

COVID-19 subject sdrop2__molpath

2021-04-17

The table below provides a summary of subject samples for which sequencing data is available.

The experiments column shows the number of sequencing experiments performed for each specimen.

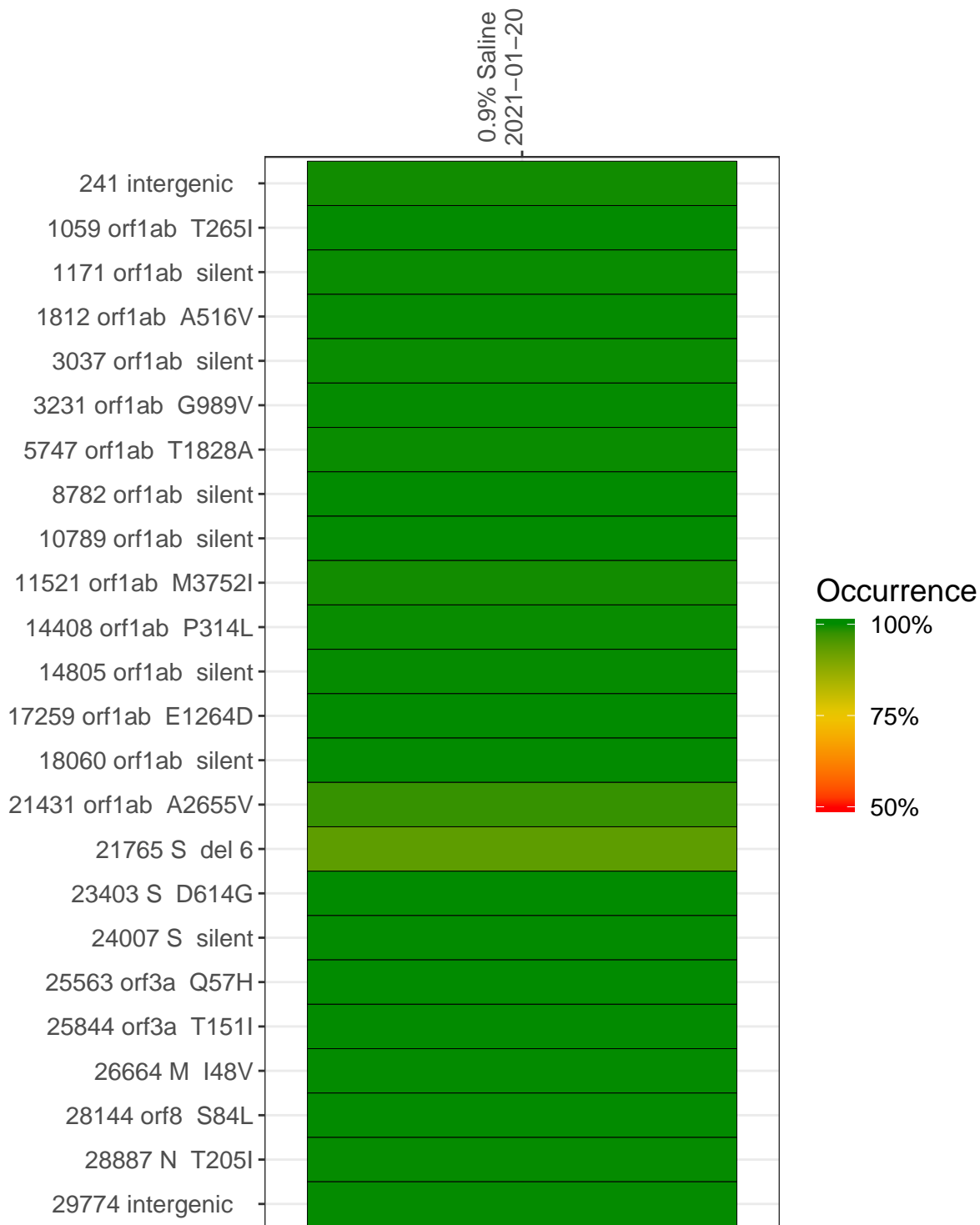
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0622	composite	NA	0.9% Saline	2021-01-20	29.66	B.1.375	99.9%	99.8%
VSP0622-1	single experiment	NA	0.9% Saline	2021-01-20	29.73	B.1.375	99.8%	99.8%
VSP0622-2	single experiment	NA	0.9% Saline	2021-01-20	29.94	B.1.375	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of read pairs and the variant yields a PHRED score > 20. Gray tiles denote positions where the variant was not the major variant or no variants were found. The relative base compositions of each experiment used to calculate tiles are shown in the following plot where the total number of position reads are shown atop of each plot.



