COVID-19 subject UPHS-1121

2021-06-23

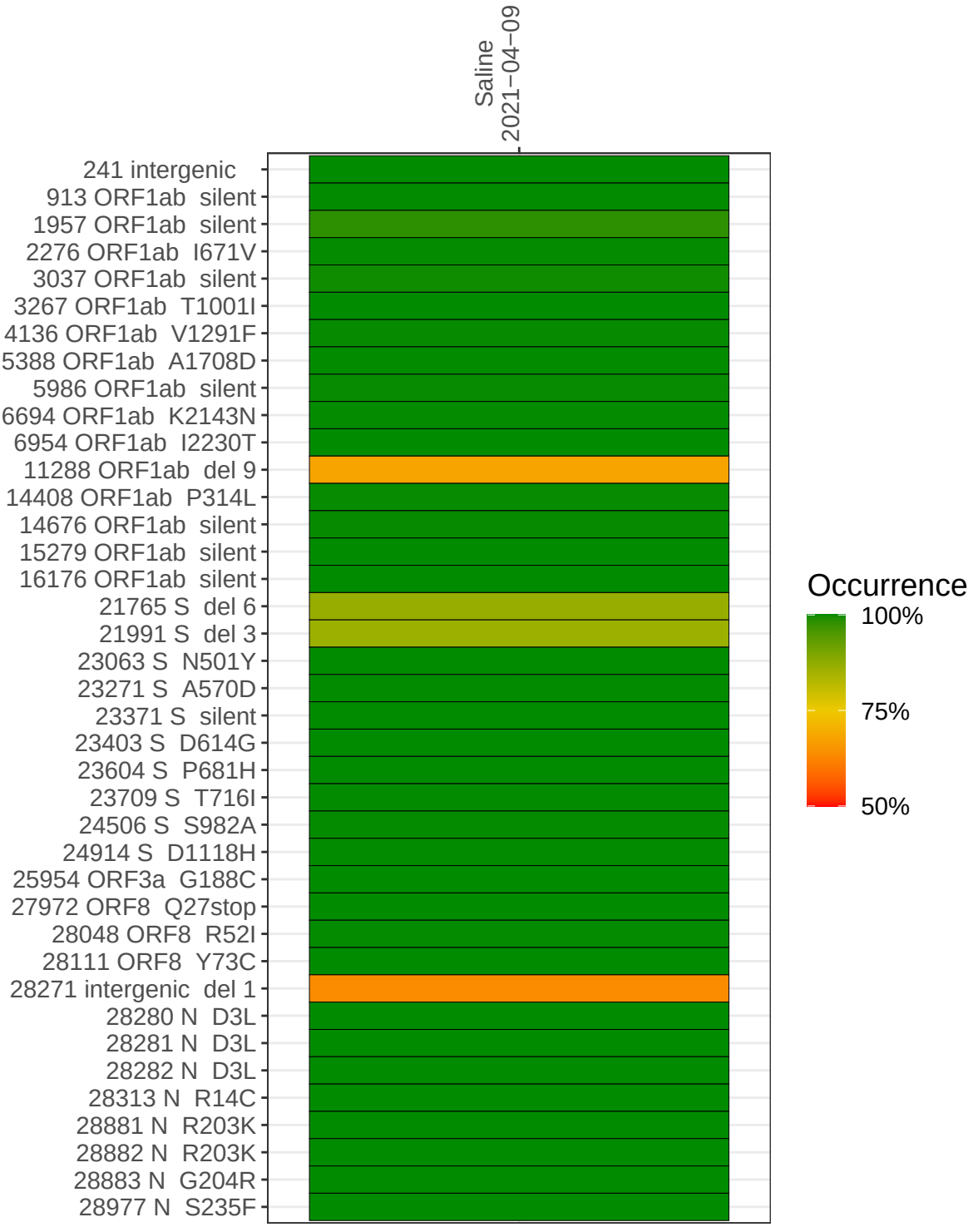
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

