

Report of Comamonas testosteroni in T33.4.4

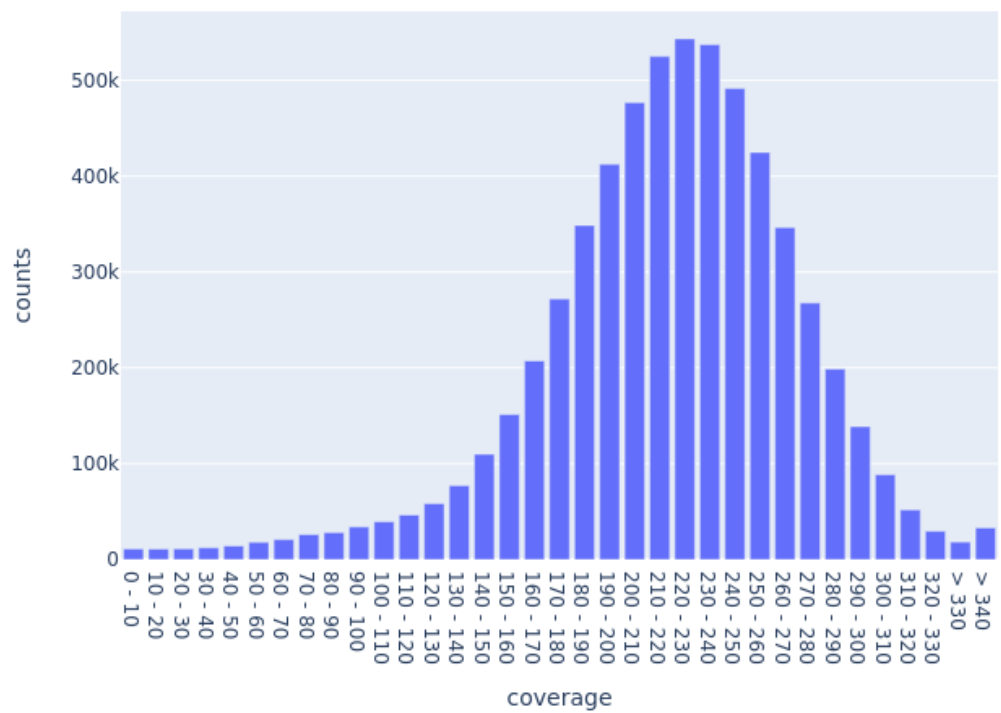
Mapping stats of Illumina reads

170533687 + 0 in total (QC-passed reads + QC-failed reads)
0 + 0 secondary
1253 + 0 supplementary
0 + 0 duplicates
9095310 + 0 mapped (5.33% : N/A)
170532434 + 0 paired in sequencing
85266217 + 0 read1
85266217 + 0 read2
8825300 + 0 properly paired (5.18% : N/A)
8832218 + 0 with itself and mate mapped
261839 + 0 singletons (0.15% : N/A)
656 + 0 with mate mapped to a different chr
378 + 0 with mate mapped to a different chr (mapQ>=5)

Coverage plot

This plots shows the coverage per position in the genome.
Average coverage: 221.17606610094586

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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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