COVID-19 subject UPHS-1340

2021-05-21

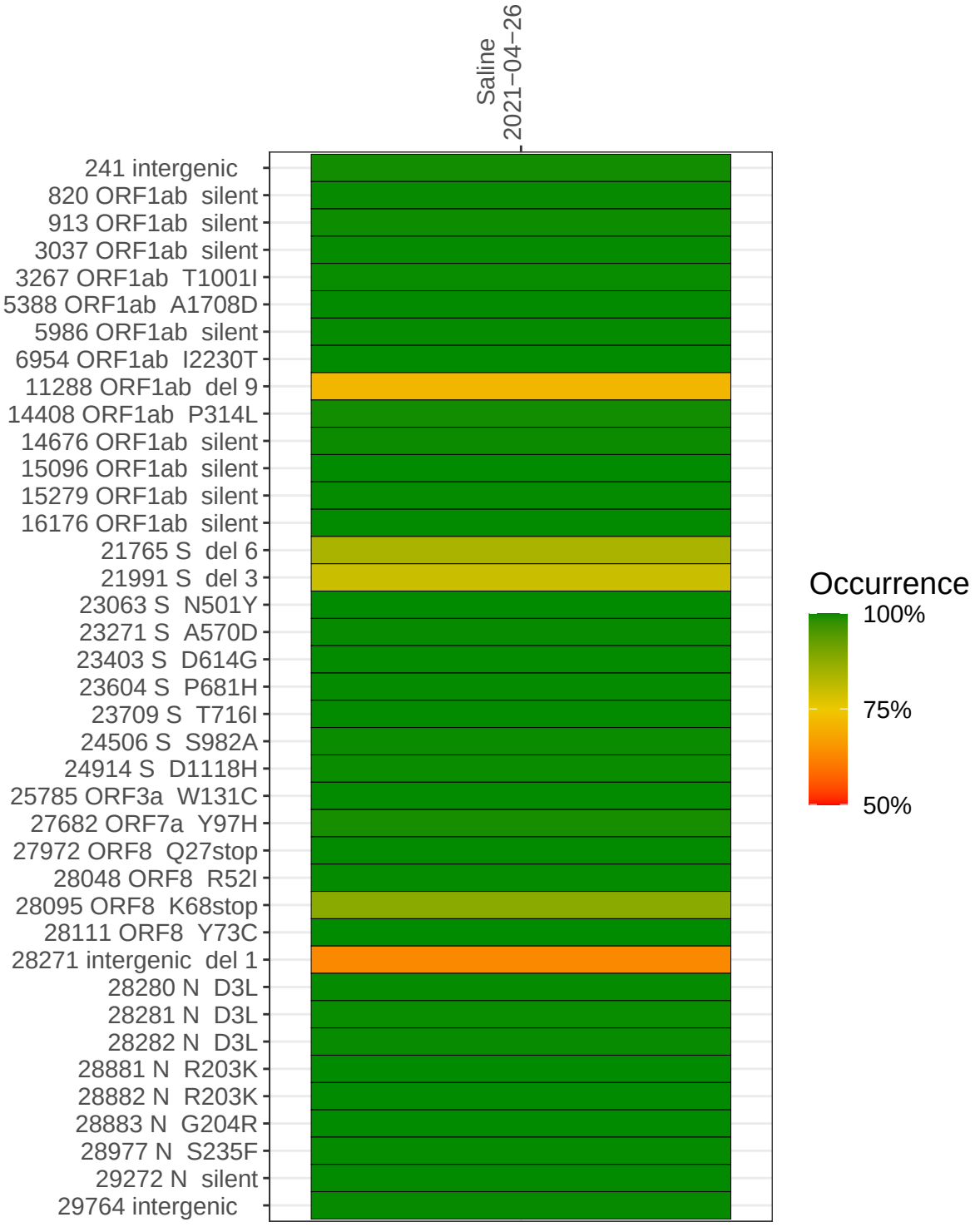
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

