

COVID-19 subject 434

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.

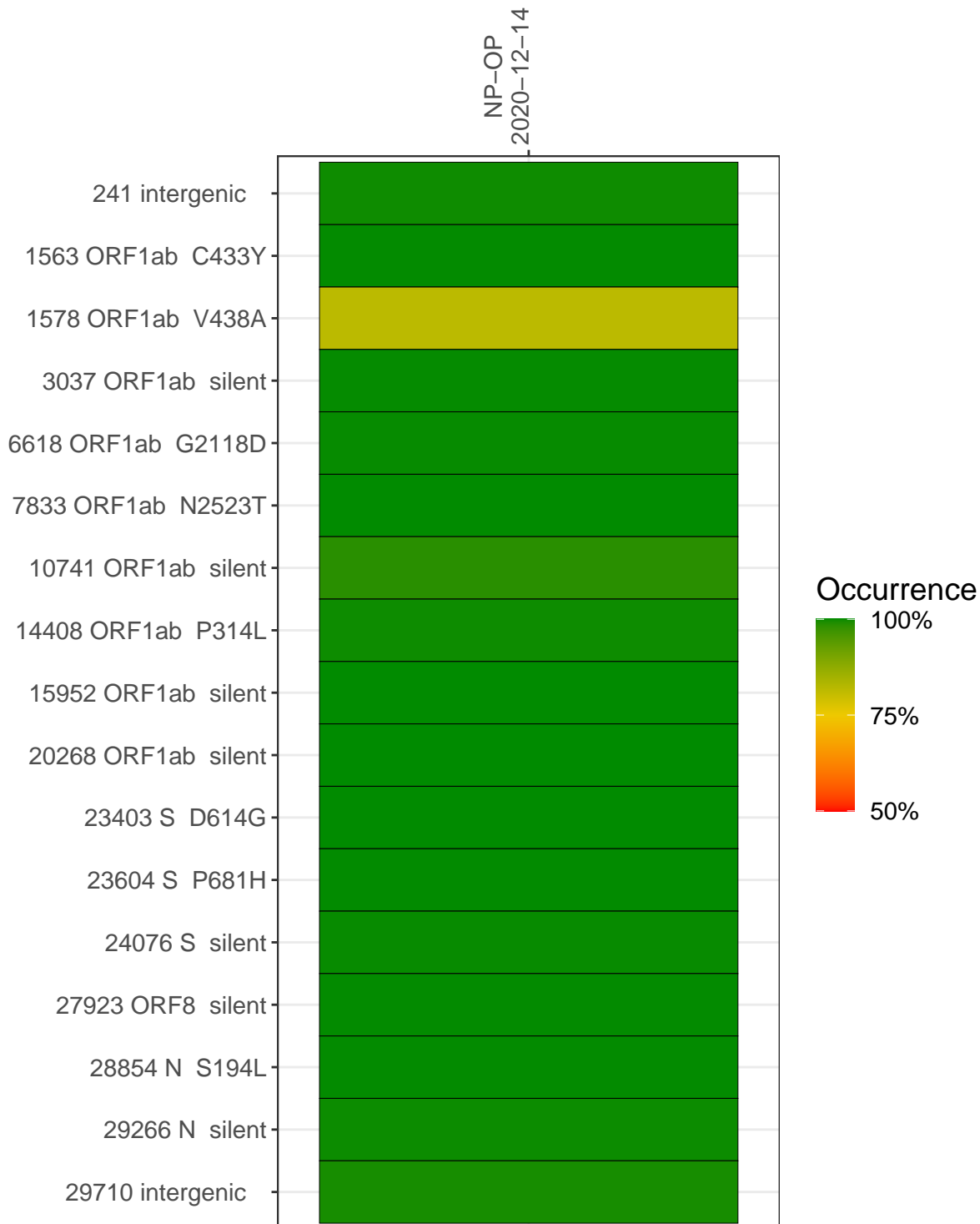
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0550	composite	NA	NP-OP	2020-12-14	21.37	B.1.243	99.9%	99.7%
VSP0550-1	single experiment	NA	NP-OP	2020-12-14	29.07	B.1.243	99.7%	99.7%
VSP0550-2	single experiment	NA	NP-OP	2020-12-14	29.91	B.1.243	99.8%	99.5%

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.



