

CFSAN/OAO
BIostatistics and Bioinformatics Staff

WASTEWATER SARS-COV2 ANALYSIS REPORT

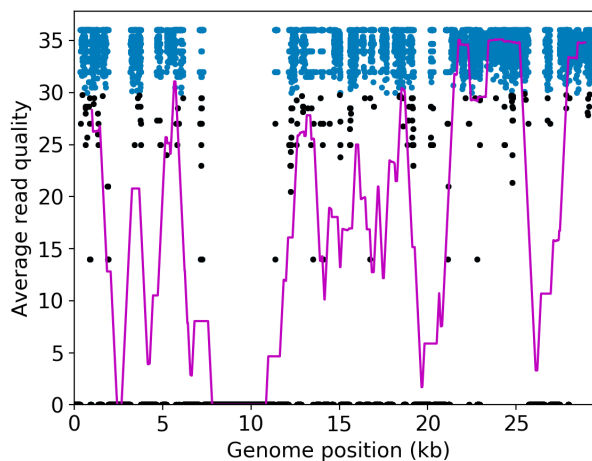
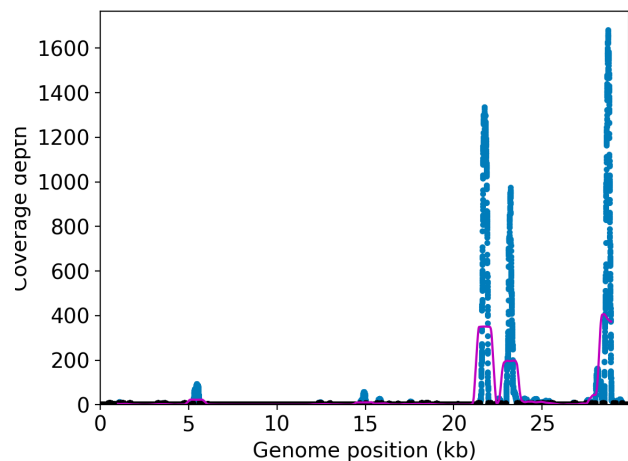
Sample name:	SRR16828016
Date generated:	2022-03-15, 14:21:28 EDT
Executed by:	Tunc Kayikcioglu (Tunc.Kayikcioglu@fda.hhs.gov)
Executed on:	172.20.44.224 (aka n224.raven.cfsan)