0.9% Saline
2021-01-20

241 intergenic	13100	5709
1059 orf1ab T265I	6702	2691
1171 orf1ab silent	7372	2850
1812 orf1ab A516V	7437	2797
3037 orf1ab silent	13509	5318
3231 orf1ab G989V	6930	2707
5747 orf1ab T1828A	22569	9282
8782 orf1ab silent	10784	4001
10789 orf1ab silent	15778	5509
11521 orf1ab M3752I	29007	10536
14408 orf1ab P314L	16679	6124
14805 orf1ab silent	15107	5406
17259 orf1ab E1264D	53686	19044
18060 orf1ab silent	8620	3073
21431 orf1ab A2655V	1181	342
21765 S del 6	5405	2138
23403 S D614G	16830	6667
24007 S silent	6574	2446
25563 orf3a Q57H	9993	3711
25844 orf3a T151I	13324	4997
26664 M I48V	11084	4316
28144 orf8 S84L	6847	2479
28887 N T205I	1250	492
29774 intergenic	718	289

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

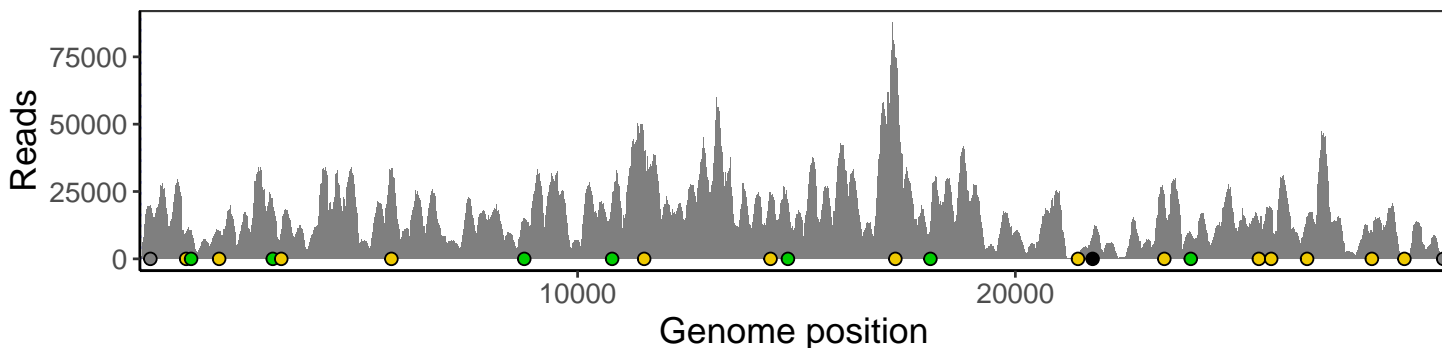
VSP0622-1

VSP0622-2

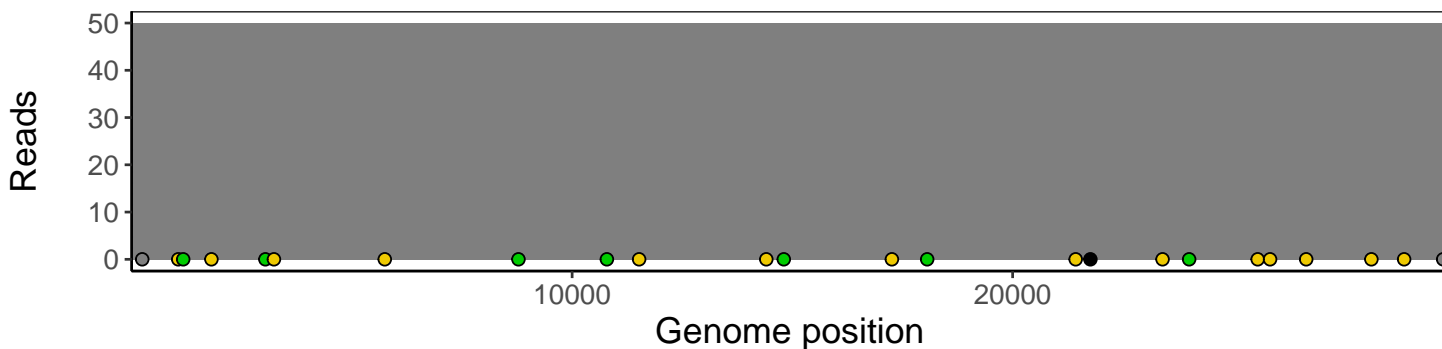
Analyses of individual experiments and composite results