NP-OP
2020-12-14

241 intergenic	17215	6533
1563 ORF1ab C433Y	1178	346
1578 ORF1ab V438A	1230	412
3037 ORF1ab silent	9060	2809
6618 ORF1ab G2118D	4061	1438
7833 ORF1ab N2523T	5517	1767
10741 ORF1ab silent	5378	1719
14408 ORF1ab P314L	9542	3024
15952 ORF1ab silent	31860	10149
20268 ORF1ab silent	245	86
23403 S D614G	28019	9987
23604 S P681H	20200	6915
24076 S silent	5089	1696
27923 ORF8 silent	3001	1044
28854 N S194L	2833	961
29266 N silent	11582	3400
29710 intergenic	119	35

Base change

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

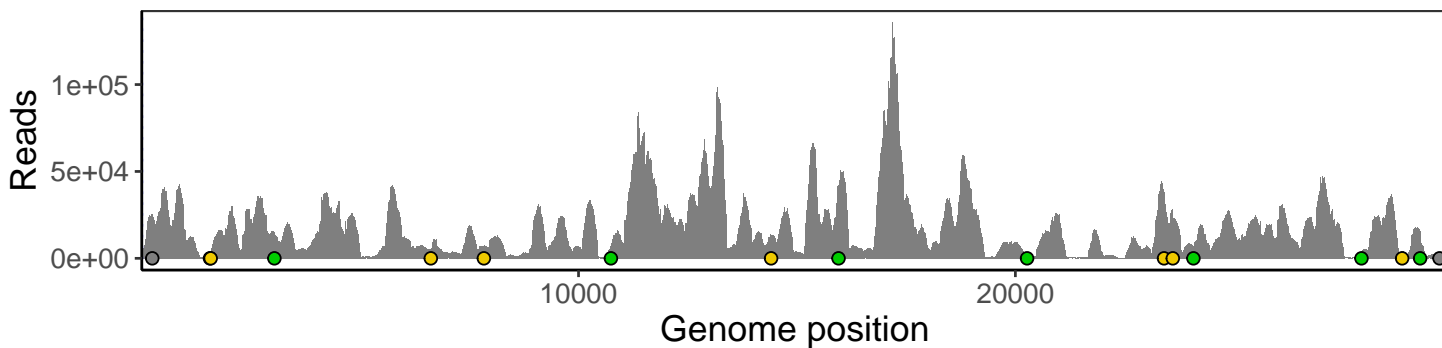
VSP0550-1

VSP0550-2

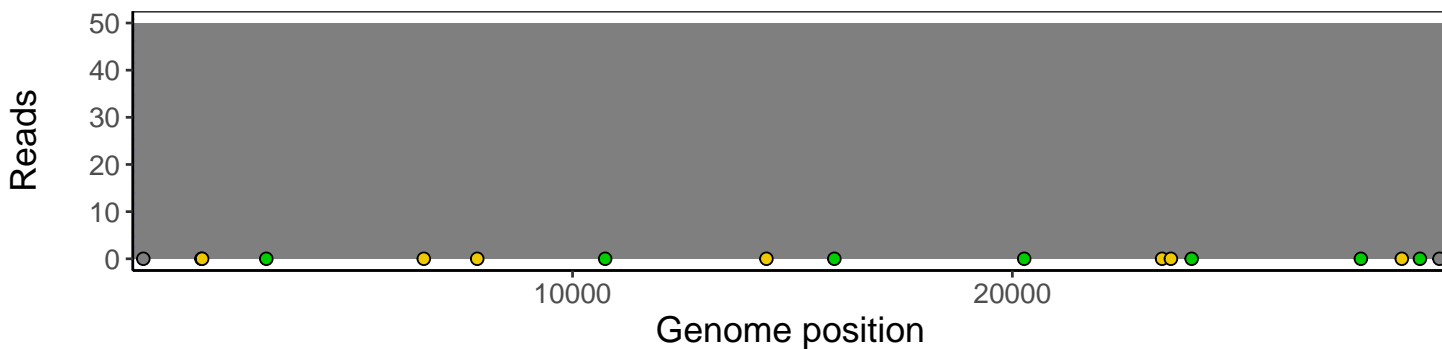
Analyses of individual experiments and composite results

