

# COVID-19 subject PQ-Seq1

*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)
VSP0770	composite	NA	Saliva	2021-02-01	29.94	B.1.2	99.9%	99.9%
VSP0770-1	single experiment	NA	Saliva	2021-02-01	29.94	B.1.2	99.9%	99.9%
VSP0770-2	single experiment	NA	Saliva	2021-02-01	3.90	NA	86.1%	77.6%

## 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	12317	39
1059 ORF1ab T265I	9225	23
3037 ORF1ab silent	9791	2
8083 ORF1ab M2606I	4416	52
10319 ORF1ab L3352F	18047	4
10874 ORF1ab N3537D	16316	15
14408 ORF1ab P314L	17594	21
14805 ORF1ab silent	4943	85
16887 ORF1ab silent	33474	0
17436 ORF1ab silent	16443	100
18424 ORF1ab N1653D	6799	85
21304 ORF1ab R2613C	2010	2
23127 S A522V	6432	9
23403 S D614G	88	0
25135 S K1191N	2705	37
25563 ORF3a Q57H	15455	9
25907 ORF3a G172V	891	111
27498 ORF7a silent	5910	127
27964 ORF8 S24L	15117	0
28376 N A35S	20609	281
28472 N P67S	50911	0
28849 N silent	216	186
28869 N P199L	206	185

VSP0770-1

VSP0770-2

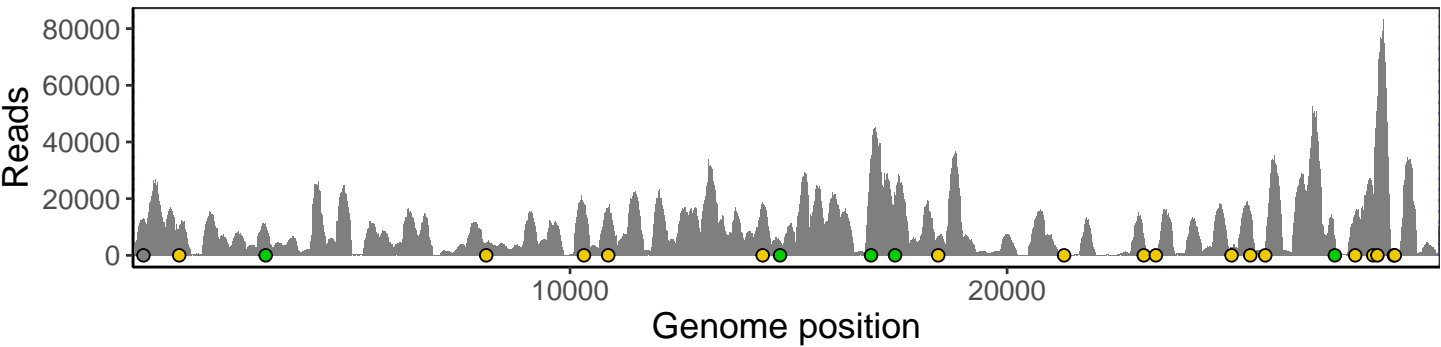
Base change

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

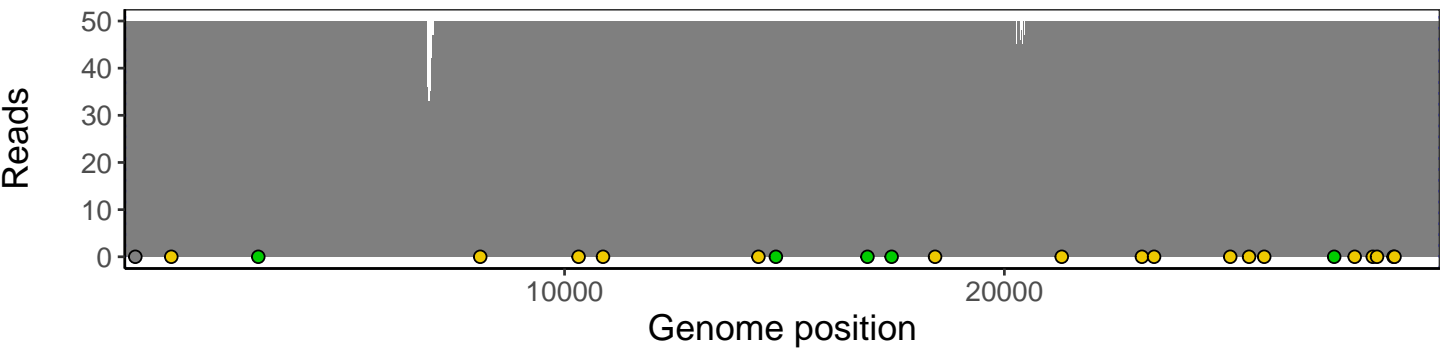
# Analyses of individual experiments and composite results

