COVID-19 subject UPHS-1030

2021-06-23

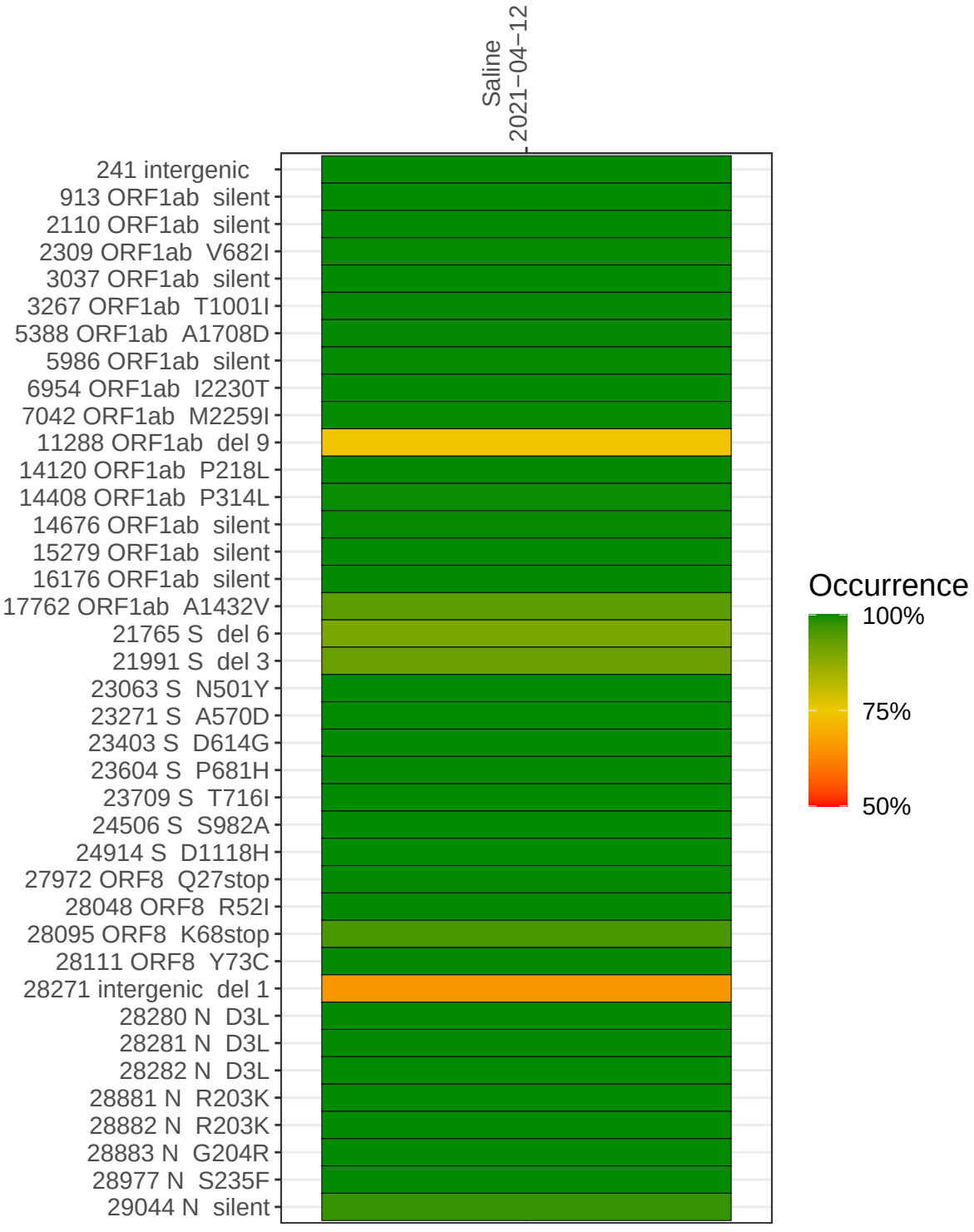
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

