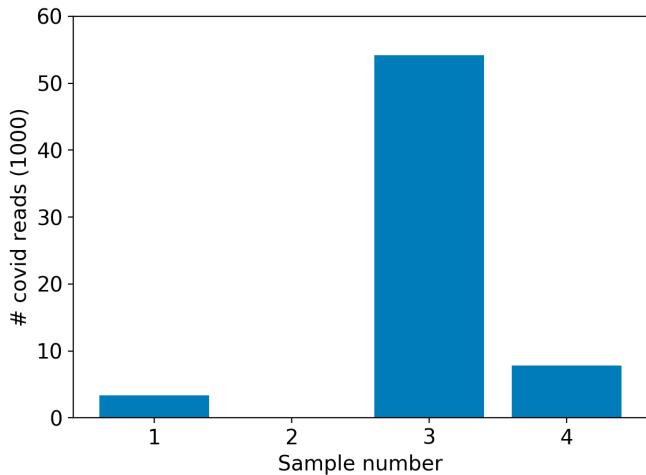




WASTEWATER SARS-COV2 ANALYSIS REPORT

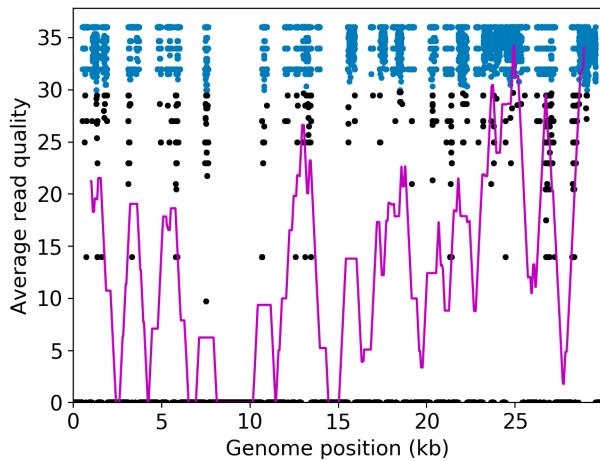
Summary

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

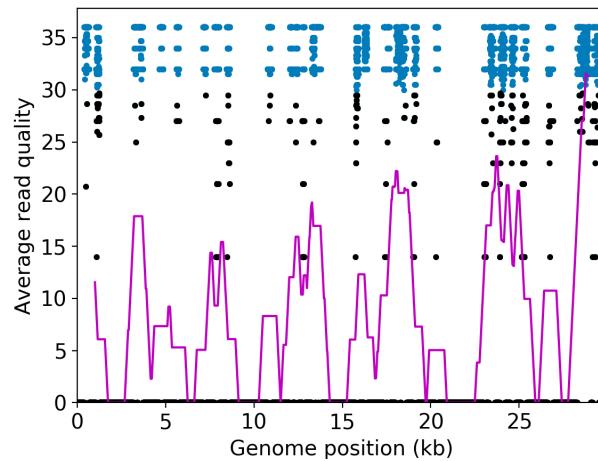


*Quantity of raw reads that align to the reference sequence and pass filter, i.e. the read length after adaptor trimming ≥ 30 and minimum read quality ≥ 20 within a sliding window of width 4. SNR refers to the ratio of SC2-mapping reads aligned that pass filter in the sample vs. that in the auto-detected 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 were included.

[SRR16828013](#)

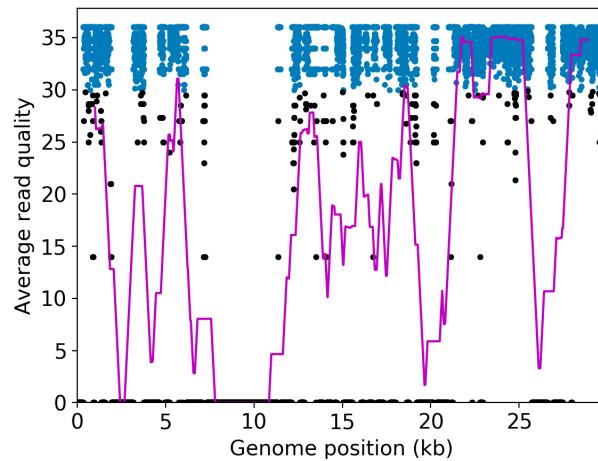
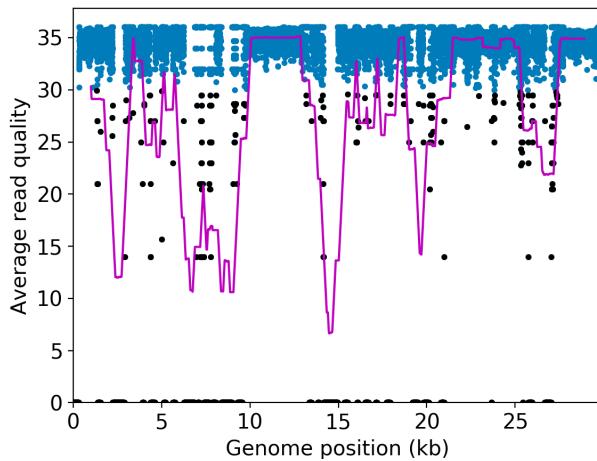


[SRR16828014](#)



[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.

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WASTEWATER SARS-COV2 ANALYSIS REPORT

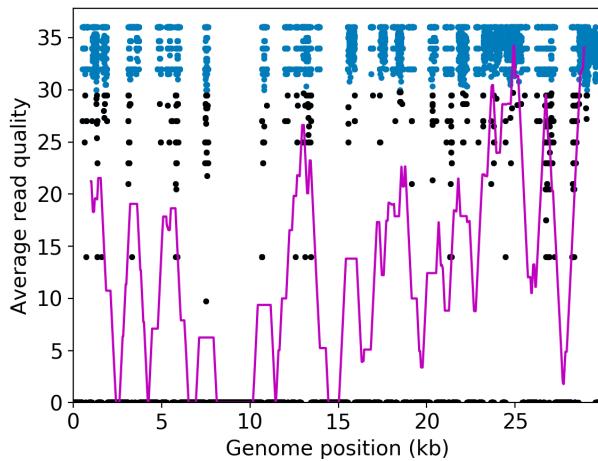
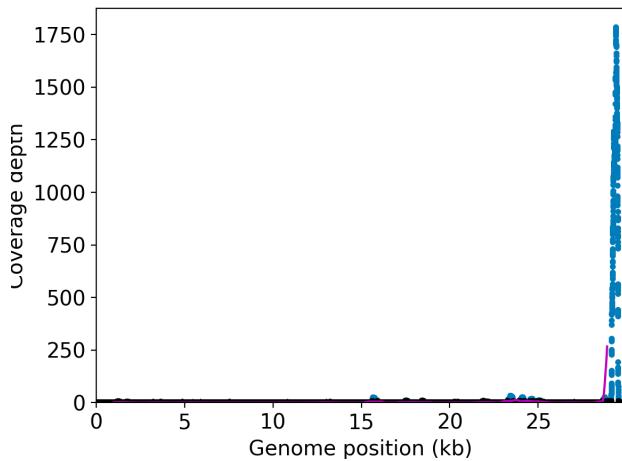
Sample name:	SRR16828013
Date generated:	2022-03-15, 14:47:48 EDT
Executed by:	Tunc Kayikcioglu (Tunc.Kayikcioglu@fda.hhs.gov)
Executed on:	172.20.44.145 (aka n145.raven.cfsan)

Sequencing summary

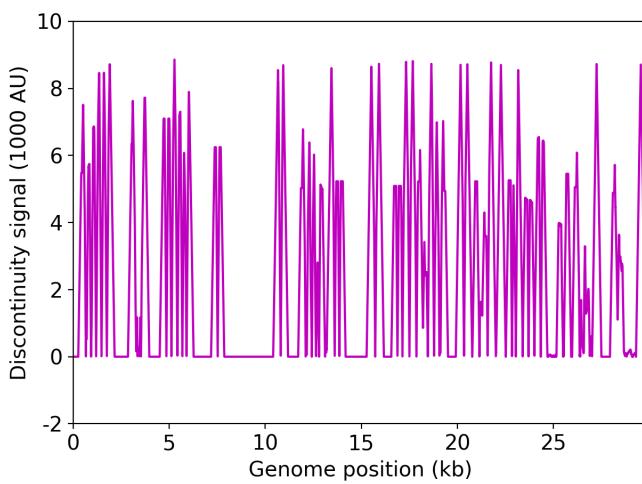
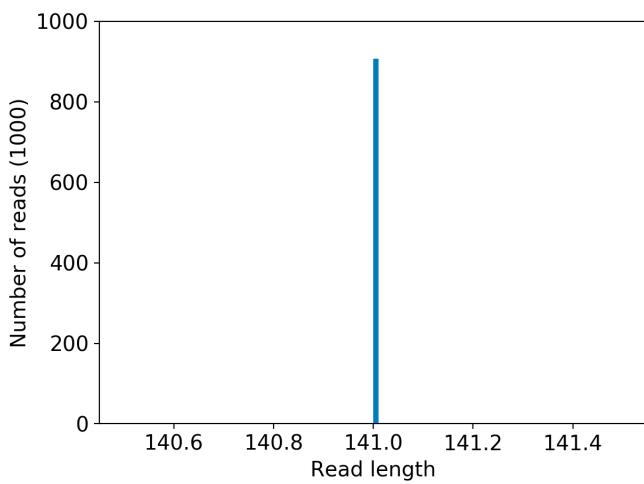
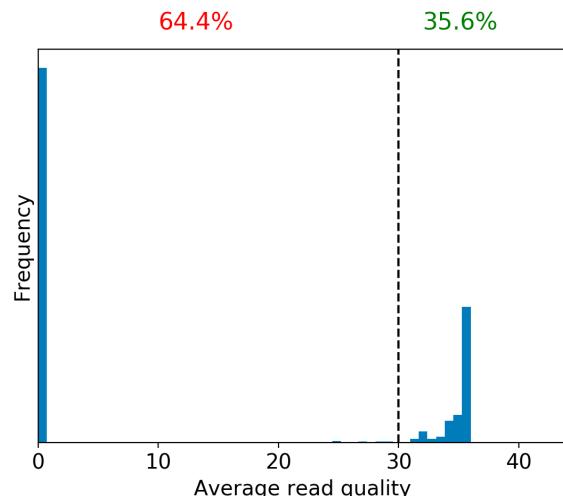
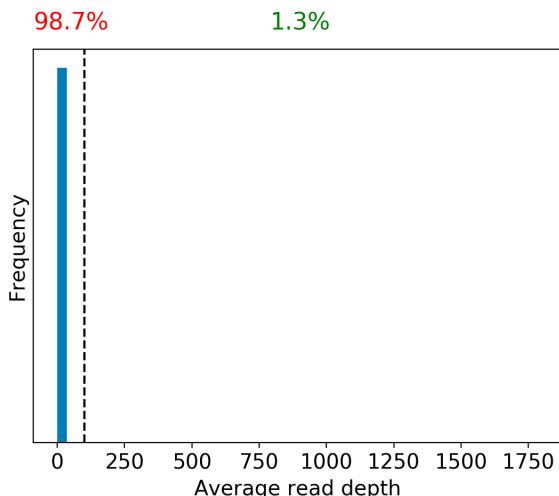
Sequencing chemistry:	AMPLICON with NextSeq 500
Source site:	USA: Washington (?,?)
Sampling date:	2021-01-11
Collected by:	Aquavitas
Sequenced by:	Missing
Total number of reads:	906676
Reads aligned:	3476 (0%)
Average read quality:	34.6
Average read length:	141
Reads passing filter:	3399 (0%)
Average read quality passing filter:	34.7
Average read length passing filter:	141
Average coverage passing filter:	16X

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.



