

COVID-19 subject PQ-Seq4

2021-04-30

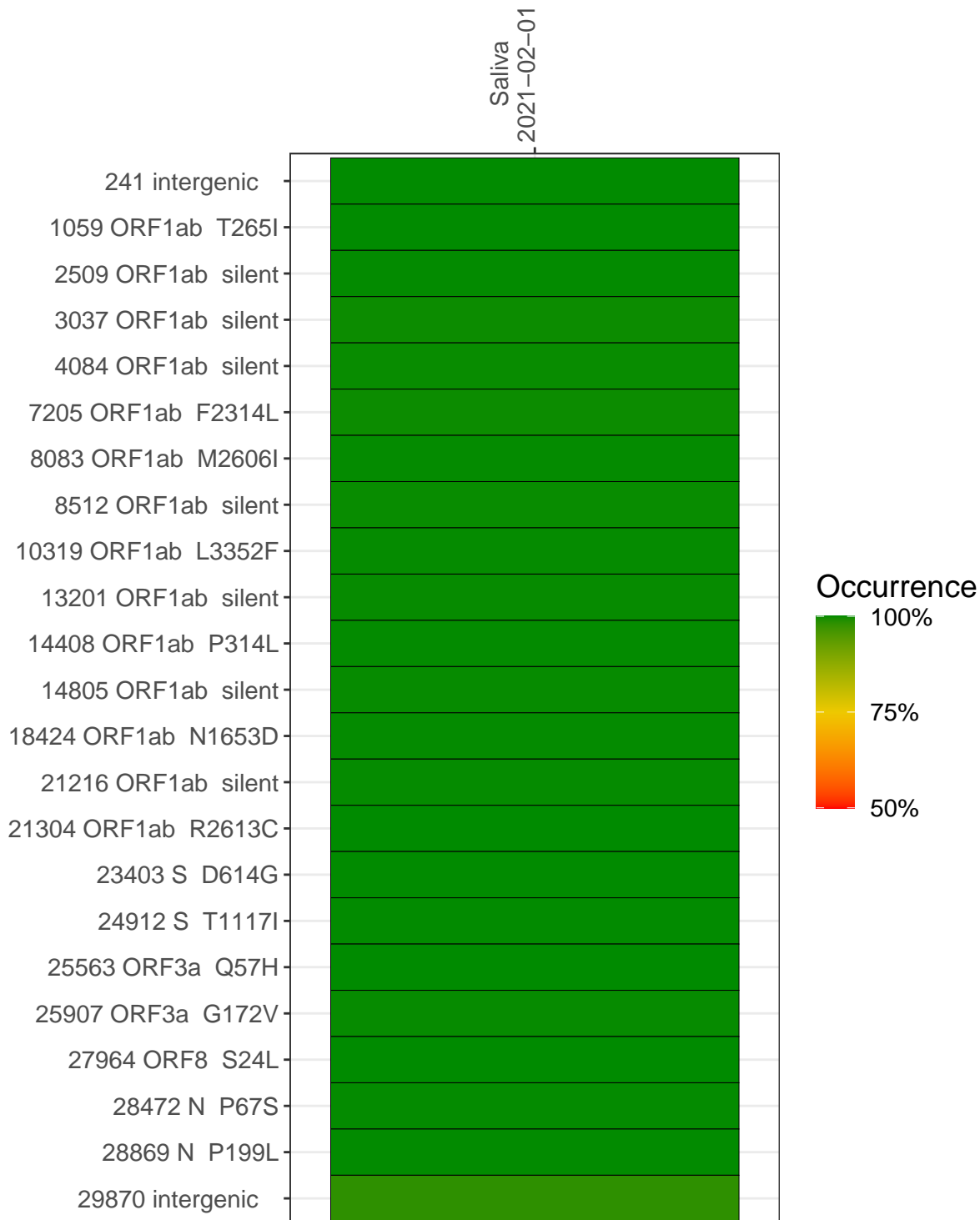
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
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/everett/projects/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.



