

COVID-19 subject MPCluster2-Seq2

2021-06-23

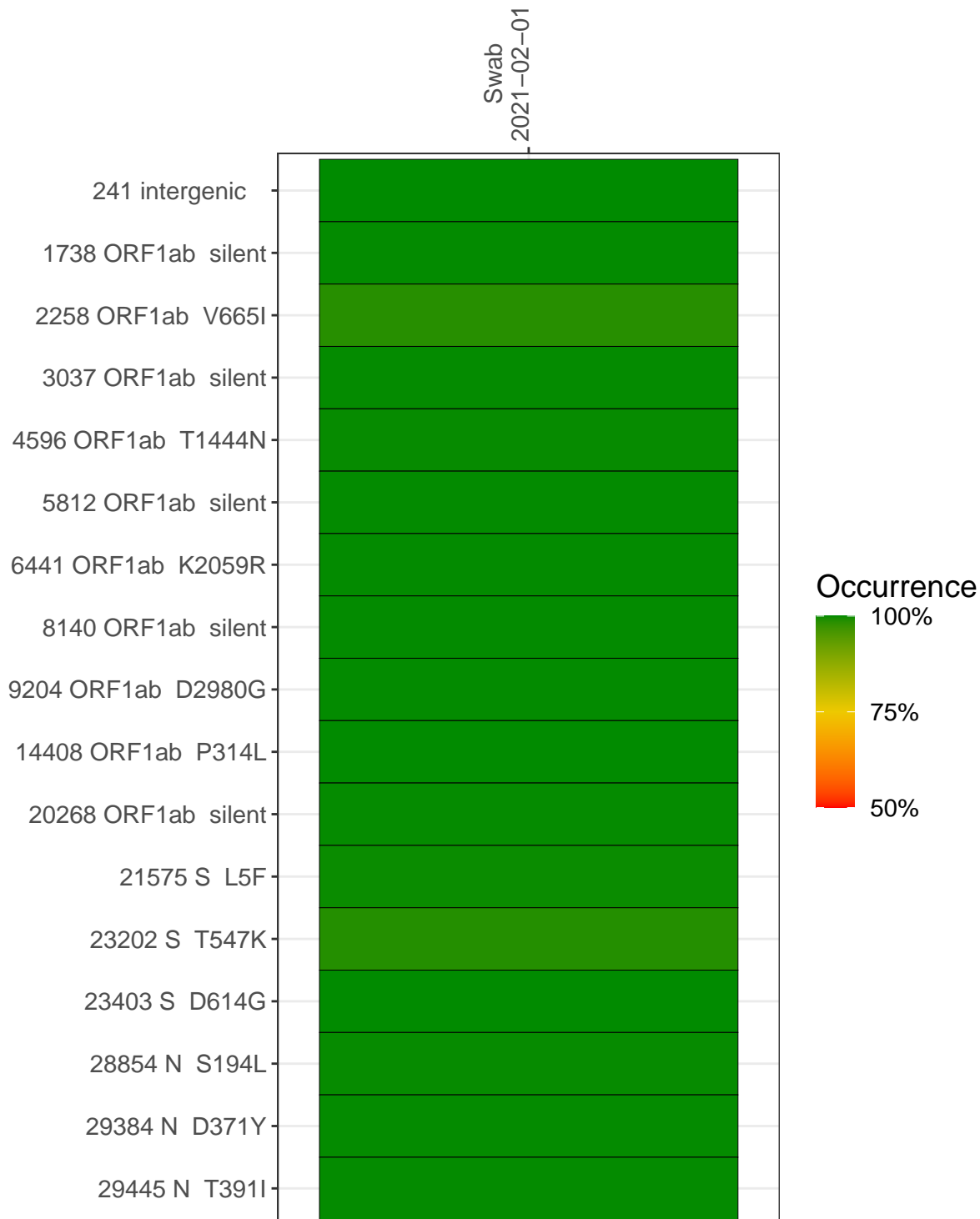
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0760	composite	NA	Swab	2021-02-01	29.94	B.1.234	99.9%	99.9%
VSP0760-1	single experiment	NA	Swab	2021-02-01	29.84	B.1.234	99.8%	99.8%
VSP0760-2	single experiment	NA	Swab	2021-02-01	29.83	B.1.234	99.9%	99.8%

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.



