COVID-19 subject UPHS-1591

2021-06-03

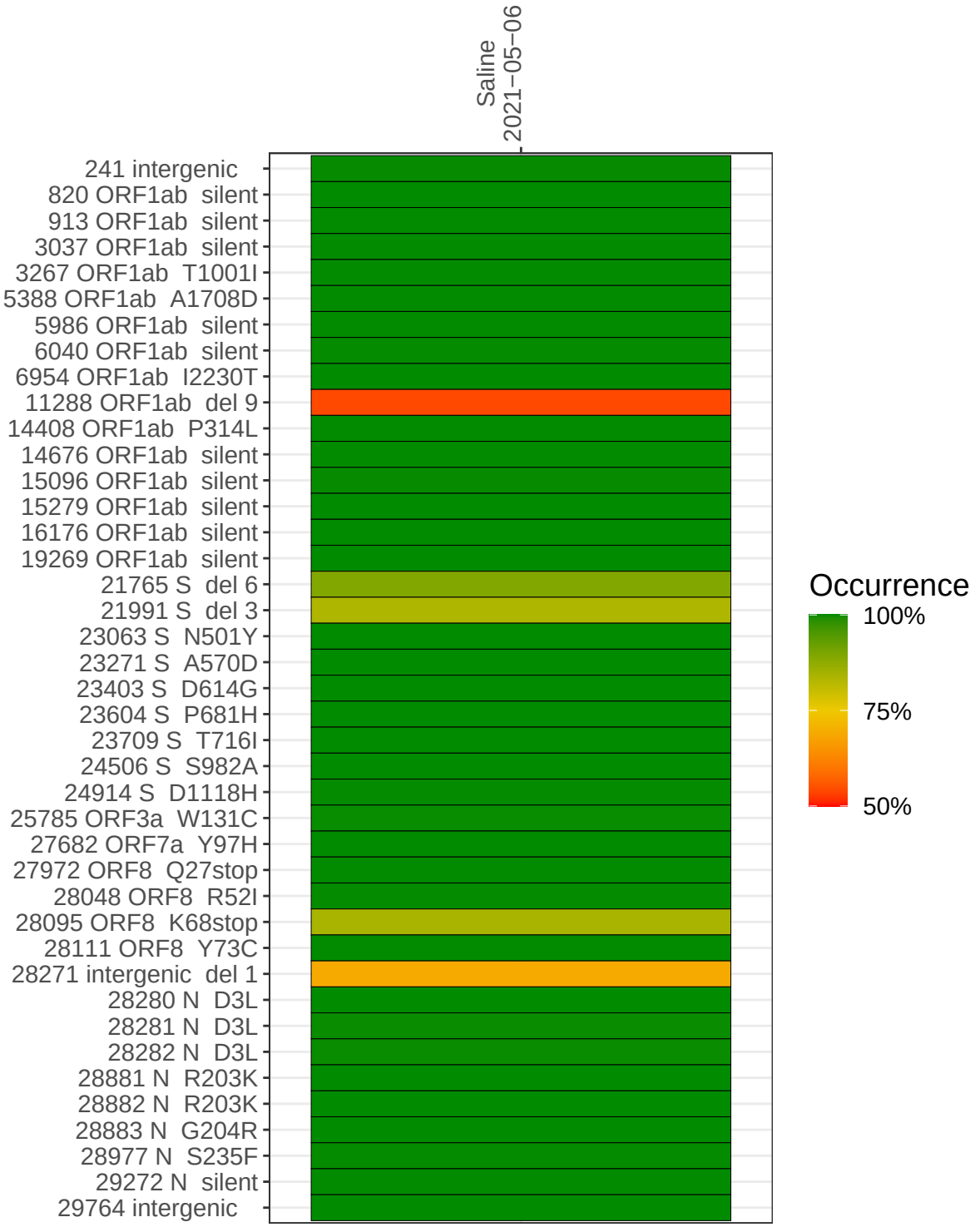
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