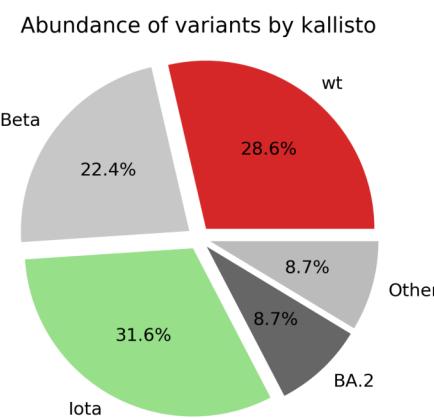
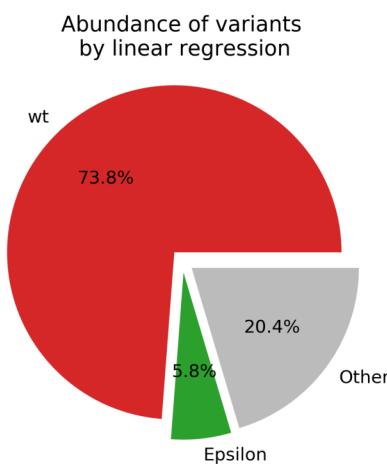
	Uncovered coordinates (0X)	Poorly covered coordinates (<10X)
# Inaccessible genomic coordinates by kit design:	-1nt (0%)	-1nt (0%)
All genomic coordinates:	18832nt (62%)	28129nt (94%)

Common SNPs:	14nt (43%)	26nt (81%)
Diverse SNPs:	117nt (23%)	504nt (99%)
Rare SNPs:	1987nt (79%)	2495nt (99%)

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):	3577 reads (0.79%)
Hits to human genome (kraken2):	1968 reads (0.43%)
Hits to synthetic sequences (kraken2, taxid 28384):	113 reads (0.02%)

Detected variants (Experimental)

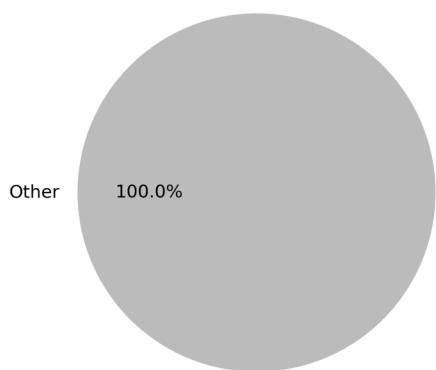


Based on deconvolution, [wt](#) is estimated to constitute 72.54% of the viral particles and hence is the most abundant variant in the sample. The R^2 for the linear regression was 0.21. Variants that were detected less than 5% were grouped under "Other"

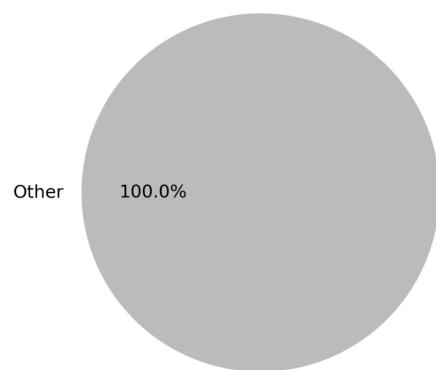
Based on the consensus sequence of the observed reads, the "ensemble-averaged sequence" most closely resembles the [B](#) lineage. If this is a sample consisting of a single source of pathogens or an overwhelming majority of the different sources are infected with the same variant, the sample is dominated 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 [Iota](#) lineage. Accuracy of this measure is expected to improve if the input data consists of long reads as opposed to convolution.

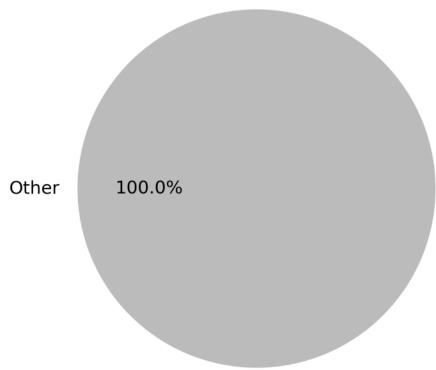
Abundance of variants by kraken2+bracken, using allCovid DB



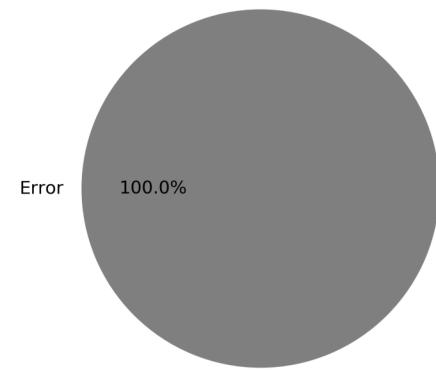
Abundance of variants by kraken2+bracken, using majorCovid DB



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)	(0 of 13)	(0 of 23)	(0 of 28)	(0 of 19)

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
23403	A	G	0.778	2.03E-07	S:D614G	B.1.1.529 , B.1.427 , C.37 , B.1.429 , B.1.526 , AV1 , B.1.621
24076	T	C	0.278	7.89E-03	NUC:T24076C	None found
29133	G	T	0.320	1.63E-03	N:G287V	None found
29135	G	T	0.342	2.67E-06	N:D288Y	None found
29136	A	G	0.225	7.92E-04	N:D288G	None found
29137	C	T	0.436	1.48E-08	NUC:C29137T	None found

29138	C	T	0.100	7.24E-03	N:Q289*		None found
29140	G	+A	0.203	1.03E-04	NUC:G29140+A		None found
29141	G	T	0.072	9.38E-03	N:E290*		None found
29142	A	T	0.093	2.13E-03	N:E290V		None found
29143	A	T	0.246	1.15E-09	N:E290D		None found
29144	C	T	0.062	3.07E-03	NUC:C29144T		None found
29145	T	G	0.267	7.94E-10	N:L291R		None found
29146	A	T	0.172	7.98E-09	NUC:A29146T		None found
29147	A	G	0.131	2.10E-06	N:I292V		None found
29148	T	A	0.143	3.37E-07	N:I292N		None found
29149	C	G	0.139	6.28E-08	N:I292M		None found
29150	A	T	0.113	3.06E-06	N:R293*		None found
29151	G	+T	0.070	7.52E-04	NUC:G29151+T		None found
29153	C	T	0.120	5.08E-10	N:Q294*		None found
29156	G	+A	0.052	3.45E-03	NUC:G29156+A		None found
29157	G	A	0.053	2.10E-05	N:G295E		None found
29158	A	G	0.050	3.28E-05	NUC:A29158G		None found
29161	T	G	0.056	4.36E-06	NUC:T29161G		None found
29276	G	T	0.052	2.80E-18	N:G335C		None found
29384	G	T	0.543	0.00E+00	N:D371Y		None found
29508	G	+C	0.055	1.61E-07	NUC:G29508+C		None found
29510	A	T	0.087	4.77E-16	N:S413C		None found
29512	T	+C	0.051	1.49E-05	NUC:T29512+C		None found
29513	G	T	0.072	1.31E-12	N:A414S		None found
29516	G	T	0.078	4.81E-11	N:D415Y		None found
29519	T	A	0.096	4.65E-13	N:S416T		None found
29520	C	+TGT	0.057	3.30E-03	NUC:C29520+TGT		None found
29521	A	T	0.132	2.92E-08	NUC:A29521T		None found
29522	A	T	0.487	1.55E-34	N:T417S		None found
29525	C	T	0.111	3.10E-07	N:Q418*		None found
29526	A	T	0.200	1.40E-07	N:Q418L		None found
29527	G	T	0.494	4.83E-23	N:Q418H		None found
29528	G	T	0.139	1.23E-04	N:A419S		None found
29530	C	T	0.404	1.45E-07	NUC:C29530T		None found
29531	T	G	0.303	1.46E-04	N:*420E		None found
29533	A	T	0.667	4.88E-08	N:*420Y		None found
29536	T	A	1.000	9.61E-08	NUC:T29536A		None found

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WASTEWATER SARS-COV2 ANALYSIS REPORT

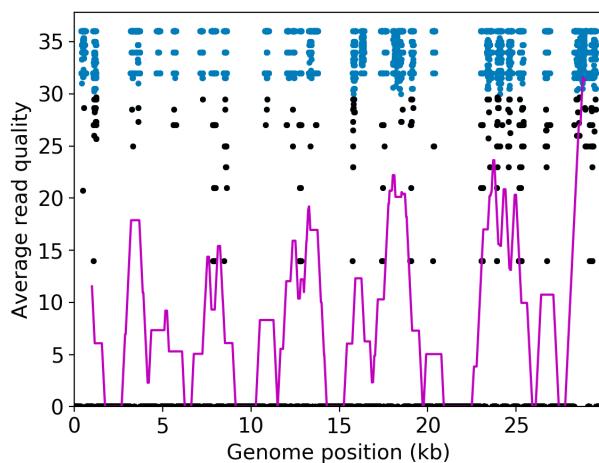
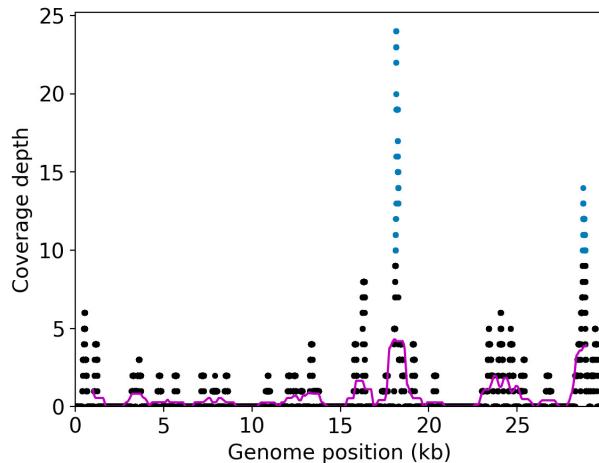
Sample name:	SRR16828014
Date generated:	2022-03-15, 14:20:14 EDT
Executed by:	Tunc Kayikcioglu (Tunc.Kayikcioglu@fda.hhs.gov)
Executed on:	172.20.44.145 (aka n145.raven.cfsan)

Sequencing summary

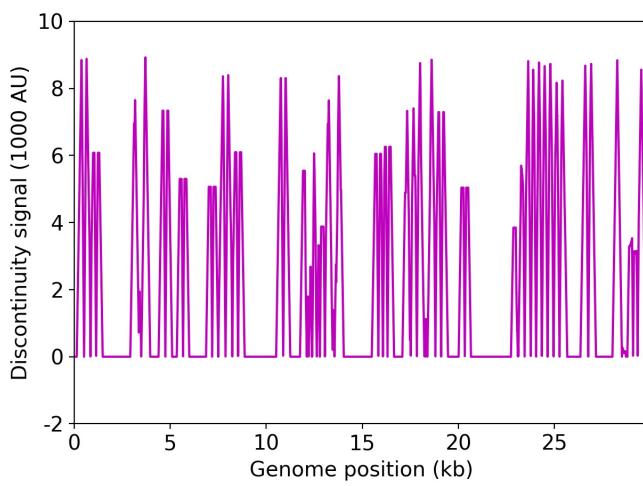
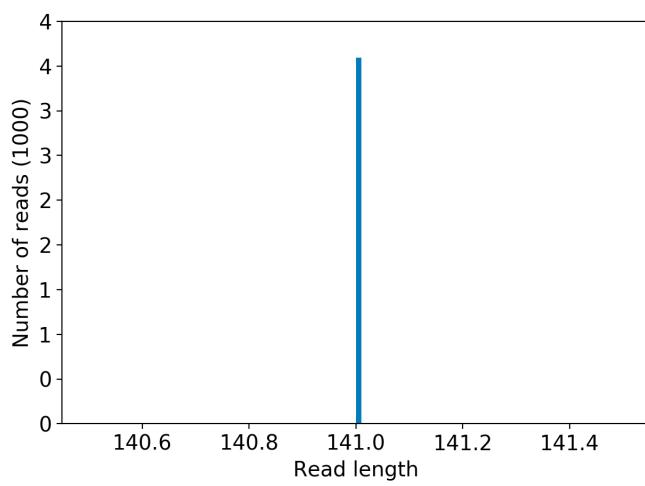
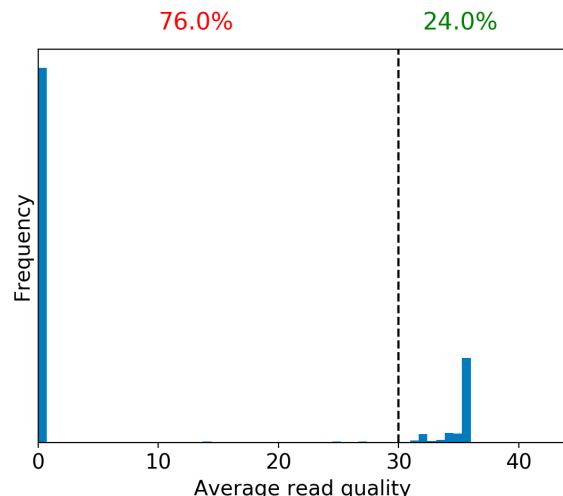
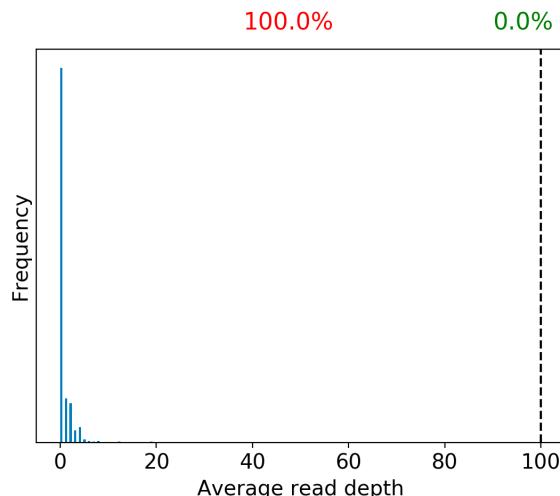
Sequencing chemistry:	AMPLICON with NextSeq 500
Source site:	USA: Washington (?,?)
Sampling date:	2021-01-04
Collected by:	Aquavitas
Sequenced by:	Missing
Total number of reads:	4096
Reads aligned:	157 (3%)
Average read quality:	34.4
Average read length:	141
Reads passing filter:	154 (3%)
Average read quality passing filter:	34.5
Average read length passing filter:	141
Average coverage passing filter:	0X

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.



