COVID-19 subject UPHS-1037

2021-06-23

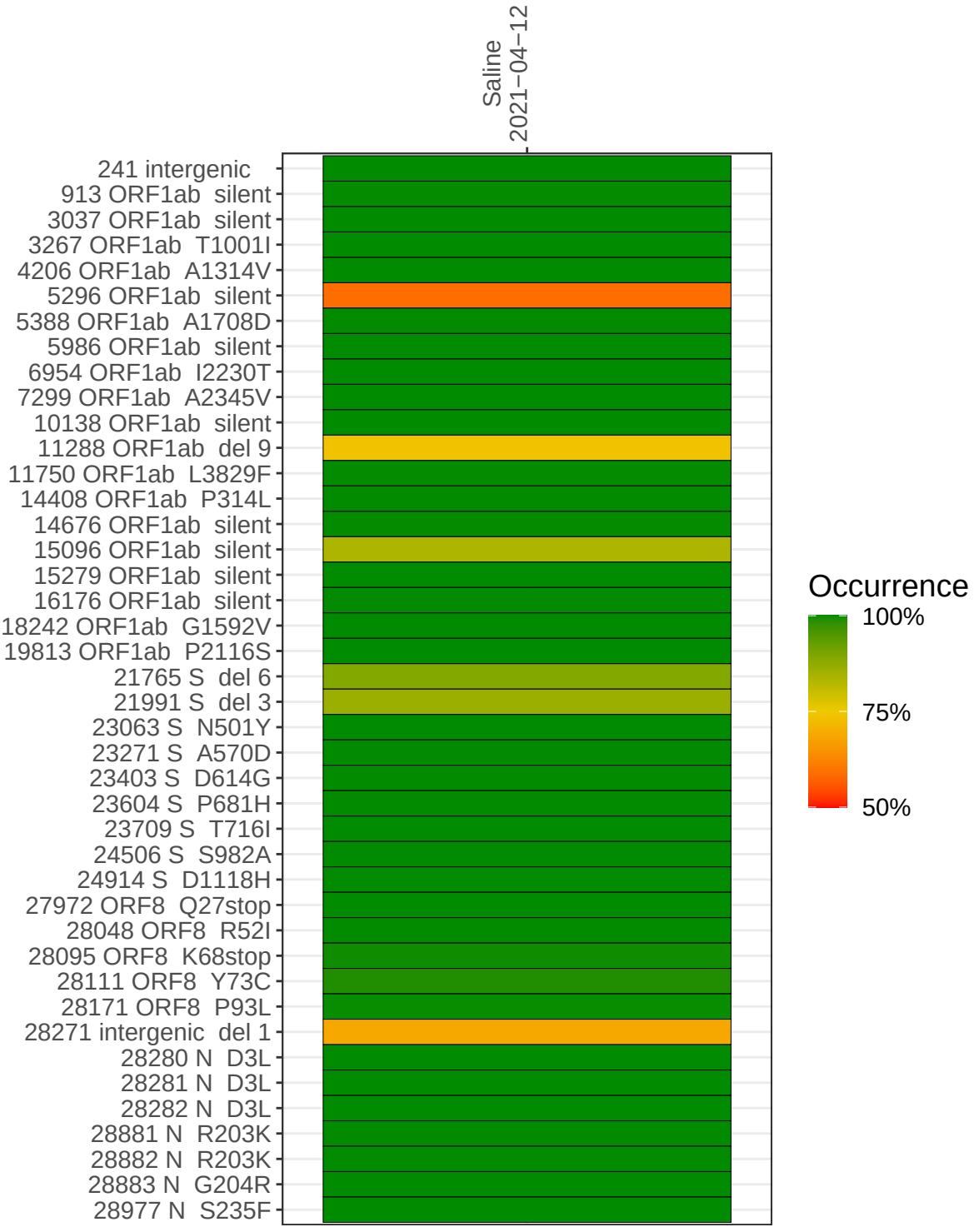
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