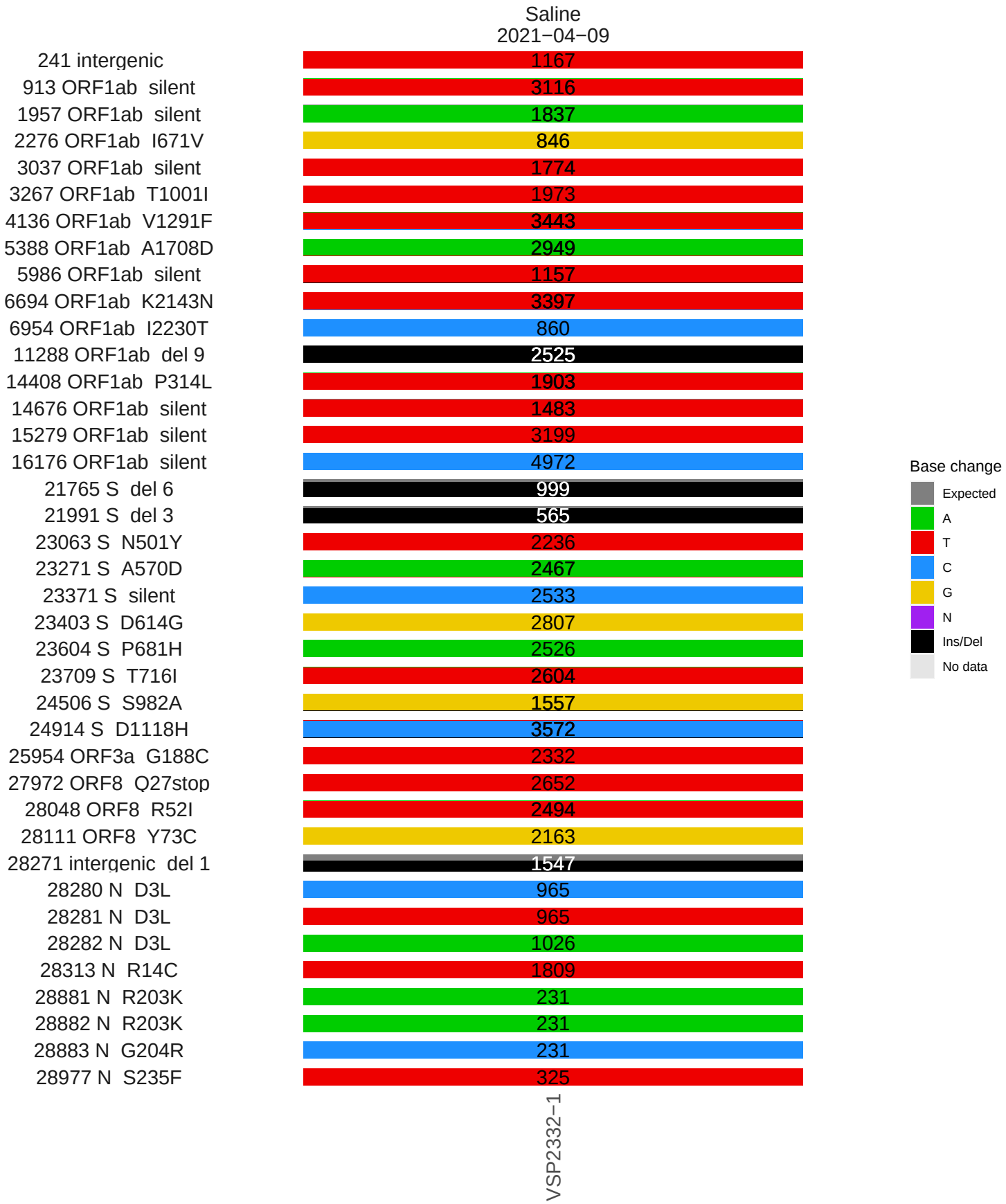
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2332-1	single experiment	NA	Saline	2021-04-09	29.86	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.