Sequencing summary

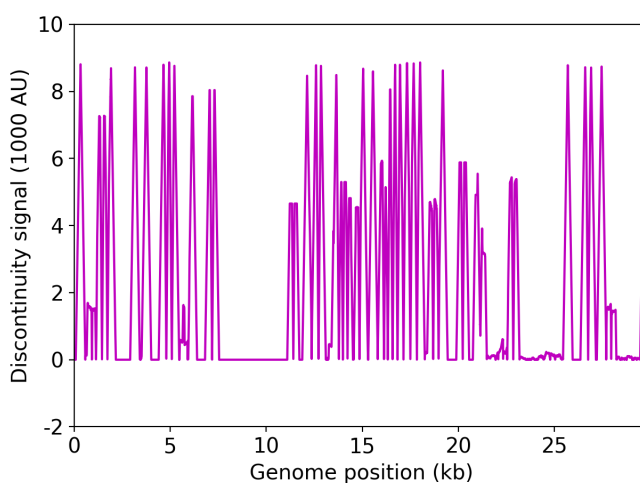
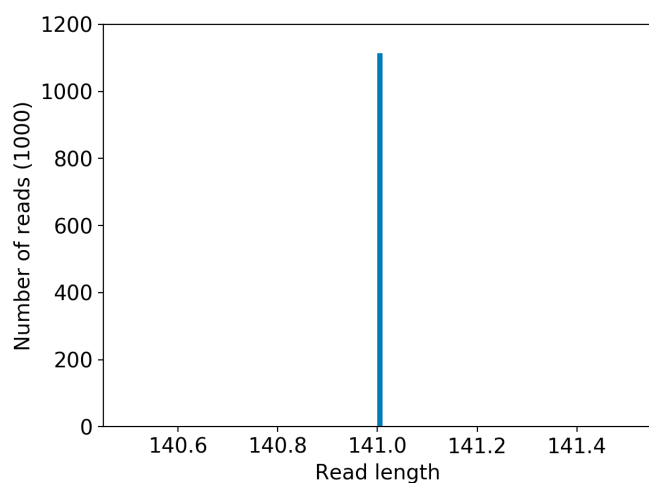
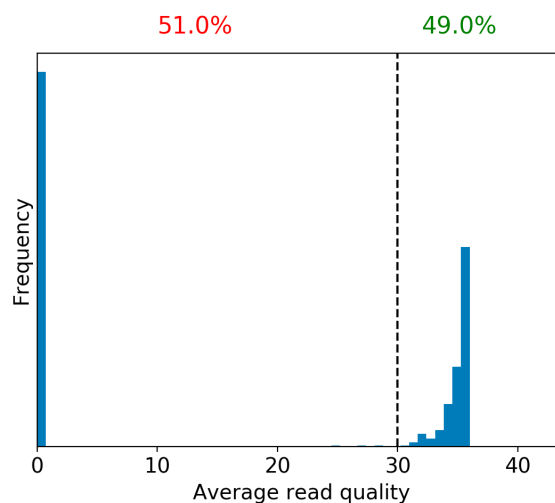
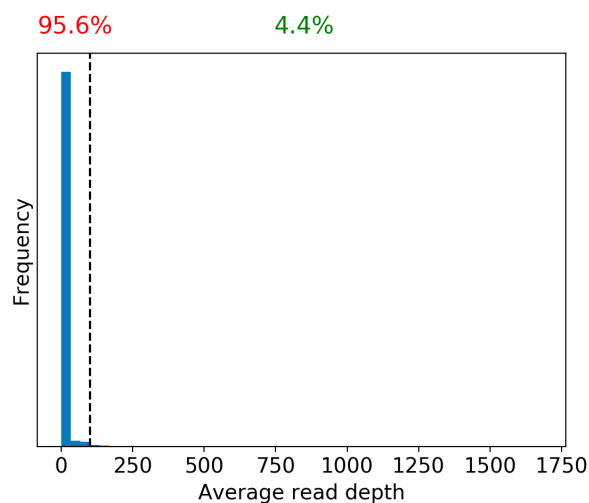
Sequencing chemistry:	AMPLICON with NextSeq 500
Source site:	USA: West Virginia (?.?)
Sampling date:	2021-02-01
Collected by:	Aquavitas
Sequenced by:	Missing
Total number of reads:	1114642
Reads aligned:	8031 (0%)
Average read quality:	34.6
Average read length:	141
Reads passing filter:	7861 (0%)
Average read quality passing filter:	34.7
Average read length passing filter:	141
Average coverage passing filter:	37X

A read passes filter if the read length after adaptor trimming ≥ 30 and minimum read quality ≥ 20 within a sliding window of width 4.

Overall sequence characteristics



NOTE: The red shaded areas marked with a (*) are not covered by the design of the library preparation kit and hence excluded from analyses. Magenta curves represent moving average with a window width of 1kb.



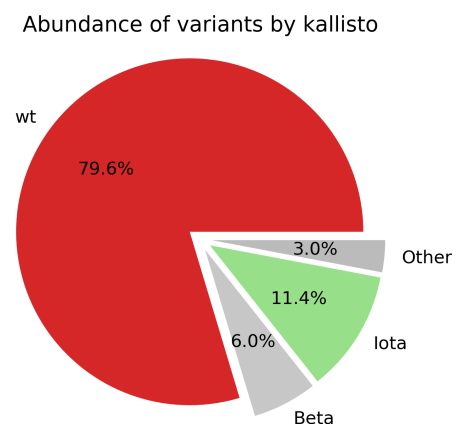
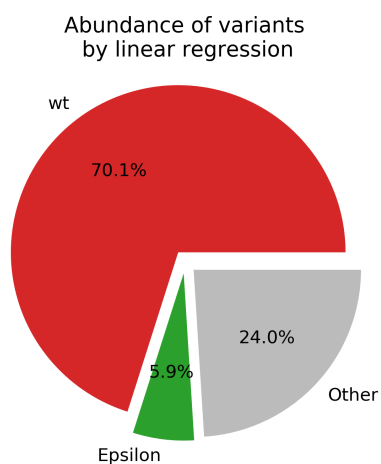
	Uncovered coordinates (0X)	Poorly covered coordinates (<10X)
# Inaccessible genomic coordinates by kit design:	-1nt (0%)	-1nt (0%)
All genomic coordinates:	15002nt (50%)	24582nt (82%)