VSP0770 | 2021-02-01 | Saliva | PQ-Seq1 | composite result

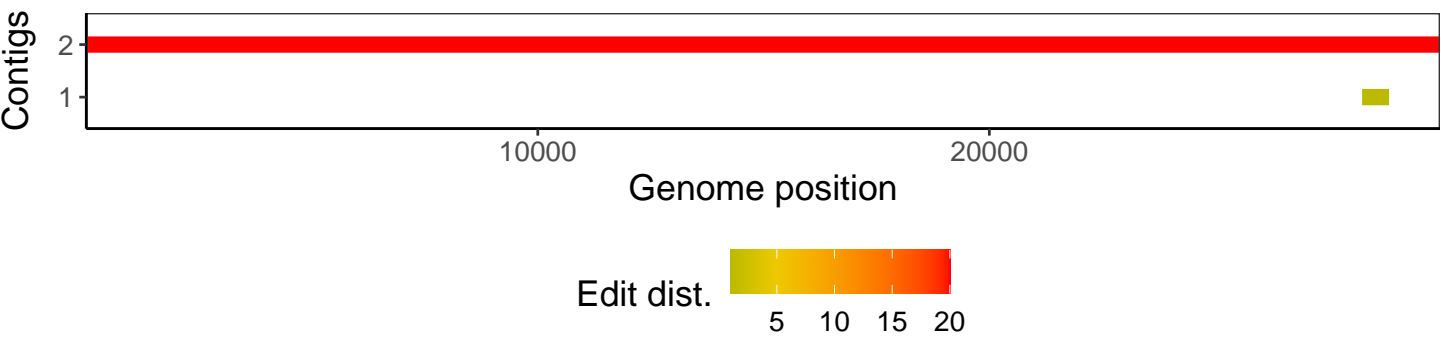
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



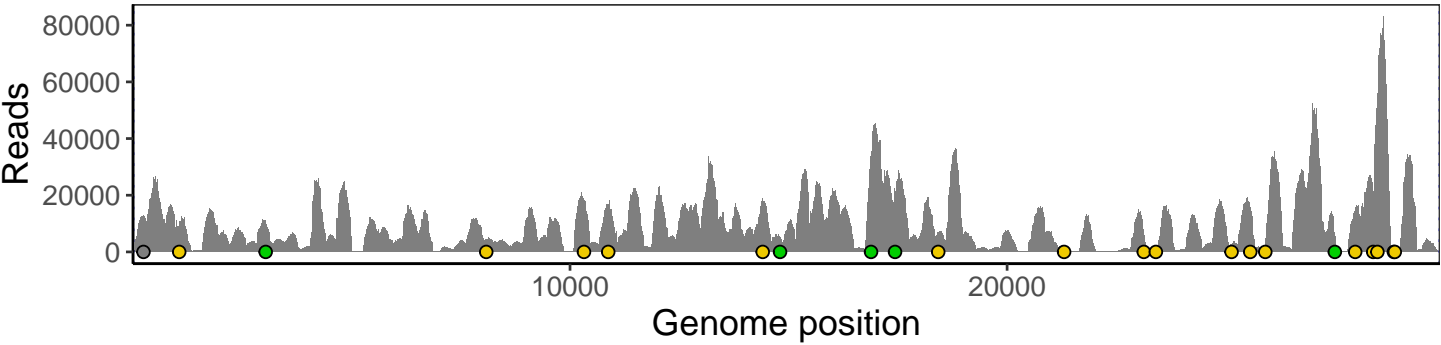
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