WARNING: The sequence coverage is very low (0X)

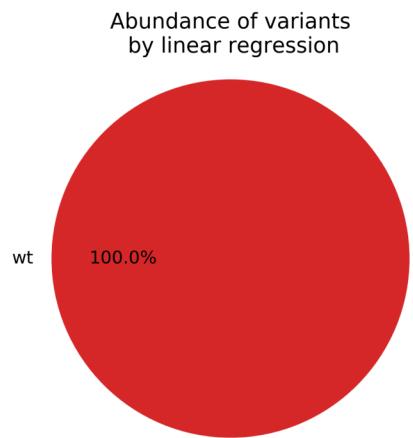
	Uncovered coordinates (0X)	Poorly covered coordinates (<10X)
# Inaccessible genomic coordinates by kit design:	-1nt (0%)	-1nt (0%)

All genomic coordinates:	22376nt (74%)	29615nt (99%)
Common SNPs:	16nt (50%)	31nt (96%)
Diverse SNPs:	491nt (97%)	505nt (100%)
Rare SNPs:	2315nt (92%)	2500nt (100%)

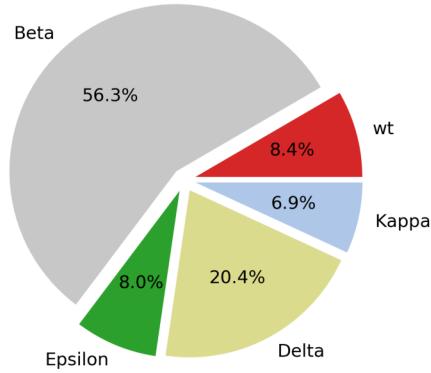
SNPs refer to the polymorphic sites currently in circulation that were detected out of recent GISAID entries. The sites that differ from the SC2 reference sequence are denoted as "common" if [90%, 100%] of the submissions carry this mutation, whereas those that are prevalent in [0%, 10%] of the submissions 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):	282 reads (13.77%)
Hits to human genome (kraken2):	302 reads (14.75%)
Hits to synthetic sequences (kraken2, taxid 28384):	0 reads (0.00%)

Detected variants (Experimental)



Abundance of variants by kallisto

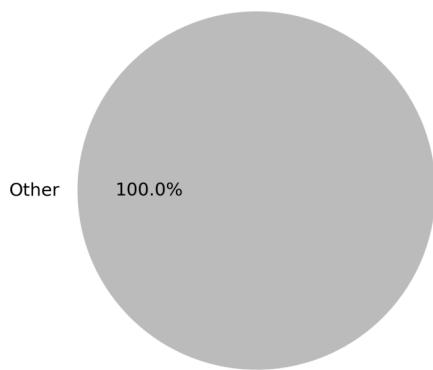


Based on deconvolution, [wt](#) is estimated to constitute 100.00% of the viral particles and hence is the most abundant variant in the sample. The R^2 for the linear regression was 1.00. Variants that were detected less than 5% were grouped under "Other"

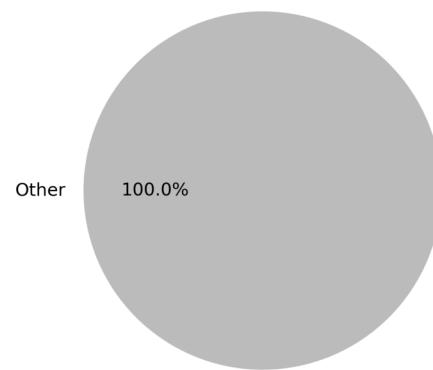
Based on the consensus sequence of the observed reads, the "ensemble-averaged sequence" most closely resembles the [Unknown](#) lineage. If this is a sample consisting of a single source of pathogens or an overwhelming majority of the different sources are infected with the same variant, the sample is 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 [Beta](#) lineage. Accuracy of this measure is expected to improve if the input data consists of long reads as opposed to convolution.

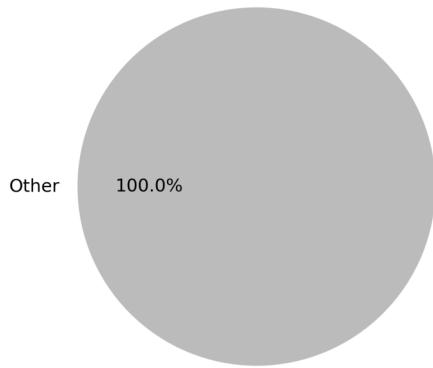
Abundance of variants by kraken2+bracken, using allCovid DB



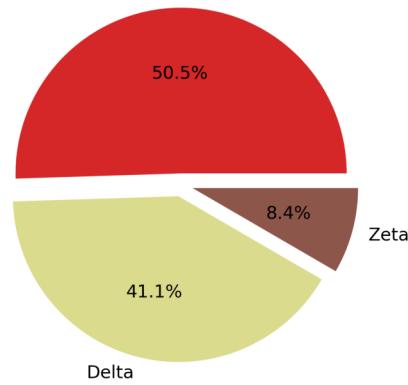
Abundance of variants by kraken2+bracken, using majorCovid DB



Abundance of variants by Freyja



Abundance of variants by LCS
B.1



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)	(0 of 13)	(0 of 23)	(0 of 28)	(0 of 19)

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
18268	G	T	0.364	5.49E-04	ORF1AB:E1601*	None found
18270	A	C	0.500	1.55E-03	ORF1AB:E1601D	None found
18271	G	T	0.385	1.62E-04	ORF1AB:E1602*	None found

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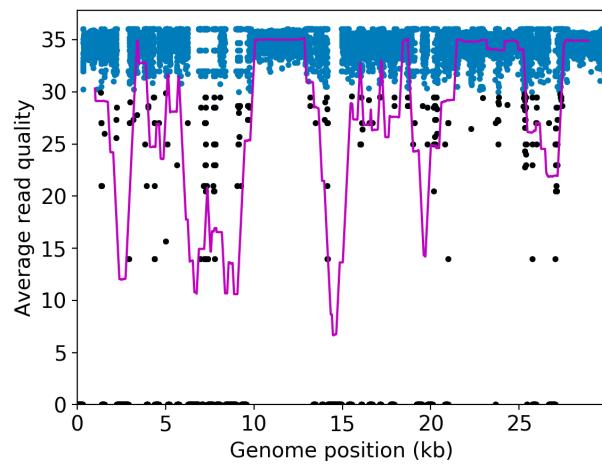
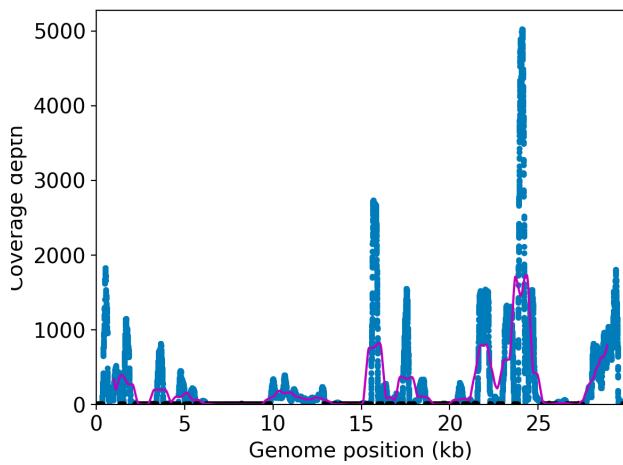
Sample name:	SRR16828015
Date generated:	2022-03-15, 14:36:25 EDT
Executed by:	Tunc Kayikcioglu (Tunc.Kayikcioglu@fda.hhs.gov)
Executed on:	172.20.44.145 (aka n145.raven.cfsan)

Sequencing summary

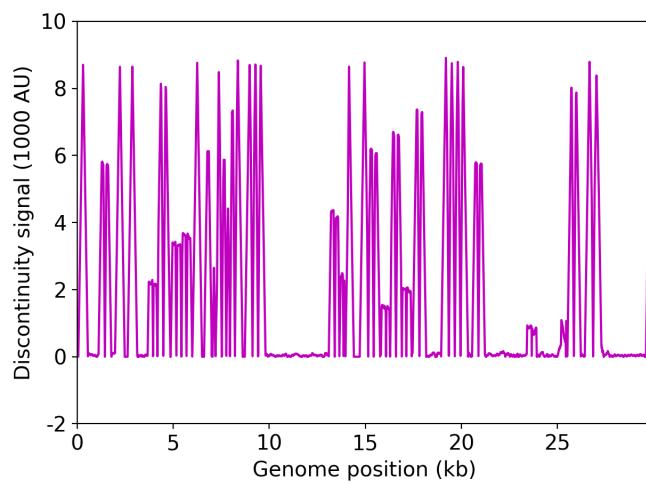
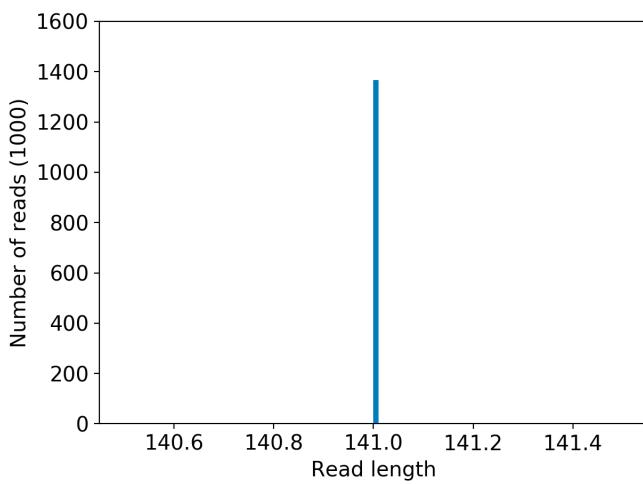
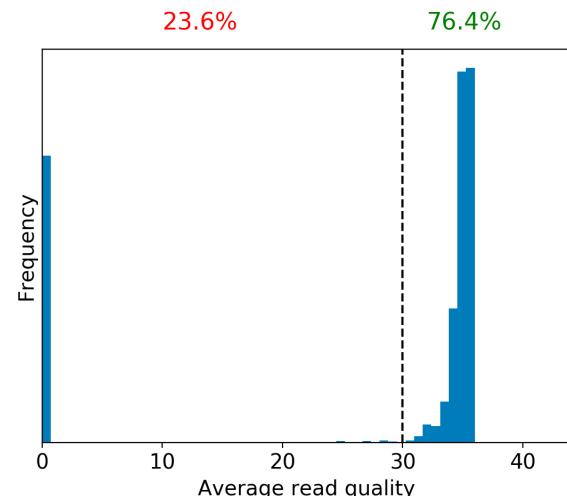
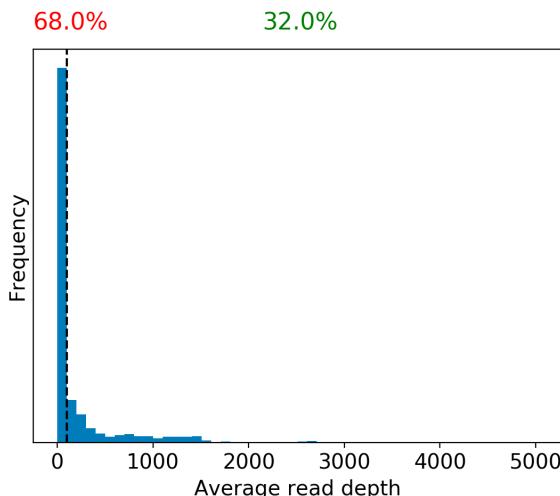
Sequencing chemistry:	AMPLICON with NextSeq 500
Source site:	USA: West Virginia (?.)
Sampling date:	2021-02-08
Collected by:	Aquavitas
Sequenced by:	Missing
Total number of reads:	1366018
Reads aligned:	55306 (4%)
Average read quality:	34.6
Average read length:	141
Reads passing filter:	54184 (3%)
Average read quality passing filter:	34.7
Average read length passing filter:	141
Average coverage passing filter:	255X

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.



