	1936x	True

001_pZX020-1_contig Coverage Map

low confidence positions are marked with orange "x"
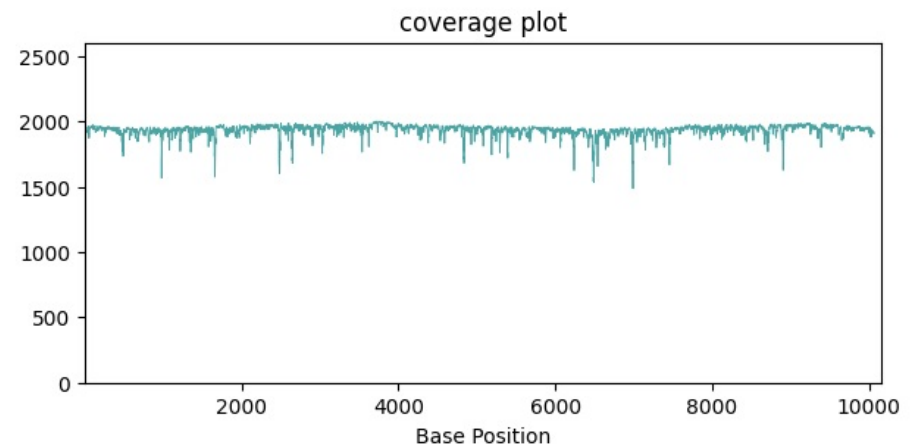
Read Length Distribution

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