

COVID-19 subject UPHS-1371

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.

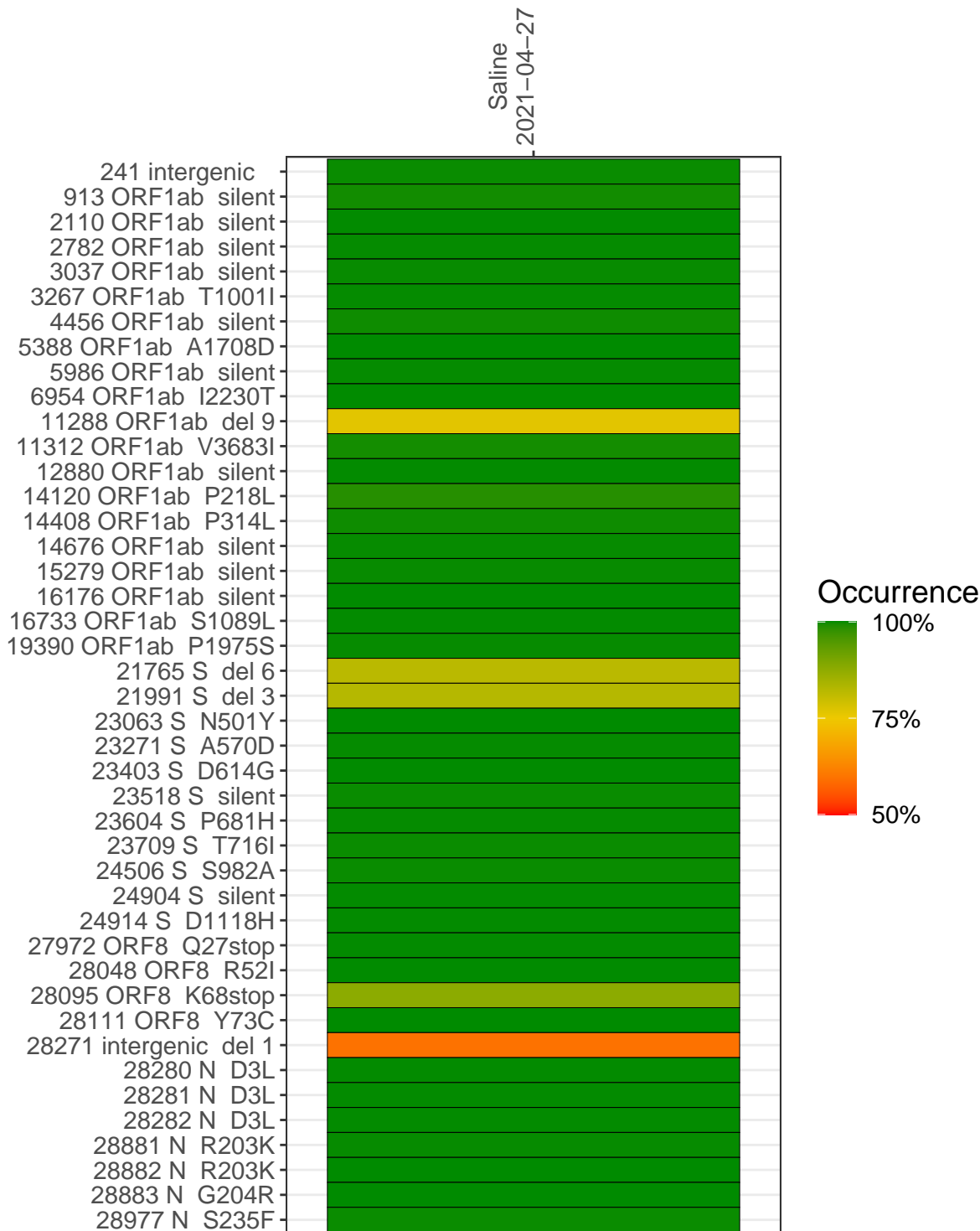
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP2626-1	single experiment	NA	Saline	2021-04-27	29.82	B.1.1.7	99.7%	99.7%

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.



	Saline 2021-04-27	
241 intergenic	2826	
913 ORF1ab silent	7025	
2110 ORF1ab silent	5139	
2782 ORF1ab silent	7954	
3037 ORF1ab silent	4026	
3267 ORF1ab T1001I	5157	
4456 ORF1ab silent	4782	
5388 ORF1ab A1708D	3982	
5986 ORF1ab silent	3372	
6954 ORF1ab I2230T	2745	
11288 ORF1ab del 9	5545	
11312 ORF1ab V3683I	8938	
12880 ORF1ab silent	7907	
14120 ORF1ab P218L	7458	
14408 ORF1ab P314L	7202	
14676 ORF1ab silent	5217	
15279 ORF1ab silent	7841	
16176 ORF1ab silent	5708	
16733 ORF1ab S1089L	5552	
19390 ORF1ab P1975S	5625	
21765 S del 6	4196	
21991 S del 3	1984	
23063 S N501Y	805	
23271 S A570D	6150	
23403 S D614G	7065	
23518 S silent	4809	
23604 S P681H	8771	
23709 S T716I	8532	
24506 S S982A	4828	
24904 S silent	6181	
24914 S D1118H	6676	
27972 ORF8 Q27stop	9627	
28048 ORF8 R52I	9070	
28095 ORF8 K68stop	7643	
28111 ORF8 Y73C	7039	
28271 intergenic del 1	4245	
28280 N D3L	2495	
28281 N D3L	2495	
28282 N D3L	2674	
28881 N R203K	709	
28882 N R203K	708	
28883 N G204R	710	
28977 N S235F	839	
	VSP2626-1	

