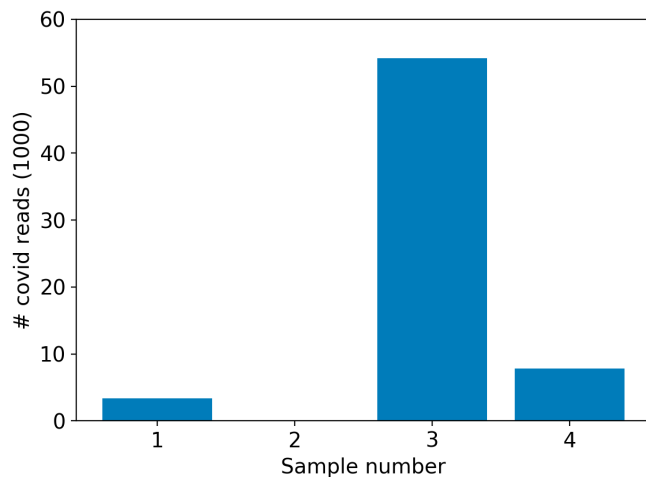


**CFSAN/OAO**  
**BIostatISTICS AND BIOinformatics STAFF**

# WASTEWATER SARS-COV2 ANALYSIS REPORT

## Summary

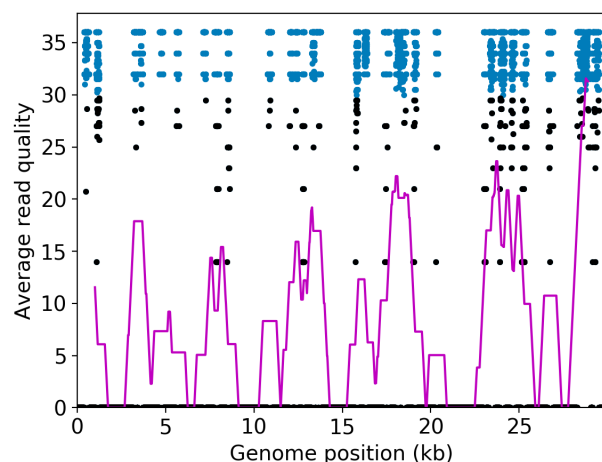
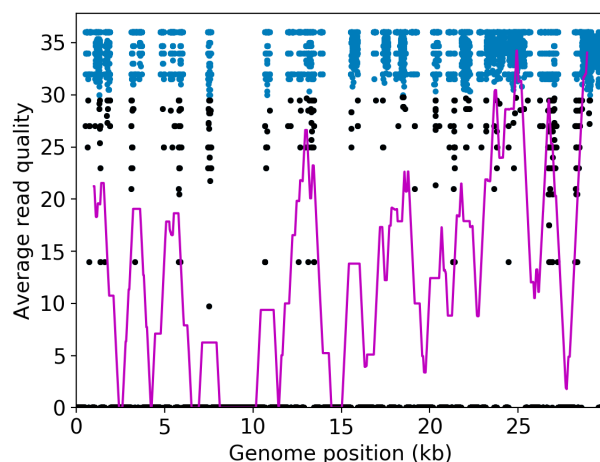
Sample#	Sample name	Total #reads	Reads aligned PF*	Genomic coordinates 0X	Genomic coordinates <10X
1	<a href="#">SRR16828013</a>	906676	3399 (0%)	18832nt (62%)	28129nt (94%)
2	<a href="#">SRR16828014</a>	4096	154 (3%)	22376nt (74%)	29615nt (99%)
3	<a href="#">SRR16828015</a>	1366018	54184 (3%)	6793nt (22%)	12997nt (43%)
4	<a href="#">SRR16828016</a>	1114642	7861 (0%)	15002nt (50%)	24582nt (82%)



\*Quantity of raw reads that align to the reference sequence and pass filter, i.e. the read length after adaptor trimming  $\geq 30$  and minimum read quality  $\geq 20$  within a sliding window of width 4. SNR refers to the ratio of SC2-mapping reads aligned that pass filter in the sample vs. that in the auto-detected negative control samples (if any). The dashed line represents the baseline level of covid reads detected from the negative control or their average if multiple negative controls we included.

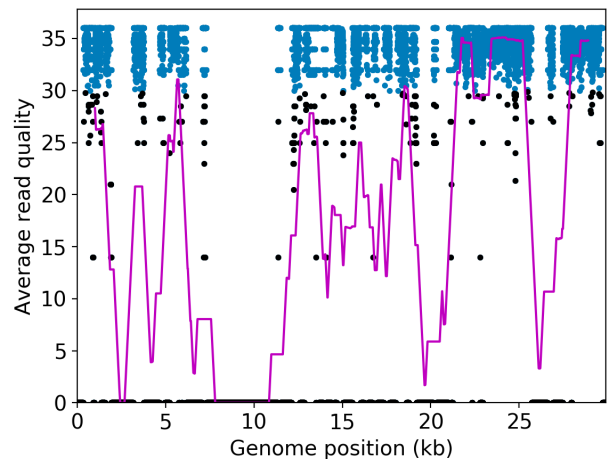
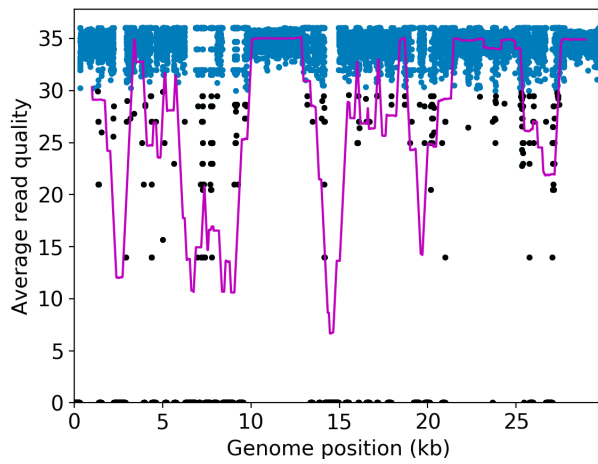
[SRR16828013](#)

[SRR16828014](#)



[SRR16828015](#)

[SRR16828016](#)



## Software configuration

Minimap2: 2.22-r1101 samtools 1.13 Using htslib 1.13, iVar version 1.3.1, Kraken version 2.1.2, kallisto, version 0.48.0. Lineage definitions were compiled on 2022-03-14 from [constellations](#). Lineage signature file was compiled on 2022-03-14 and includes lineages: A.23.1, A.23.1+E484K, AV1, AY.4, AY.4.2, B.1.1.318, B.1.1.529, B.1.1.7, B.1.1.7+E484K, B.1.351, B.1.427, B.1.429, B.1.525, B.1.526, B.1.617.1, B.1.617.2, B.1.617.2+K417N, B.1.617.3, B.1.621, BA.1, BA.2, BA.3, C.37, P.1, P.2, P.3, wt. Lineage assignment to the consensus sequence was performed by pangolin 3.1.20 using the classification tree of pangolEARN 2022-02-28.