Common SNPs:	7nt (21%)	17nt (53%)
Diverse SNPs:	419nt (82%)	448nt (88%)
Rare SNPs:	1140nt (45%)	1852nt (74%)

SNPs refer to the polymorphic sites currently in circulation that were detected out of recent GISAID entries. The sites that differ from the SC2 reference sequence are denoted as "common" if [90%, 100%] of the submissions carry this mutation, whereas those that are prevalent in [0%,10%] of the submissions are grouped under the "rare" category. The population is still diverse at the mutation sites that are observed in (10%,90%) of the entries and these coordinates are grouped under the "diverse" category.

Hits to SARS-Cov2 genome (kraken2):	9351 reads (1.68%)
Hits to human genome (kraken2):	3710 reads (0.67%)
Hits to synthetic sequences (kraken2, taxid 28384):	63 reads (0.01%)

Detected variants (Experimental)

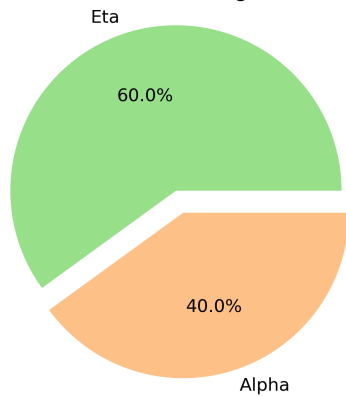


Based on deconvolution, [wt](#) is estimated to constitute 69.31% of the viral particles and hence is the most abundant variant in the sample. The R^2 for the linear regression was 0.15. Variants that were detected less than 5% were grouped under "Other"

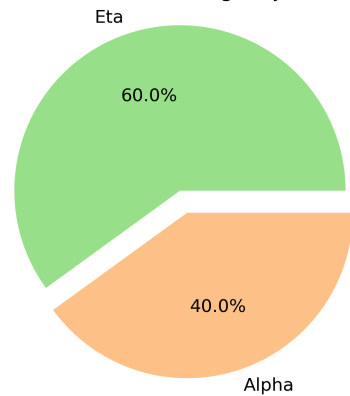
Based on the consensus sequence of the observed reads, the "ensemble-averaged sequence" most closely resembles the [B.1](#) lineage. If this is a sample consisting of a single source of pathogens or an overwhelming majority of the different sources are infected with the same variant, the sample is dominated by this variant.

Based on mapping individual reads to the variant consensus sequences in the reference database, kallisto predicts that the sample is dominated by [wt](#) lineage. Accuracy of this measure is expected to improve if the input data consists of long reads as opposed to convolution.

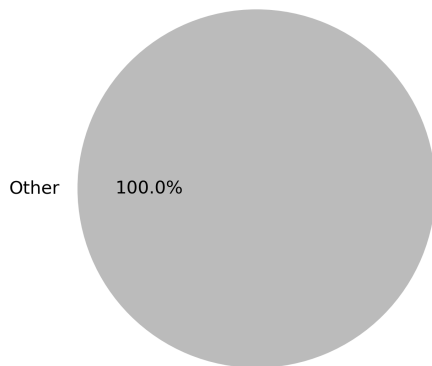
Abundance of variants by
kraken2+bracken, using allCovid DB