VSP0622 | 2021-01-20 | 0.9% Saline | molpath-sdrop2 | composite result

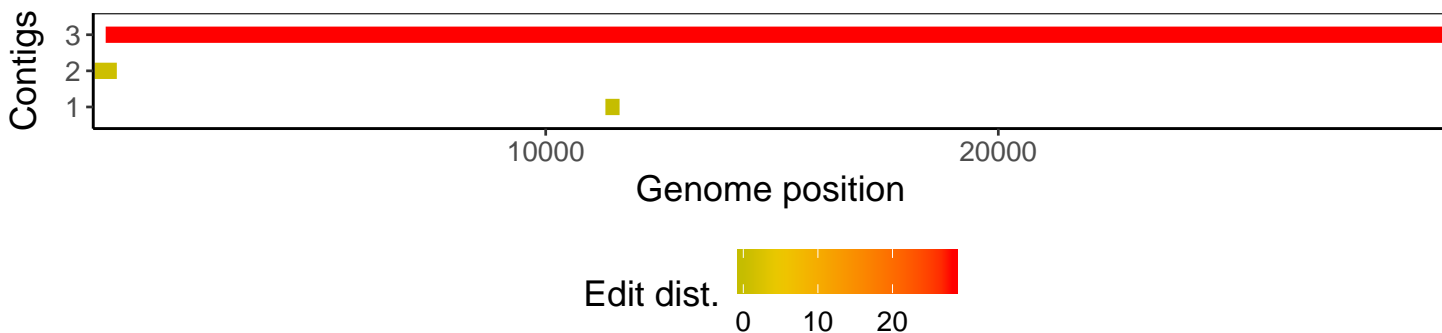
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



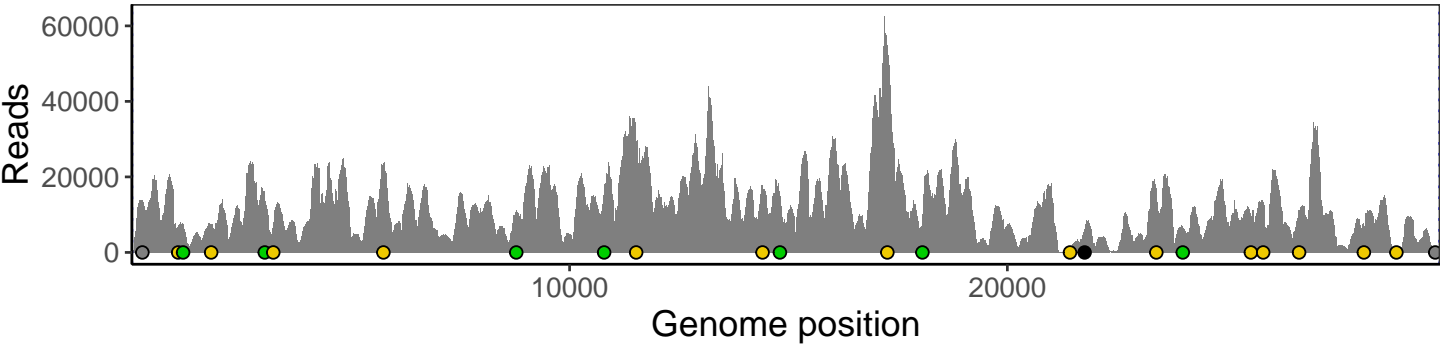
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



