

# COVID-19 subject PQ-Seq4

*2021-06-23*

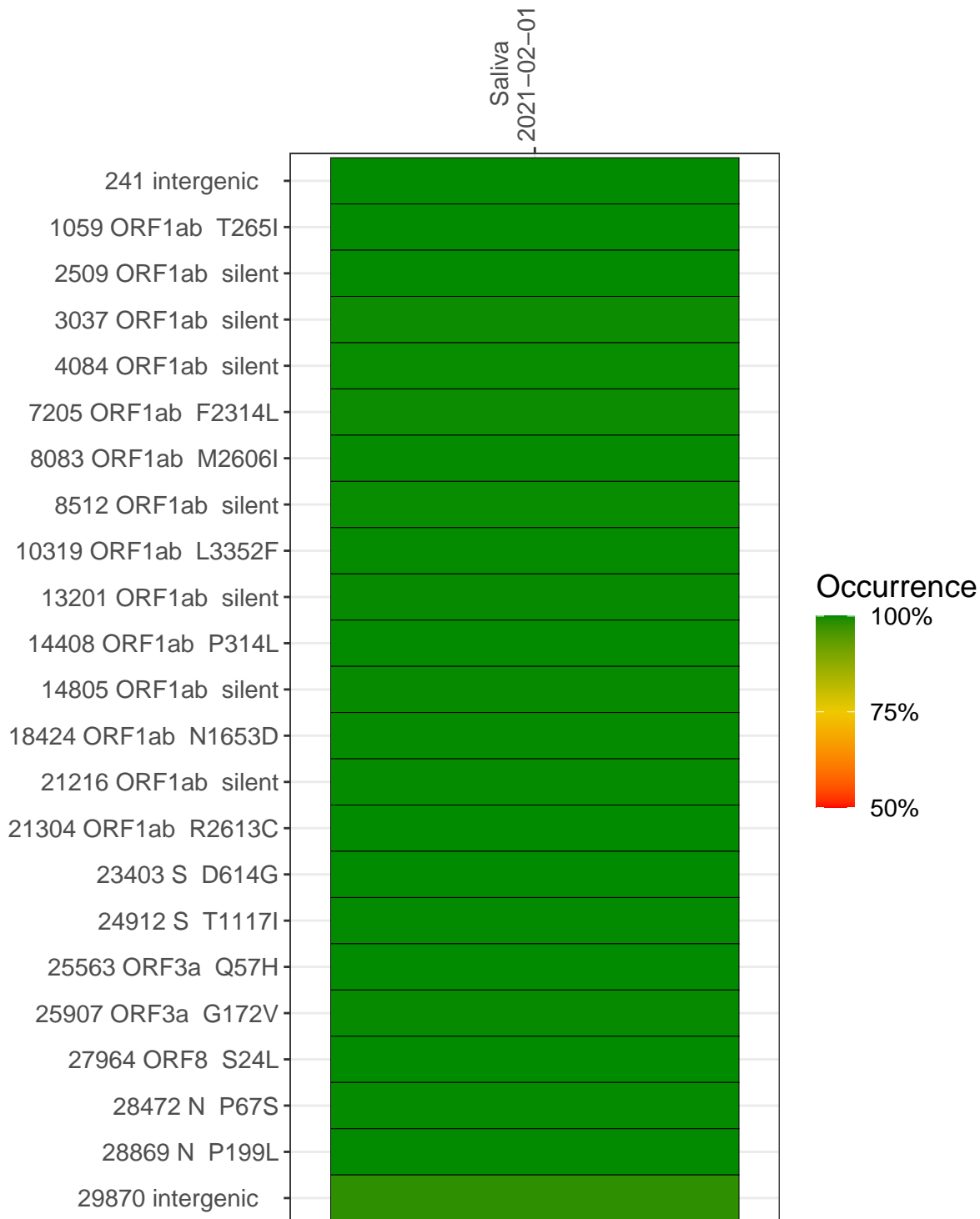
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads)
VSP0773	composite	NA	Saliva	2021-02-01	29.82	B.1.2	99.9%	99.9%
VSP0773-1	single experiment	NA	Saliva	2021-02-01	29.84	B.1.2	99.8%	99.8%
VSP0773-2	single experiment	NA	Saliva	2021-02-01	7.91	NA	97.6%	90.3%