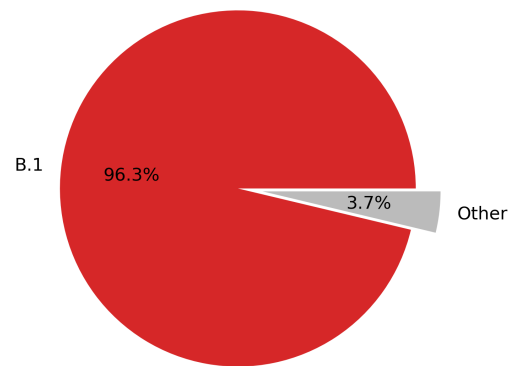
Abundance of variants by
kraken2+bracken, using majorCovid DB



Abundance of variants by Freyja



Abundance of variants by LCS



Under the assumption that the presence of a variant requires the detection of all respective mutations of the variant, the characteristic mutations which support the presence of the respective variant are indicated in the respective column of the table. Numbers show the number of mutations detected, if any, and the number of mutations expected to be present based on the variant definitions.

VOC	AY.4	AY.4.2	B.1.617.2	BA.1	BA.2	BA.3
Characteristic mutations detected	(0 of 19)	(0 of 3)	(1 of 13) N:D377Y	(1 of 23) S:A67V	(1 of 28) S:T19I	(1 of 19) S:A67V

Detected mutations

Only genomic coordinates with at least 10X coverage were considered.

Position	Ref. base	Alt. base	Alt. freq	p-value	Mutation name	Compatible lineages
5428	A	T	0.091	6.54E-03	NUC:A5428T	None found
5433	G	C	0.100	2.30E-03	ORF1AB:G1723A	None found
14805	C	T	1.000	9.51E-13	NUC:C14805T	None found
14864	T	A	0.188	6.91E-03	ORF1AB:V466D	None found
14987	A	C	0.292	4.70E-03	ORF1AB:Y507S	None found
21478	C	G	0.500	5.22E-03	ORF1AB:L2671V	None found
21537	T	G	0.300	5.77E-05	ORF1AB:D2690E	None found

21538	G	A	0.209	5.95E-04	ORF1AB:V2691I	None found
21539	T	G	0.318	4.62E-06	ORF1AB:V2691G	None found
21540	T	G	0.182	7.28E-04	NUC:T21540G	None found
21542	T	G	0.107	5.18E-03	ORF1AB:L2692R	None found
21543	T	G	0.115	4.23E-03	NUC:T21543G	None found
21546	T	A	0.110	1.05E-03	NUC:T21546A	None found
21548	A	G	0.089	2.41E-03	ORF1AB:N2694S	None found
21551	A	G	0.081	5.06E-04	ORF1AB:N2695S	None found
21555	A	T	0.085	2.76E-04	ORF1AB:*2696Y	None found
21557	C	A	0.092	7.75E-05	NUC:C21557A	None found
21559	A	+G	0.072	2.27E-03	NUC:A21559+G	None found
21562	A	+G	0.069	2.38E-03	NUC:A21562+G	None found
21581	T	G	0.056	2.29E-04	S:L7V	None found
21587	C	A	0.083	2.93E-07	S:P9T	None found
21588	C	G	0.089	8.70E-08	S:P9R	None found
21590	C	-T	0.059	2.79E-04	DEL:21590:1	None found
21591	T	A	0.052	5.74E-05	S:L10Q	None found
21622	C	G	0.053	1.55E-10	NUC:C21622G	None found
21628	T	G	0.058	1.20E-12	NUC:T21628G	None found
21633	T	A	0.058	3.60E-15	S:L24*	None found
21777	G	A	0.106	5.87E-37	S:G72E	None found
21798	T	G	0.071	4.92E-24	S:F79C	None found
21898	G	T	0.097	3.23E-19	NUC:G21898T	None found
21899	A	T	0.113	3.76E-22	S:K113*	None found
21901	G	T	0.091	2.31E-16	S:K113N	None found
21904	C	A	0.084	3.91E-14	NUC:C21904A	None found
21915	T	C	0.068	1.96E-08	S:L118P	None found
21917	A	G	0.121	7.30E-12	S:I119V	None found
21918	T	C	0.056	7.34E-05	S:I119T	None found
21921	T	C	0.077	2.10E-05	S:V120A	None found
21923	A	T	0.274	1.21E-14	S:N121Y	None found
21924	A	T	0.082	3.69E-05	S:N121I	None found
21925	T	C	0.092	3.02E-04	NUC:T21925C	None found
21926	A	G	0.442	3.79E-18	S:N122D	None found
21927	A	C	0.098	8.94E-04	S:N122T	None found
21928	C	A	0.075	5.48E-03	S:N122K	None found
21929	G	T	0.112	3.24E-04	S:A123S	None found
21931	T	+GCCG	0.253	3.51E-07	NUC:T21931+GCCG	None found
21932	A	G	0.368	5.15E-11	S:T124A	None found
21934	T	G	0.388	5.06E-16	NUC:T21934G	None found