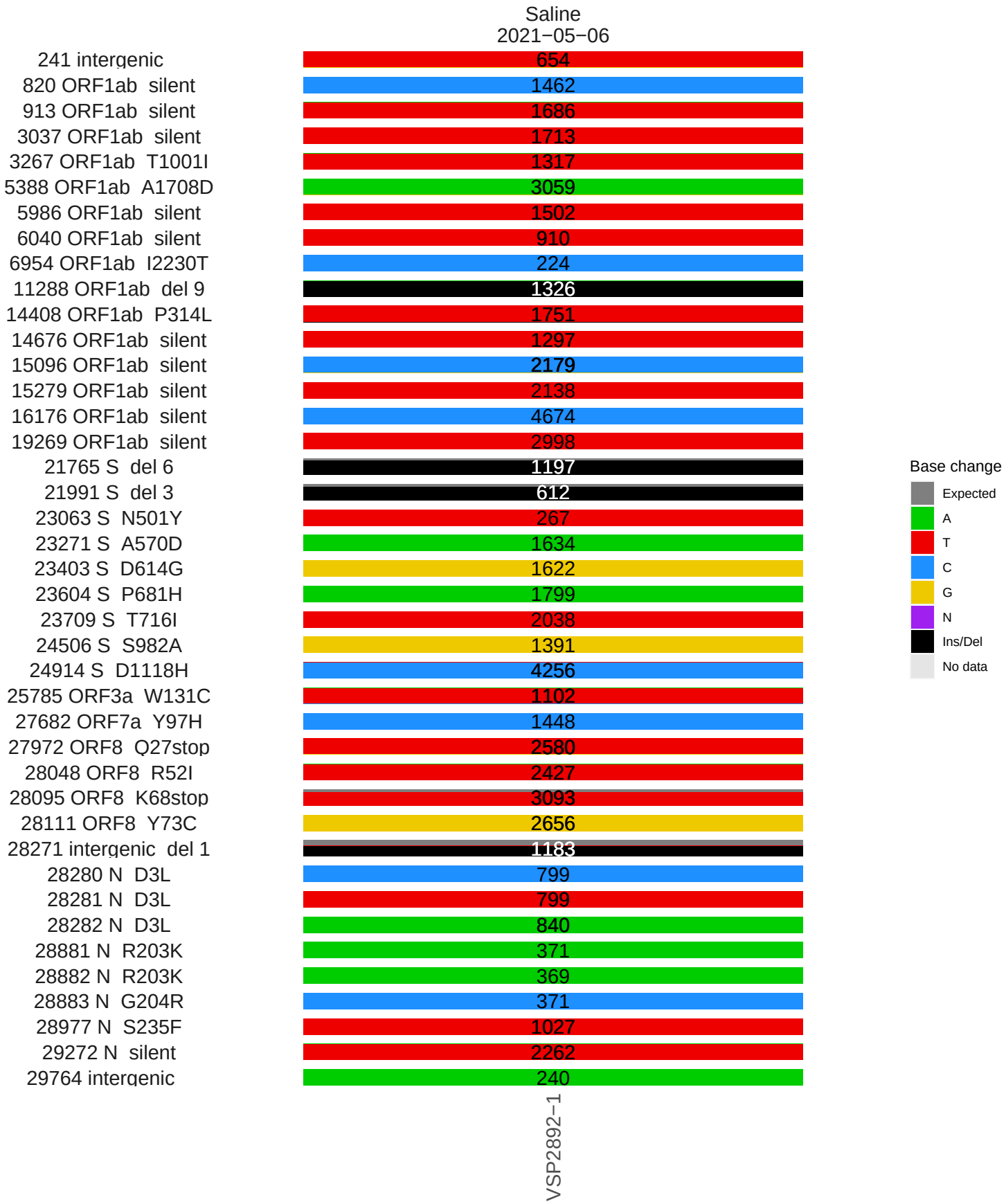
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2892-1	single experiment	NA	Saline	2021-05-06	29.84	B.1.1.7	99.8%	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.

