

COVID-19 subject 272

2021-06-23

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.

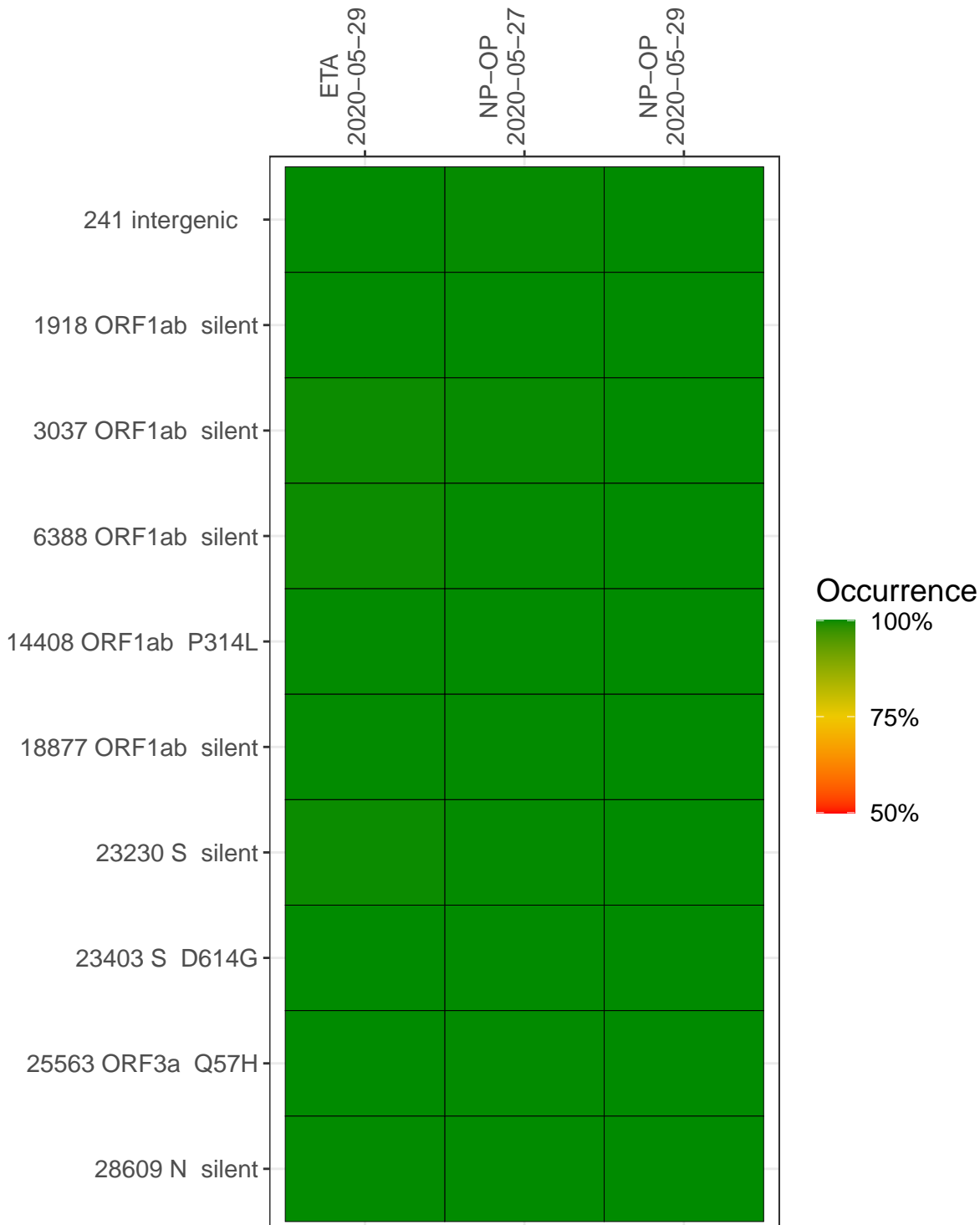
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0179-1	single experiment	14500	NP-OP	2020-05-27	29.41	B.1.439	99.9%	99.8%
VSP0195-1	single experiment	1530000	ETA	2020-05-29	25.63	B.1.439	99.9%	99.3%
VSP0196-1	single experiment	14300	NP-OP	2020-05-29	22.29	B.1.439	99.5%	99.0%
VSP0260-1	single experiment	NA	Stool	2020-06-17	NA	NA	3.5%	0.0%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.



