

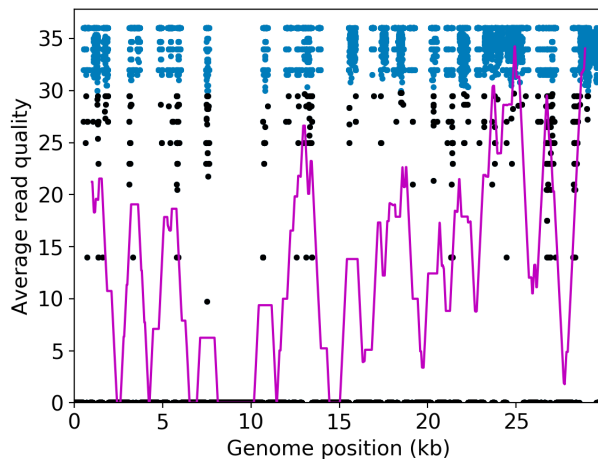
CFSAN/OAO
BIostatISTICS AND BIOinformatics STAFF

WASTEWATER SARS-COV2 ANALYSIS REPORT

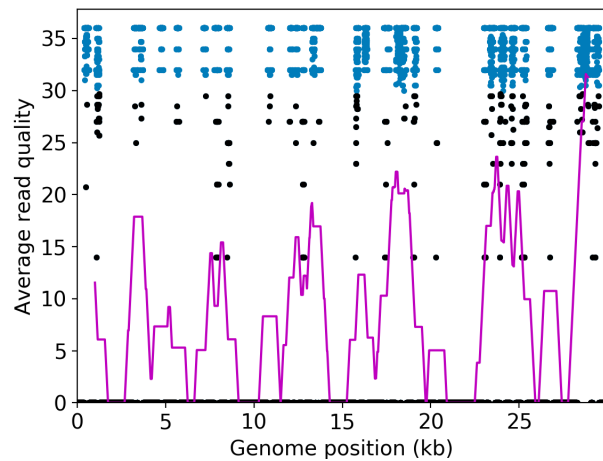
SUMMARY

Sample#	Sample name	Total #reads	% covid hits	Genomic coordinates 0X	Genomic coordinates <10X
1	SRR16828013	906676	0.79	18832	28129
2	SRR16828014	4096	13.77	22376	29615
3	SRR16828015	1366018	8.62	6793	12997
4	SRR16828016	1114642	1.68	15002	24582

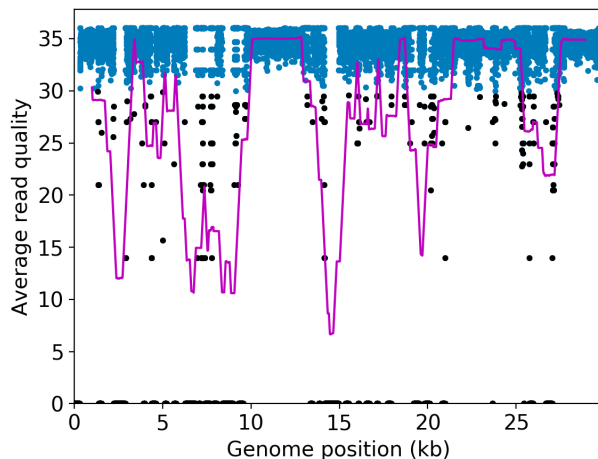
[SRR16828013](#)



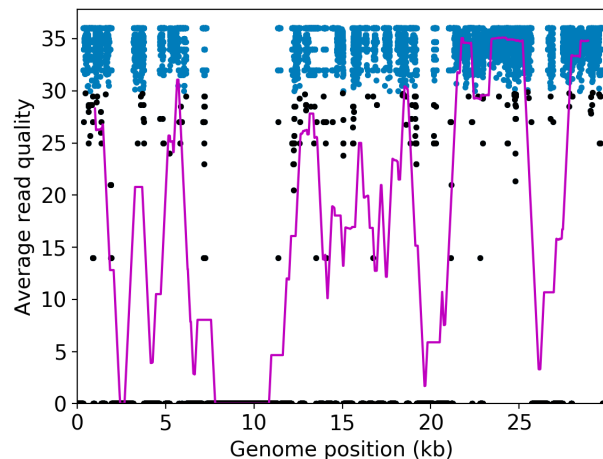
[SRR16828014](#)



[SRR16828015](#)



[SRR16828016](#)



Software configuration

Minimap2: 2.22-r1101 samtools 1.13 Using htlib 1.13, iVar version 1.3.1, Kraken version 2.1.2, kallisto, version 0.48.0. Lineage definitions were compiled on 2022-02-09 from [constellations](#). Lineage signature file was compiled on 2022-02-09 and includes lineages: A.23.1, A.23.1+E484K, AV1, AY.4, AY.4.2, Alpha, B.1.1.318, B.1.1.7+E484K, B.1.617.1, B.1.617.2+K417N, B.1.617.3, Beta, Delta, Epsilon, Eta, Gamma, Iota, Lambda, Mu, Omicron, Theta, Zeta, wt. Lineage assignment to the consensus sequence was performed by pangolin 3.1.20 using the classification tree of pangoLEARN 2022-02-02.