Swab
2021-02-01

241 intergenic	12805	2797
1738 ORF1ab silent	9518	5923
2258 ORF1ab V665I	2345	4105
3037 ORF1ab silent	2976	5613
4596 ORF1ab T1444N	9204	8025
5812 ORF1ab silent	11335	15094
6441 ORF1ab K2059R	11154	7942
8140 ORF1ab silent	6567	7251
9204 ORF1ab D2980G	4694	5642
14408 ORF1ab P314L	8907	11057
20268 ORF1ab silent	1192	3039
21575 S L5F	919	2136
23202 S T547K	8874	4953
23403 S D614G	20774	10753
28854 N S194L	1521	451
29384 N D371Y	1405	1836
29445 N T391I	2071	2654

Base change

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

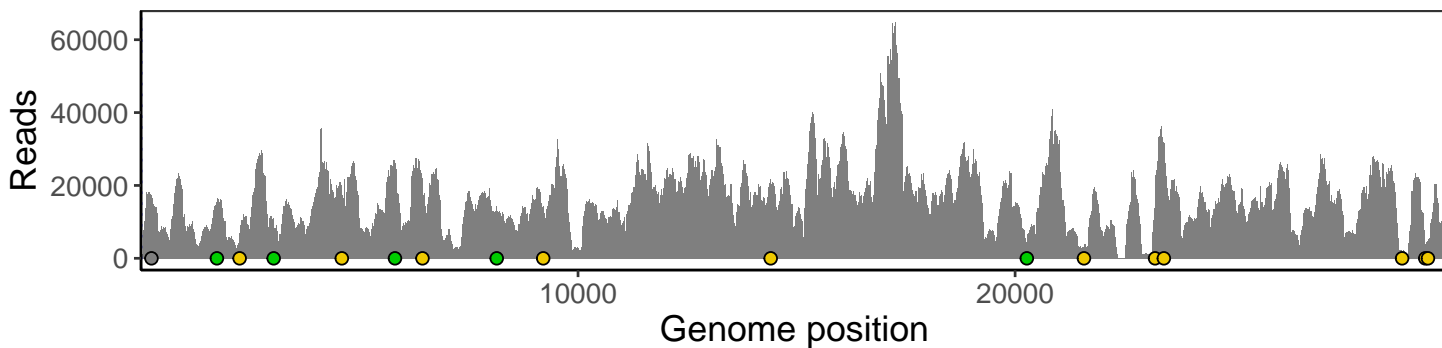
VSP0760-1

VSP0760-2

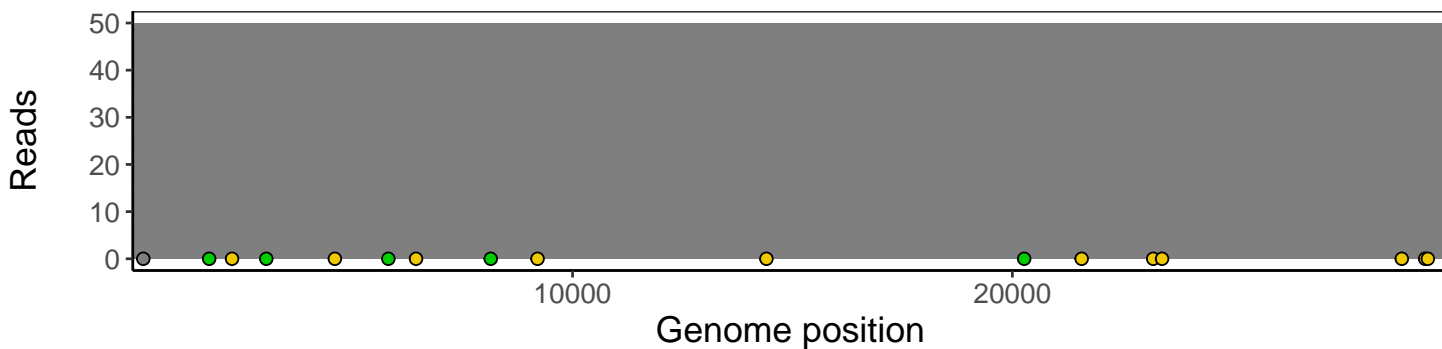
Analyses of individual experiments and composite results