VSP0550 | 2020-12-14 | NP-OP | 434no | composite result

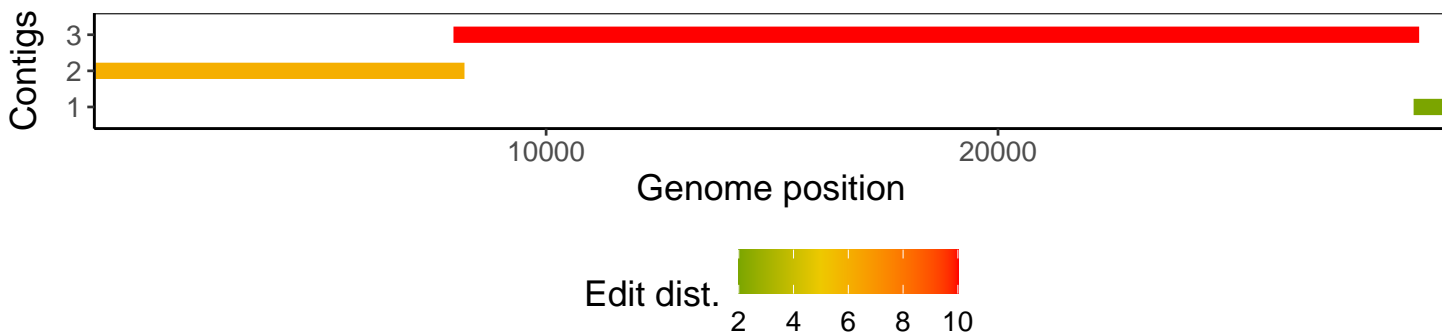
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



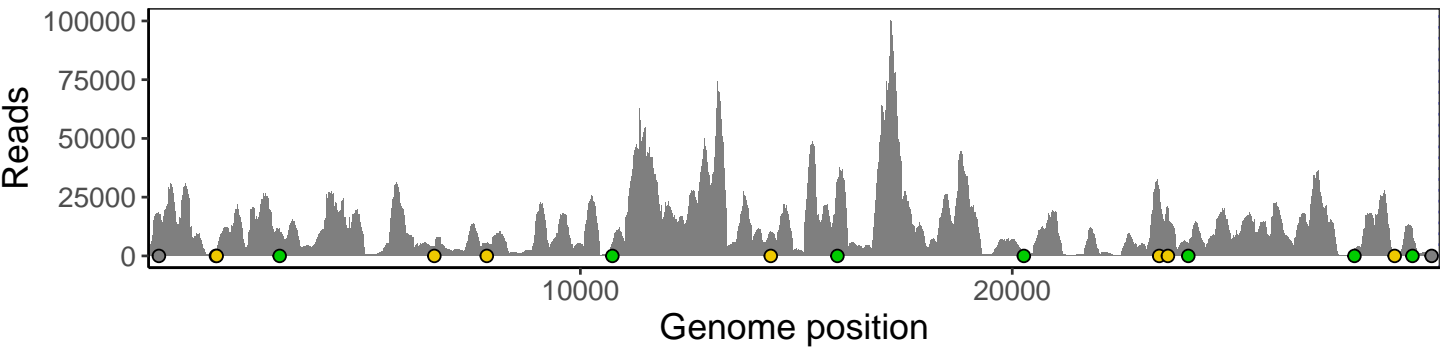
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