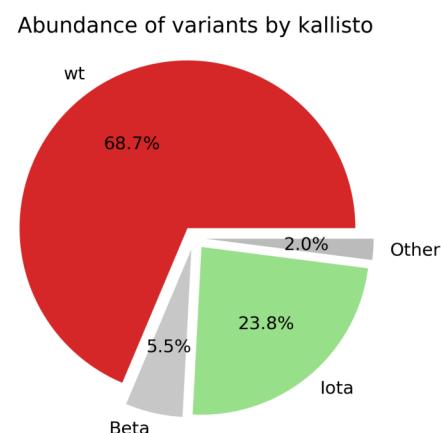
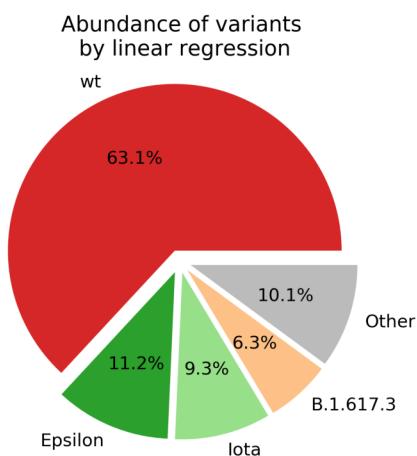
	Uncovered coordinates (0X)	Poorly covered coordinates (<10X)
# Inaccessible genomic coordinates by kit design:	-1nt (0%)	-1nt (0%)
All genomic coordinates:	6793nt (22%)	12997nt (43%)

Common SNPs:	3nt (9%)	5nt (15%)
Diverse SNPs:	96nt (19%)	414nt (81%)
Rare SNPs:	773nt (30%)	1155nt (46%)

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):	58859 reads (8.62%)
Hits to human genome (kraken2):	5951 reads (0.87%)
Hits to synthetic sequences (kraken2, taxid 28384):	167 reads (0.02%)

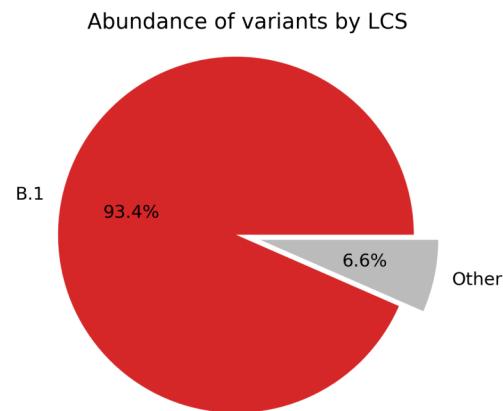
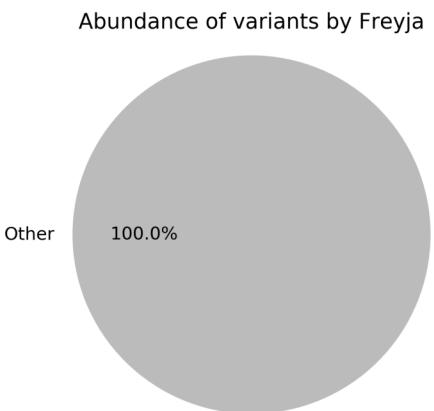
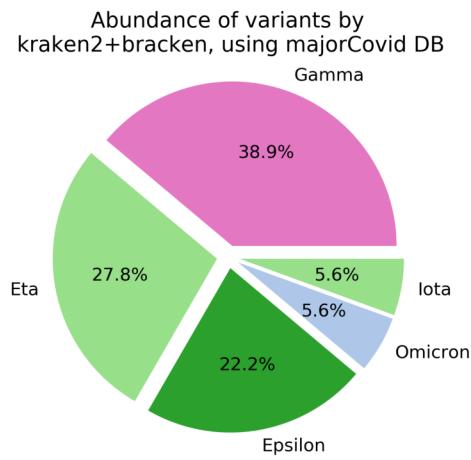
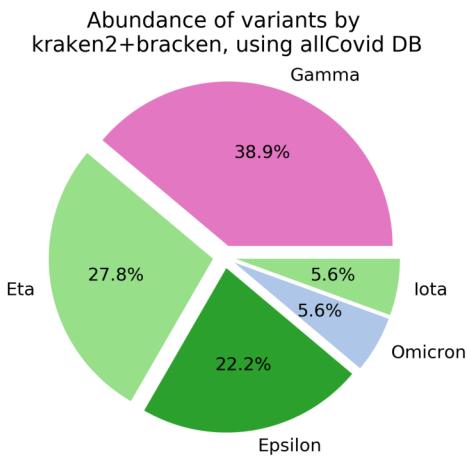
Detected variants (Experimental)



Based on deconvolution, [wt](#) is estimated to constitute 62.55% 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.1.2](#) 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.



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	BA.1.617.2	BA.1	BA.2	BA.3
Characteristic mutations detected	(0 of 19)	(0 of 3)	(2 of 13) ORF7A:T120I S:P681R	(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
337	C	A	0.500	5.16E-04	NUC:C337A	None found
339	A	T	0.261	4.42E-03	ORF1AB:D25V	None found
340	C	T	0.231	7.71E-03	NUC:C340T	None found
342	T	G	0.090	3.85E-03	ORF1AB:V26G	None found
347	G	A	0.097	2.10E-04	ORF1AB:V28I	None found
348	T	G	0.112	4.83E-05	ORF1AB:V28G	None found

350	C	T	0.114	1.23E-05	ORF1AB:R29C	None found
354	G	T	0.065	6.23E-04	ORF1AB:G30V	None found
355	C	A	0.060	1.06E-03	NUC:C355A	None found
357	T	A	0.065	5.29E-04	ORF1AB:F31Y	None found
358	T	A	0.052	2.48E-03	ORF1AB:F31L	None found
360	G	C	0.075	1.07E-04	ORF1AB:G32A	None found
367	C	T	0.280	3.41E-22	NUC:C367T	None found
372	A	C	0.071	2.80E-06	ORF1AB:E36A	None found
377	G	A	0.103	1.34E-10	ORF1AB:V38I	None found
378	T	G	0.103	1.95E-10	ORF1AB:V38G	None found
379	C	G	0.109	7.34E-12	NUC:C379G	None found
384	C	A	0.149	3.40E-18	ORF1AB:S40*	None found
389	G	A	0.140	2.47E-18	ORF1AB:A42T	None found
391	A	+G	0.115	4.41E-12	NUC:A391+G	None found
627	T	C	0.229	6.38E-36	ORF1AB:V121A	None found
629	C	G	0.140	2.18E-19	ORF1AB:L122V	None found
632	C	A	0.116	1.61E-15	ORF1AB:L123I	None found
634	T	C	0.057	2.13E-08	NUC:T634C	None found
637	T	C	0.108	2.29E-13	NUC:T637C	None found
638	A	G	0.070	2.63E-08	ORF1AB:K125E	None found
641	A	C	0.088	3.43E-09	ORF1AB:N126H	None found
642	A	C	0.086	5.48E-09	ORF1AB:N126T	None found
693	T	C	0.081	5.82E-03	ORF1AB:F143S	None found
944	G	T	0.116	1.41E-03	ORF1AB:G227C	None found
953	T	A	0.097	7.64E-03	ORF1AB:C230S	None found
956	T	A	0.113	8.06E-03	ORF1AB:C231S	None found
959	C	T	0.115	4.57E-03	ORF1AB:R232C	None found
963	A	C	0.075	9.50E-03	ORF1AB:E233A	None found
978	T	G	0.057	4.56E-03	ORF1AB:I238S	None found
982	T	C	0.051	3.51E-03	NUC:T982C	None found
983	T	A	0.051	4.03E-03	ORF1AB:W240R	None found
988	C	T	0.069	7.21E-05	NUC:C988T	None found
990	C	A	0.064	9.59E-05	ORF1AB:T242K	None found
995	C	G	0.054	1.43E-04	ORF1AB:R244G	None found
1059	C	T	0.940	6.57E-202	ORF1AB:T265I	B.1.351 , B.1.427 , B.1.429 , B.1.526
1207	A	G	0.065	8.40E-09	NUC:A1207G	None found
1335	G	C	0.097	1.17E-03	ORF1AB:C357S	None found
1337	G	T	0.113	8.04E-04	ORF1AB:G358C	None found
1340	T	C	0.241	3.60E-05	ORF1AB:Y359H	None found
1341	A	T	0.288	5.73E-06	ORF1AB:Y359F	None found

1343	T	C	0.178	1.67E-03	NUC:T1343C	None found
1344	T	G	0.256	1.04E-04	ORF1AB:L360*	None found
1346	C	G	0.333	7.23E-05	ORF1AB:P361A	None found
1351	A	C	0.375	4.55E-03	ORF1AB:Q362H	None found
1352	A	G	0.538	2.29E-03	ORF1AB:N363D	None found
1545	C	T	0.167	8.77E-04	ORF1AB:A427V	None found
1546	T	G	0.158	4.94E-03	NUC:T1546G	None found
1549	C	A	0.192	3.32E-04	ORF1AB:S428R	None found
1551	C	T	0.083	6.42E-03	ORF1AB:A429V	None found
1552	T	G	0.111	3.80E-03	NUC:T1552G	None found
1554	A	G	0.096	8.58E-05	ORF1AB:N430S	None found
1555	C	G	0.095	9.99E-06	ORF1AB:N430K	None found
1556	A	G	0.065	3.99E-04	ORF1AB:I431V	None found
1557	T	G	0.094	7.49E-06	ORF1AB:I431R	None found
1558	A	G	0.056	6.46E-04	ORF1AB:I431M	None found
1855	G	C	0.097	7.98E-15	NUC:G1855C	None found
1856	A	T	0.088	1.11E-12	ORF1AB:S531C	None found
1864	T	+A	0.081	4.50E-08	NUC:T1864+A	None found
1867	T	C	0.095	4.85E-11	NUC:T1867C	None found
1868	G	A	0.133	4.22E-15	ORF1AB:A535T	None found
1872	T	C	0.093	6.79E-09	ORF1AB:F536S	None found
1874	G	C	0.052	3.39E-05	ORF1AB:A537P	None found
1879	A	T	0.068	3.80E-06	NUC:A1879T	None found
1882	G	C	0.062	2.32E-05	ORF1AB:E539D	None found
1925	A	+C	0.085	2.86E-03	NUC:A1925+C	None found
1928	G	+T	0.167	6.19E-04	NUC:G1928+T	None found
1931	C	+TTAT	0.180	7.45E-04	NUC:C1931+TTAT	None found
1933	A	C	0.190	2.59E-04	ORF1AB:Q556H	None found
1935	A	C	0.232	4.36E-05	ORF1AB:N557T	None found
1936	T	A	0.211	1.03E-04	ORF1AB:N557K	None found
1944	G	C	0.250	2.37E-03	ORF1AB:R560P	None found
3411	C	A	0.072	9.68E-03	ORF1AB:A1049D	None found
3413	A	C	0.080	5.18E-03	ORF1AB:K1050Q	None found
3415	A	G	0.090	2.27E-03	NUC:A3415G	None found
3416	A	G	0.089	2.64E-03	ORF1AB:K1051E	None found
3417	A	T	0.083	2.14E-03	ORF1AB:K1051M	None found
3419	G	A	0.061	6.29E-03	ORF1AB:V1052I	None found
3420	T	C	0.067	2.92E-03	ORF1AB:V1052A	None found
3422	A	T	0.121	5.33E-06	ORF1AB:K1053*	None found
3425	C	G	0.113	9.52E-07	ORF1AB:P1054A	None found
3426	C	A	0.076	6.58E-05	ORF1AB:P1054Q	None found

3427	A	G	0.132	2.62E-08	NUC:A3427G	None found
3428	A	G	0.052	1.19E-03	ORF1AB:T1055A	B.1.621
3443	G	A	0.076	2.89E-07	ORF1AB:A1060T	None found
3444	C	G	0.051	3.98E-05	ORF1AB:A1060G	None found
3486	C	T	0.595	8.38E-109	ORF1AB:A1074V	None found
3491	A	G	0.349	5.90E-60	ORF1AB:N1076D	None found
3626	A	G	0.075	1.82E-16	ORF1AB:N1121D	None found
3634	C	G	0.066	5.46E-15	ORF1AB:N1123K	None found
3637	A	G	0.080	2.77E-18	NUC:A3637G	None found
3665	G	+TCT	0.051	9.04E-08	NUC:G3665+TCT	None found
3671	G	A	0.077	1.45E-16	ORF1AB:E1136K	None found
3672	A	C	0.078	1.36E-16	ORF1AB:E1136A	None found
3674	A	C	0.073	2.17E-15	ORF1AB:N1137H	None found
3677	T	C	0.065	1.34E-13	ORF1AB:F1138L	None found
3756	T	C	0.055	2.45E-04	ORF1AB:V1164A	None found
3759	G	C	0.059	1.35E-04	ORF1AB:C1165S	None found
3761	G	C	0.066	5.56E-05	ORF1AB:V1166L	None found
3764	G	T	0.115	6.76E-08	ORF1AB:D1167Y	None found
3766	T	C	0.059	3.72E-04	NUC:T3766C	None found
3767	A	+C	0.150	9.02E-08	NUC:A3767+C	None found
3769	T	C	0.088	3.05E-04	NUC:T3769C	None found
3770	G	T	0.082	4.05E-04	ORF1AB:V1169F	None found
3771	T	G	0.097	2.82E-04	ORF1AB:V1169G	None found
3772	T	C	0.068	5.49E-03	NUC:T3772C	None found
3773	C	+TTAT	0.093	4.45E-03	NUC:C3773+TTAT	None found
3774	G	T	0.438	2.19E-20	ORF1AB:R1170L	None found
3775	C	T	0.261	4.67E-10	NUC:C3775T	None found
3777	C	T	0.200	8.38E-06	ORF1AB:T1171I	None found
3779	A	T	0.236	1.62E-07	ORF1AB:N1172Y	None found
3780	A	C	0.250	2.02E-05	ORF1AB:N1172T	None found
3781	T	C	0.273	1.17E-05	NUC:T3781C	None found
3782	G	C	0.140	1.48E-03	ORF1AB:V1173L	None found
3785	T	+G	0.222	1.02E-03	NUC:T3785+G	None found
3786	A	G	0.256	1.27E-04	ORF1AB:Y1174C	None found
3788	T	G	0.333	1.49E-06	ORF1AB:L1175V	None found
3789	T	G	0.250	5.31E-04	ORF1AB:L1175*	None found
3790	A	T	0.389	7.71E-04	ORF1AB:L1175F	None found
4651	T	A	0.370	1.68E-04	NUC:T4651A	None found
4653	C	A	0.290	9.94E-04	ORF1AB:A1463D	None found
4654	T	C	0.212	4.83E-03	NUC:T4654C	None found
4655	C	A	0.237	6.16E-04	NUC:C4655A	None found

