Report of Microbacterium saperdae in T33.3.5

Mapping stats of Illumina reads

161880773 + 0 in total (QC-passed reads + QC-failed reads)
0 + 0 secondary
95 + 0 supplementary
0 + 0 duplicates
1292500 + 0 mapped (0.80% : N/A)
161880678 + 0 paired in sequencing
80940339 + 0 read1
80940339 + 0 read2
1208870 + 0 properly paired (0.75% : N/A)
1211212 + 0 with itself and mate mapped
81193 + 0 singletons (0.05% : N/A)
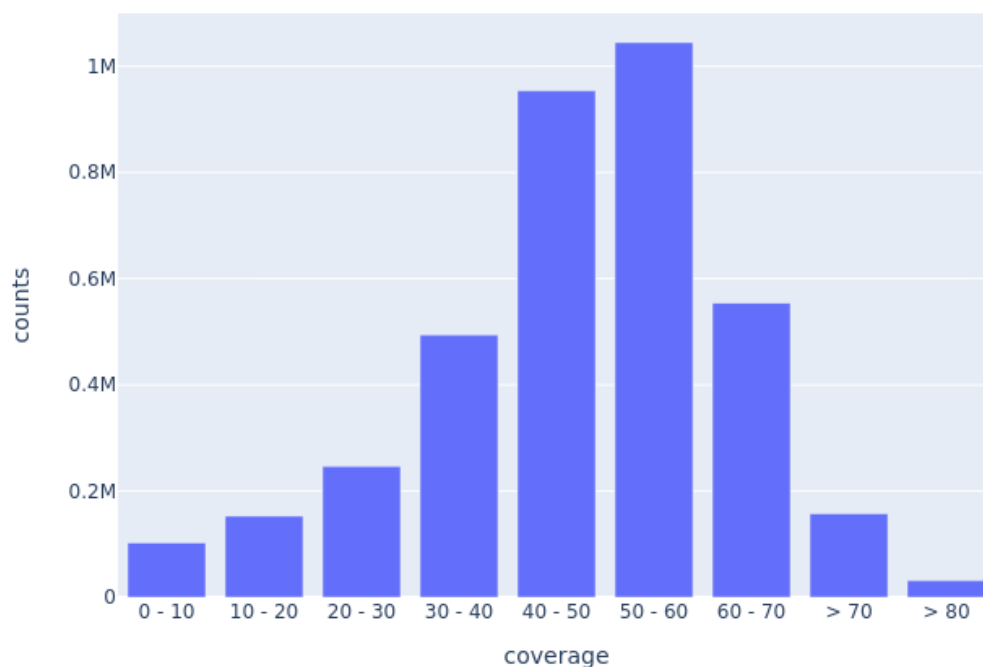0 + 0 with mate mapped to a different chr
0 + 0 with mate mapped to a different chr (mapQ>=5)

Coverage plot

This plots shows the coverage per position in the genome.
Average coverage: 49.04336038067126

Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

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