Whole Plasmid Sequencing Report: 003_pZX021-1

| Name	Reads	Bases
Total DNA	835	4460961
Host Genomic DNA	22 (2.63%)	108903 (2.44%)

Assembly Status: form 1 contig

Contig	Length (bp)	Reads Mapped	Bases Mapped	Multimer	Coverage	Is Circular
003_pZX021-1_contig	9713	646 (77.37%)	4184324 (93.80%)	2.06%	421x	True

003_pZX021-1_contig Coverage Map

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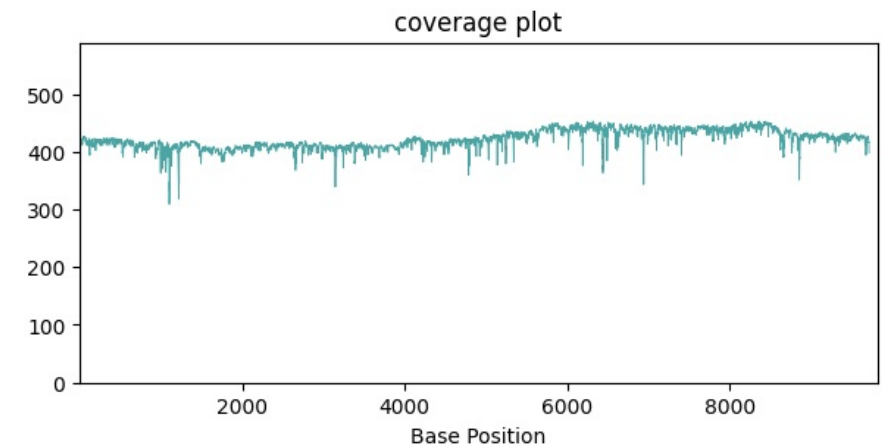
Read Length Distribution
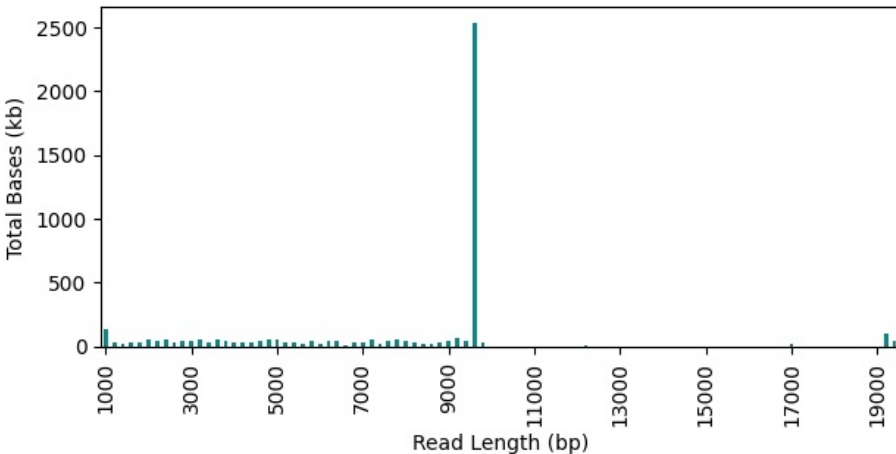
Files Included:

- 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