	ETA 2020-05-29	NP-OP 2020-05-27	NP-OP 2020-05-29
241 intergenic	487	3572	60
1918 ORF1ab silent	5043	3229	53
3037 ORF1ab silent	2148	2920	78
6388 ORF1ab silent	1071	5330	230
14408 ORF1ab P314L	1877	5734	90
18877 ORF1ab silent	3600	4784	87
23230 S silent	1554	5315	227
23403 S D614G	2122	7246	267
25563 ORF3a Q57H	4872	3767	41
28609 N silent	3531	12130	401
	VSP0195-1	VSP0179-1	VSP0196-1

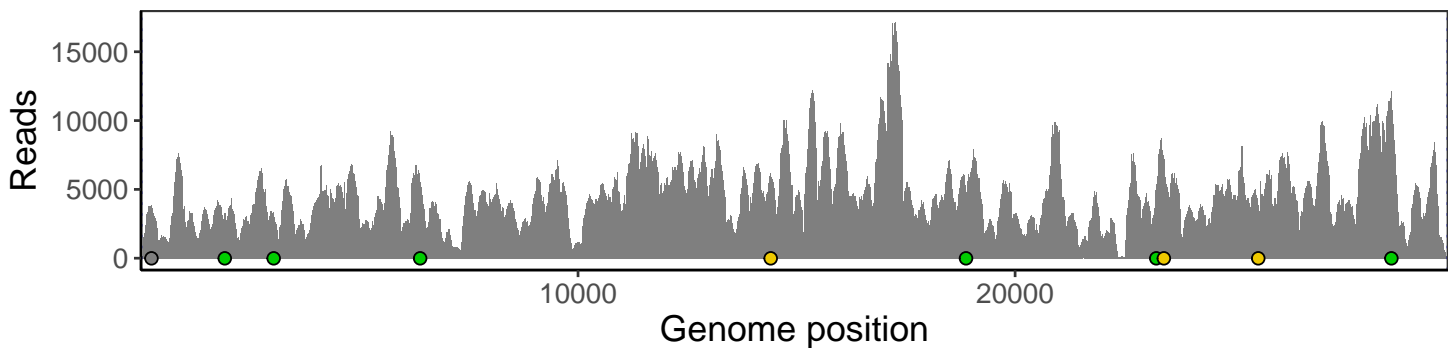
Base change

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

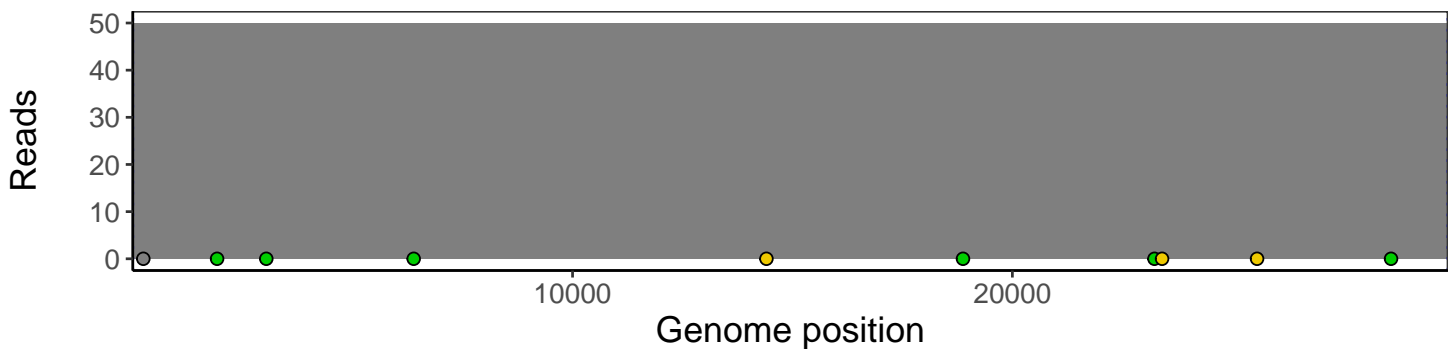
Analyses of individual experiments and composite results

VSP0179-1 | 2020-05-27 | NP-OP | 272no-q | 14500 genomes | single experiment

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.