## 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.



Saliva  
2021-02-01

241 intergenic	15386	36
1059 ORF1ab T265I	6897	100
2509 ORF1ab silent	4689	4
3037 ORF1ab silent	7260	9
4084 ORF1ab silent	13493	328
7205 ORF1ab F2314L	1326	38
8083 ORF1ab M2606I	9767	75
8512 ORF1ab silent	3656	3
10319 ORF1ab L3352F	12826	72
13201 ORF1ab silent	25772	175
14408 ORF1ab P314L	14398	55
14805 ORF1ab silent	14663	100
18424 ORF1ab N1653D	19392	97
21216 ORF1ab silent	1637	66
21304 ORF1ab R2613C	1863	51
23403 S D614G	23108	230
24912 S T1117I	12631	61
25563 ORF3a Q57H	9538	84
25907 ORF3a G172V	6351	110
27964 ORF8 S24L	8399	1
28472 N P67S	15297	2
28869 N P199L	1854	146
29870 intergenic	13	1687

Base change

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

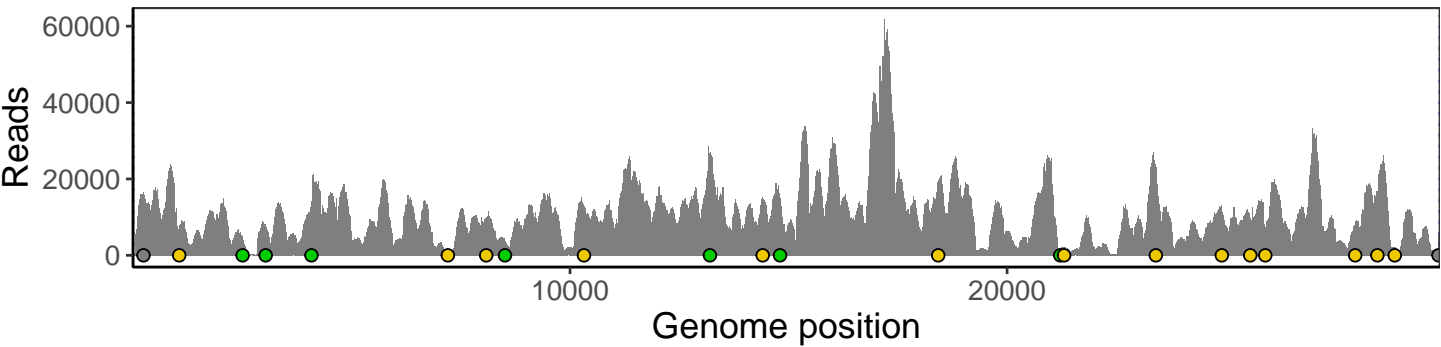
VSP0773-1

VSP0773-2

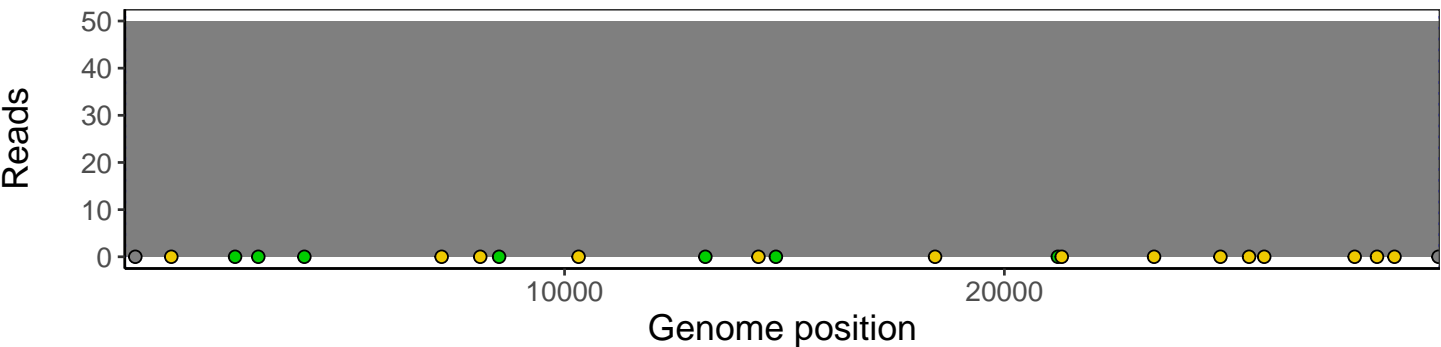
# Analyses of individual experiments and composite results