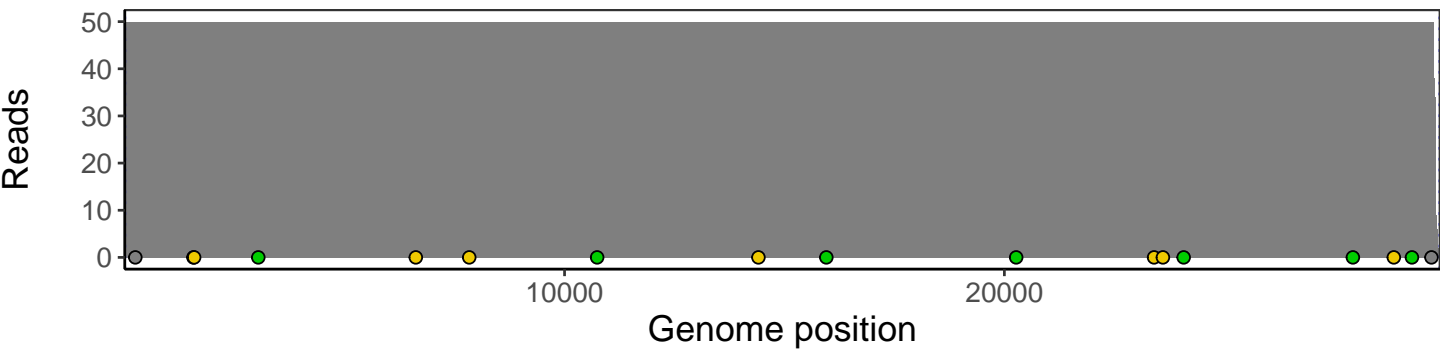
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



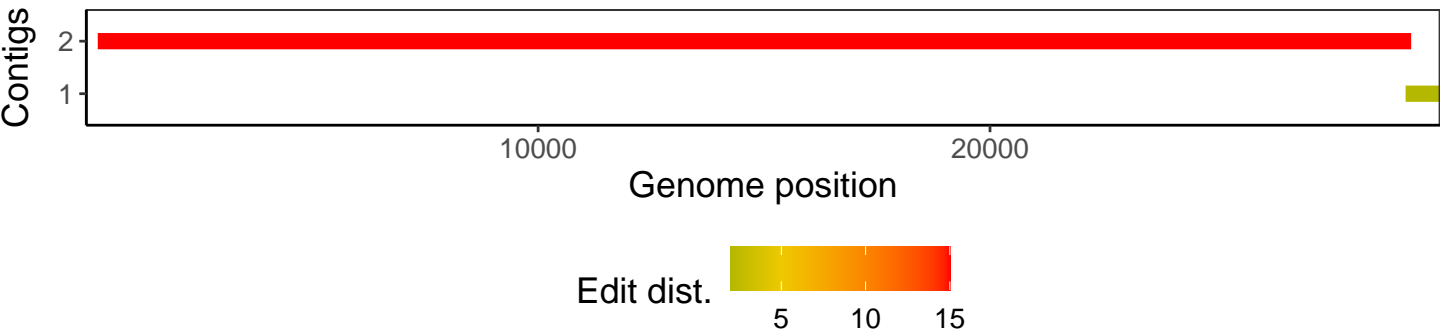
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



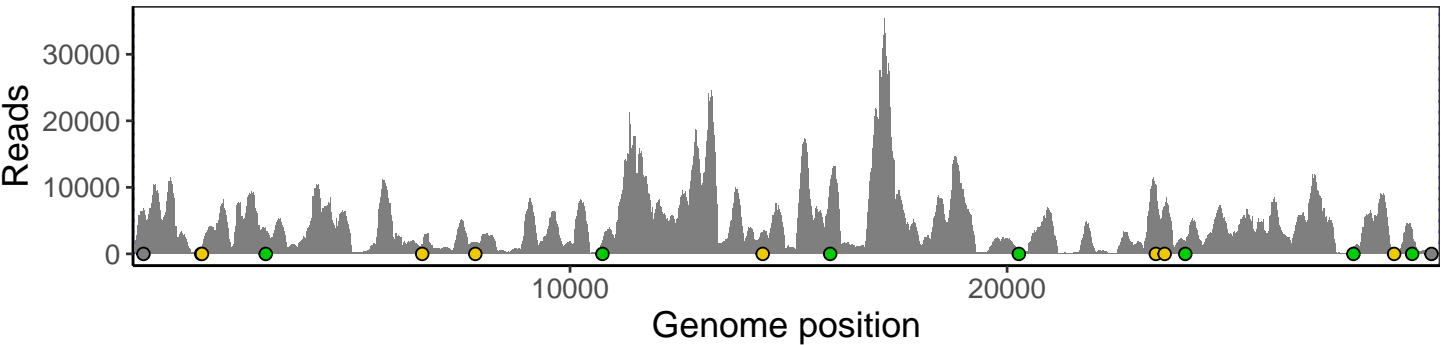
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