4679	C	A	0.053	5.35E-04	ORF1AB:P1472T	None found
4845	T	G	0.084	1.13E-08	ORF1AB:F1527C	None found
4856	G	T	0.099	2.68E-10	ORF1AB:G1531C	None found
4859	G	C	0.061	6.66E-06	ORF1AB:D1532H	None found
4864	A	G	0.067	1.69E-06	NUC:A4864G	None found
4973	G	+C	0.082	2.74E-04	NUC:G4973+C	None found
4976	T	+CTC	0.089	1.85E-03	NUC:T4976+CTC	None found
4980	C	T	0.124	7.64E-06	ORF1AB:T1572I	None found
4981	A	+C	0.085	3.23E-03	NUC:A4981+C	None found
4985	G	T	0.075	2.60E-03	ORF1AB:V1574L	None found
4986	T	C	0.111	2.57E-04	ORF1AB:V1574A	None found
4988	G	T	0.093	1.26E-03	ORF1AB:D1575Y	None found
4997	A	G	0.111	7.97E-03	ORF1AB:N1578D	None found
5002	C	G	0.179	5.06E-03	NUC:C5002G	None found
5003	C	T	0.269	4.15E-03	ORF1AB:H1580Y	None found
5239	C	G	0.600	2.26E-03	ORF1AB:Y1658*	None found
5299	T	G	0.083	1.39E-03	NUC:T5299G	None found
5414	T	G	0.052	1.55E-03	ORF1AB:Y1717D	None found
5563	A	C	0.073	8.15E-03	ORF1AB:E1766D	None found
5567	G	C	0.094	9.54E-03	ORF1AB:V1768L	None found
9821	A	G	0.176	9.39E-03	ORF1AB:N3186D	None found
9870	C	A	0.077	8.81E-03	ORF1AB:T3202K	None found
9928	G	T	0.124	1.07E-09	ORF1AB:M3221I	None found
10114	A	C	0.064	9.99E-04	NUC:A10114C	None found
10115	A	T	0.062	2.14E-03	ORF1AB:T3284S	None found
10319	C	T	0.915	8.81E-45	ORF1AB:L3352F	None found
10328	G	T	0.073	6.83E-03	ORF1AB:D3355Y	None found
10507	C	G	0.063	8.26E-03	ORF1AB:N3414K	None found
10529	T	G	0.079	2.58E-04	ORF1AB:F3422V	None found
10533	G	A	0.056	2.70E-03	ORF1AB:C3423Y	None found
10537	C	G	0.053	3.01E-03	ORF1AB:Y3424*	None found
10623	C	G	0.053	6.42E-06	ORF1AB:T3453R	None found
10749	T	C	0.066	3.78E-05	ORF1AB:L3495P	None found
10751	G	C	0.085	9.74E-05	ORF1AB:V3496L	None found
10754	G	T	0.097	1.48E-05	ORF1AB:A3497S	None found
10757	A	C	0.106	7.88E-06	ORF1AB:M3498L	None found
10759	G	T	0.071	3.89E-04	ORF1AB:M3498I	None found
10761	A	T	0.094	4.10E-05	ORF1AB:K3499M	None found
10762	G	A	0.080	2.19E-04	NUC:G10762A	None found
10763	T	C	0.089	7.88E-05	ORF1AB:Y3500H	None found
10767	A	T	0.082	8.93E-05	ORF1AB:N3501I	None found

10768	T	C	0.077	1.66E-04	NUC:T10768C	None found
10770	A	C	0.097	1.24E-05	ORF1AB:Y3502S	None found
10771	T	C	0.078	1.42E-04	NUC:T10771C	None found
10774	A	G	0.074	2.19E-04	NUC:A10774G	None found
10775	C	T	0.068	3.12E-04	ORF1AB:P3504S	None found
10780	A	T	0.054	3.25E-03	NUC:A10780T	None found
10782	C	T	0.050	3.66E-03	ORF1AB:T3506I	None found
10786	A	T	0.070	8.55E-04	ORF1AB:Q3507H	None found
10904	A	T	0.075	2.31E-03	ORF1AB:S3547C	None found
10907	G	T	0.064	7.02E-03	ORF1AB:A3548S	None found
10910	T	C	0.068	7.44E-03	NUC:T10910C	None found
10918	A	C	0.081	3.05E-03	ORF1AB:E3551D	None found
10920	A	C	0.072	6.92E-03	ORF1AB:D3552A	None found
11074	C	-T	0.461	7.46E-15	DEL:11074:1	None found
11089	A	C	0.065	6.37E-03	ORF1AB:E3608D	None found
11091	A	C	0.074	2.48E-03	ORF1AB:N3609T	None found
11106	T	C	0.066	2.22E-03	ORF1AB:F3614S	None found
11107	T	G	0.062	2.21E-03	ORF1AB:F3614L	None found
11109	C	A	0.063	2.12E-03	ORF1AB:A3615D	None found
11131	T	C	0.556	4.93E-36	NUC:T11131C	None found
11186	T	A	0.057	4.52E-04	ORF1AB:L3641I	None found
11214	T	A	0.054	1.65E-03	ORF1AB:F3650Y	None found
11234	G	C	0.072	2.63E-04	ORF1AB:A3657P	None found
11247	T	C	0.055	3.23E-03	ORF1AB:M3661T	None found
11312	G	C	0.067	4.70E-03	ORF1AB:V3683L	None found
11314	T	C	0.069	4.63E-03	NUC:T11314C	None found
11315	A	T	0.068	3.36E-03	ORF1AB:M3684L	None found
11317	G	A	0.067	4.88E-03	ORF1AB:M3684I	None found
11320	T	C	0.062	9.59E-03	NUC:T11320C	None found
11321	G	A	0.072	4.69E-03	ORF1AB:A3686T	None found
11341	A	T	0.067	7.42E-03	NUC:A11341T	None found
11344	C	A	0.068	8.53E-03	NUC:C11344A	None found
11346	T	A	0.070	8.99E-03	ORF1AB:L3694H	None found
11350	G	C	0.070	9.79E-03	ORF1AB:M3695I	None found
12158	G	A	0.102	6.88E-03	ORF1AB:E3965K	None found
12316	A	G	0.156	2.34E-04	NUC:A12316G	None found
12317	T	G	0.159	1.50E-04	ORF1AB:S4018A	None found
12525	C	T	0.836	4.62E-34	ORF1AB:T4087I	None found
12656	T	C	0.059	6.53E-03	NUC:T12656C	None found
12727	T	G	0.057	5.60E-03	ORF1AB:C4154W	None found
12729	C	A	0.064	2.89E-03	ORF1AB:A4155D	None found

12732	C	A	0.053	6.29E-03	ORF1AB:A4156D	None found
12733	C	T	0.052	6.29E-03	NUC:C12733T	None found
12738	C	T	0.079	2.47E-04	ORF1AB:T4158I	None found
12739	T	A	0.081	2.14E-04	NUC:T12739A	None found
12741	C	G	0.072	5.19E-04	ORF1AB:T4159R	None found
12743	C	G	0.078	2.54E-04	ORF1AB:Q4160E	None found
12746	A	G	0.062	1.08E-03	ORF1AB:T4161A	None found
12864	A	C	0.063	1.70E-03	ORF1AB:D4200A	None found
12868	A	C	0.070	1.62E-03	NUC:A12868C	None found
12887	G	C	0.164	5.68E-05	ORF1AB:E4208Q	None found
12889	A	T	0.213	2.95E-05	ORF1AB:E4208D	None found
12893	G	A	0.146	3.47E-03	ORF1AB:E4210K	None found
12894	A	C	0.176	9.69E-04	ORF1AB:E4210A	None found
15529	T	C	0.769	2.02E-05	ORF1AB:C688R	None found
15533	A	C	0.250	3.22E-03	ORF1AB:Q689P	None found
15535	G	T	0.286	1.76E-03	ORF1AB:A690S	None found
15536	C	G	0.394	5.70E-08	ORF1AB:A690G	None found
15538	G	+TGTA	0.214	2.38E-03	NUC:G15538+TGTA	None found
15540	C	G	0.130	2.61E-04	NUC:C15540G	None found
15542	C	G	0.667	1.83E-21	ORF1AB:T692R	None found
15543	G	C	0.068	2.83E-03	NUC:G15543C	None found
15545	C	T	0.074	9.05E-05	ORF1AB:A693V	None found
15548	A	G	0.093	1.06E-06	ORF1AB:N694S	None found
15549	T	G	0.053	9.04E-05	ORF1AB:N694K	None found
15551	T	+GTA	0.091	1.22E-06	NUC:T15551+GTA	None found
15555	T	G	0.138	1.21E-14	ORF1AB:N696K	None found
15556	G	A	0.144	8.44E-16	ORF1AB:A697T	None found
15557	C	G	0.097	7.21E-11	ORF1AB:A697G	None found
15558	A	+G	0.061	1.07E-04	NUC:A15558+G	None found
15559	C	+A	0.059	3.39E-05	NUC:C15559+A	None found
15560	T	G	0.075	1.65E-10	ORF1AB:L698R	None found
15593	A	T	0.054	1.81E-15	ORF1AB:K709M	None found
15599	T	A	0.050	8.32E-15	ORF1AB:V711D	None found
15603	C	A	0.056	6.79E-18	NUC:C15603A	None found
15605	A	G	0.084	3.48E-29	ORF1AB:N713S	None found
15607	T	G	0.078	1.85E-29	ORF1AB:L714V	None found
15610	C	T	0.077	1.27E-29	ORF1AB:Q715*	None found
15613	C	G	0.116	6.92E-48	ORF1AB:H716D	None found
15615	C	G	0.061	4.35E-25	ORF1AB:H716Q	None found
15751	G	A	0.052	1.07E-37	ORF1AB:A762T	None found
15772	A	G	0.052	1.54E-34	ORF1AB:S769G	None found

15780	G	C	0.054	2.01E-36	ORF1AB:K771N	None found
15782	A	T	0.052	1.40E-35	ORF1AB:N772I	None found
15905	A	C	0.066	1.65E-18	ORF1AB:Q813P	None found
15906	G	T	0.077	5.44E-22	ORF1AB:Q813H	None found
15907	G	T	0.065	5.55E-17	ORF1AB:G814C	None found
15908	G	C	0.134	5.81E-35	ORF1AB:G814A	None found
15910	G	T	0.073	4.64E-18	ORF1AB:D815Y	None found
15912	T	C	0.061	1.37E-14	NUC:T15912C	None found
15913	G	A	0.062	2.19E-14	ORF1AB:D816N	None found
15914	A	C	0.084	1.81E-18	ORF1AB:D816A	None found
15915	T	C	0.078	3.06E-15	NUC:T15915C	None found
15916	T	C	0.083	2.15E-14	ORF1AB:Y817H	None found
15917	A	G	0.069	6.99E-12	ORF1AB:Y817C	None found
15919	G	C	0.136	8.89E-23	ORF1AB:V818L	None found
15921	G	C	0.062	7.85E-09	NUC:G15921C	None found
15923	A	T	0.064	5.55E-08	ORF1AB:Y819F	None found
15924	C	T	0.143	1.63E-14	NUC:C15924T	None found
15925	C	A	0.064	1.63E-05	ORF1AB:L820I	None found
15926	T	C	0.064	3.62E-05	ORF1AB:L820P	None found
15927	T	G	0.122	1.02E-09	NUC:T15927G	None found
15928	C	T	0.219	8.20E-15	ORF1AB:P821S	None found
15929	C	T	0.102	2.81E-06	ORF1AB:P821L	None found
15930	T	G	0.096	4.65E-05	NUC:T15930G	None found
15931	T	G	0.213	1.74E-08	ORF1AB:Y822D	None found
15932	A	G	0.065	5.73E-03	ORF1AB:Y822C	None found
15933	C	T	0.327	7.87E-12	NUC:C15933T	None found
15936	A	T	0.235	9.98E-05	NUC:A15936T	None found
15937	G	T	0.190	5.25E-05	ORF1AB:D824Y	None found
15941	C	T	0.250	9.16E-03	ORF1AB:P825L	None found
15942	A	T	0.182	7.12E-03	NUC:A15942T	None found
15943	T	G	0.263	4.66E-03	ORF1AB:S826A	None found
16134	C	G	0.222	8.16E-03	ORF1AB:H889Q	None found
16209	T	G	0.053	1.45E-03	NUC:T16209G	None found
16283	G	C	0.058	1.37E-04	ORF1AB:C939S	None found
16285	G	C	0.065	4.74E-05	ORF1AB:G940R	None found
16291	T	C	0.051	3.20E-04	ORF1AB:C942R	None found
16295	T	G	0.056	1.43E-04	ORF1AB:I943R	None found
16297	C	T	0.055	1.47E-04	ORF1AB:R944C	None found
16304	C	A	0.068	2.20E-05	ORF1AB:P946Q	None found
16305	A	G	0.067	2.51E-05	NUC:A16305G	None found
16407	C	T	0.261	5.20E-18	NUC:C16407T	None found