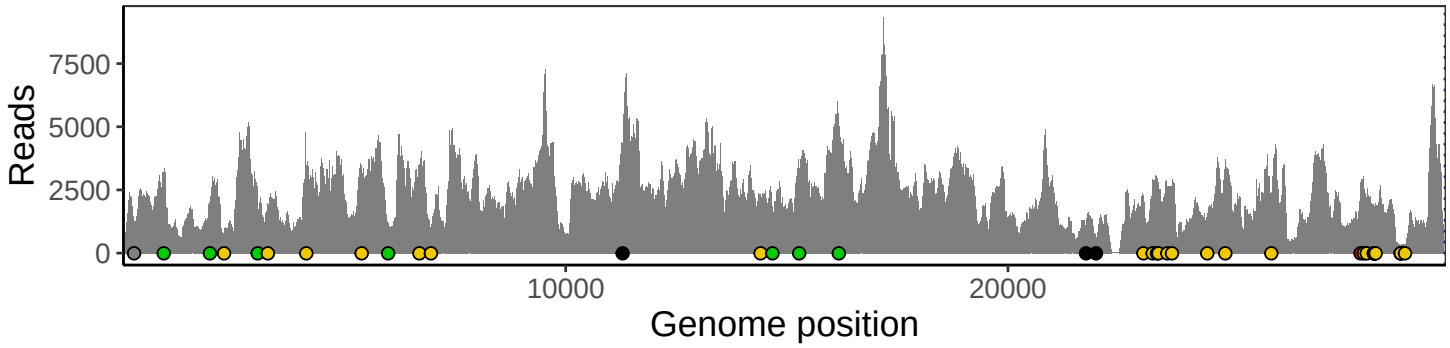



Saline
2021−04−09
241 intergenic 1167
913 ORF1ab silent 3116
1957 ORF1ab silent 1837
2276 ORF1ab I671V 846
3037 ORF1ab silent 1774
3267 ORF1ab T1001I 1973
4136 ORF1ab V1291F 3443
5388 ORF1ab A1708D 2949
5986 ORF1ab silent 1157
6694 ORF1ab K2143N 3397
6954 ORF1ab I2230T 860
11288 ORF1ab del 9 2525
14408 ORF1ab P314L 1903
14676 ORF1ab silent 1483
15279 ORF1ab silent 3199
16176 ORF1ab silent 4972
21765 S del 6 999
21991 S del 3 565
23063 S N501Y 2236
23271 S A570D 2467
23371 S silent 2533
23403 S D614G 2807
23604 S P681H 2526
23709 S T716I 2604
24506 S S982A 1557
24914 S D1118H 3572
25954 ORF3a G188C 2332
27972 ORF8 Q27stop 2652
28048 ORF8 R52I 2494
28111 ORF8 Y73C 2163
28271 intergenic del 1 1547
28280 N D3L 965
28281 N D3L 965
28282 N D3L 1026
28313 N R14C 1809
28881 N R203K 231
28882 N R203K 231
28883 N G204R 231
28977 N S235F 325
VSP2332−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

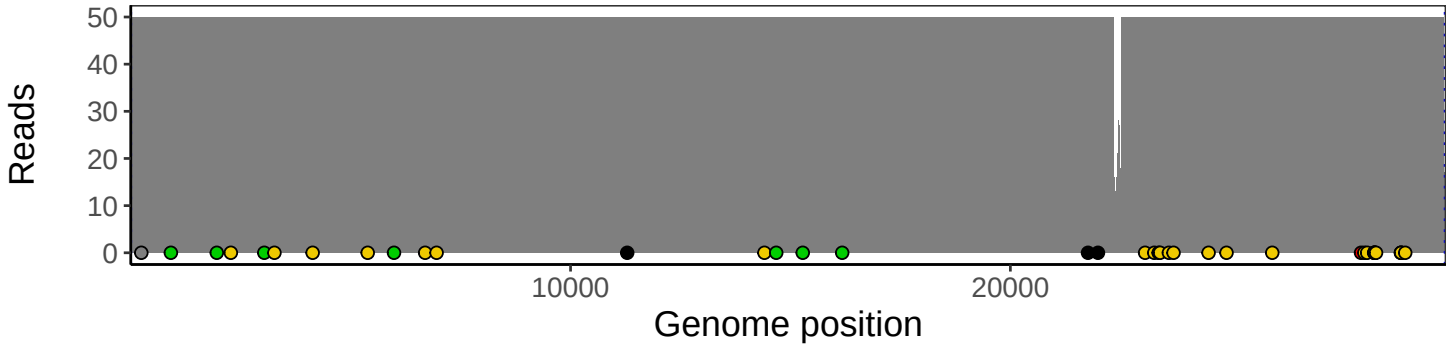
Analyses of individual experiments and composite results

VSP2332-1 | 2021-04-09 | Saline | UPHS-1121 | genomes | single experiment

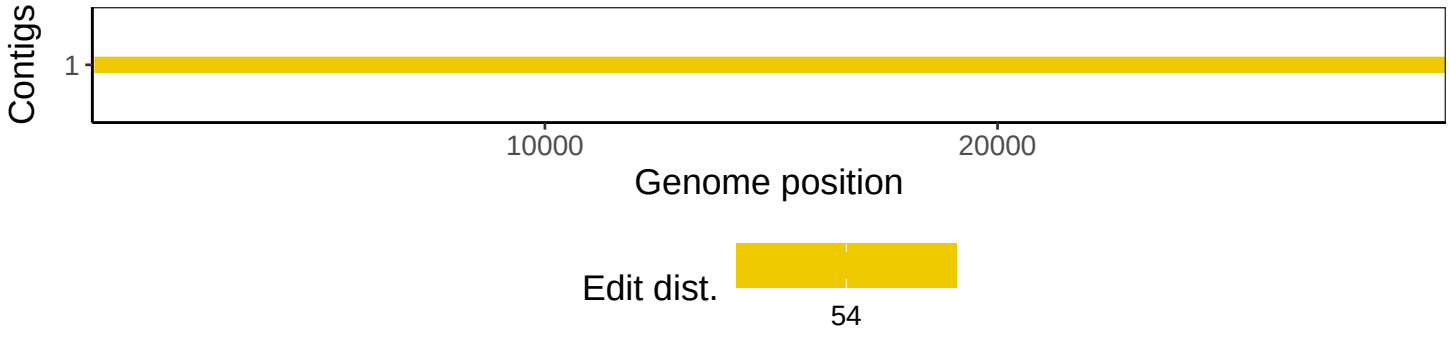
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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