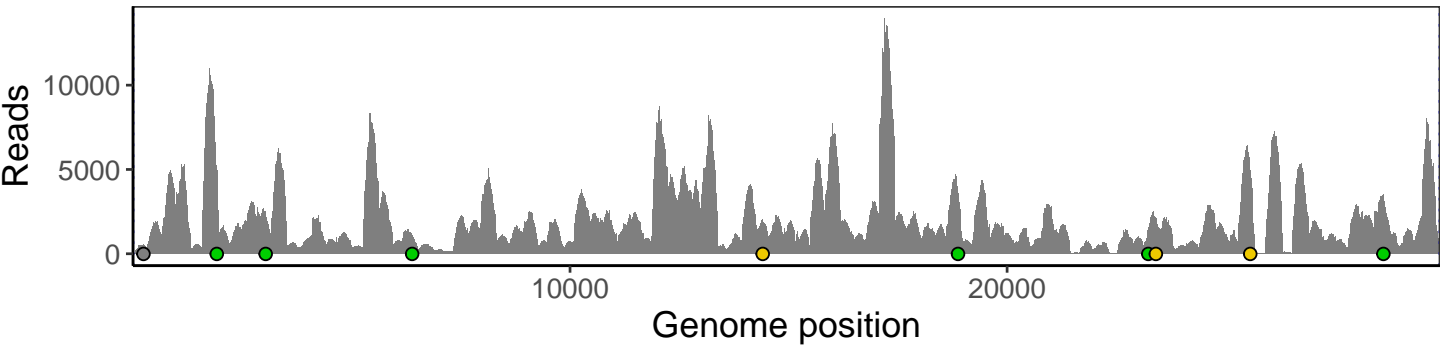
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



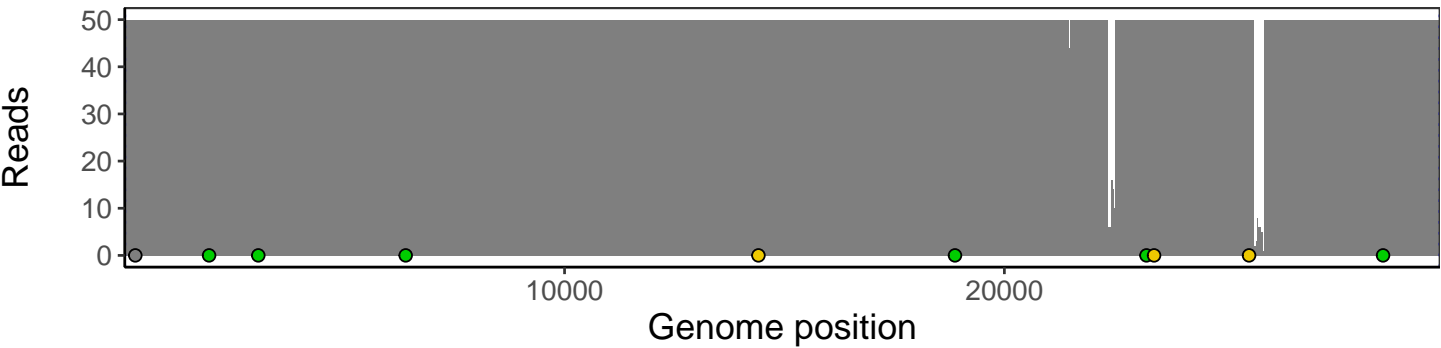
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