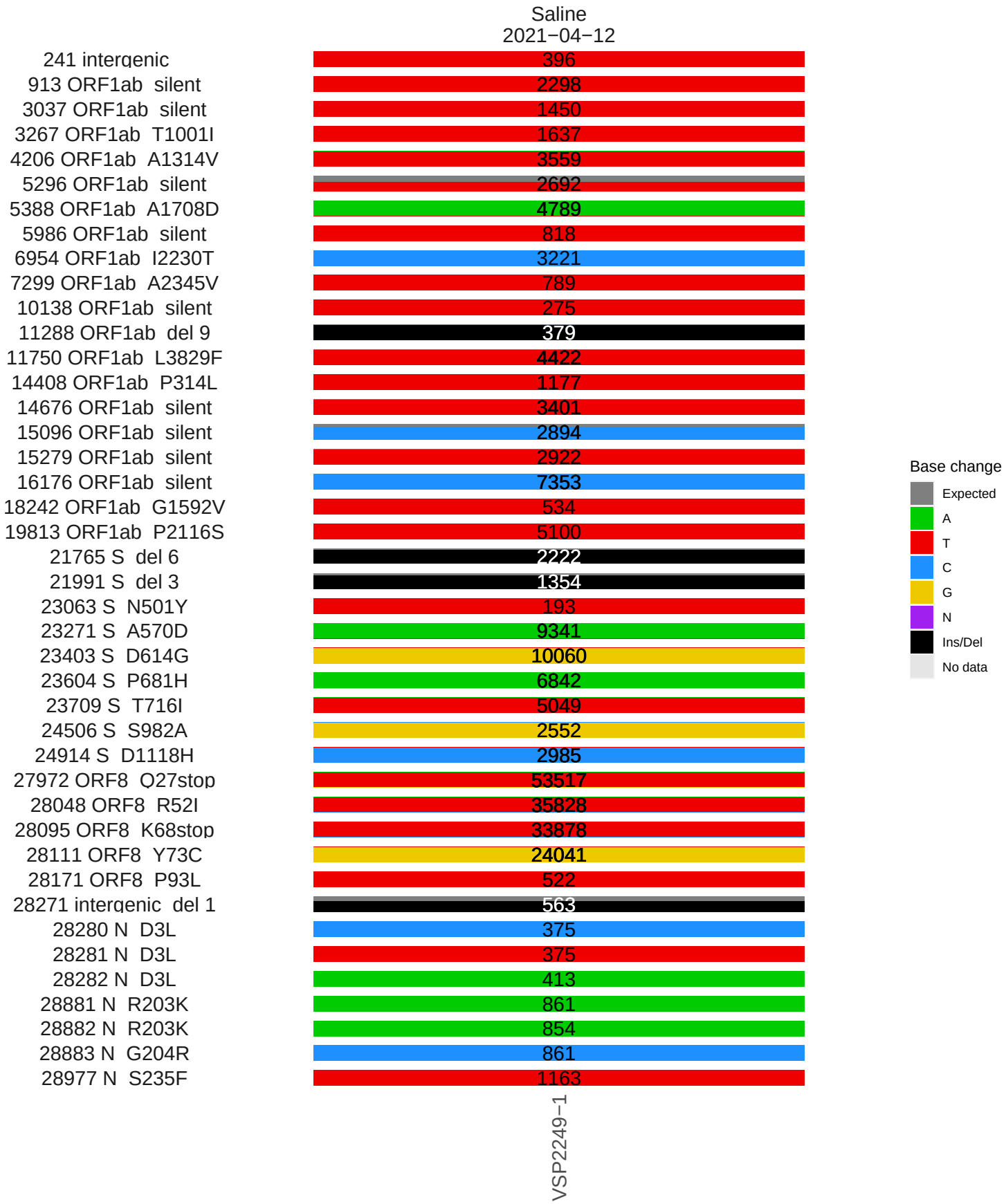
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2249-1	single experiment	NA	Saline	2021-04-12	25.96	B.1.1.7	97.5%	97.5%

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.