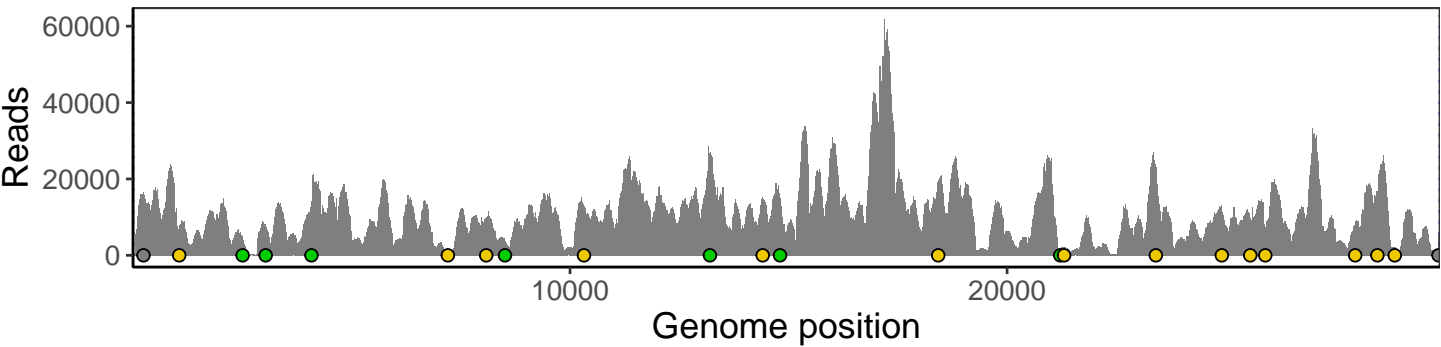
Saliva
2021-02-01

	VSP0773-1	VSP0773-2
inter.) N I 2 N DRF RF3 S T S [F1at RF1; RF1e RF1; F1a RF1e RF1e RF1e RF1a iterg	13	1687
	1854	146
	15297	2
	8399	1
	6351	110
	9538	84
	12631	61
	23108	230
	1863	51
	1637	66
	19392	97
	14663	100
	14398	55
	25772	175
	12826	72
	3656	3
	9767	75
	1326	38
	13493	328
	7260	9
	4689	4
	6897	100
	15386	36

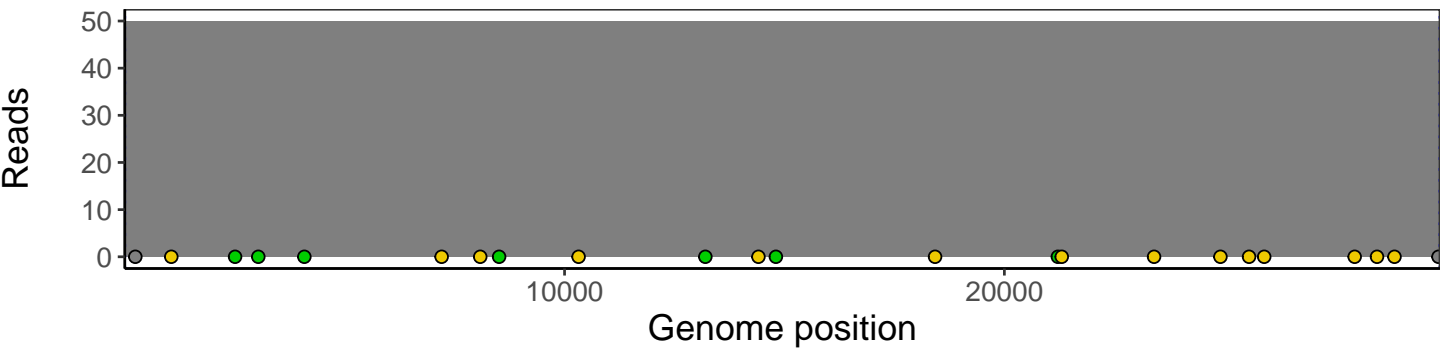
Analyses of individual experiments and composite results