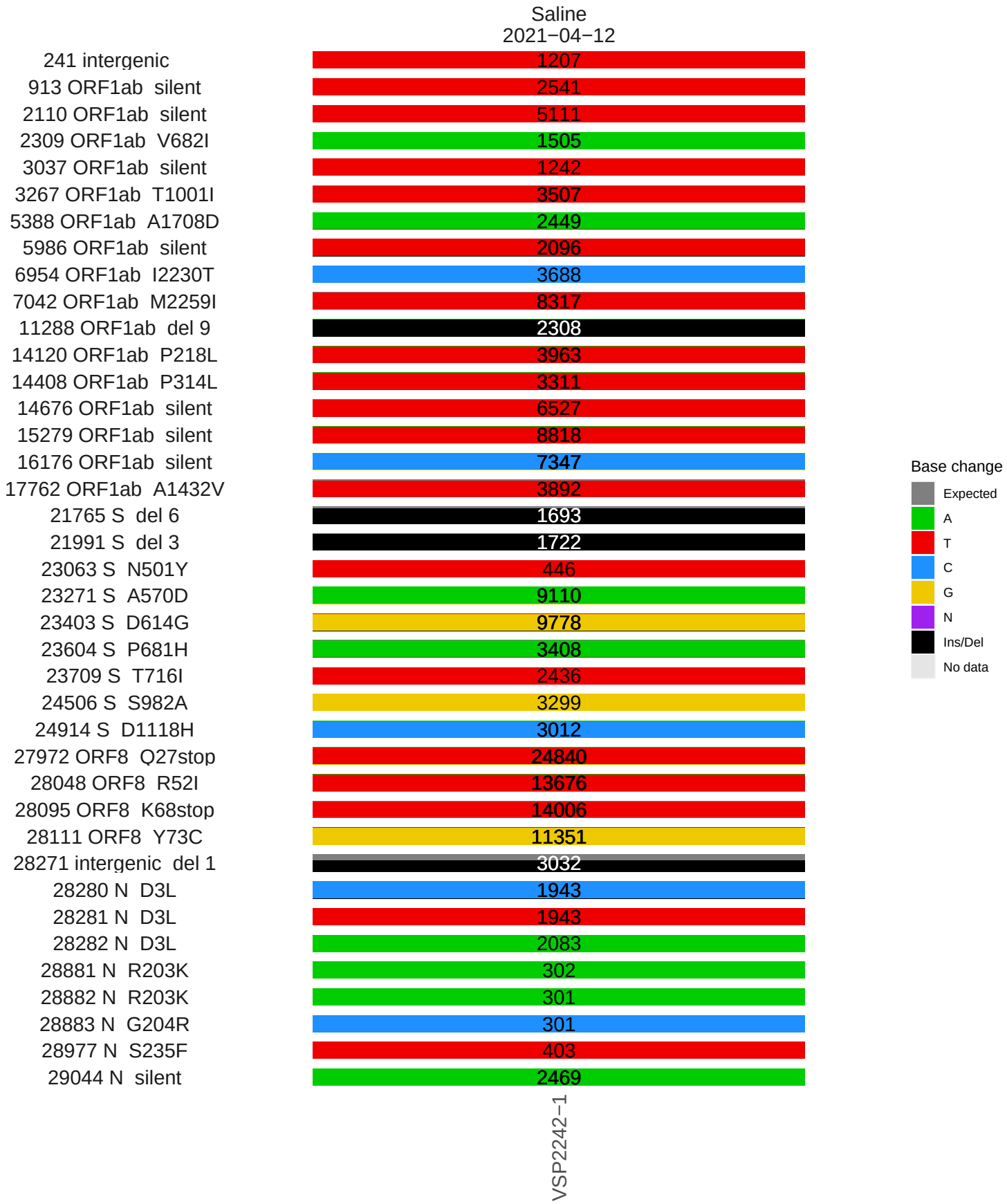
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2242-1	single experiment	NA	Saline	2021-04-12	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.