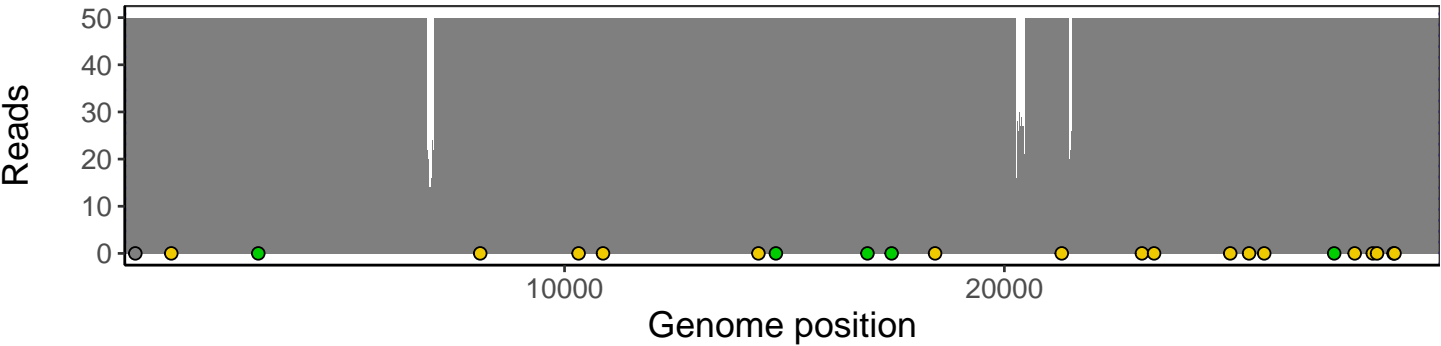
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



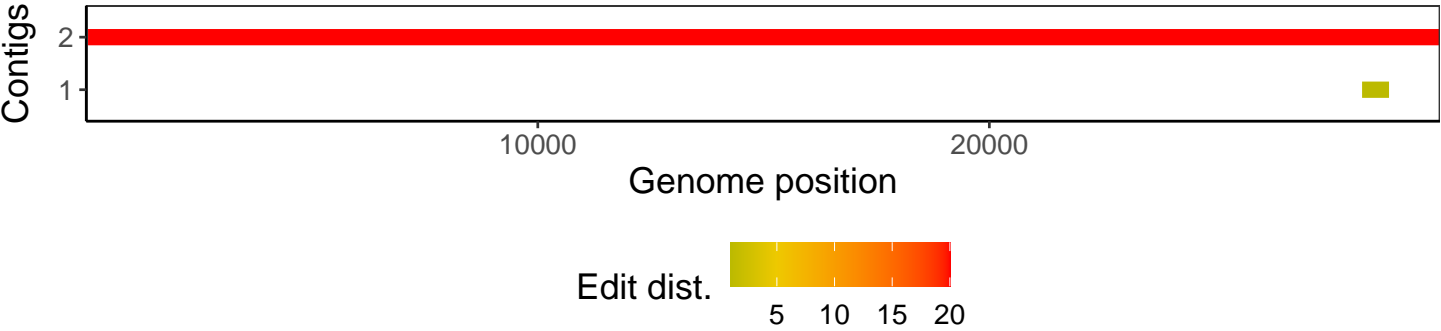
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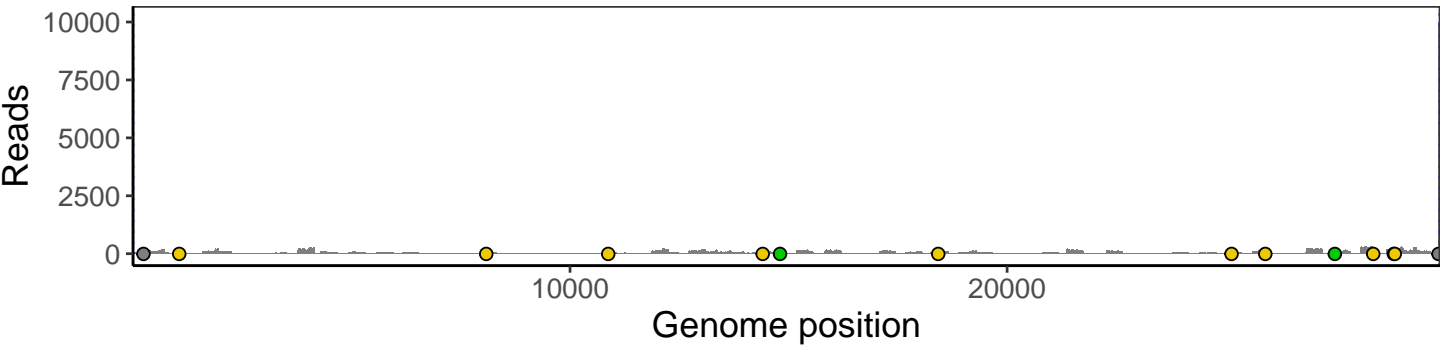
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