21935	A	G	0.191	8.87E-04	S:N125D	None found
21937	T	C	0.241	5.90E-03	NUC:T21937C	None found
22959	G	C	0.350	4.16E-03	S:R466T	None found
22964	A	G	0.368	1.41E-05	S:I468V	None found
22965	T	+G	0.225	2.68E-03	NUC:T22965+G	None found
22966	T	G	0.255	4.86E-05	S:I468M	None found
22967	T	A	0.224	1.26E-04	S:S469T	None found
22968	C	T	0.185	2.35E-04	S:S469L	None found
22969	A	G	0.170	1.13E-03	NUC:A22969G	None found
22970	A	G	0.190	1.49E-04	S:T470A	None found
22971	C	G	0.167	5.47E-04	S:T470S	None found
22972	T	A	0.311	1.09E-07	NUC:T22972A	None found
22975	A	T	0.176	2.49E-05	S:E471D	None found
22976	A	G	0.194	4.75E-05	S:I472V	None found
22977	T	G	0.118	2.46E-03	S:I472S	None found
22978	C	G	0.160	6.58E-05	S:I472M	None found
22981	T	A	0.093	5.34E-03	S:Y473*	None found
22982	C	G	0.117	8.54E-04	S:Q474E	None found
22985	G	A	0.136	1.15E-04	S:A475T	None found
22987	C	A	0.095	1.14E-03	NUC:C22987A	None found
23081	C	A	0.061	2.08E-08	S:P507T	None found
23082	C	G	0.088	7.63E-13	S:P507R	None found
23084	T	G	0.109	1.64E-17	S:Y508D	None found
23086	C	G	0.062	1.34E-10	S:Y508*	None found
23087	A	+G	0.068	3.62E-09	NUC:A23087+G	None found
23106	T	A	0.059	1.38E-12	S:F515Y	None found
23108	G	A	0.060	6.39E-13	S:E516K	None found
23109	A	C	0.056	4.43E-12	S:E516A	None found
23112	T	A	0.057	5.36E-13	S:L517H	None found
23205	G	A	0.061	3.84E-17	S:G548D	None found
23222	G	+C	0.059	5.21E-11	NUC:G23222+C	None found
23223	A	T	0.134	5.85E-30	S:E554V	None found
23224	G	C	0.061	1.28E-13	S:E554D	None found
23228	A	T	0.064	7.48E-14	S:N556Y	None found
23229	A	T	0.055	3.25E-11	S:N556I	None found
23230	C	T	0.079	1.26E-15	NUC:C23230T	None found
23234	A	C	0.069	1.30E-12	S:K558Q	None found
23328	C	-A	0.099	5.62E-05	DEL:23328:1	None found
23332	T	+C	0.125	4.64E-07	NUC:T23332+C	None found
23335	T	+TATACACA	0.080	3.70E-04	NUC:T23335+TATACACA	None found
23337	T	C	0.107	1.72E-06	S:F592S	None found