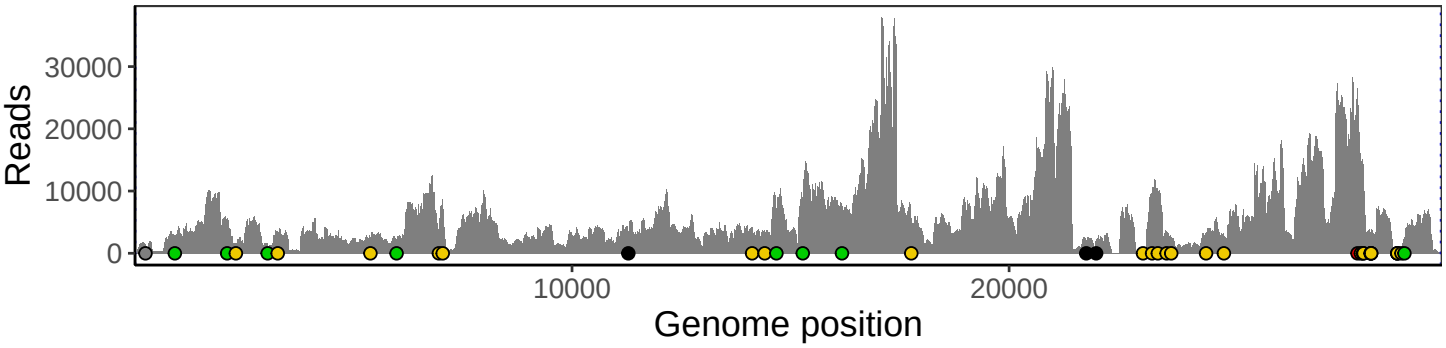



Saline
2021−04−12
241 intergenic 1207
913 ORF1ab silent 2541
2110 ORF1ab silent 5111
2309 ORF1ab V682I 1505
3037 ORF1ab silent 1242
3267 ORF1ab T1001I 3507
5388 ORF1ab A1708D 2449
5986 ORF1ab silent 2096
6954 ORF1ab I2230T 3688
7042 ORF1ab M2259I 8317
11288 ORF1ab del 9 2308
14120 ORF1ab P218L 3963
14408 ORF1ab P314L 3311
14676 ORF1ab silent 6527
15279 ORF1ab silent 8818
16176 ORF1ab silent 7347
17762 ORF1ab A1432V 3892
21765 S del 6 1693
21991 S del 3 1722
23063 S N501Y 446
23271 S A570D 9110
23403 S D614G 9778
23604 S P681H 3408
23709 S T716I 2436
24506 S S982A 3299
24914 S D1118H 3012
27972 ORF8 Q27stop 24840
28048 ORF8 R52I 13676
28095 ORF8 K68stop 14006
28111 ORF8 Y73C 11351
28271 intergenic del 1 3032
28280 N D3L 1943
28281 N D3L 1943
28282 N D3L 2083
28881 N R203K 302
28882 N R203K 301
28883 N G204R 301
28977 N S235F 403
29044 N silent 2469
VSP2242−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

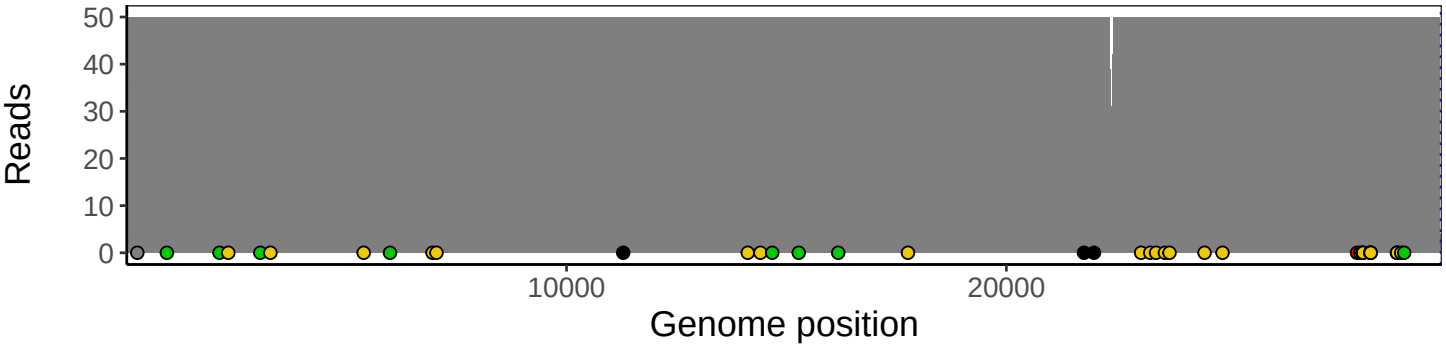
Analyses of individual experiments and composite results

VSP2242-1 | 2021-04-12 | Saline | UPHS-1030 | genomes | single experiment

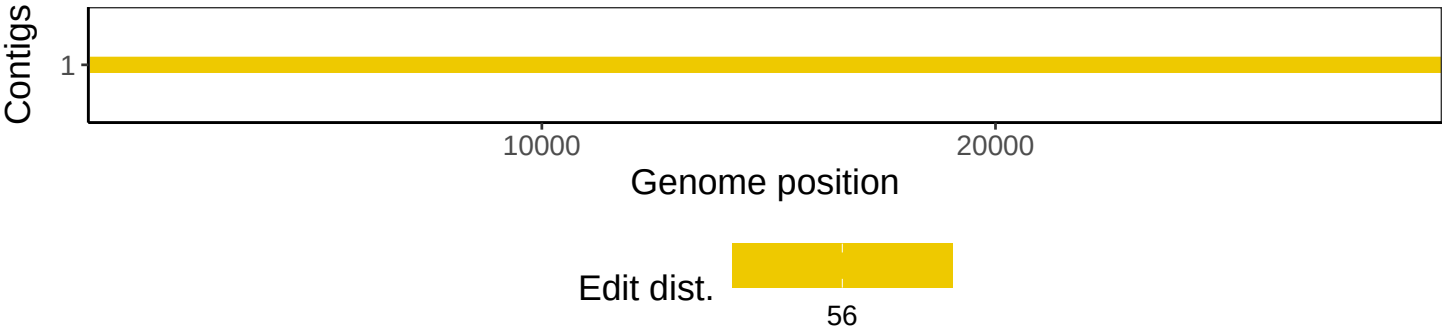
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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