VSP0773 | 2021-02-01 | Saliva | PQ-Seq4 | composite result

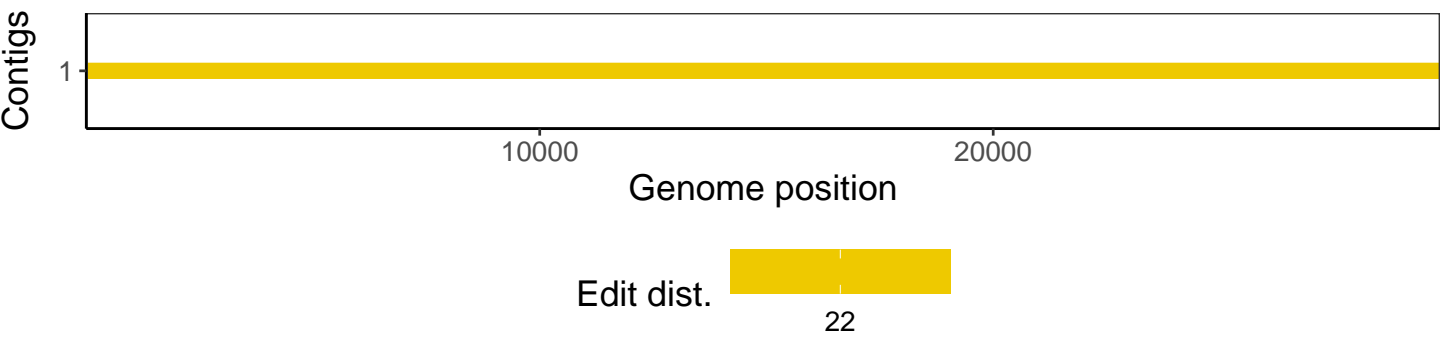
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



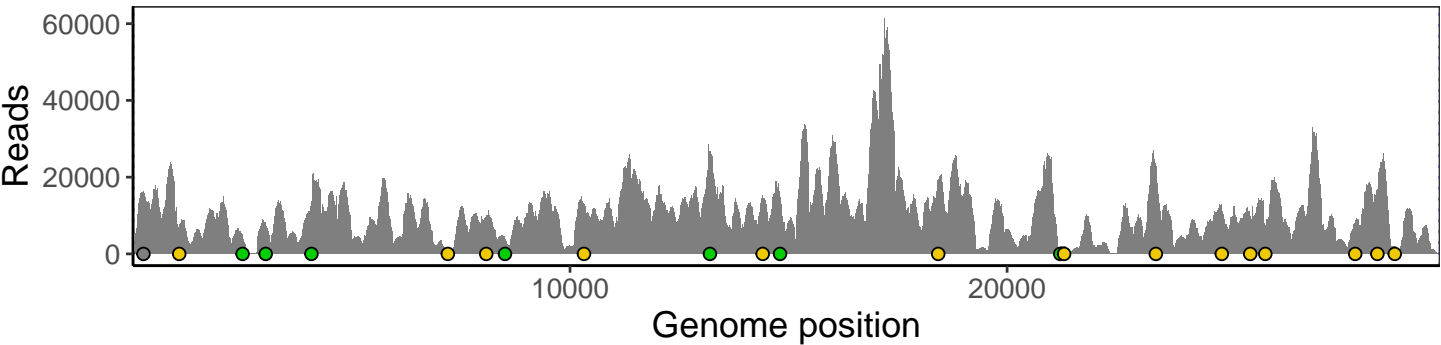
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