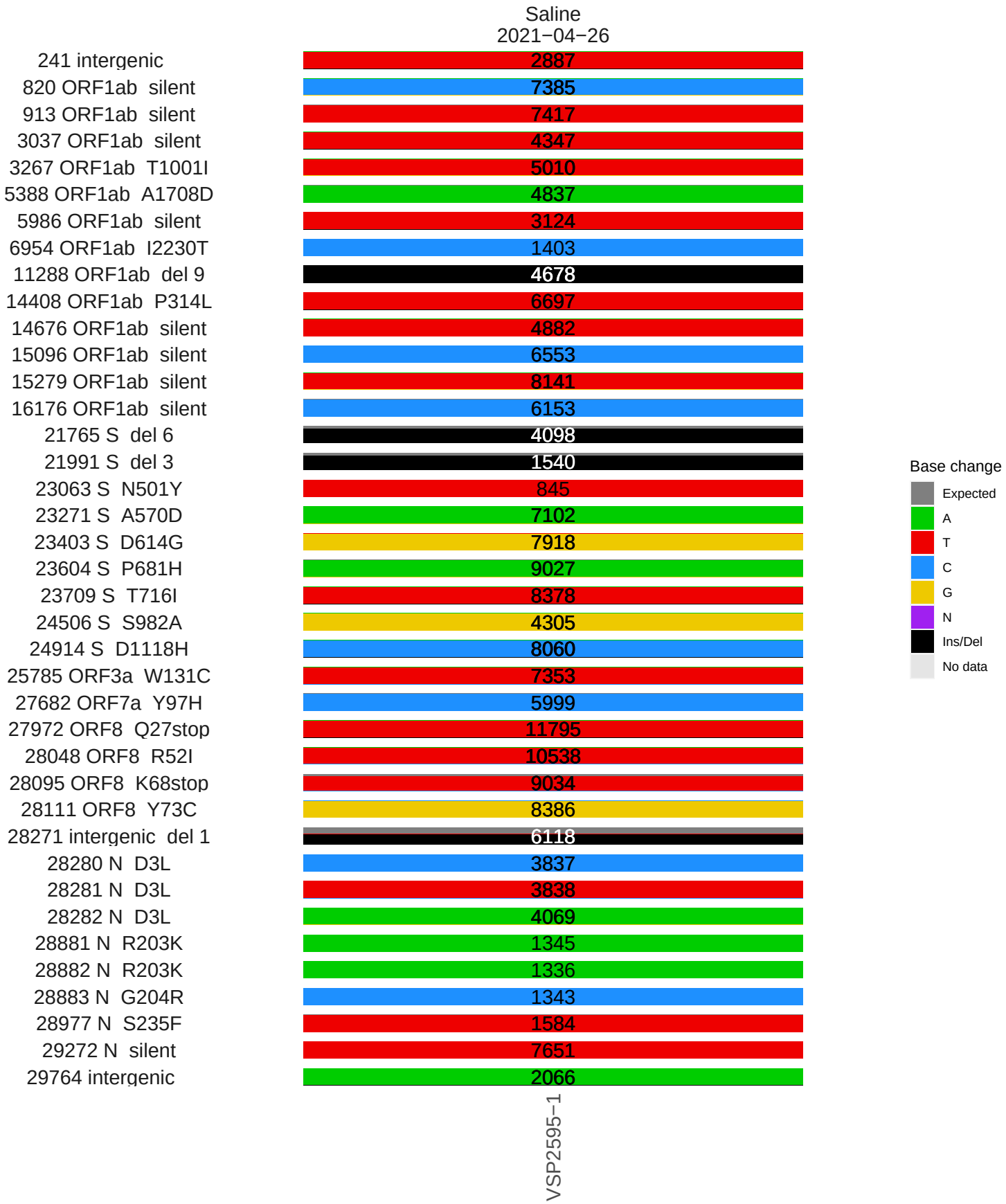
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2595-1	single experiment	NA	Saline	2021-04-26	29.80	B.1.1.7	99.9%	99.8%

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.