VSP0760 | 2021-02-01 | Swab | MPCluster2-Seq2 | composite result

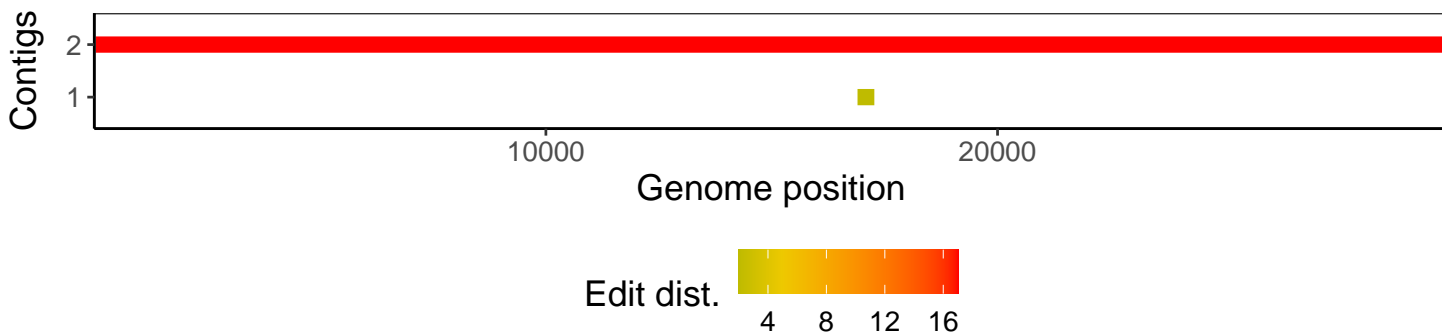
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



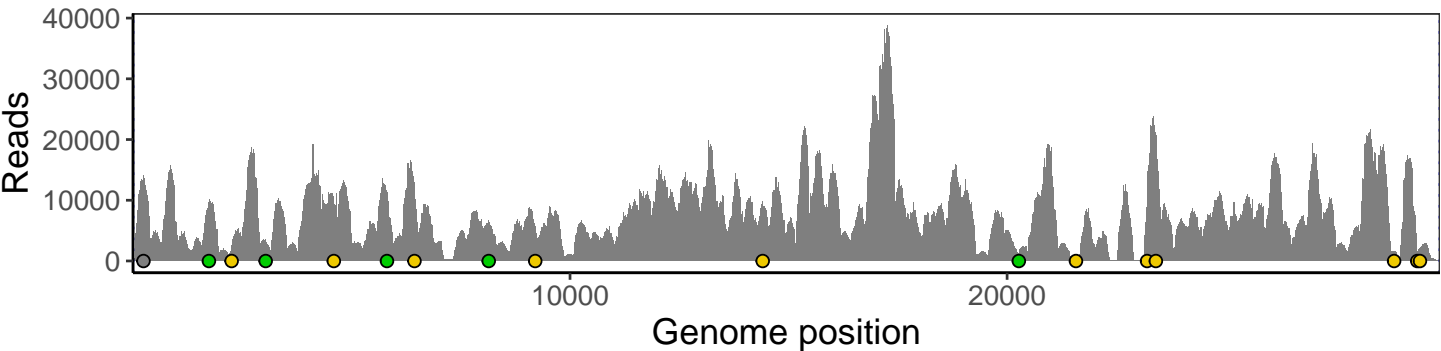
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