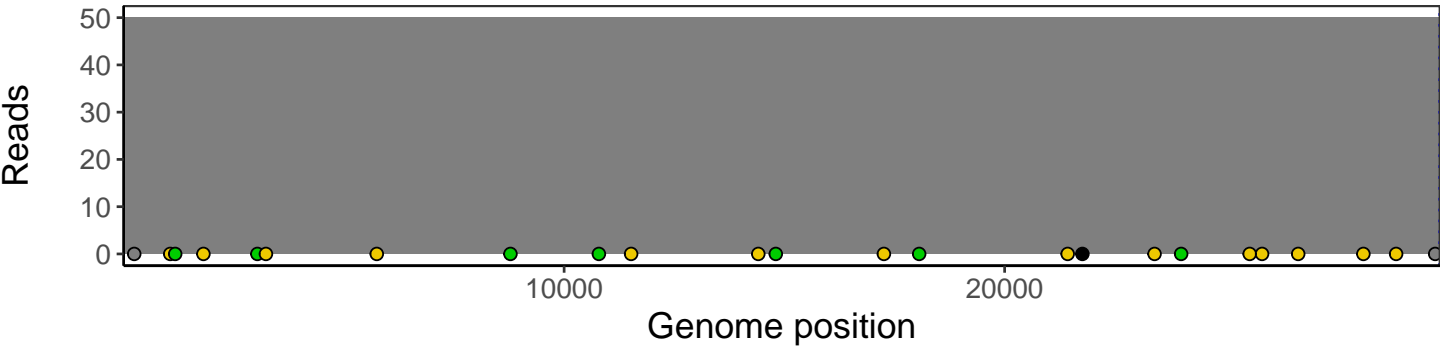
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



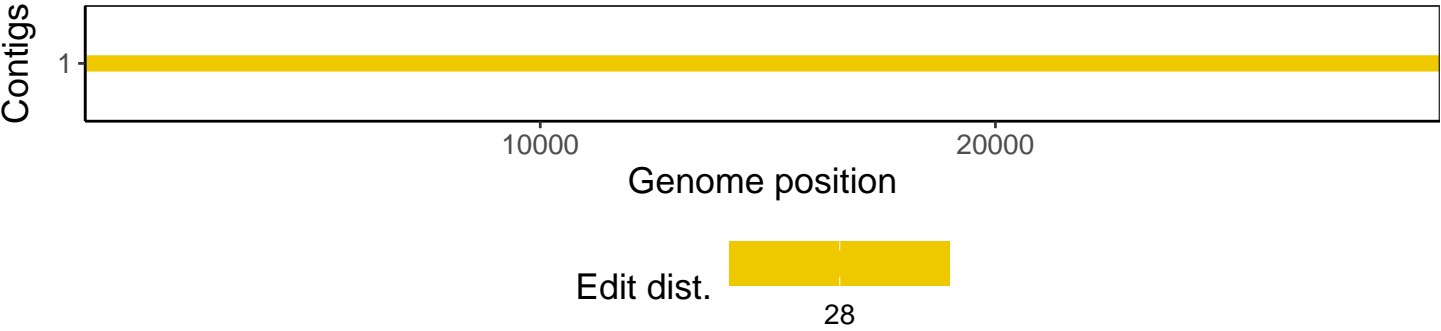
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



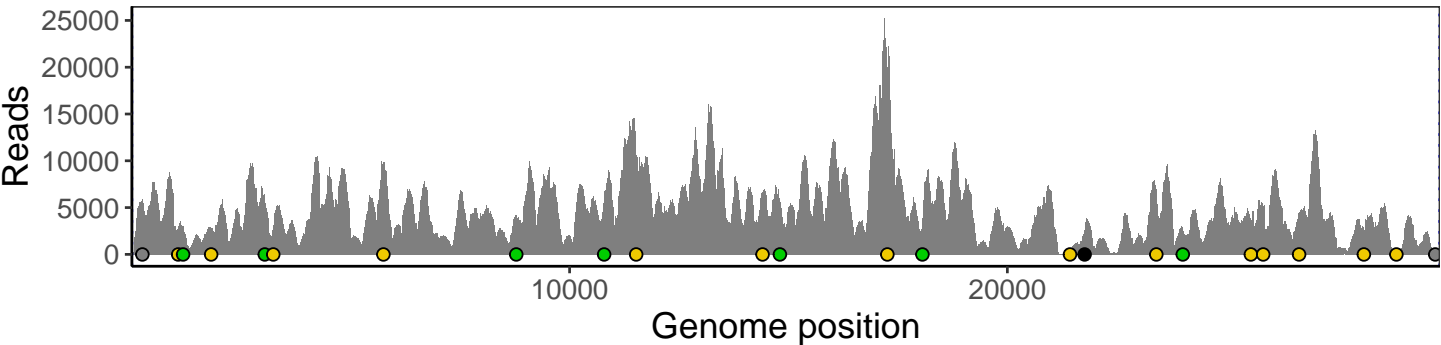
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