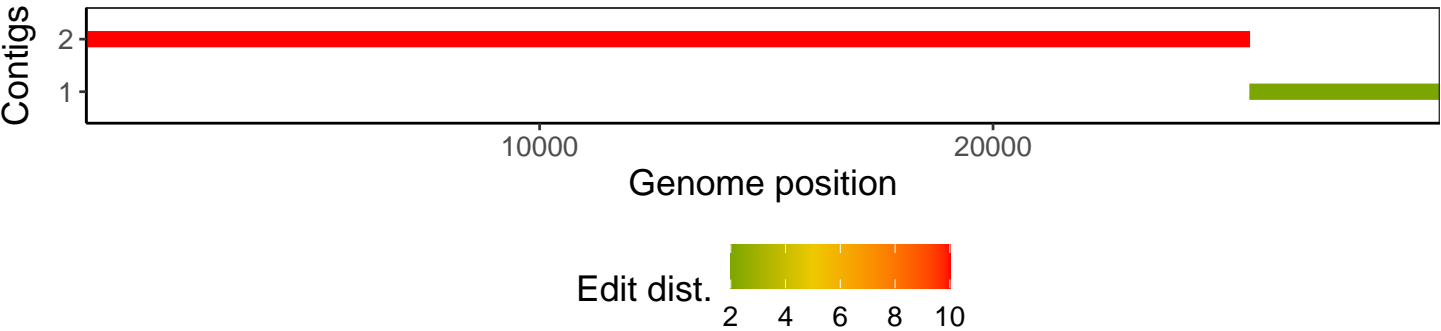
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



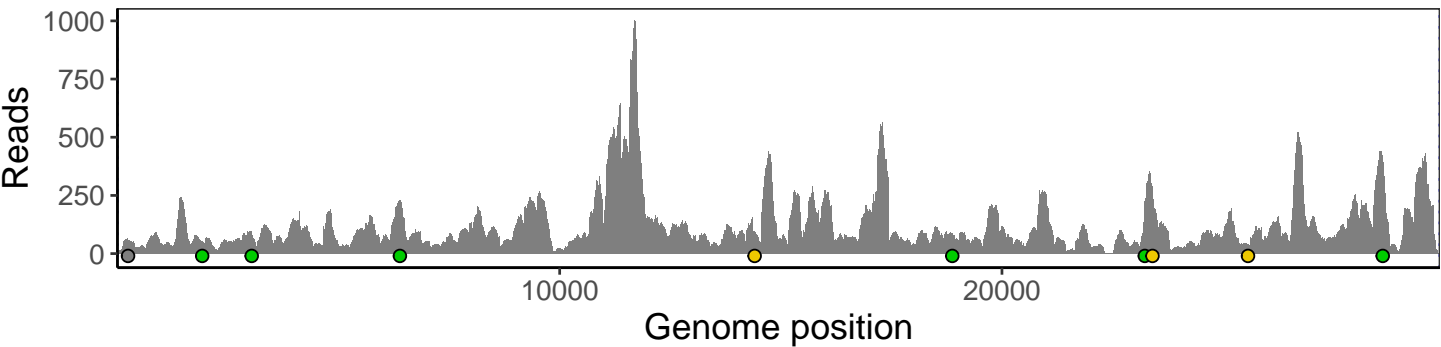
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



