COVID-19 subject UPHS-1381

2021-06-03

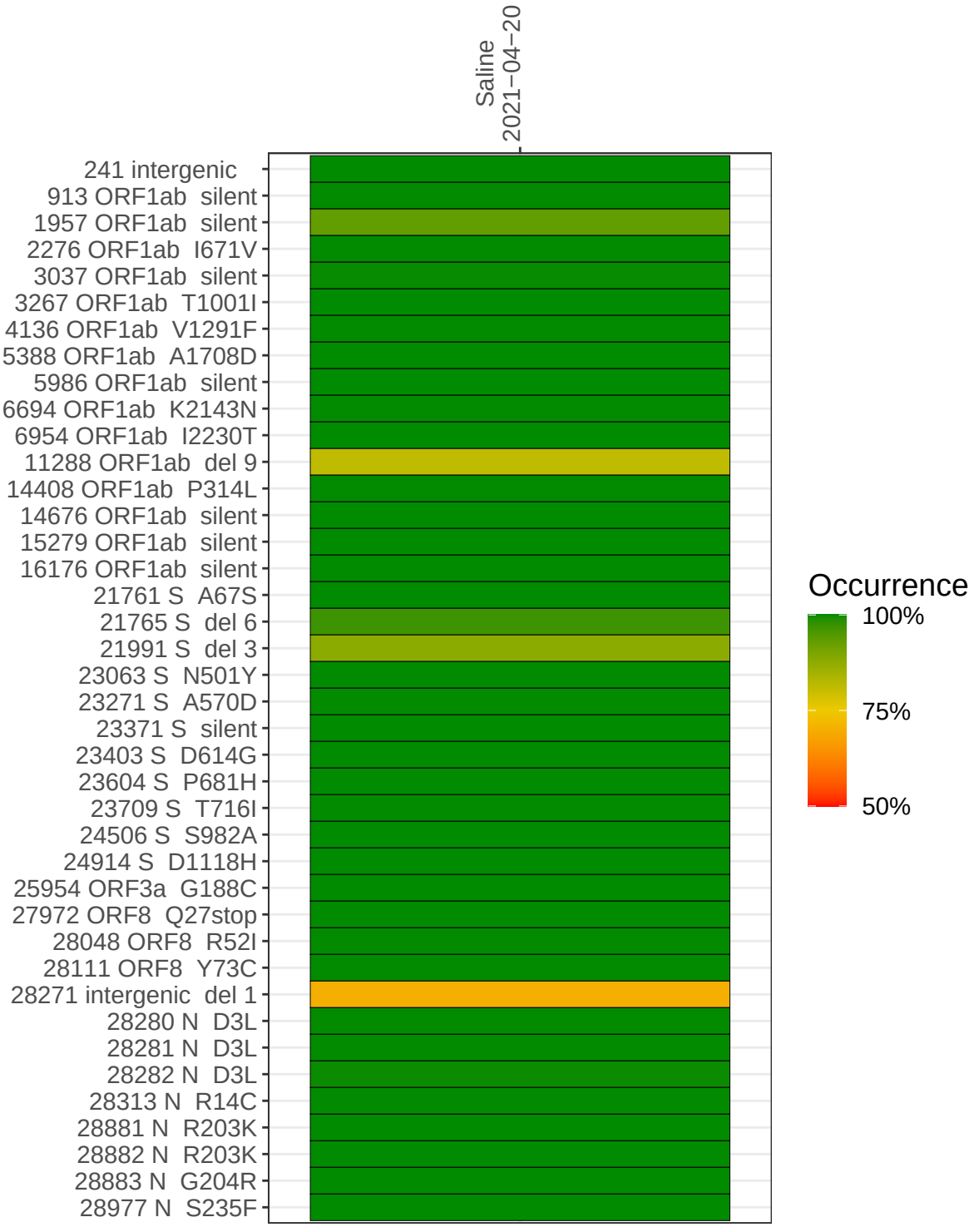
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