16422	A	T	0.062	7.00E-04	ORF1AB:Q985H	None found
16428	C	T	0.367	7.26E-21	NUC:C16428T	None found
16445	A	C	0.058	8.34E-03	ORF1AB:Y993S	None found
16453	A	T	0.101	1.56E-03	ORF1AB:K996*	None found
16455	A	T	0.104	1.38E-03	ORF1AB:K996N	None found
16456	T	A	0.104	1.66E-03	ORF1AB:S997T	None found
16463	A	C	0.086	7.06E-03	ORF1AB:K999T	None found
16467	A	G	0.092	9.12E-03	NUC:A16467G	None found
16859	C	G	0.083	3.16E-03	ORF1AB:A1131G	None found
16861	G	C	0.098	1.46E-03	ORF1AB:V1132L	None found
16863	T	G	0.084	3.42E-03	NUC:T16863G	None found
16944	T	A	0.110	1.08E-03	ORF1AB:S1159R	None found
16956	A	C	0.075	2.59E-03	NUC:A16956C	None found
16958	T	A	0.058	7.94E-03	ORF1AB:V1164E	None found
16960	C	G	0.115	2.86E-05	ORF1AB:P1165A	None found
16961	C	T	0.162	5.74E-07	ORF1AB:P1165L	None found
16963	C	T	0.217	4.34E-09	ORF1AB:Q1166*	None found
16969	C	A	0.198	1.03E-08	ORF1AB:H1168N	None found
16970	A	C	0.196	1.70E-08	ORF1AB:H1168P	None found
16971	C	A	0.193	2.25E-08	ORF1AB:H1168Q	None found
16972	T	G	0.209	4.18E-09	ORF1AB:Y1169D	None found
17086	C	T	0.193	1.93E-04	ORF1AB:P1207S	None found
17090	G	A	0.234	1.93E-04	ORF1AB:G1208D	None found
17091	T	C	0.200	1.02E-03	NUC:T17091C	None found
17092	A	G	0.205	8.87E-04	ORF1AB:T1209A	None found
17095	G	+TCT	0.250	4.10E-03	NUC:G17095+TCT	None found
17096	G	C	0.531	7.74E-08	ORF1AB:G1210A	None found
17097	T	C	0.290	9.94E-04	NUC:T17097C	None found
17098	A	T	0.300	9.66E-05	ORF1AB:K1211*	None found
17100	G	T	0.500	2.29E-05	ORF1AB:K1211N	None found
17102	G	C	0.882	1.31E-07	ORF1AB:S1212T	None found
17103	T	A	0.588	3.33E-05	ORF1AB:S1212R	None found
17107	T	C	0.714	5.38E-05	ORF1AB:F1214L	None found
17109	T	G	0.545	5.42E-03	ORF1AB:F1214L	None found
17323	T	G	0.438	2.45E-03	ORF1AB:L1286V	None found
17324	T	C	0.350	9.57E-04	ORF1AB:L1286S	None found
17326	C	T	0.469	1.87E-07	ORF1AB:P1287S	None found
17327	C	G	0.278	8.66E-05	ORF1AB:P1287R	None found
17328	T	G	0.176	2.79E-03	NUC:T17328G	None found
17329	G	C	0.333	4.34E-07	ORF1AB:E1288Q	None found
17332	A	-C	0.131	2.83E-03	DEL:17332:1	None found

17333	C	T	0.296	9.57E-09	ORF1AB:T1289M	None found
17334	G	+TGTATA	0.138	1.56E-03	NUC:G17334+TGTATA	None found
17335	A	G	0.136	1.18E-03	ORF1AB:T1290A	None found
17336	C	G	0.216	2.53E-07	ORF1AB:T1290R	None found
17337	A	G	0.074	6.20E-03	NUC:A17337G	None found
17338	G	+A	0.089	8.21E-04	NUC:G17338+A	None found
17339	C	A	0.054	1.25E-03	ORF1AB:A1291E	None found
17414	C	A	0.059	9.75E-14	ORF1AB:A1316D	None found
17483	C	T	0.391	7.68E-152	ORF1AB:T1339I	None found
17658	G	C	0.051	2.27E-09	ORF1AB:M1397I	None found
17671	G	C	0.085	5.49E-10	ORF1AB:V1402L	None found
17685	T	C	0.053	1.38E-03	NUC:T17685C	None found
17687	T	C	0.056	2.67E-03	ORF1AB:V1407A	None found
17691	A	T	0.056	5.53E-03	NUC:A17691T	None found
17693	C	A	0.061	7.11E-03	ORF1AB:S1409Y	None found
17695	G	+T	0.095	5.74E-03	NUC:G17695+T	None found
17697	A	T	0.121	2.54E-03	NUC:A17697T	None found
17698	A	C	0.138	1.45E-03	ORF1AB:I1411L	None found
17704	A	C	0.500	1.93E-03	NUC:A17704C	None found
17705	G	T	0.643	7.04E-05	ORF1AB:R1413M	None found
18252	C	G	0.212	1.64E-05	ORF1AB:N1595K	None found
18257	T	G	0.183	5.73E-06	ORF1AB:F1597C	None found
18261	C	A	0.151	2.38E-05	NUC:C18261A	None found
18262	A	G	0.095	1.04E-03	ORF1AB:T1599A	None found
18263	C	G	0.209	6.61E-08	ORF1AB:T1599S	None found
18264	C	A	0.065	7.45E-03	NUC:C18264A	None found
18265	C	T	0.052	8.37E-03	ORF1AB:R1600C	None found
18267	C	T	0.051	7.37E-03	NUC:C18267T	None found
18268	G	-A	0.068	7.55E-03	DEL:18268:1	None found
18269	A	T	0.055	4.76E-03	ORF1AB:E1601V	None found
18271	G	C	0.094	8.84E-05	ORF1AB:E1602Q	None found
18273	A	T	0.142	9.13E-08	ORF1AB:E1602D	None found
18274	G	+T	0.105	3.99E-05	NUC:G18274+T	None found
18275	C	G	0.095	1.10E-06	ORF1AB:A1603G	None found
18394	G	+C	0.088	9.78E-08	NUC:G18394+C	None found
18399	A	C	0.073	4.96E-07	NUC:A18399C	None found
18400	C	T	0.130	2.74E-12	ORF1AB:P1645S	None found
18403	A	C	0.076	2.16E-07	ORF1AB:T1646P	None found
18406	G	T	0.057	4.28E-06	ORF1AB:G1647C	None found
18407	G	C	0.094	2.84E-09	ORF1AB:G1647A	None found
18408	T	C	0.110	2.26E-10	NUC:T18408C	None found

18409	T	C	0.079	3.83E-07	ORF1AB:Y1648H	None found
18410	A	G	0.054	7.04E-05	ORF1AB:Y1648C	None found
18415	G	T	0.070	4.94E-06	ORF1AB:D1650Y	None found
18417	T	G	0.061	3.35E-05	ORF1AB:D1650E	None found
18424	A	G	0.940	1.02E-115	ORF1AB:N1653D	None found
18492	A	G	0.052	1.49E-05	NUC:A18492G	None found
20369	T	G	0.700	1.03E-03	ORF1AB:L2301R	None found
20370	A	T	0.700	1.03E-03	NUC:A20370T	None found
20372	T	A	0.636	1.35E-03	ORF1AB:L2302Q	None found
20380	C	T	0.500	9.57E-03	NUC:C20380T	None found
20381	T	A	0.545	1.55E-03	ORF1AB:L2305Q	None found
20566	A	G	0.064	7.85E-06	ORF1AB:K2367E	None found
20575	A	T	0.063	2.54E-05	ORF1AB:K2370*	None found
20579	T	A	0.069	1.14E-05	ORF1AB:V2371E	None found
20705	A	C	0.071	2.68E-03	ORF1AB:K2413T	None found
20707	A	C	0.064	6.13E-03	ORF1AB:M2414L	None found
20711	A	C	0.065	5.56E-03	ORF1AB:Q2415P	None found
20779	A	C	0.350	2.87E-03	ORF1AB:M2438L	None found
21534	T	A	0.333	7.62E-03	ORF1AB:S2689R	None found
21540	T	G	0.179	7.32E-03	NUC:T21540G	None found
21542	T	G	0.175	3.82E-03	ORF1AB:L2692R	None found
21545	T	G	0.098	8.45E-03	ORF1AB:V2693G	None found
21546	T	A	0.109	4.57E-03	NUC:T21546A	None found
21548	A	G	0.106	5.63E-03	ORF1AB:N2694S	None found
21550	A	G	0.067	6.36E-03	ORF1AB:N2695D	None found
21557	C	A	0.061	2.48E-03	NUC:C21557A	None found
21584	T	G	0.072	7.39E-06	S:L8V	None found
21587	C	A	0.107	8.75E-10	S:P9T	None found
21588	C	G	0.076	3.65E-07	S:P9R	None found
21633	T	A	0.057	7.48E-16	S:L24*	None found
21637	C	A	0.057	2.17E-17	NUC:C21637A	None found
21642	C	T	0.051	5.52E-16	S:A27V	None found
21776	G	T	0.057	1.93E-21	S:G72W	None found
21777	G	A	0.123	4.95E-47	S:G72E	None found
21781	C	A	0.056	1.38E-20	NUC:C21781A	None found
21798	T	G	0.060	4.46E-21	S:F79C	None found
21812	C	T	0.892	0.00E+00	NUC:C21812T	None found
21826	T	-G	0.067	3.13E-16	DEL:21826:1	None found
21898	G	T	0.078	4.62E-21	NUC:G21898T	None found
21899	A	T	0.059	2.91E-16	S:K113*	None found
21904	C	A	0.089	3.44E-23	NUC:C21904A	None found

21912	T	G	0.057	9.31E-17	S:L117R	None found
21915	T	A	0.061	4.83E-19	S:L118H	None found
21916	T	G	0.052	3.31E-15	NUC:T21916G	None found
21918	T	+G	0.064	2.65E-13	NUC:T21918+G	None found
21920	G	C	0.055	1.83E-16	S:V120L	None found
21921	T	+A	0.066	3.04E-13	NUC:T21921+A	None found
21923	A	T	0.052	9.84E-16	S:N121Y	None found
21924	A	C	0.052	9.34E-16	S:N121T	None found
21925	T	G	0.082	8.48E-25	S:N121K	None found
21928	C	A	0.052	1.34E-14	S:N122K	None found
22046	A	T	0.063	1.92E-23	S:S162C	None found
22050	C	T	0.065	5.30E-21	S:A163V	None found
22052	A	T	0.119	3.65E-39	S:N164Y	None found
22057	T	G	0.053	8.18E-17	S:N165K	None found
22059	G	A	0.063	9.17E-21	S:C166Y	None found
22201	G	T	0.054	4.94E-14	NUC:G22201T	None found
22202	C	T	0.052	2.21E-12	S:R214C	None found
22203	G	T	0.061	4.30E-14	S:R214L	None found
22205	G	C	0.107	3.01E-23	S:D215H	None found
22265	A	C	0.071	7.42E-04	S:I235L	None found
22267	C	G	0.269	2.17E-05	S:I235M	None found
22268	A	T	0.725	6.75E-19	S:T236S	None found
22270	T	G	0.143	6.69E-03	NUC:T22270G	None found
22271	A	C	0.400	2.72E-07	NUC:A22271C	None found
22272	G	T	0.378	2.99E-11	S:R237M	None found
22273	G	T	0.375	1.22E-08	S:R237S	None found
22274	T	A	0.385	4.11E-06	S:F238I	None found
22275	T	C	0.368	1.72E-05	S:F238S	None found
22276	T	A	0.400	6.64E-06	S:F238L	None found
22279	A	C	0.593	1.03E-07	S:Q239H	None found
22281	C	T	0.440	8.57E-05	S:T240I	None found
22282	T	C	0.600	1.86E-05	NUC:T22282C	None found
22284	T	G	0.600	1.86E-05	S:L241*	None found
22947	A	G	0.812	2.72E-06	S:K462R	None found
22949	C	T	0.625	5.00E-05	S:P463S	None found
22950	C	G	0.706	3.22E-06	S:P463R	None found
22952	T	G	0.214	8.70E-03	S:F464V	None found
22953	T	G	0.167	3.19E-03	S:F464C	None found
22954	T	A	0.333	3.77E-05	S:F464L	None found
22956	A	G	0.152	5.56E-03	S:E465G	None found
22957	G	C	0.158	1.16E-03	S:E465D	None found