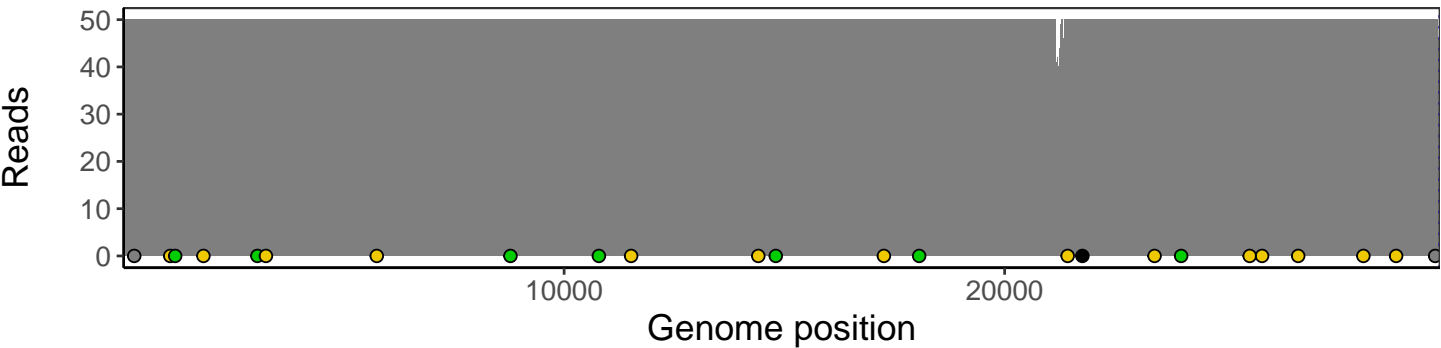
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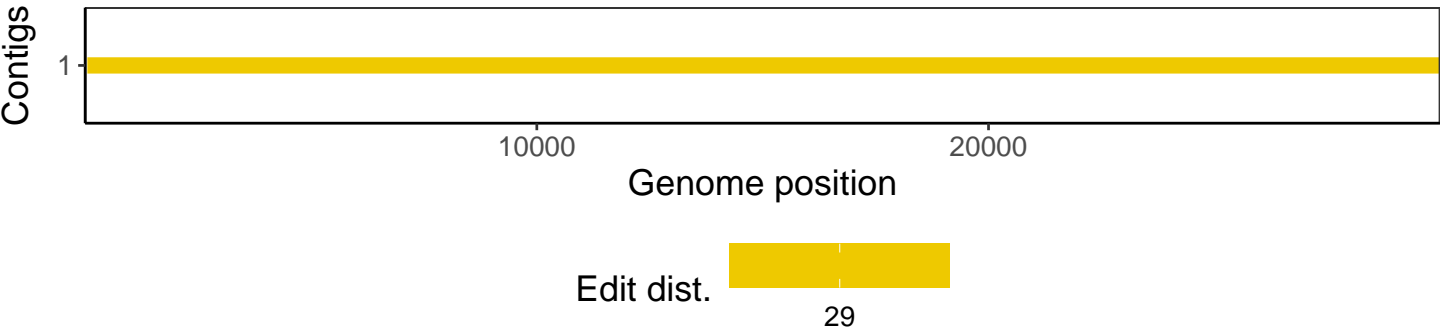
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Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3
pangolin	2.3.8
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1