COVID-19 subject UPHS-1196

2021-06-23

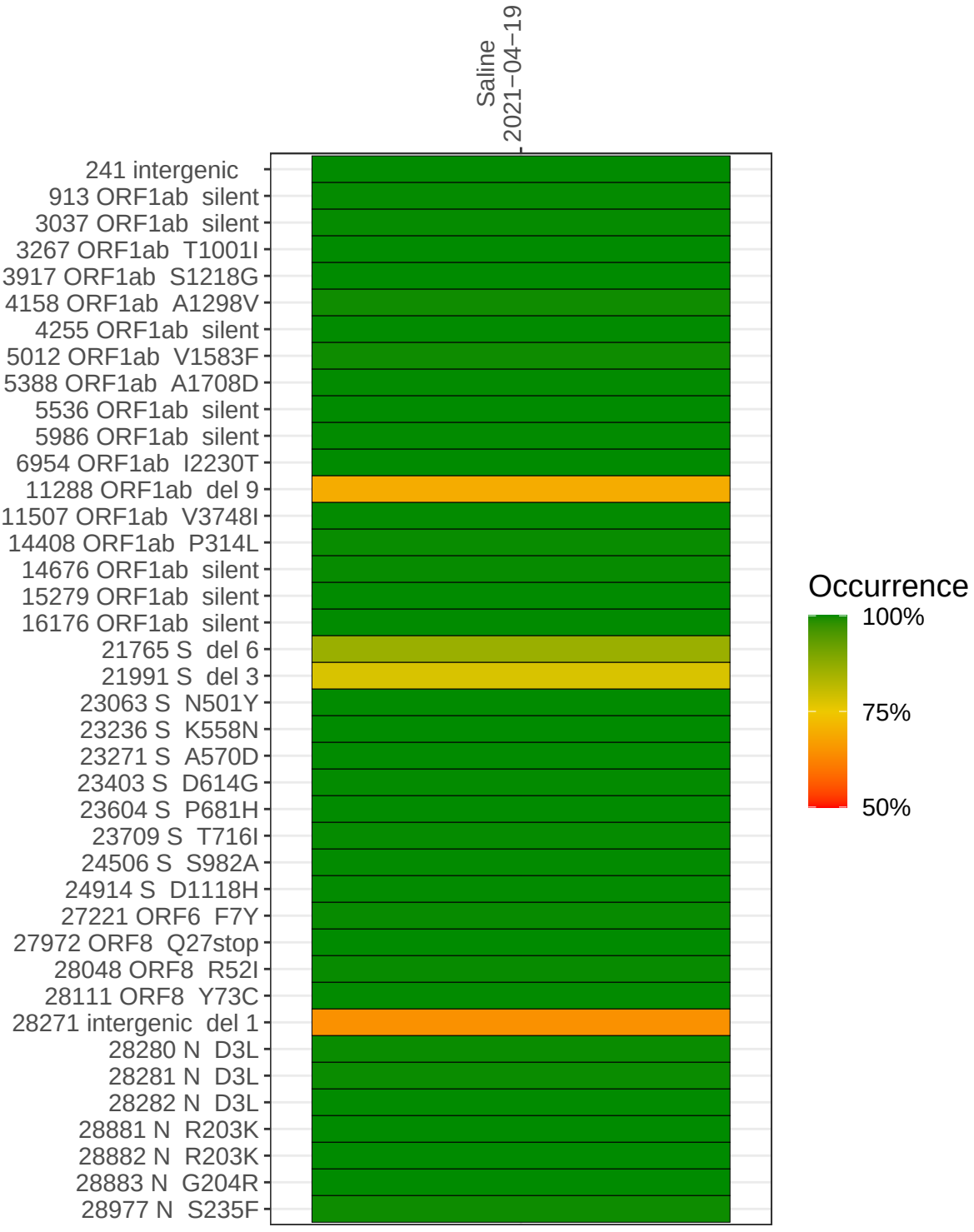
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