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

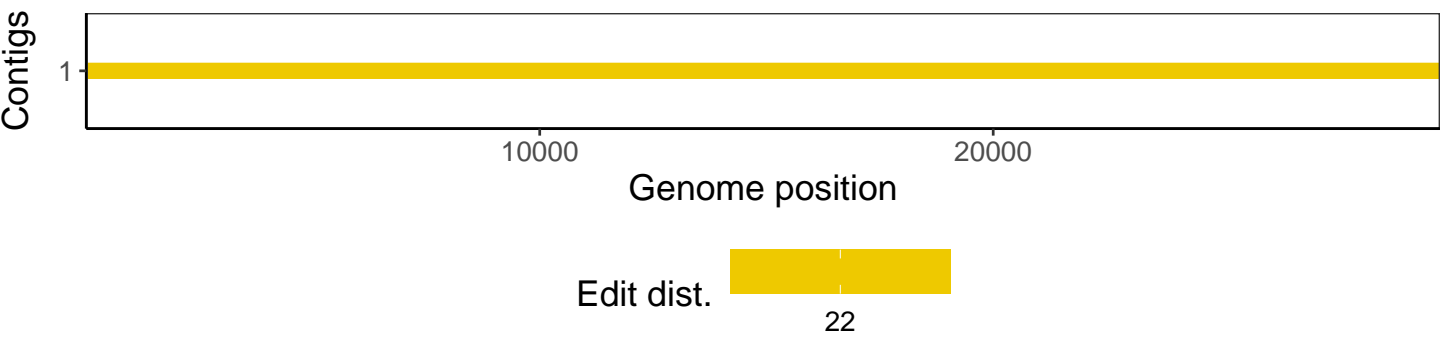
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



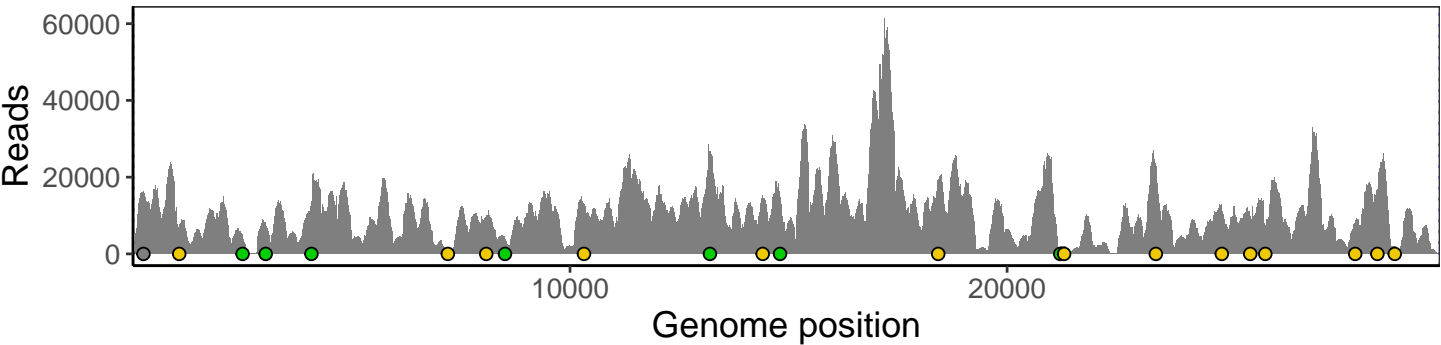
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