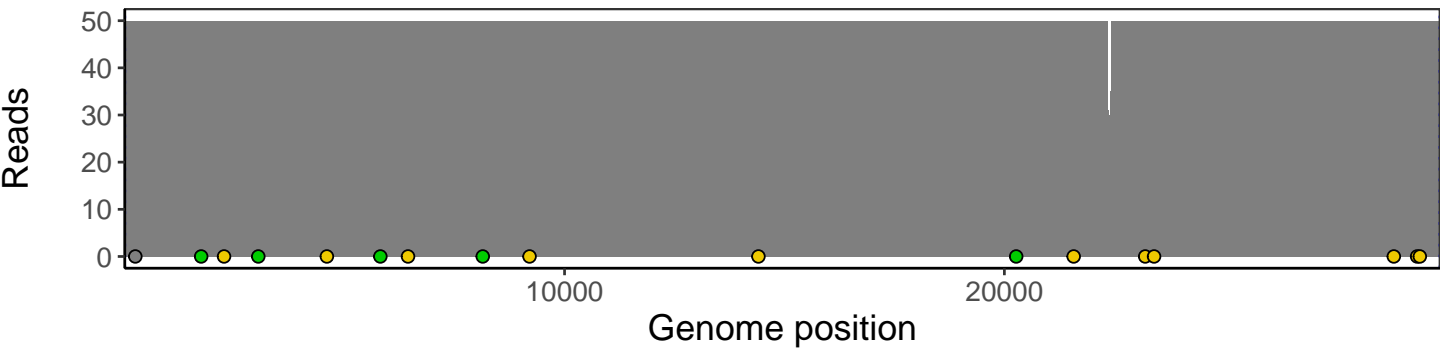
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