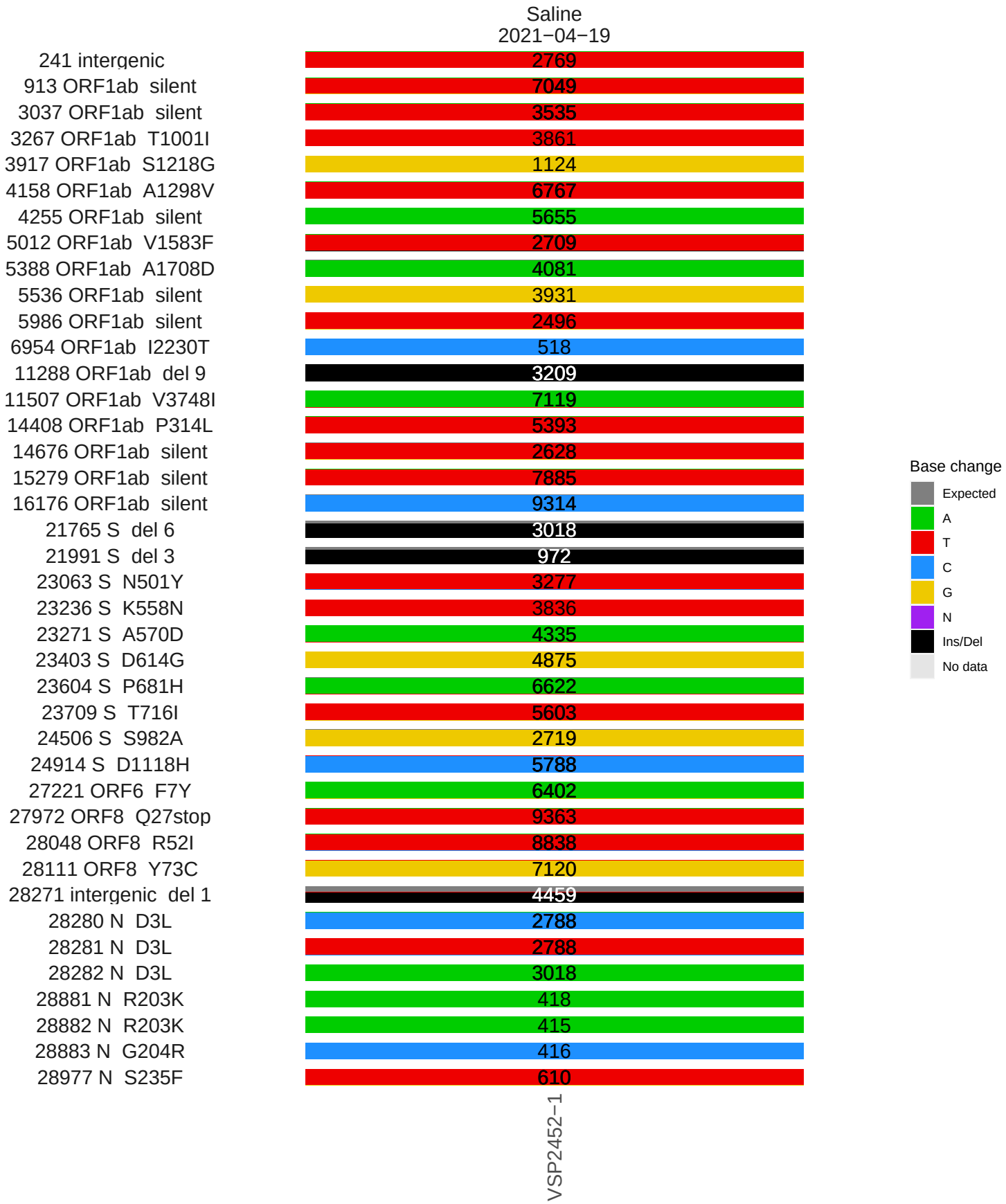
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2452-1	single experiment	NA	Saline	2021-04-19	29.85	B.1.1.7	99.9%	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.