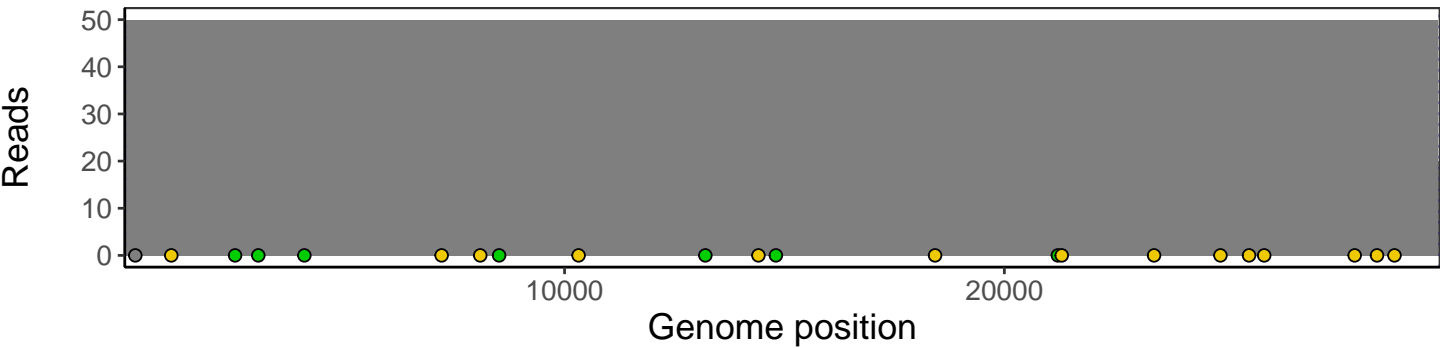
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



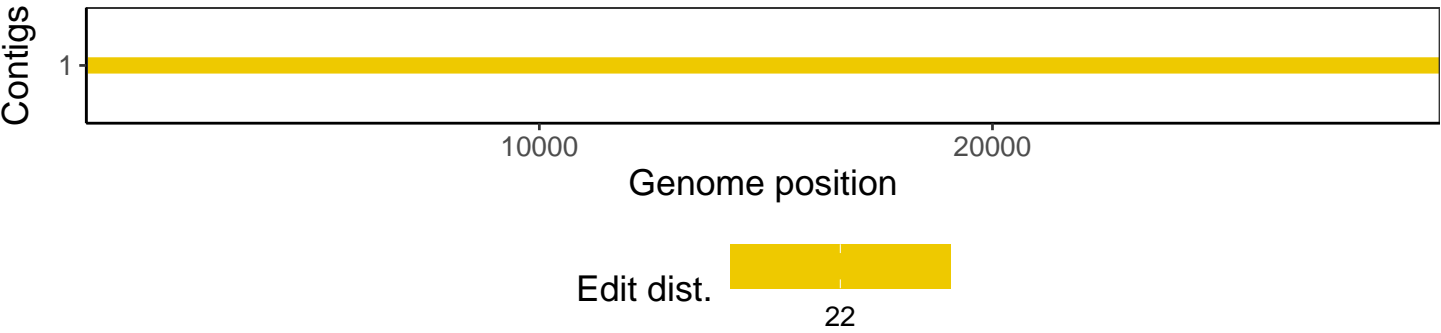
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