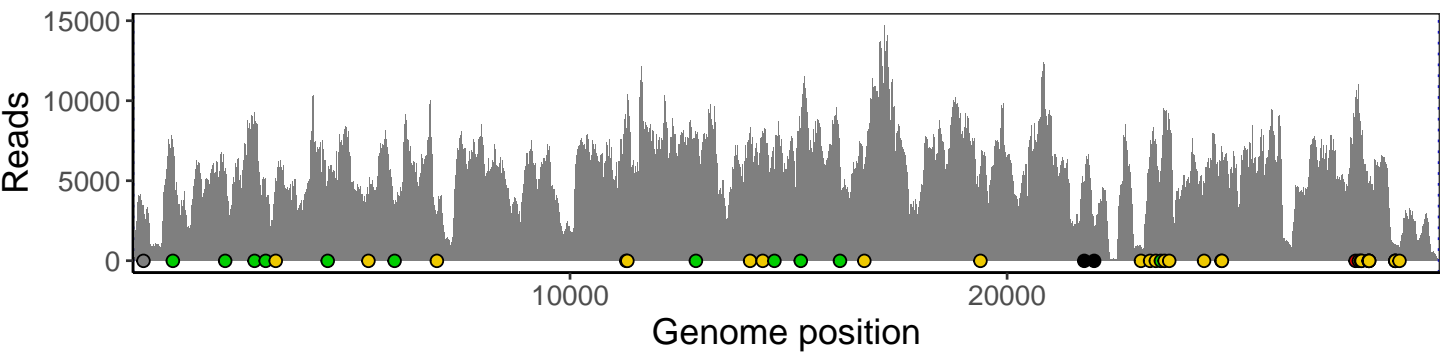
Base change

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

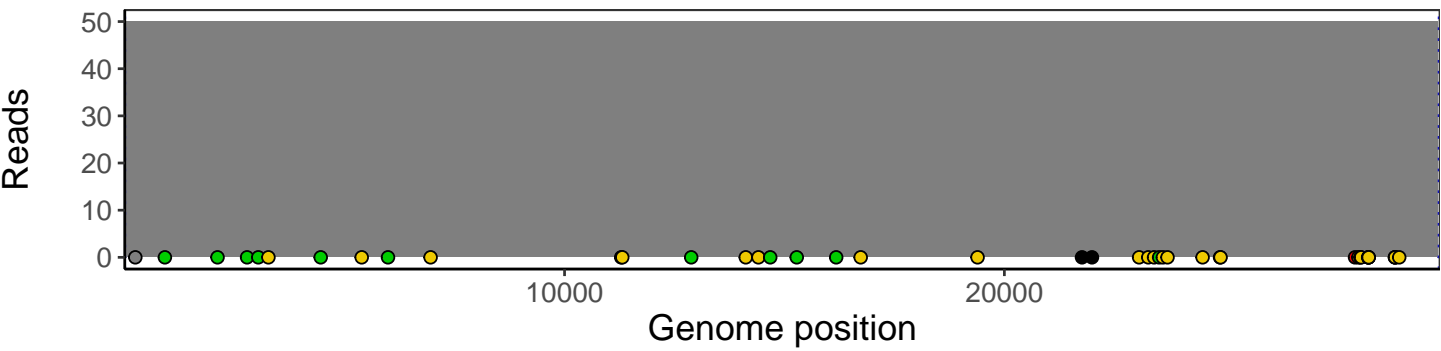
Analyses of individual experiments and composite results

VSP2626-1 | 2021-04-27 | Saline | UPHS-1371 | genomes | single experiment

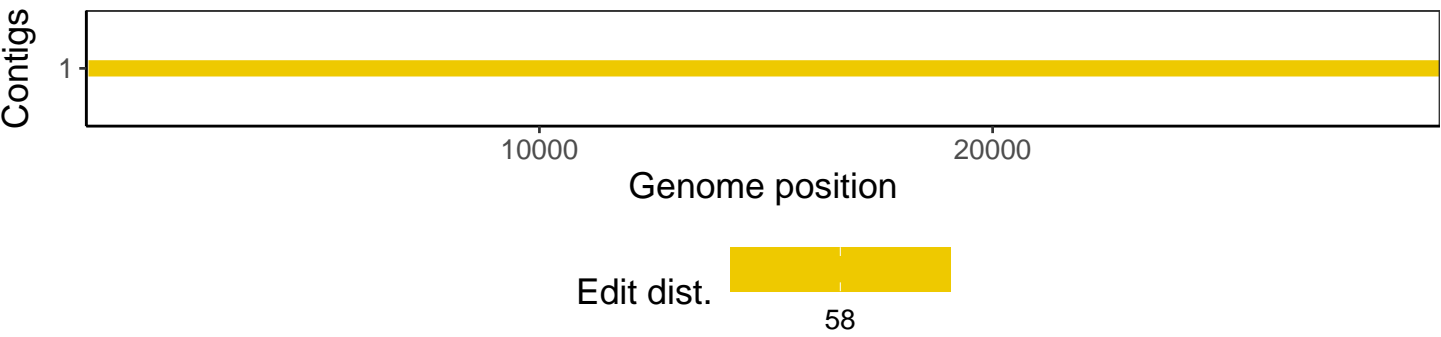
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



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