COVID-19 subject UPHS-1033

2021-06-23

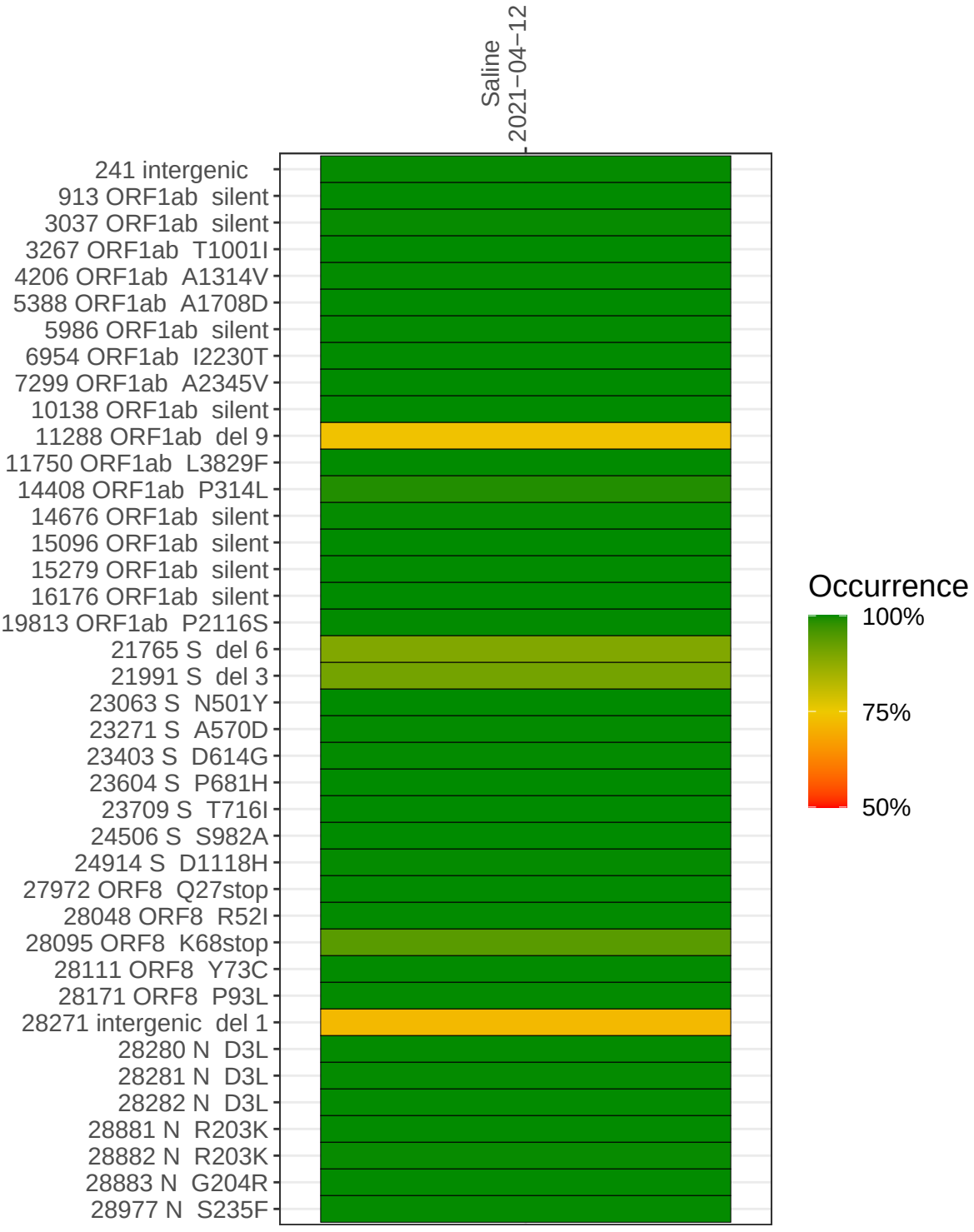
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