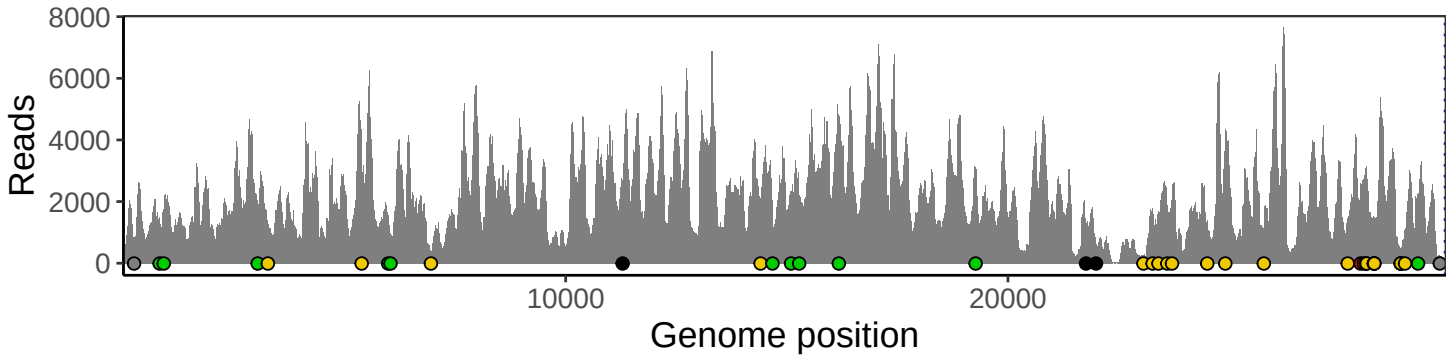



Saline
2021−05−06
241 intergenic 654
820 ORF1ab silent 1462
913 ORF1ab silent 1686
3037 ORF1ab silent 1713
3267 ORF1ab T1001I 1317
5388 ORF1ab A1708D 3059
5986 ORF1ab silent 1502
6040 ORF1ab silent 910
6954 ORF1ab I2230T 224
11288 ORF1ab del 9 1326
14408 ORF1ab P314L 1751
14676 ORF1ab silent 1297
15096 ORF1ab silent 2179
15279 ORF1ab silent 2138
16176 ORF1ab silent 4674
19269 ORF1ab silent 2998
21765 S del 6 1197
21991 S del 3 612
23063 S N501Y 267
23271 S A570D 1634
23403 S D614G 1622
23604 S P681H 1799
23709 S T716I 2038
24506 S S982A 1391
24914 S D1118H 4256
25785 ORF3a W131C 1102
27682 ORF7a Y97H 1448
27972 ORF8 Q27stop 2580
28048 ORF8 R52I 2427
28095 ORF8 K68stop 3093
28111 ORF8 Y73C 2656
28271 intergenic del 1 1183
28280 N D3L 799
28281 N D3L 799
28282 N D3L 840
28881 N R203K 371
28882 N R203K 369
28883 N G204R 371
28977 N S235F 1027
29272 N silent 2262
29764 intergenic 240
VSP2892−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

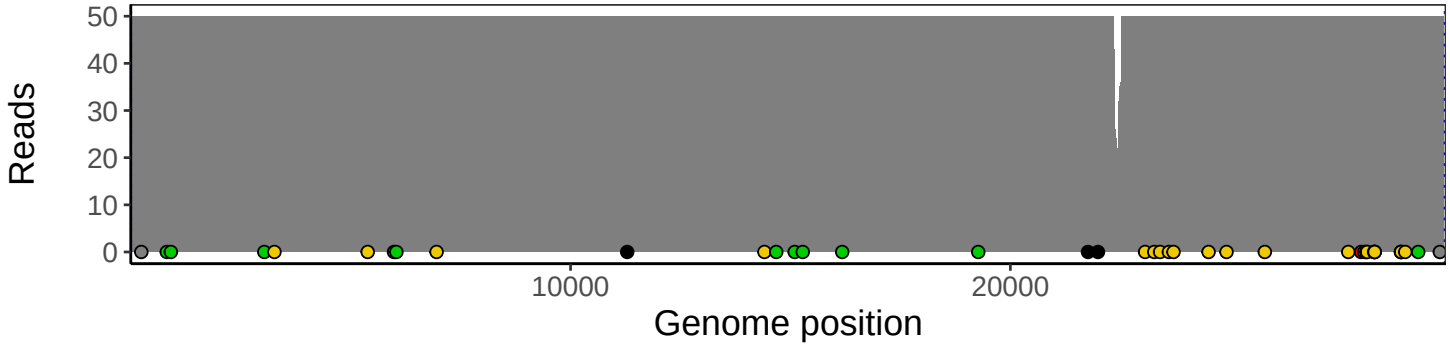
Analyses of individual experiments and composite results

VSP2892-1 | 2021-05-06 | Saline | UPHS-1591 | genomes | single experiment

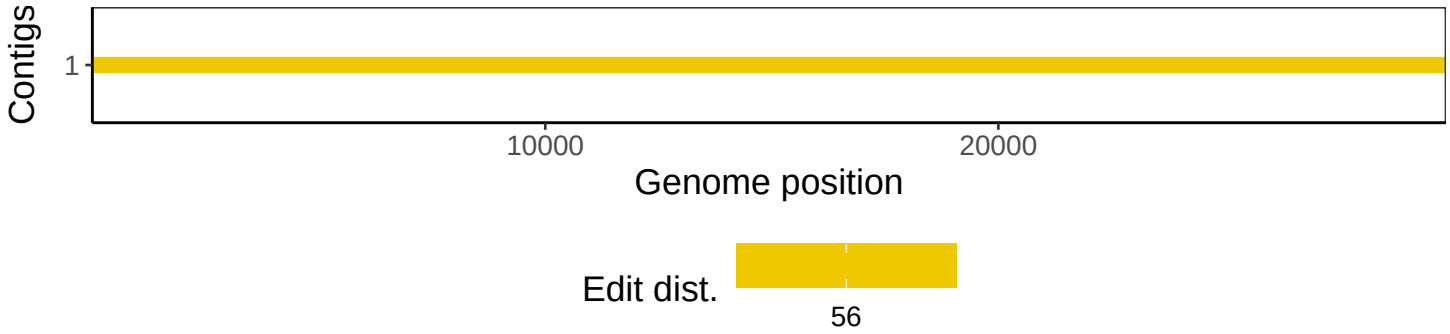
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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