22959	G	C	0.119	2.46E-03	S:R466T	None found
22962	A	+G	0.074	6.68E-03	NUC:A22962+G	None found
22964	A	G	0.216	4.78E-08	S:I468V	None found
22965	T	+G	0.100	3.39E-03	NUC:T22965+G	None found
22966	T	G	0.084	8.63E-04	S:I468M	None found
22967	T	A	0.134	1.12E-05	S:S469T	None found
22968	C	T	0.116	3.00E-05	S:S469L	None found
22969	A	G	0.091	3.35E-04	NUC:A22969G	None found
22970	A	G	0.065	2.23E-03	S:T470A	None found
22971	C	G	0.116	1.37E-05	S:T470S	None found
22972	T	G	0.055	2.63E-03	NUC:T22972G	None found
22975	A	T	0.050	3.22E-03	S:E471D	None found
22976	A	G	0.064	1.41E-03	S:I472V	None found
22977	T	G	0.087	1.28E-04	S:I472S	None found
22978	C	G	0.072	2.67E-04	S:I472M	None found
22981	T	A	0.069	3.21E-04	S:Y473*	None found
22982	C	G	0.088	2.61E-05	S:Q474E	None found
22985	G	A	0.100	3.34E-06	S:A475T	None found
22987	C	A	0.071	5.79E-05	NUC:C22987A	None found
23071	T	A	0.060	2.10E-10	NUC:T23071A	None found
23074	T	A	0.062	1.85E-11	NUC:T23074A	None found
23075	T	G	0.063	1.40E-11	S:Y505D	None found
23078	C	A	0.050	4.05E-10	S:Q506K	None found
23082	C	G	0.052	1.98E-12	S:P507R	None found
23084	T	G	0.055	7.50E-14	S:Y508D	None found
23101	T	C	0.056	1.27E-16	NUC:T23101C	None found
23106	T	A	0.057	5.28E-17	S:F515Y	None found
23108	G	A	0.063	5.85E-19	S:E516K	None found
23109	A	C	0.064	2.66E-19	S:E516A	None found
23112	T	A	0.051	8.39E-15	S:L517H	None found
23114	C	T	0.248	3.19E-84	NUC:C23114T	None found
23223	A	T	0.094	9.88E-28	S:E554V	None found
23228	A	T	0.054	3.18E-15	S:N556Y	None found
23230	C	T	0.055	5.50E-16	NUC:C23230T	None found
23234	A	C	0.050	1.16E-13	S:K558Q	None found
23271	C	G	0.053	1.77E-15	S:A570G	None found
23272	T	A	0.072	2.85E-21	NUC:T23272A	None found
23276	A	+G	0.064	2.49E-13	NUC:A23276+G	None found
23295	A	+T	0.253	1.08E-72	NUC:A23295+T	None found
23395	T	G	0.059	2.30E-63	NUC:T23395G	None found

23403	A	G	0.890	0.00E+00	S:D614G	B.1.1.529 , B.1.427 , C.37 , B.1.429 , B.1.526 , AV1 , B.1.621
23412	G	A	0.051	5.31E-18	S:C617Y	None found
23517	G	C	0.061	2.76E-18	S:G652A	None found
23518	G	T	0.057	5.45E-17	NUC:G23518T	None found
23579	A	T	0.052	2.23E-07	S:S673C	None found
23580	G	C	0.080	7.35E-11	S:S673T	None found
23623	A	C	0.061	2.88E-03	NUC:A23623C	None found
23624	G	T	0.109	3.96E-05	S:A688S	None found
23626	T	C	0.224	6.93E-07	NUC:T23626C	None found
23627	A	T	0.328	1.47E-09	S:S689C	None found
23628	G	T	0.155	2.03E-04	S:S689I	None found
23629	T	A	0.143	1.32E-03	S:S689R	None found
23630	C	+TCT	0.500	6.85E-09	NUC:C23630+TCT	None found
23631	A	T	0.776	9.46E-21	S:Q690L	None found
23633	T	C	0.123	6.01E-03	S:S691P	None found
23634	C	A	0.768	6.09E-20	S:S691Y	None found
23636	A	-T	0.500	2.66E-07	DEL:23636:1	None found
23637	T	C	0.222	2.53E-03	S:I692T	None found
23639	A	T	0.175	2.07E-03	S:I693F	None found
23640	T	C	0.194	2.81E-03	S:I693T	None found
23641	T	C	0.194	2.81E-03	NUC:T23641C	None found
23642	G	T	0.194	4.13E-03	S:A694S	None found
23645	T	G	0.769	1.06E-10	S:Y695D	None found
23851	A	G	0.125	2.46E-03	NUC:A23851G	None found
23852	A	C	0.372	2.24E-06	S:N764H	None found
23853	A	G	0.484	6.56E-12	S:N764S	None found
23854	C	T	0.187	7.24E-12	NUC:C23854T	None found
23855	C	T	0.272	1.32E-14	S:R765C	None found
23856	G	C	0.079	1.51E-04	S:R765P	None found
23857	T	G	0.130	1.48E-09	NUC:T23857G	None found
23858	G	C	0.144	8.08E-10	S:A766P	None found
23859	C	T	0.193	2.36E-18	S:A766V	None found
23860	T	G	0.255	8.99E-23	NUC:T23860G	None found
23861	T	G	0.281	9.97E-26	S:L767V	None found
23862	T	G	0.132	8.31E-15	S:L767*	None found
23863	A	G	0.083	2.53E-09	NUC:A23863G	None found
23864	A	T	0.120	2.78E-16	S:T768S	None found
23865	C	G	0.126	1.02E-20	S:T768S	None found
23866	T	G	0.055	3.23E-10	NUC:T23866G	None found
23867	G	+TGTATAA	0.076	3.42E-09	NUC:G23867+TGTATAA	None found

23869	A	G	0.102	5.49E-26	NUC:A23869G	None found
23871	T	G	0.051	6.33E-15	S:I770R	None found
23874	C	A	0.070	1.22E-24	S:A771D	None found
23878	T	A	0.079	6.65E-30	NUC:T23878A	None found
23880	A	+G	0.055	4.30E-13	NUC:A23880+G	None found
24066	A	G	0.052	1.95E-64	S:K835R	None found
24193	G	T	0.059	8.28E-42	NUC:G24193T	None found
24199	G	T	0.054	2.38E-33	NUC:G24199T	None found
24200	G	T	0.059	1.05E-35	S:G880C	None found
24201	G	A	0.056	1.18E-31	S:G880D	None found
24209	A	T	0.050	9.34E-24	S:T883S	None found
24217	T	C	0.050	1.69E-18	NUC:T24217C	None found
24219	G	C	0.050	3.17E-17	S:W886S	None found
24220	G	T	0.065	2.02E-22	S:W886C	None found
24223	C	A	0.052	1.16E-15	NUC:C24223A	None found
24225	T	C	0.106	6.60E-33	S:F888S	None found
24227	G	T	0.050	7.07E-15	S:G889C	None found
24228	G	A	0.065	5.10E-19	S:G889D	None found
24230	G	A	0.061	9.12E-17	S:A890T	None found
24243	T	C	0.062	1.04E-09	S:L894S	None found
24244	A	T	0.054	2.15E-08	S:L894F	None found
24246	A	T	0.053	1.08E-07	S:Q895L	None found
24247	A	T	0.063	4.01E-09	S:Q895H	None found
24248	A	C	0.124	2.46E-09	S:I896L	None found
24250	A	G	0.083	1.16E-05	S:I896M	None found
24251	C	T	0.082	2.88E-05	S:P897S	None found
24253	A	G	0.068	1.72E-03	NUC:A24253G	None found
24255	T	C	0.673	1.94E-32	S:F898S	None found
24256	T	C	0.065	5.44E-03	NUC:T24256C	None found
24257	G	C	0.151	4.05E-06	S:A899P	None found
24258	C	T	0.117	1.15E-04	S:A899V	None found
24259	T	G	0.419	3.91E-17	NUC:T24259G	None found
24260	A	C	0.427	1.76E-14	S:M900L	None found
24262	G	A	0.136	6.95E-04	S:M900I	None found
24264	A	C	0.357	2.98E-08	S:Q901P	None found
24265	A	G	0.255	2.02E-05	NUC:A24265G	None found
24415	G	C	0.102	5.54E-03	NUC:G24415C	None found
24417	T	G	0.169	1.55E-04	S:V952G	None found
24420	A	G	0.235	5.93E-07	S:N953S	None found
24422	C	T	0.116	1.15E-03	S:Q954*	None found

24424	A	T	0.122	4.75E-04	S:Q954H	B.1.1.529
24425	A	T	0.079	4.65E-03	S:N955Y	None found
24426	A	G	0.152	6.63E-05	S:N955S	None found
24427	T	G	0.125	3.20E-04	S:N955K	None found
24428	G	A	0.094	1.97E-03	S:A956T	None found
24429	C	T	0.183	4.49E-07	S:A956V	None found
24431	C	T	0.172	2.56E-06	S:Q957*	None found
24432	A	C	0.093	1.60E-03	S:Q957P	None found
24433	A	G	0.289	1.89E-10	NUC:A24433G	None found
24437	T	A	0.065	5.08E-05	S:L959I	None found
24442	C	G	0.061	3.04E-05	S:N960K	None found
24719	C	T	0.068	8.43E-21	S:P1053S	None found
24725	T	A	0.059	6.34E-17	S:S1055T	None found
24751	G	A	0.053	2.18E-11	NUC:G24751A	None found
24757	G	C	0.055	5.52E-10	NUC:G24757C	None found
24758	A	T	0.056	3.15E-10	S:T1066S	None found
24771	C	T	0.054	9.44E-08	S:A1070V	None found
24772	A	C	0.071	4.28E-10	NUC:A24772C	None found
24775	A	T	0.052	2.56E-07	S:Q1071H	None found
24791	A	T	0.053	3.89E-06	S:T1077S	None found
24798	C	T	0.052	4.47E-05	S:P1079L	None found
24827	T	C	0.144	1.97E-06	S:F1089L	None found
24828	T	G	0.064	3.89E-03	S:F1089C	None found
24829	T	G	0.154	1.24E-06	S:F1089L	None found
24830	C	T	0.160	8.29E-07	S:P1090S	None found
24832	T	A	0.094	6.67E-04	NUC:T24832A	None found
24834	G	T	0.117	4.16E-05	S:R1091L	None found
24836	G	A	0.144	1.82E-05	S:E1092K	P.3
24837	A	T	0.114	2.15E-04	S:E1092V	None found
24838	A	C	0.135	5.66E-05	S:E1092D	None found
24839	G	C	0.114	2.57E-04	S:G1093R	None found
24840	G	C	0.081	1.70E-03	S:G1093A	None found
24841	T	C	0.102	5.51E-04	NUC:T24841C	None found
24842	G	A	0.103	4.14E-04	S:V1094I	None found
24846	T	G	0.093	2.05E-03	S:F1095C	None found
26115	A	C	0.931	3.63E-17	ORF3A:E241D	None found
26412	T	A	0.176	7.26E-03	E:F56L	None found
27752	C	T	0.114	1.09E-03	ORF7A:T120I	B.1.617.2+K417N, B.1.617.2
27843	T	G	0.053	5.93E-04	NUC:T27843G	None found
27845	C	A	0.065	1.53E-04	NUC:C27845A	None found

27932	A	C	0.058	5.93E-04	NUC:A27932C	None found
27964	C	T	0.848	1.99E-60	ORF8:S24L	None found
27972	C	T	0.052	5.82E-03	ORF8:Q27*	B.1.1.7, B.1.1.7+E484K
27980	A	C	0.057	5.19E-03	ORF8:Q29H	None found
27998	C	T	0.065	8.20E-03	NUC:C27998T	None found
28000	C	T	0.079	3.00E-03	ORF8:P36L	None found
28003	G	A	0.112	3.05E-04	ORF8:C37Y	None found
28006	C	A	0.198	3.89E-08	ORF8:P38H	None found
28007	T	G	0.206	2.49E-08	NUC:T28007G	None found
28009	T	G	0.078	4.50E-04	ORF8:I39S	None found
28010	T	A	0.075	4.99E-04	NUC:T28010A	None found
28012	A	+G	0.057	7.80E-03	NUC:A28012+G	None found
28013	C	G	0.065	1.17E-04	ORF8:H40Q	None found
28014	T	G	0.069	3.70E-05	ORF8:F41V	None found
28016	C	G	0.067	5.14E-05	ORF8:F41L	None found
28021	C	A	0.060	2.96E-05	ORF8:S43Y	None found
28026	T	A	0.058	1.56E-05	ORF8:W45R	None found
28195	G	T	0.051	8.78E-07	ORF8:R101L	None found
28395	G	T	0.056	1.29E-06	N:R41L	None found
28410	C	G	0.074	7.62E-09	N:P46R	None found
28429	G	A	0.050	4.59E-06	N:W52*	None found
28431	T	A	0.051	3.88E-06	N:F53Y	None found
28472	C	T	0.979	1.78E-174	N:P67S	B.1.617.3
28519	C	G	0.054	1.28E-05	N:D82E	None found
28532	T	G	0.051	1.43E-05	N:Y87D	None found
28544	A	G	0.053	1.93E-05	N:T91A	None found
28545	C	T	0.116	6.78E-11	N:T91I	None found
28547	A	T	0.110	5.35E-10	N:R92*	None found
28548	G	T	0.081	1.55E-07	N:R92I	None found
28549	A	T	0.051	6.42E-05	N:R92S	None found
28585	C	G	0.051	1.96E-04	NUC:C28585G	None found
28586	A	T	0.051	1.92E-04	N:S105C	None found
28589	C	A	0.066	9.31E-06	N:P106T	None found
28590	C	T	0.067	8.23E-06	N:P106L	None found
28854	C	T	0.051	3.57E-09	N:S194L	None found
28869	C	T	0.902	1.38E-260	N:P199L	B.1.526
29093	T	-TC	0.159	8.00E-30	DEL:29093:2	None found
29104	T	-G	0.133	4.17E-23	DEL:29104:1	None found
29510	A	T	0.080	3.63E-13	N:S413C	None found
29513	G	T	0.066	2.25E-10	N:A414S	None found