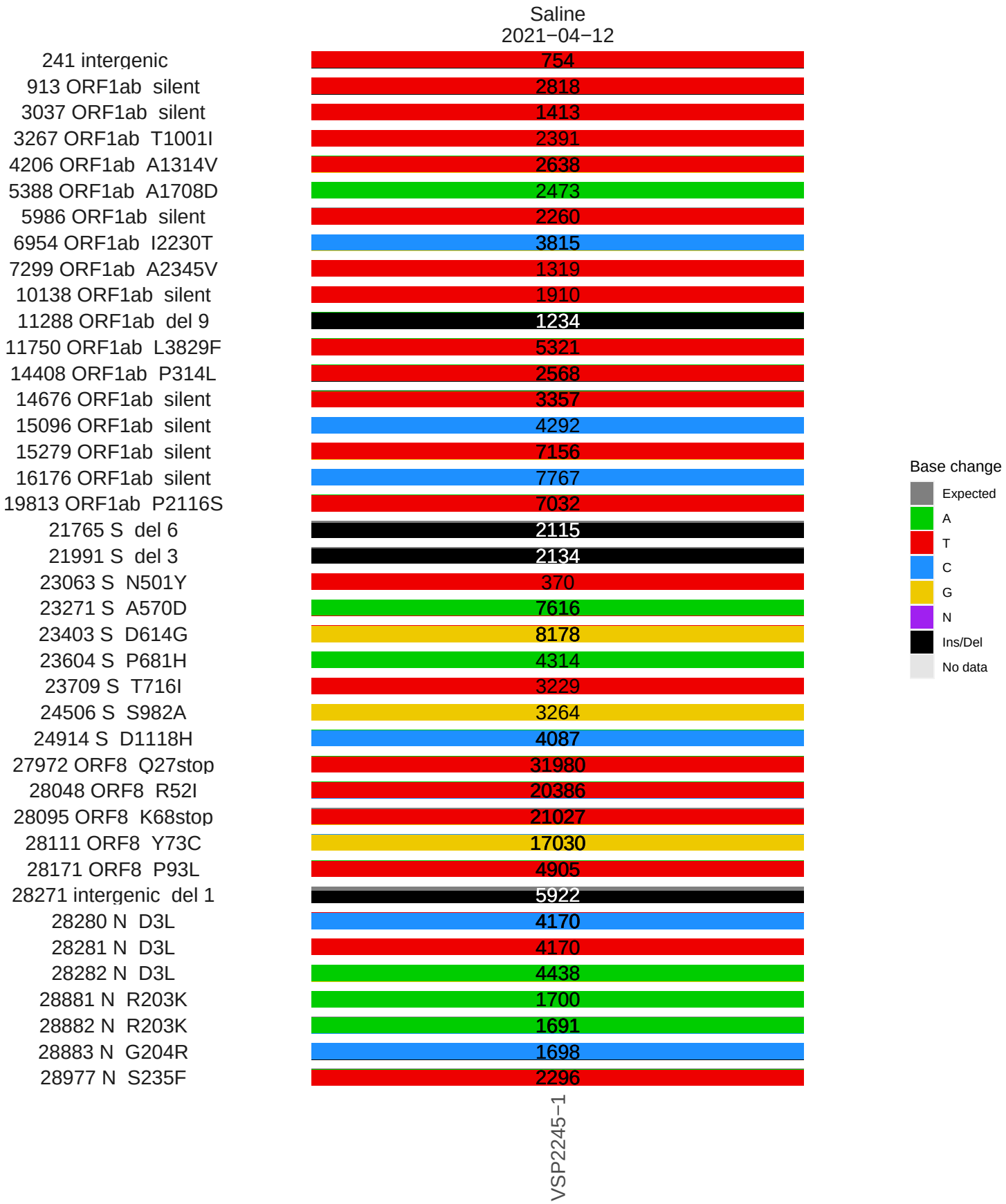
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2245-1	single experiment	NA	Saline	2021-04-12	29.80	B.1.1.7	99.8%	99.8%

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.