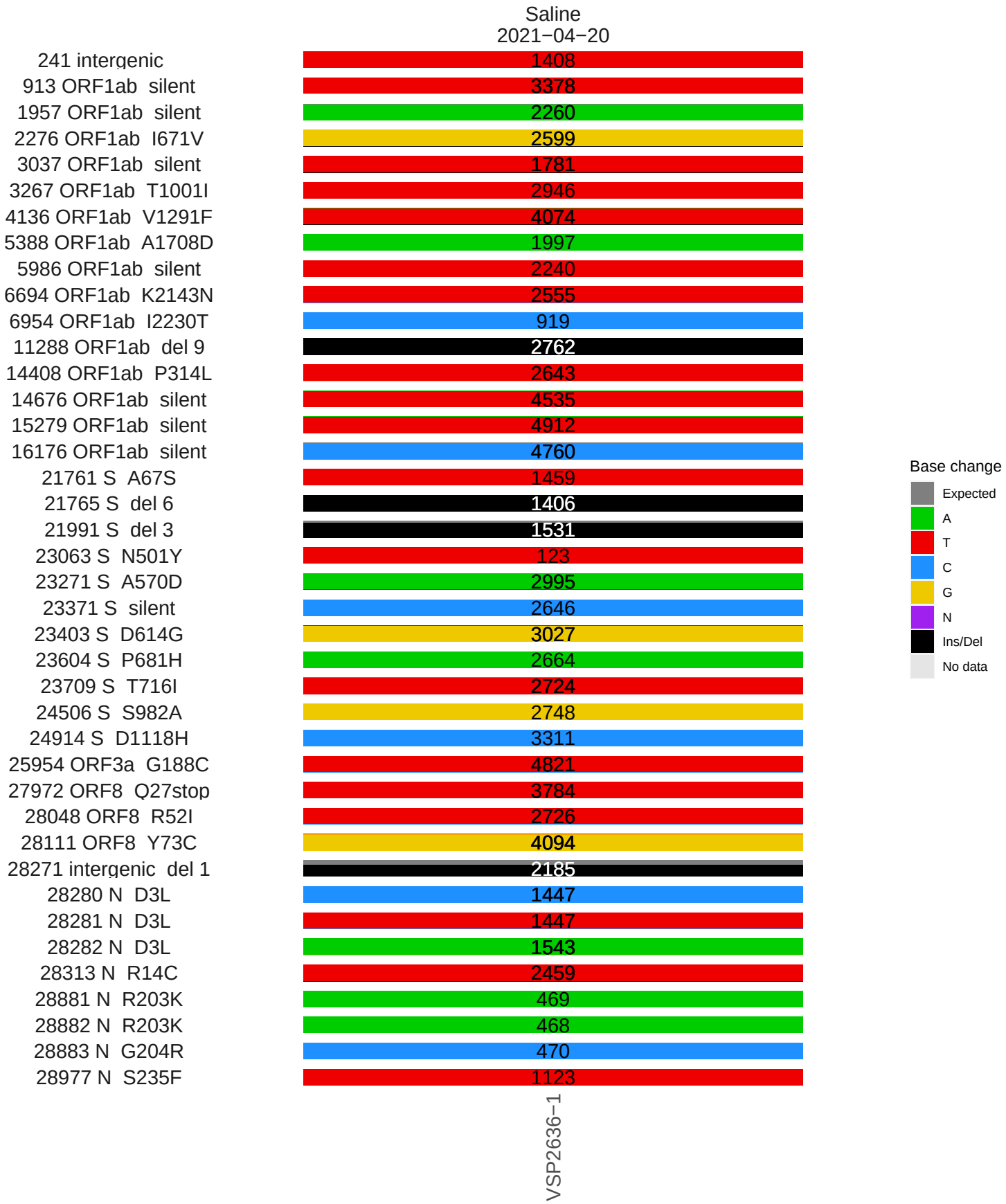
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2636-1	single experiment	NA	Saline	2021-04-20	29.80	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.