23339	G	A	0.065	1.42E-03	S:G593S	None found
23340	G	C	0.184	2.96E-08	S:G593A	None found
23341	T	C	0.147	4.09E-06	NUC:T23341C	P.3
23342	G	C	0.124	1.18E-04	S:G594R	None found
23343	G	C	0.364	5.77E-14	S:G594A	None found
23344	T	C	0.086	4.42E-03	NUC:T23344C	None found
23345	G	C	0.087	3.76E-03	S:V595L	None found
23347	C	-AG	0.244	4.58E-07	DEL:23347:2	None found
23351	G	C	0.344	3.14E-09	S:V597L	None found
23356	A	+C	0.169	1.20E-04	NUC:A23356+C	None found
23360	C	T	0.130	3.05E-03	S:P600S	None found
23403	A	G	0.932	7.42E-28	S:D614G	B.1.1.529 , B.1.427 , C.37 , B.1.429 , B.1.526 , AV1 , B.1.621
25122	A	G	0.462	5.80E-03	S:N1187S	None found
28136	T	C	0.062	2.04E-03	NUC:T28136C	None found
28150	T	A	0.058	4.96E-03	ORF8:F86Y	None found
28158	A	C	0.063	5.10E-03	ORF8:N89H	None found
28250	T	+CTG	0.798	1.82E-23	NUC:T28250+CTG	None found
28253	C	-A	0.812	6.08E-23	DEL:28253:1	None found
28254	A	C	0.429	4.08E-07	ORF8:I121L	None found
28297	T	C	0.904	6.83E-42	NUC:T28297C	None found
28509	G	+C	0.250	5.22E-03	NUC:G28509+C	None found
28510	T	G	0.561	2.84E-10	N:S79R	None found
28511	C	T	0.450	1.04E-08	N:P80S	None found
28517	G	+TGTATA	0.200	6.47E-04	NUC:G28517+TGTATA	None found
28518	A	T	0.370	1.31E-08	N:D82V	None found
28519	C	T	0.071	3.19E-03	NUC:C28519T	None found
28520	C	T	0.364	4.97E-11	N:Q83*	None found
28521	A	G	0.227	1.25E-05	N:Q83R	None found
28522	A	T	0.111	1.67E-03	N:Q83H	None found
28523	A	C	0.195	2.60E-06	N:I84L	None found
28524	T	G	0.198	2.02E-07	N:I84S	None found
28525	T	G	0.333	6.92E-12	N:I84M	None found
28527	G	T	0.075	4.36E-04	N:G85V	None found
28528	C	A	0.123	3.72E-06	NUC:C28528A	None found
28529	T	A	0.130	9.38E-07	N:Y86N	None found
28530	A	G	0.127	1.17E-06	N:Y86C	None found
28531	C	A	0.056	5.96E-04	N:Y86*	None found
28532	T	G	0.112	1.46E-07	N:Y87D	None found
28590	C	T	0.062	3.54E-11	N:P106L	None found
28842	G	T	0.379	6.69E-82	N:S190I	None found

28869	C	T	0.503	8.62E-71	N:P199L	B.1.526
28885	A	C	0.052	5.13E-04	NUC:A28885C	None found
28888	T	C	0.063	9.69E-04	NUC:T28888C	None found
28890	C	G	0.081	2.72E-04	N:S206C	None found
28892	C	+T	0.067	7.86E-03	NUC:C28892+T	None found
28895	G	T	0.088	4.98E-04	N:A208S	None found
28896	C	A	0.115	2.09E-04	N:A208D	None found
28899	G	T	0.074	7.51E-03	N:R209I	None found
28900	A	+C	0.096	3.62E-03	NUC:A28900+C	None found
28901	A	C	0.107	2.59E-03	N:M210L	None found
28904	G	T	0.145	1.76E-03	N:A211S	None found
28908	G	A	0.167	5.80E-03	N:G212D	None found
28911	A	C	0.290	6.31E-04	N:N213T	None found
29402	G	T	0.368	1.56E-03	N:D377Y	B.1.617.3 , B.1.617.2+K417N , B.1.617.2