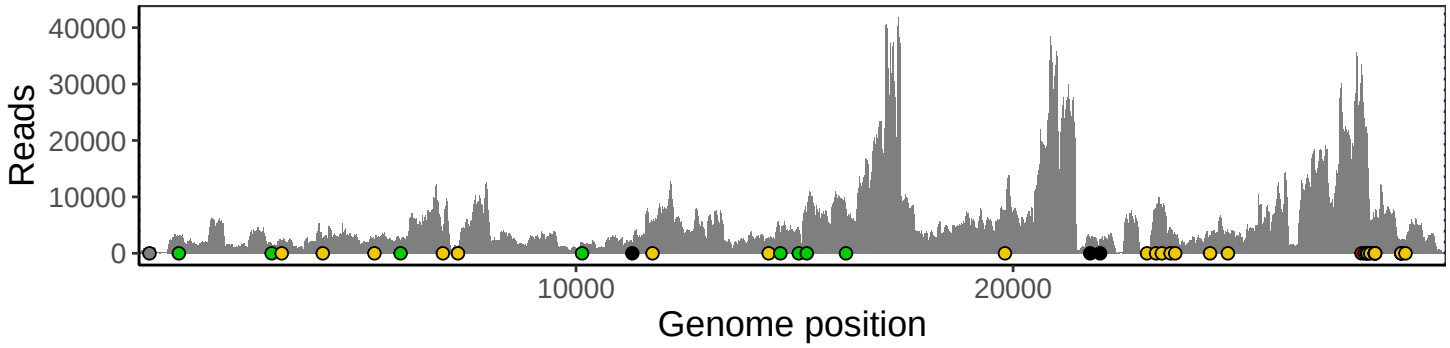



Saline
2021−04−12
241 intergenic 754
913 ORF1ab silent 2818
3037 ORF1ab silent 1413
3267 ORF1ab T1001I 2391
4206 ORF1ab A1314V 2638
5388 ORF1ab A1708D 2473
5986 ORF1ab silent 2260
6954 ORF1ab I2230T 3815
7299 ORF1ab A2345V 1319
10138 ORF1ab silent 1910
11288 ORF1ab del 9 1234
11750 ORF1ab L3829F 5321
14408 ORF1ab P314L 2568
14676 ORF1ab silent 3357
15096 ORF1ab silent 4292
15279 ORF1ab silent 7156
16176 ORF1ab silent 7767
19813 ORF1ab P2116S 7032
21765 S del 6 2115
21991 S del 3 2134
23063 S N501Y 370
23271 S A570D 7616
23403 S D614G 8178
23604 S P681H 4314
23709 S T716I 3229
24506 S S982A 3264
24914 S D1118H 4087
27972 ORF8 Q27stop 31980
28048 ORF8 R52I 20386
28095 ORF8 K68stop 21027
28111 ORF8 Y73C 17030
28171 ORF8 P93L 4905
28271 intergenic del 1 5922
28280 N D3L 4170
28281 N D3L 4170
28282 N D3L 4438
28881 N R203K 1700
28882 N R203K 1691
28883 N G204R 1698
28977 N S235F 2296
VSP2245−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

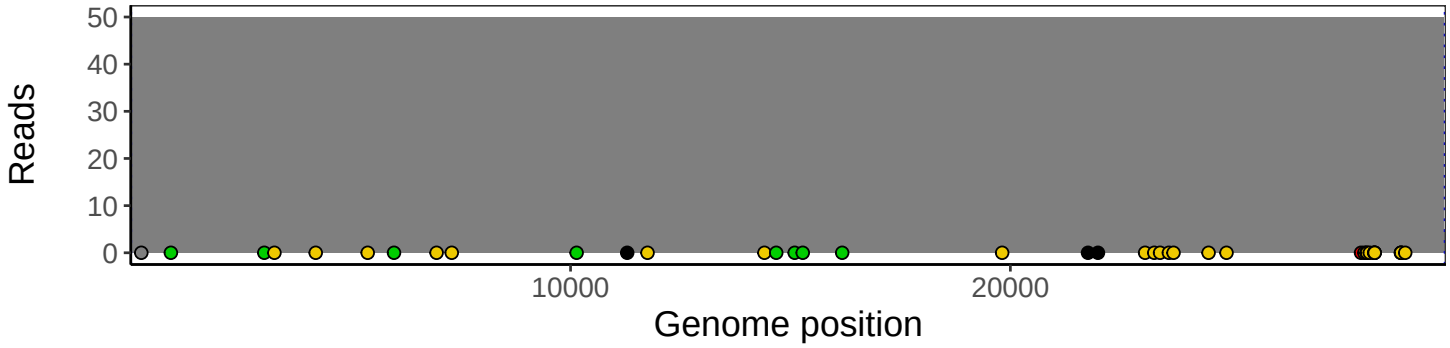
Analyses of individual experiments and composite results

VSP2245-1 | 2021-04-12 | Saline | UPHS-1033 | genomes | single experiment

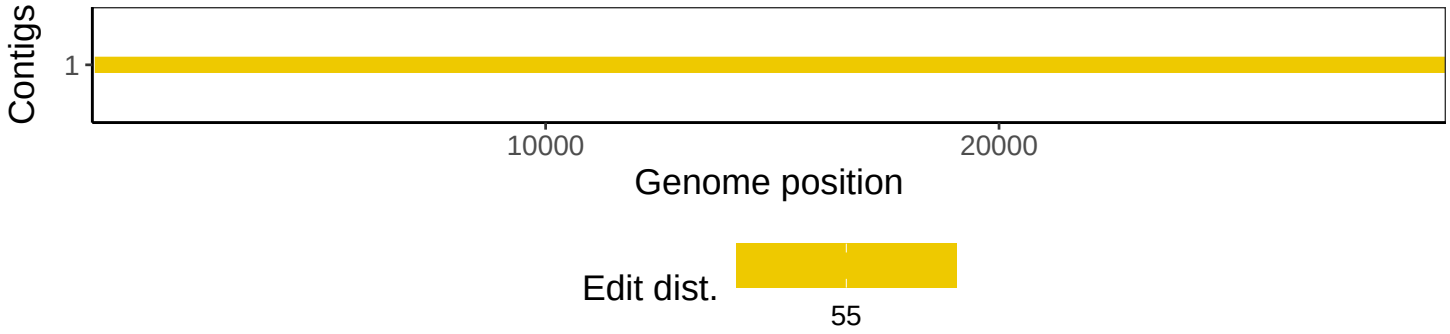
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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