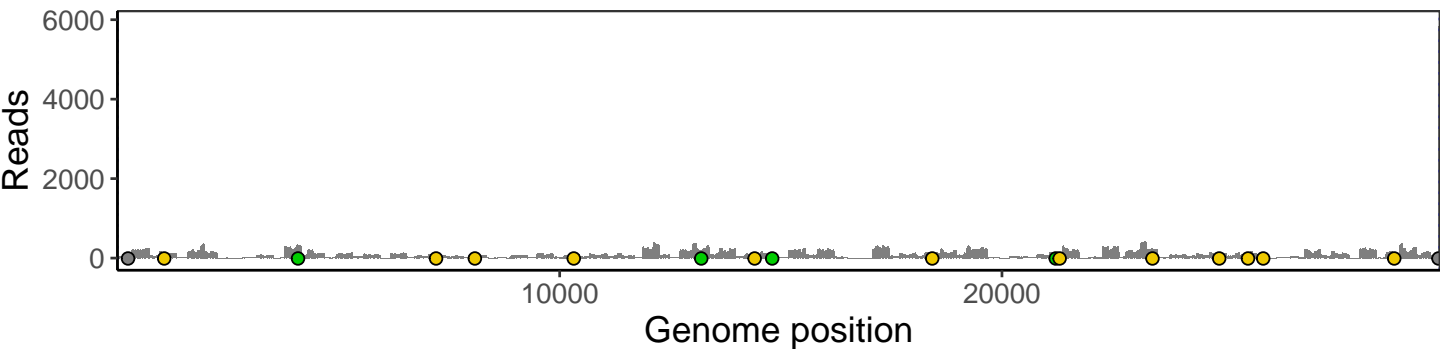
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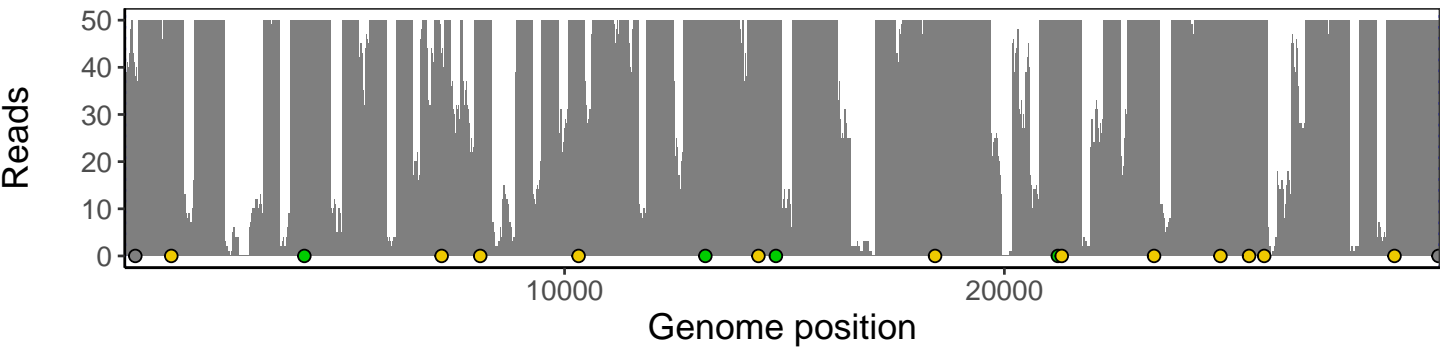
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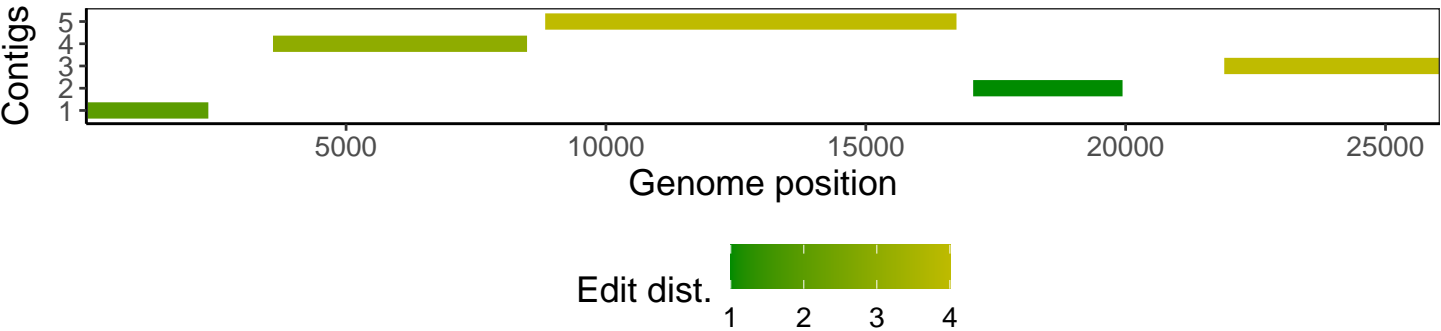
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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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