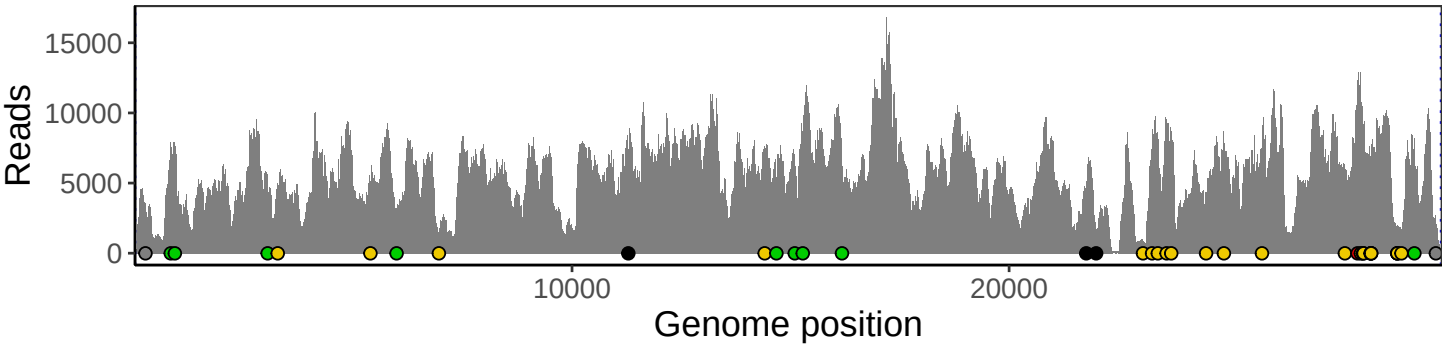



Saline
2021−04−26
241 intergenic 2887
820 ORF1ab silent 7385
913 ORF1ab silent 7417
3037 ORF1ab silent 4347
3267 ORF1ab T1001I 5010
5388 ORF1ab A1708D 4837
5986 ORF1ab silent 3124
6954 ORF1ab I2230T 1403
11288 ORF1ab del 9 4678
14408 ORF1ab P314L 6697
14676 ORF1ab silent 4882
15096 ORF1ab silent 6553
15279 ORF1ab silent 8141
16176 ORF1ab silent 6153
21765 S del 6 4098
21991 S del 3 1540
23063 S N501Y 845
23271 S A570D 7102
23403 S D614G 7918
23604 S P681H 9027
23709 S T716I 8378
24506 S S982A 4305
24914 S D1118H 8060
25785 ORF3a W131C 7353
27682 ORF7a Y97H 5999
27972 ORF8 Q27stop 11795
28048 ORF8 R52I 10538
28095 ORF8 K68stop 9034
28111 ORF8 Y73C 8386
28271 intergenic del 1 6118
28280 N D3L 3837
28281 N D3L 3838
28282 N D3L 4069
28881 N R203K 1345
28882 N R203K 1336
28883 N G204R 1343
28977 N S235F 1584
29272 N silent 7651
29764 intergenic 2066
VSP2595−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

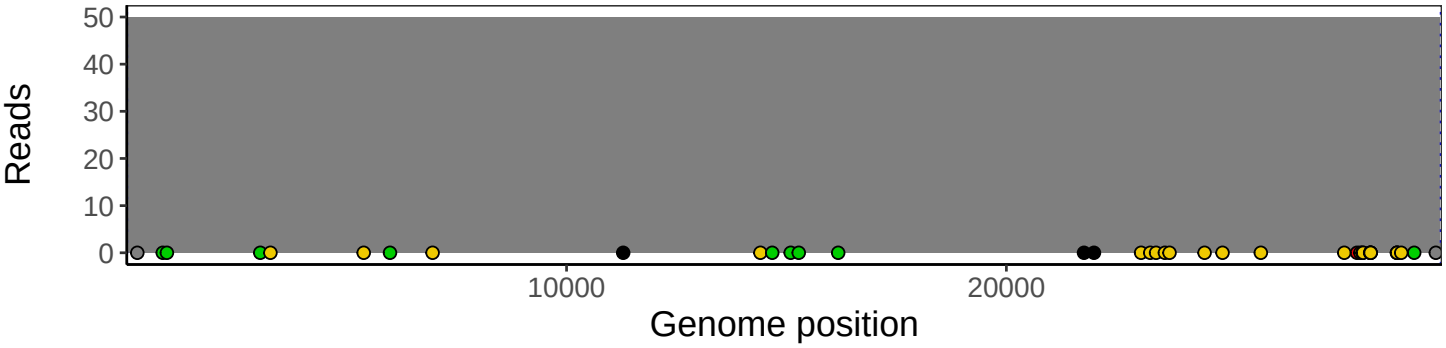
Analyses of individual experiments and composite results

VSP2595-1 | 2021-04-26 | Saline | UPHS-1340 | genomes | single experiment

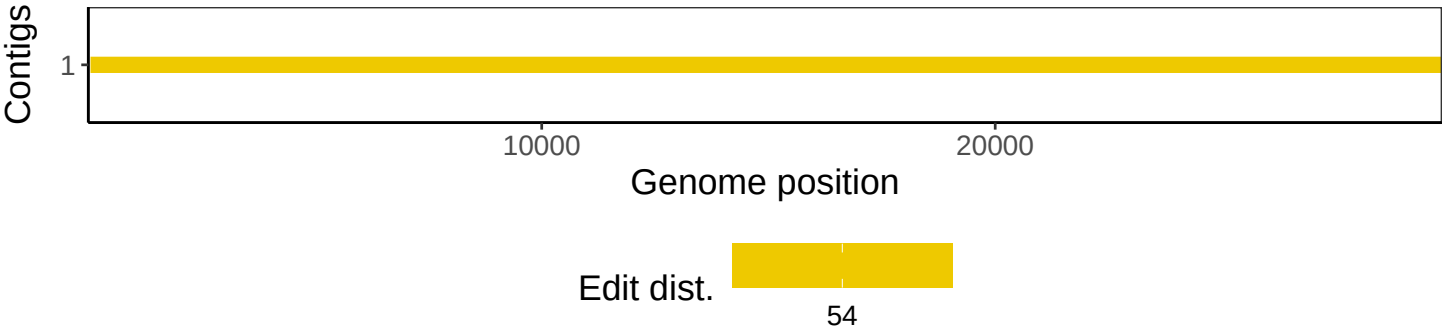
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htslib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htslib 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	3.3.3
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