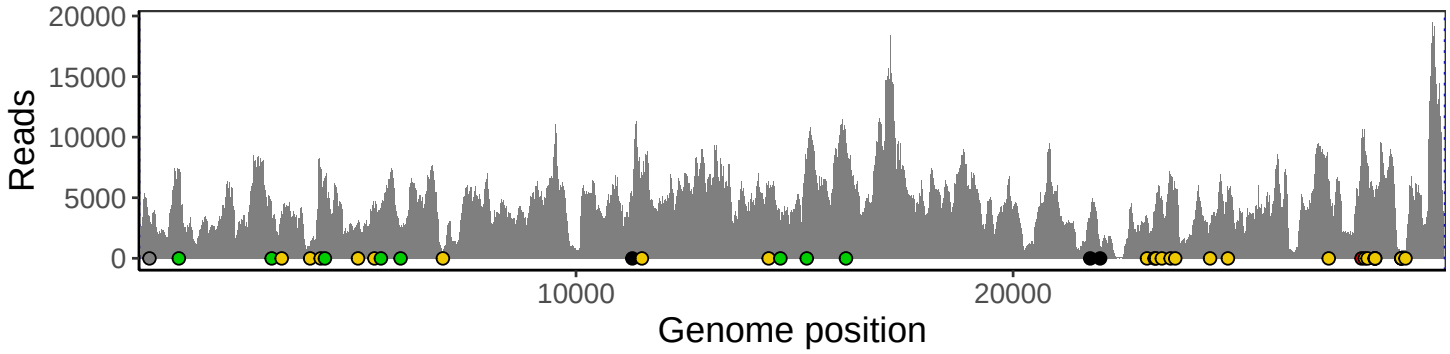



Saline
2021−04−19
241 intergenic 2769
913 ORF1ab silent 7049
3037 ORF1ab silent 3535
3267 ORF1ab T1001I 3861
3917 ORF1ab S1218G 1124
4158 ORF1ab A1298V 6767
4255 ORF1ab silent 5655
5012 ORF1ab V1583F 2709
5388 ORF1ab A1708D 4081
5536 ORF1ab silent 3931
5986 ORF1ab silent 2496
6954 ORF1ab I2230T 518
11288 ORF1ab del 9 3209
11507 ORF1ab V3748I 7119
14408 ORF1ab P314L 5393
14676 ORF1ab silent 2628
15279 ORF1ab silent 7885
16176 ORF1ab silent 9314
21765 S del 6 3018
21991 S del 3 972
23063 S N501Y 3277
23236 S K558N 3836
23271 S A570D 4335
23403 S D614G 4875
23604 S P681H 6622
23709 S T716I 5603
24506 S S982A 2719
24914 S D1118H 5788
27221 ORF6 F7Y 6402
27972 ORF8 Q27stop 9363
28048 ORF8 R52I 8838
28111 ORF8 Y73C 7120
28271 intergenic del 1 4459
28280 N D3L 2788
28281 N D3L 2788
28282 N D3L 3018
28881 N R203K 418
28882 N R203K 415
28883 N G204R 416
28977 N S235F 610
VSP2452−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

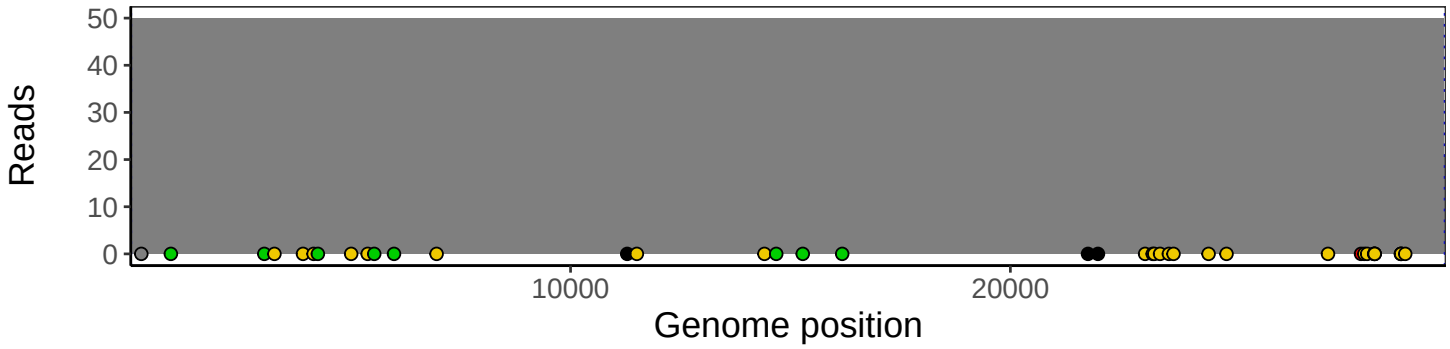
Analyses of individual experiments and composite results

VSP2452-1 | 2021-04-19 | Saline | UPHS-1196 | genomes | single experiment

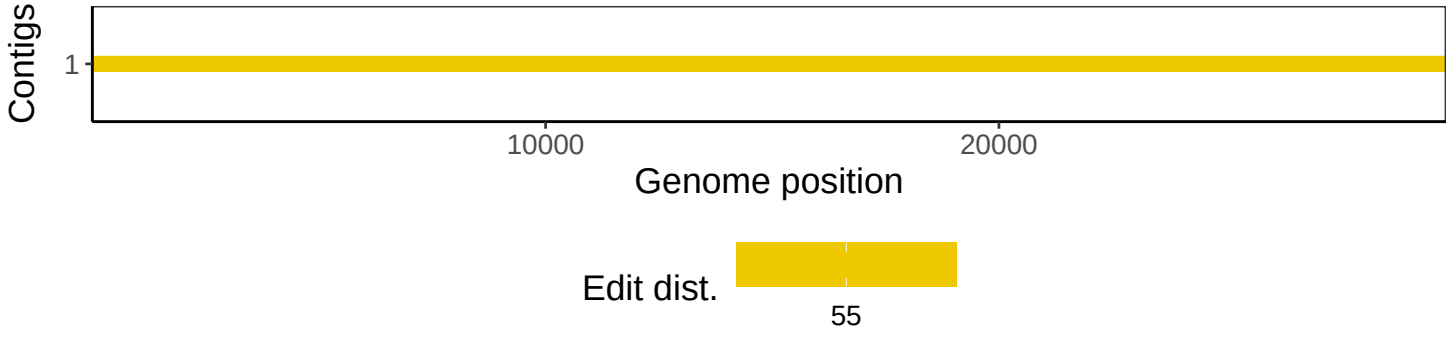
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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