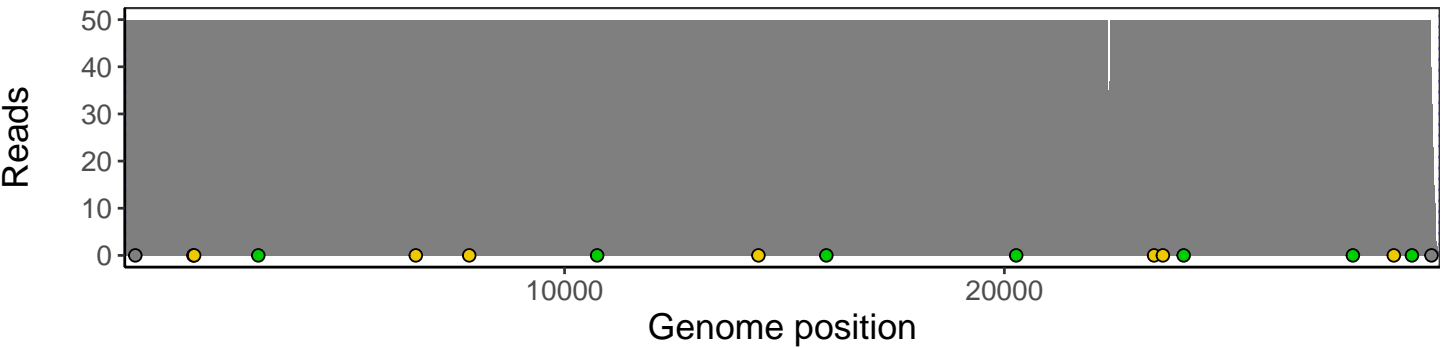
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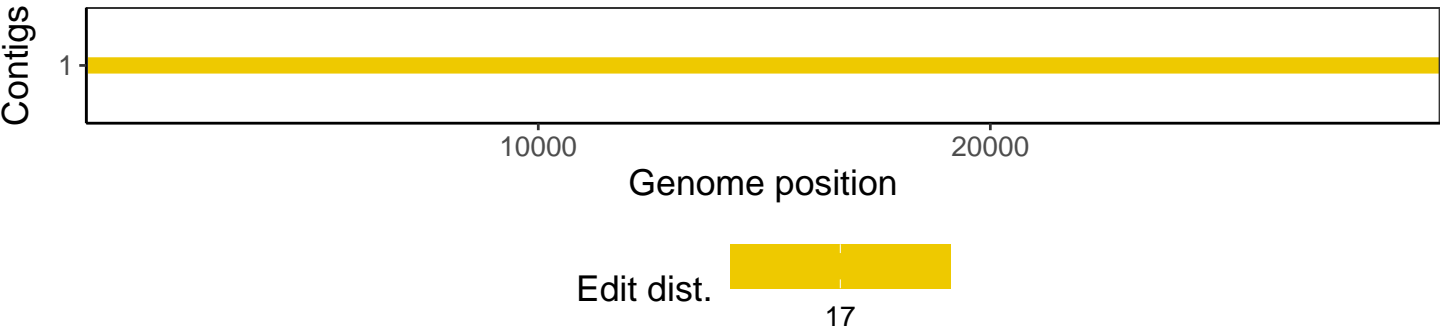
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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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	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