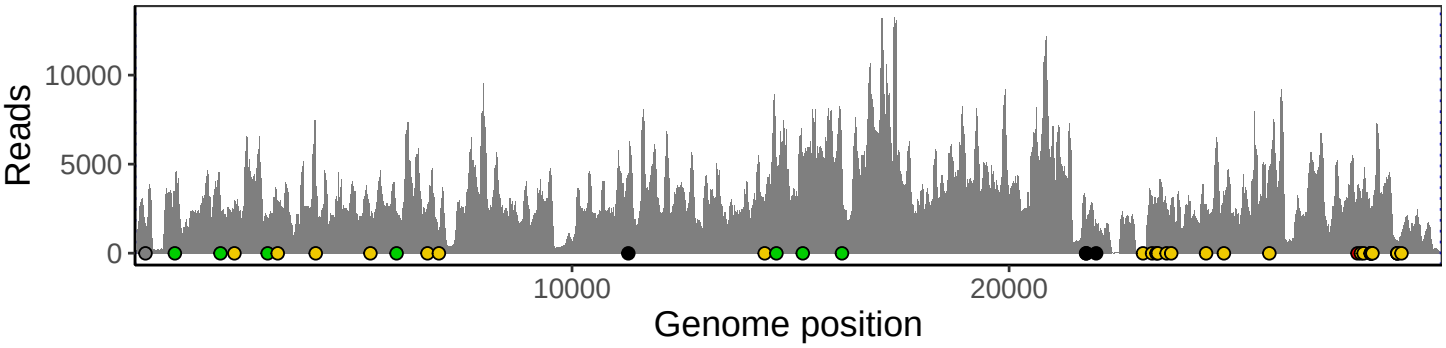



Saline
2021−04−20
241 intergenic 1408
913 ORF1ab silent 3378
1957 ORF1ab silent 2260
2276 ORF1ab I671V 2599
3037 ORF1ab silent 1781
3267 ORF1ab T1001I 2946
4136 ORF1ab V1291F 4074
5388 ORF1ab A1708D 1997
5986 ORF1ab silent 2240
6694 ORF1ab K2143N 2555
6954 ORF1ab I2230T 919
11288 ORF1ab del 9 2762
14408 ORF1ab P314L 2643
14676 ORF1ab silent 4535
15279 ORF1ab silent 4912
16176 ORF1ab silent 4760
21761 S A67S 1459
21765 S del 6 1406
21991 S del 3 1531
23063 S N501Y 123
23271 S A570D 2995
23371 S silent 2646
23403 S D614G 3027
23604 S P681H 2664
23709 S T716I 2724
24506 S S982A 2748
24914 S D1118H 3311
25954 ORF3a G188C 4821
27972 ORF8 Q27stop 3784
28048 ORF8 R52I 2726
28111 ORF8 Y73C 4094
28271 intergenic del 1 2185
28280 N D3L 1447
28281 N D3L 1447
28282 N D3L 1543
28313 N R14C 2459
28881 N R203K 469
28882 N R203K 468
28883 N G204R 470
28977 N S235F 1123
VSP2636−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

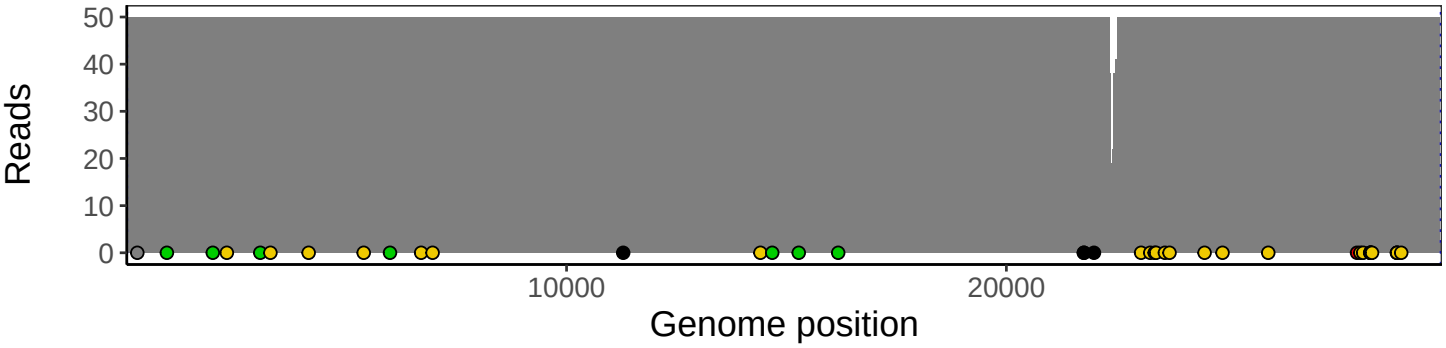
Analyses of individual experiments and composite results

VSP2636-1 | 2021-04-20 | Saline | UPHS-1381 | genomes | single experiment

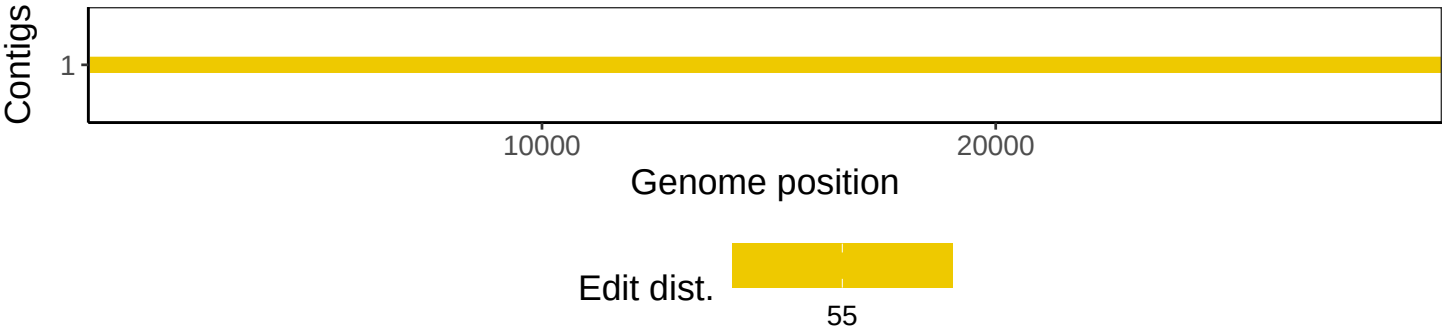
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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