29516	G	T	0.063	3.29E-08	N:D415Y	None found
29519	T	A	0.093	1.76E-11	N:S416T	None found
29521	A	T	0.104	1.48E-06	NUC:A29521T	None found
29522	A	T	0.406	1.47E-27	N:T417S	None found
29523	C	A	0.054	1.39E-03	N:T417N	None found
29526	A	T	0.144	1.64E-06	N:Q418L	None found
29527	G	T	0.450	8.90E-21	N:Q418H	None found
29528	G	T	0.118	2.12E-04	N:A419S	None found
29530	C	T	0.261	9.29E-07	NUC:C29530T	None found
29531	T	G	0.278	3.30E-06	N:*420E	None found
29533	A	T	0.415	1.37E-07	N:*420Y	None found
29536	T	A	0.548	2.62E-07	NUC:T29536A	None found
29542	A	C	0.308	8.30E-04	NUC:A29542C	None found

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WASTEWATER SARS-COV2 ANALYSIS REPORT

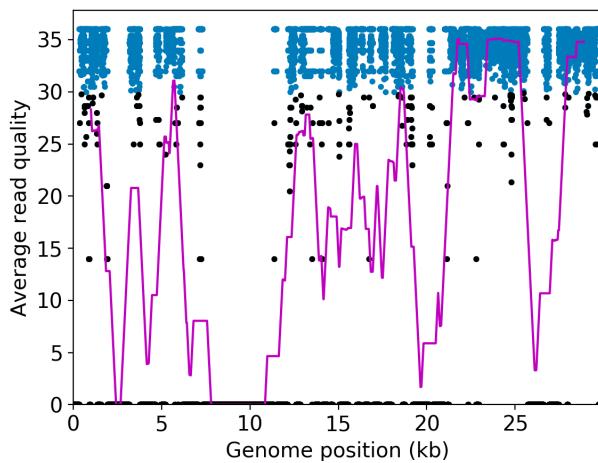
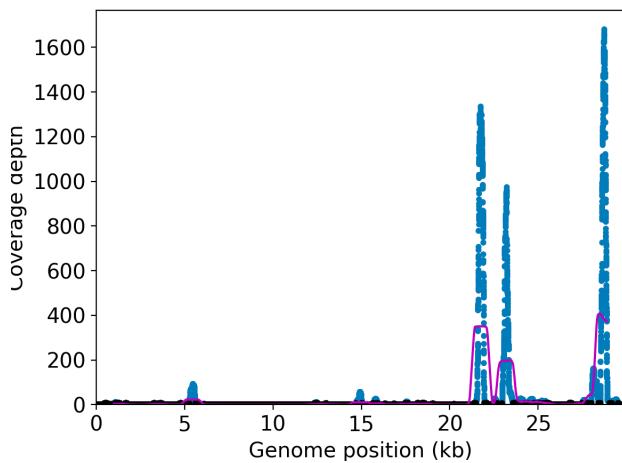
Sample name:	SRR16828016
Date generated:	2022-03-15, 14:21:28 EDT
Executed by:	Tunc Kayikcioglu (Tunc.Kayikcioglu@fda.hhs.gov)
Executed on:	172.20.44.224 (aka n224.raven.cfsan)

Sequencing summary

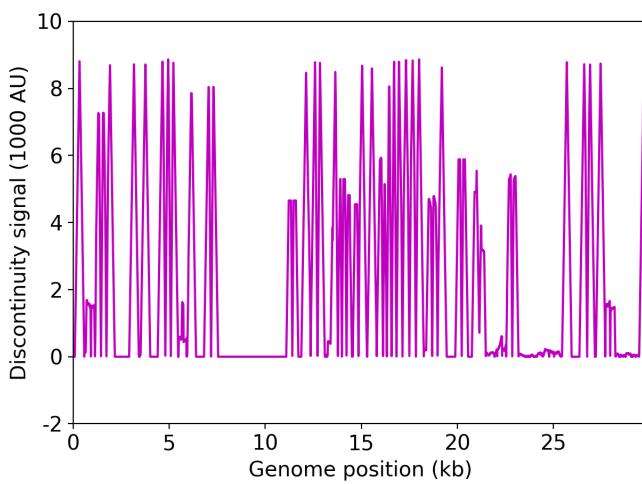
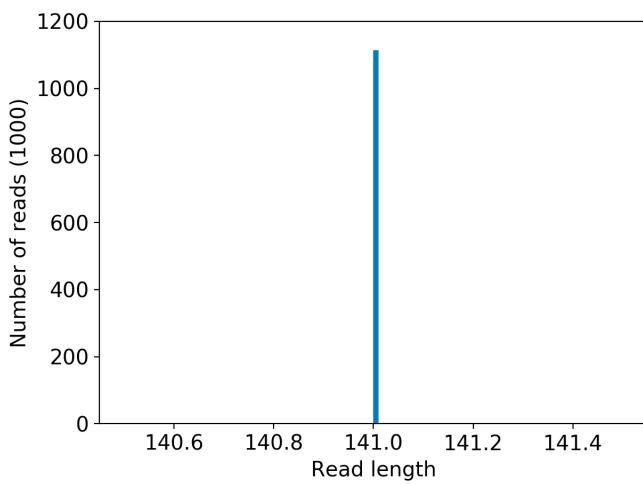
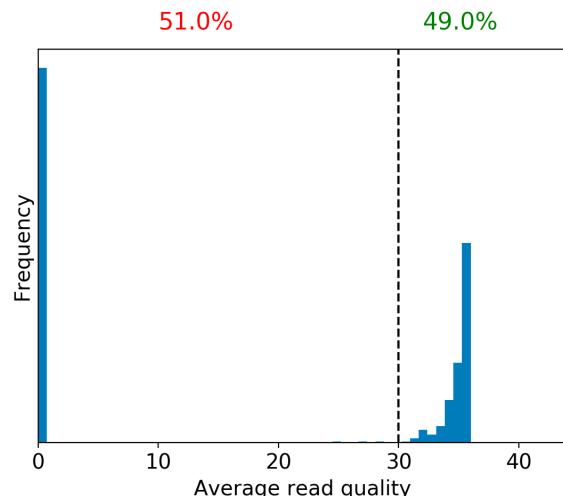
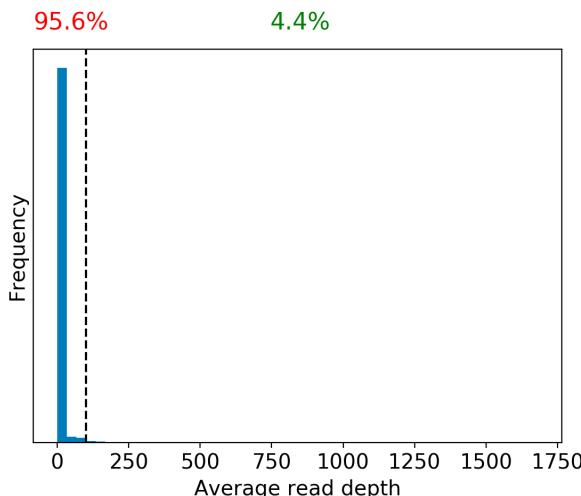
Sequencing chemistry:	AMPLICON with NextSeq 500
Source site:	USA: West Virginia (?.)
Sampling date:	2021-02-01
Collected by:	Aquavitas
Sequenced by:	Missing
Total number of reads:	1114642
Reads aligned:	8031 (0%)
Average read quality:	34.6
Average read length:	141
Reads passing filter:	7861 (0%)
Average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



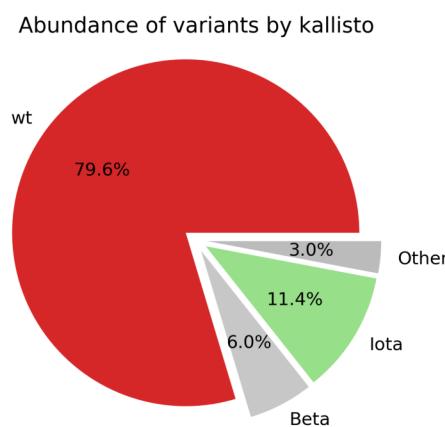
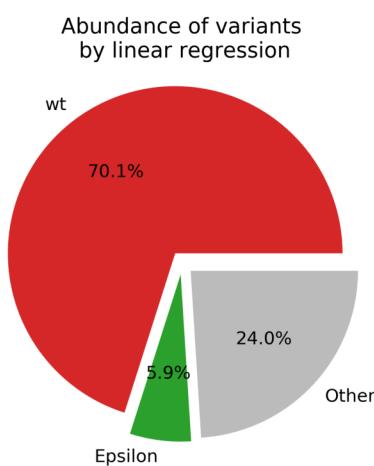
	Uncovered coordinates (0X)	Poorly covered coordinates (<10X)
# Inaccessible genomic coordinates by kit design:	-1nt (0%)	-1nt (0%)
All genomic coordinates:	15002nt (50%)	24582nt (82%)

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%)

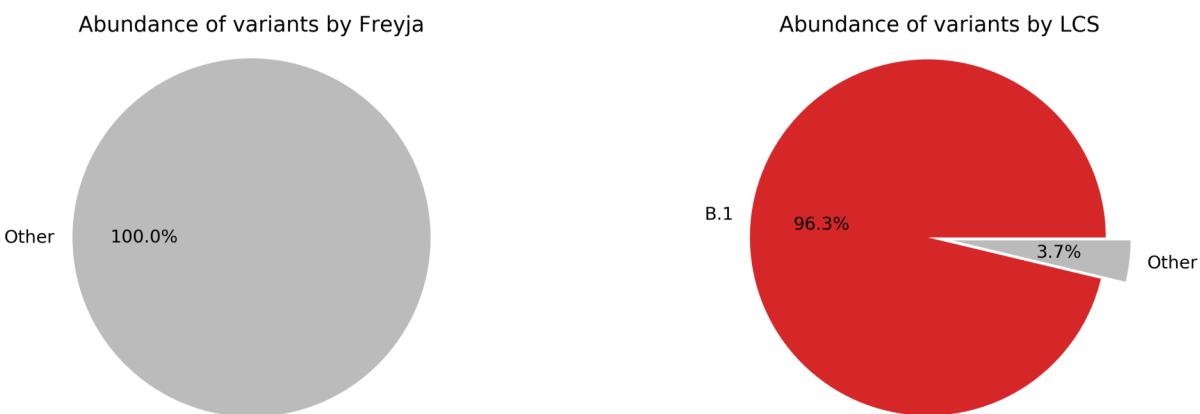
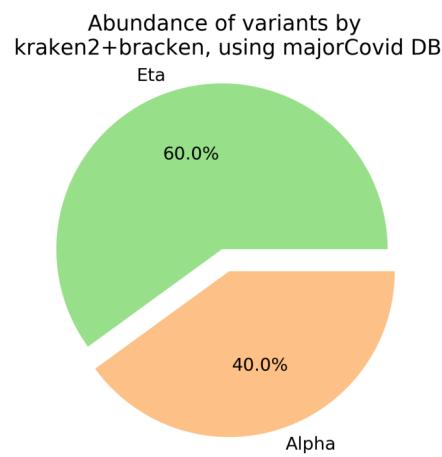
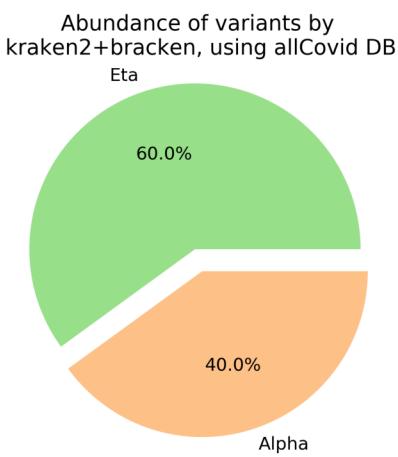
Detected variants (Experimental)



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.



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