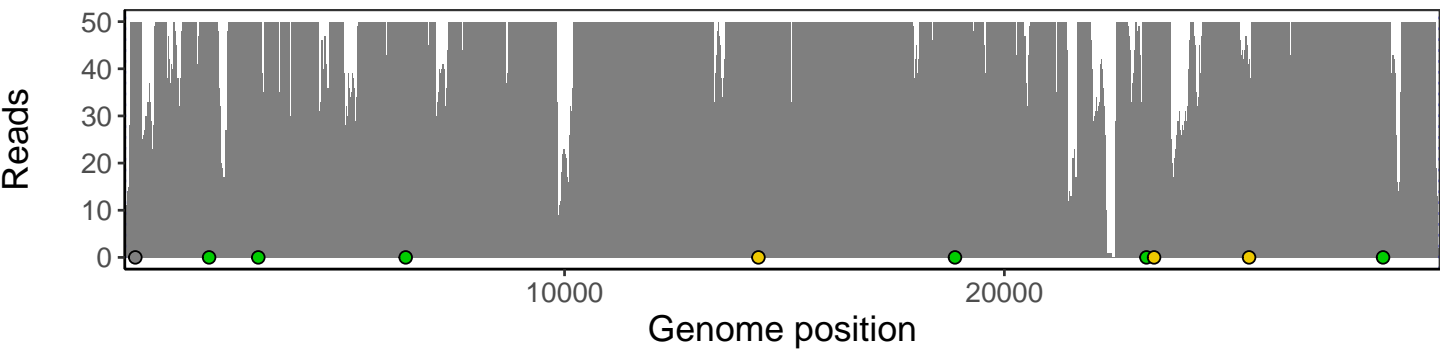
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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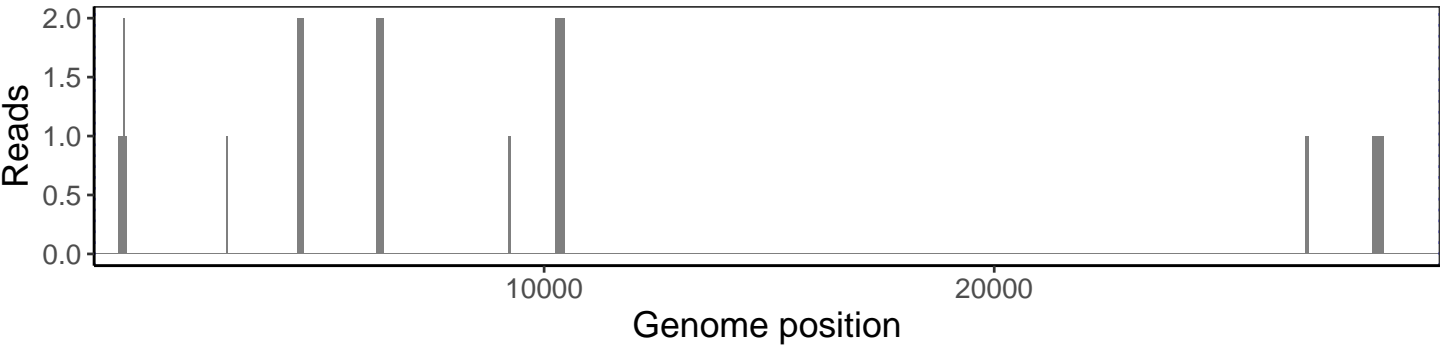
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



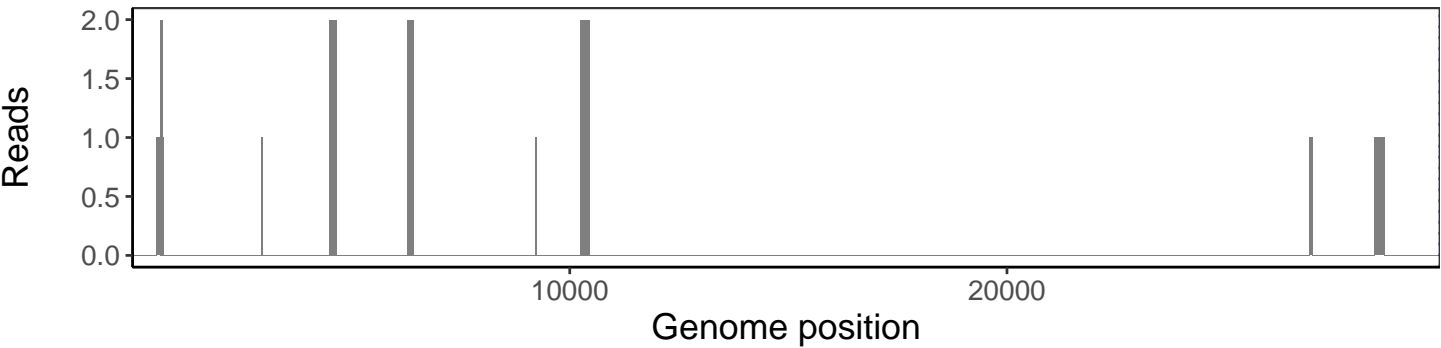
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



No contig data available.

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	3.1.3
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	3.3.3
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