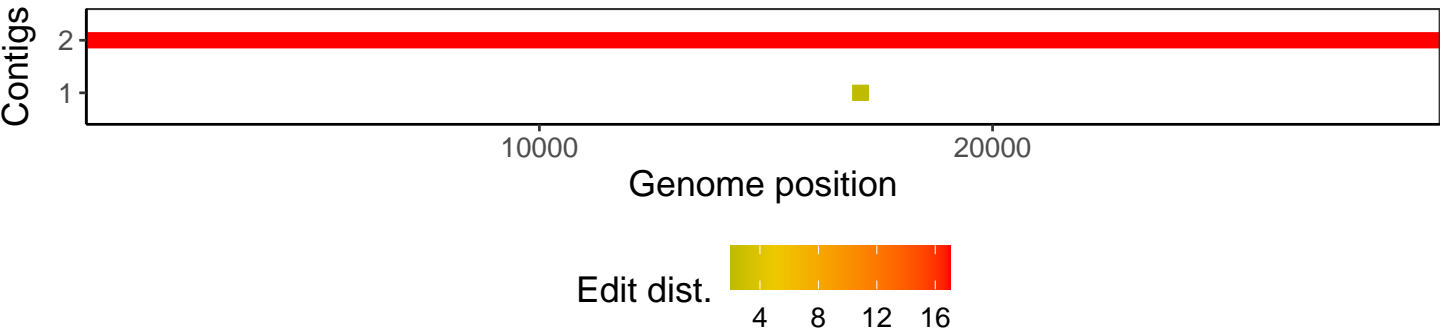
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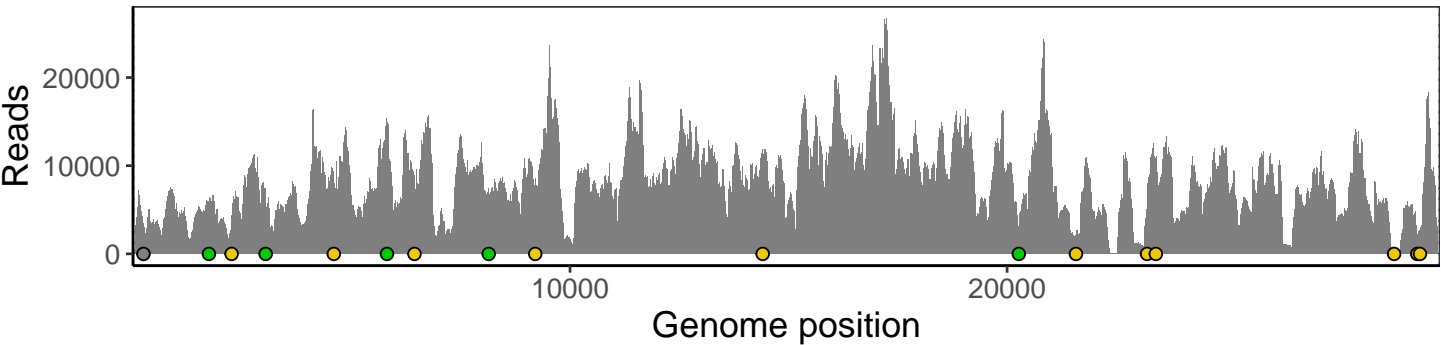
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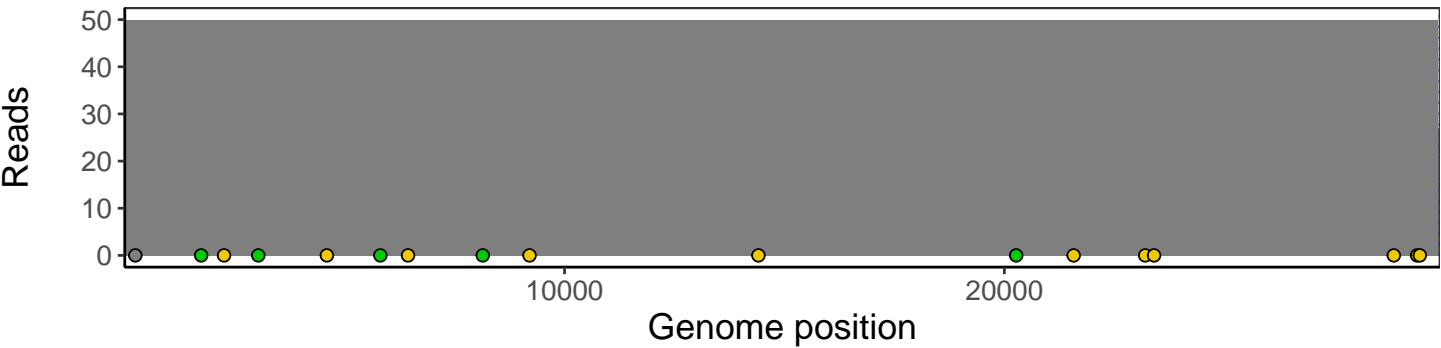
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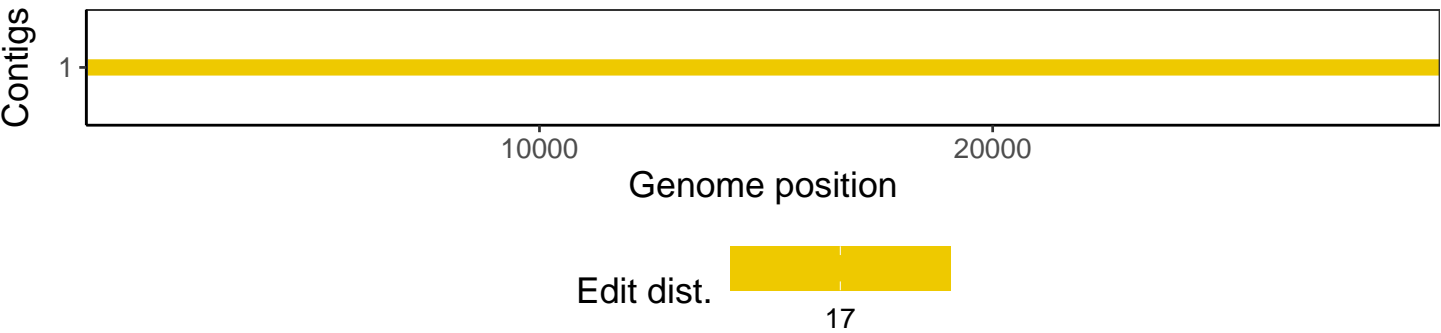
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Software environment

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	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