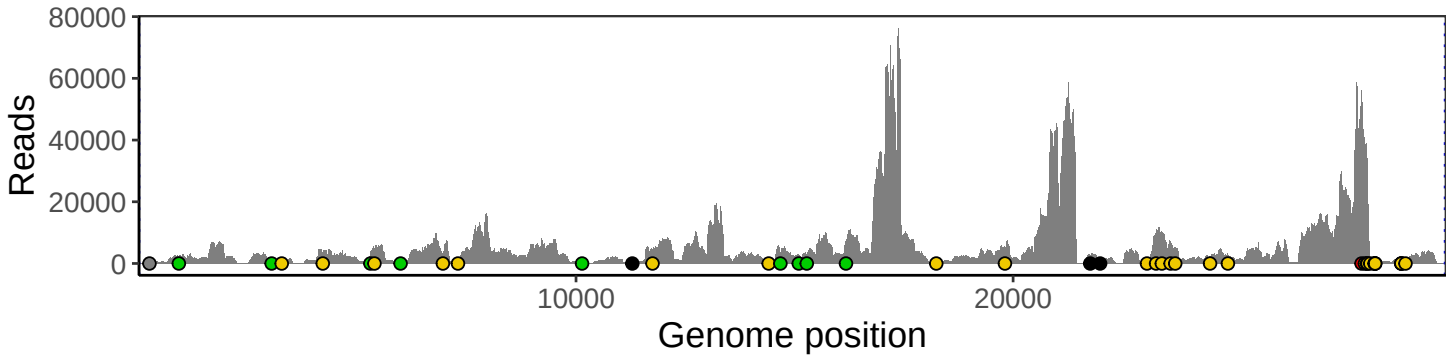



Saline
2021−04−12
241 intergenic 396
913 ORF1ab silent 2298
3037 ORF1ab silent 1450
3267 ORF1ab T1001I 1637
4206 ORF1ab A1314V 3559
5296 ORF1ab silent 2692
5388 ORF1ab A1708D 4789
5986 ORF1ab silent 818
6954 ORF1ab I2230T 3221
7299 ORF1ab A2345V 789
10138 ORF1ab silent 275
11288 ORF1ab del 9 379
11750 ORF1ab L3829F 4422
14408 ORF1ab P314L 1177
14676 ORF1ab silent 3401
15096 ORF1ab silent 2894
15279 ORF1ab silent 2922
16176 ORF1ab silent 7353
18242 ORF1ab G1592V 534
19813 ORF1ab P2116S 5100
21765 S del 6 2222
21991 S del 3 1354
23063 S N501Y 193
23271 S A570D 9341
23403 S D614G 10060
23604 S P681H 6842
23709 S T716I 5049
24506 S S982A 2552
24914 S D1118H 2985
27972 ORF8 Q27stop 53517
28048 ORF8 R52I 35828
28095 ORF8 K68stop 33878
28111 ORF8 Y73C 24041
28171 ORF8 P93L 522
28271 intergenic del 1 563
28280 N D3L 375
28281 N D3L 375
28282 N D3L 413
28881 N R203K 861
28882 N R203K 854
28883 N G204R 861
28977 N S235F 1163
VSP2249−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

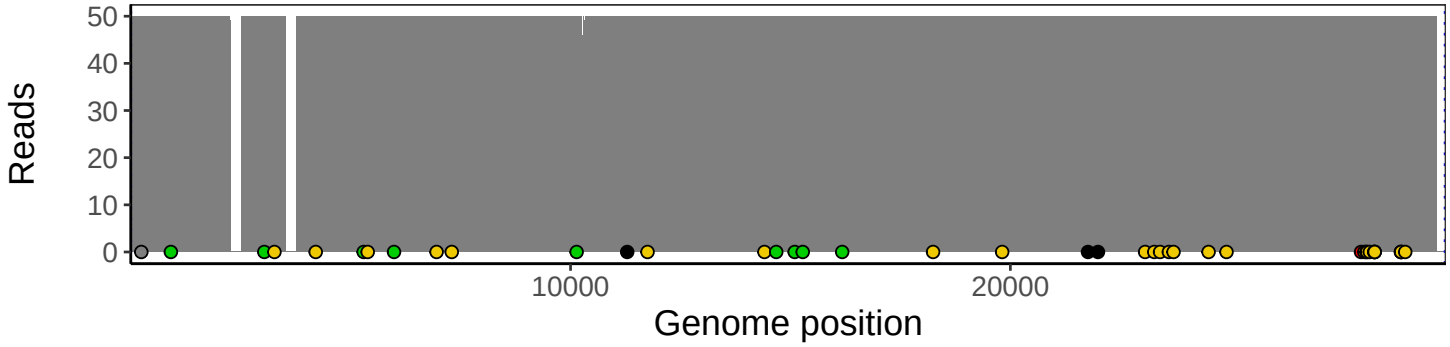
Analyses of individual experiments and composite results

VSP2249-1 | 2021-04-12 | Saline | UPHS-1037 | genomes | single experiment

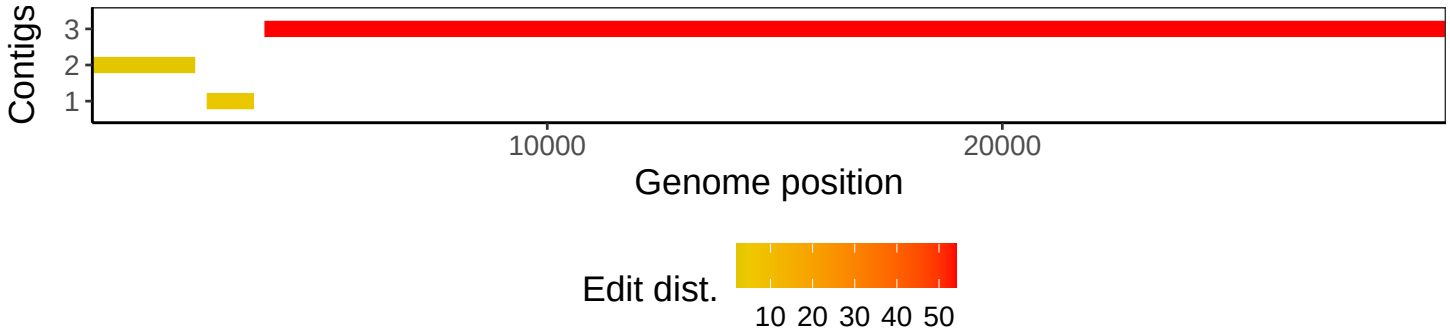
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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