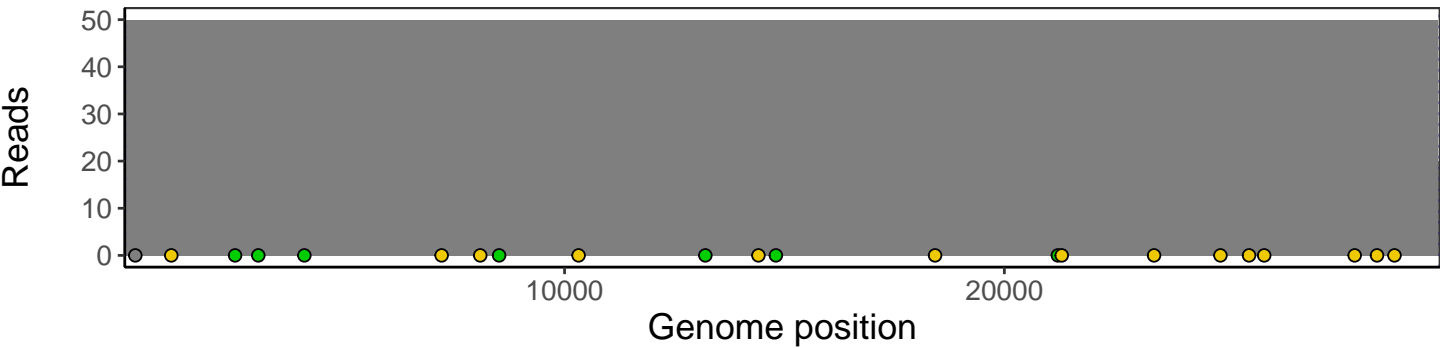
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



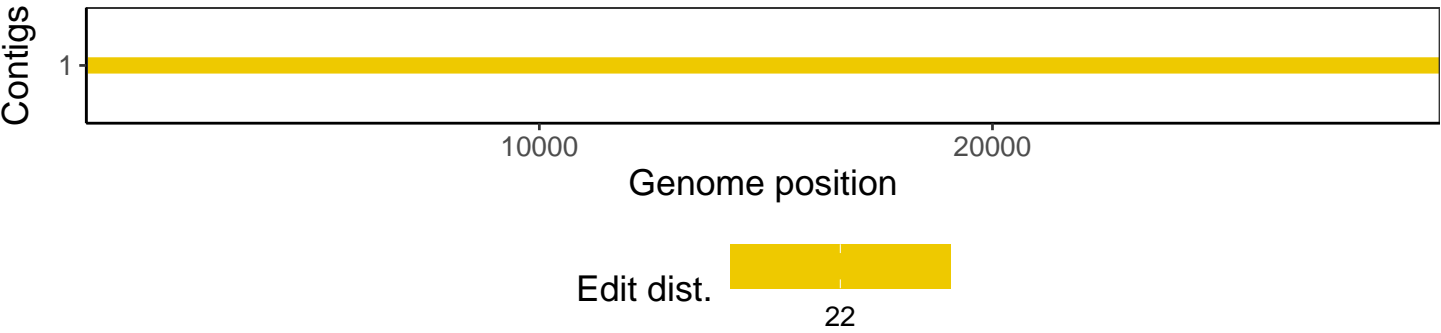
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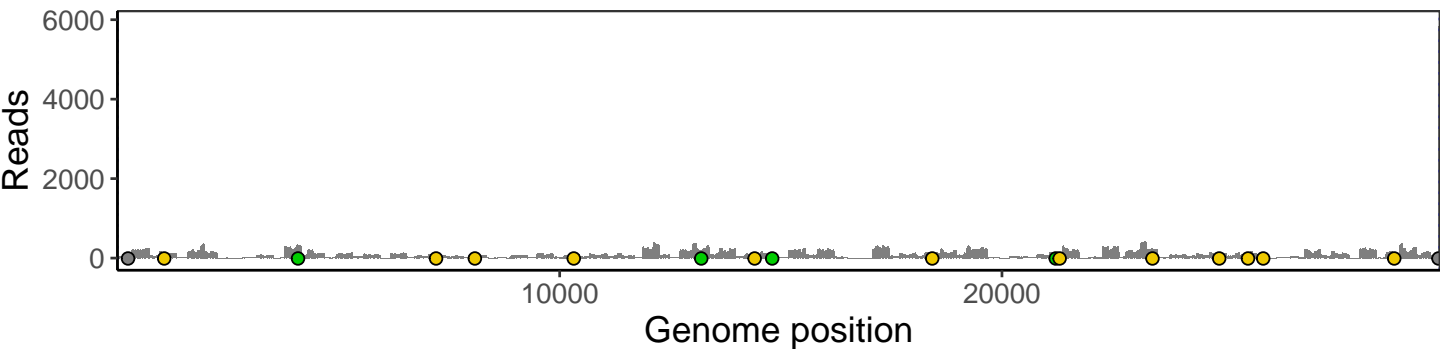
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