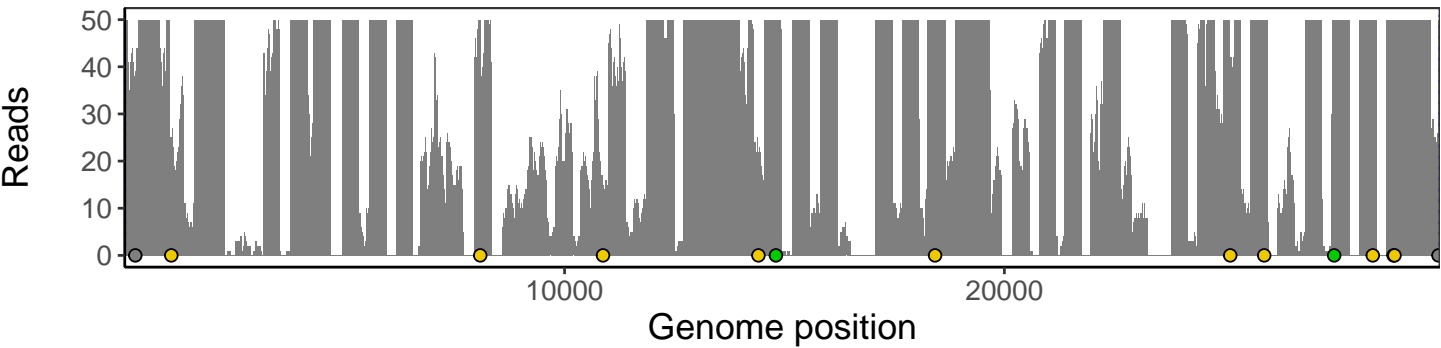
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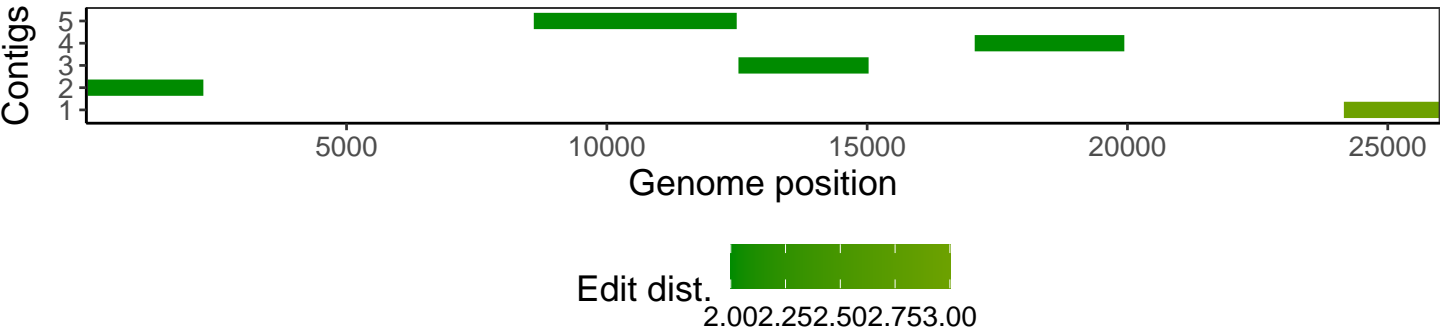
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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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