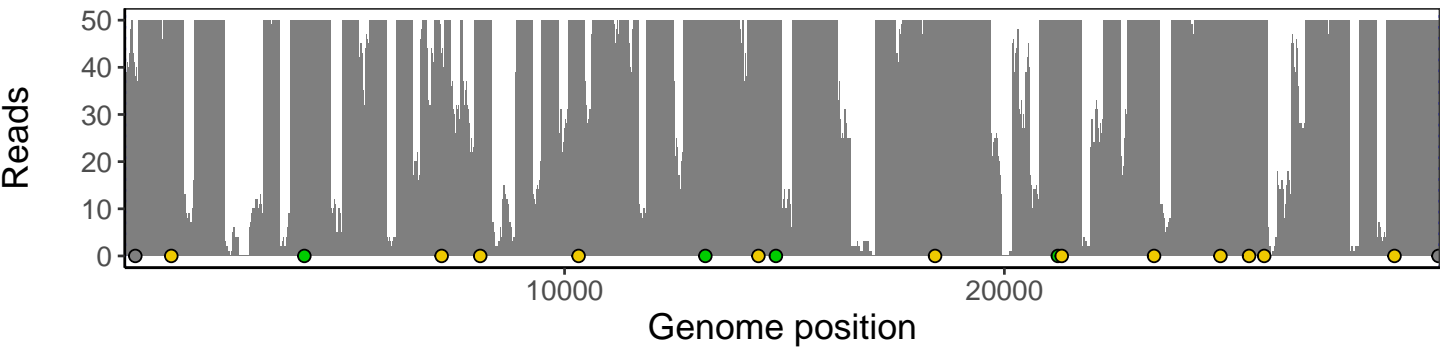
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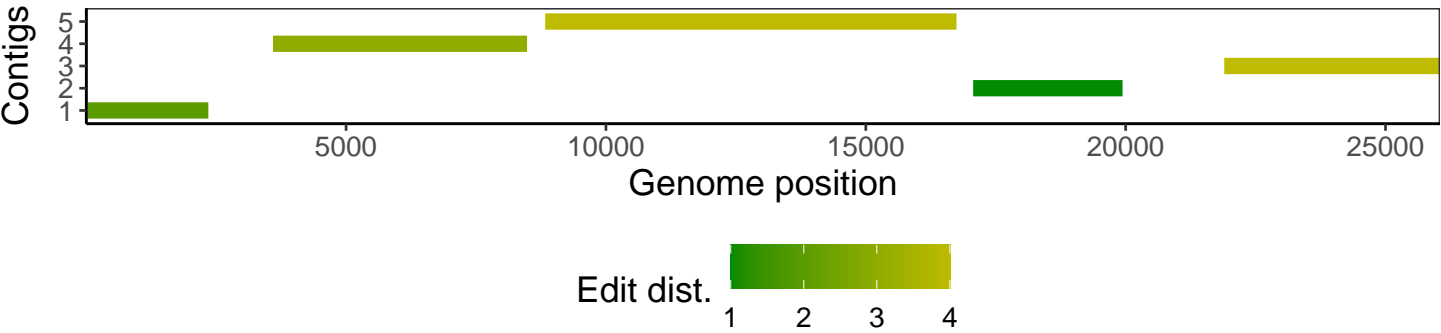
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Software environment

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	2.3.8
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	3.0.0
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