COVID-19 subject UPHS-1010

2021-05-10

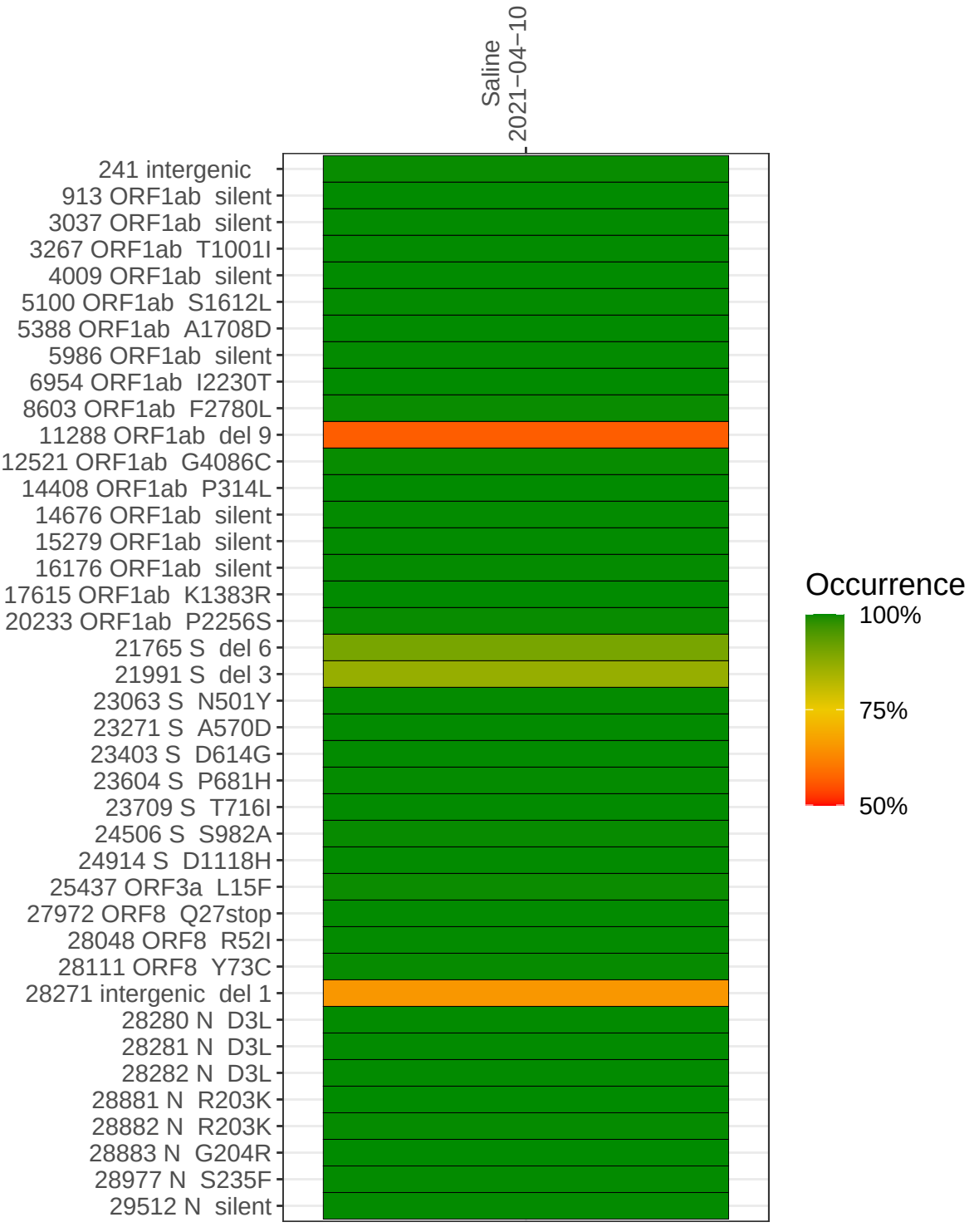
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

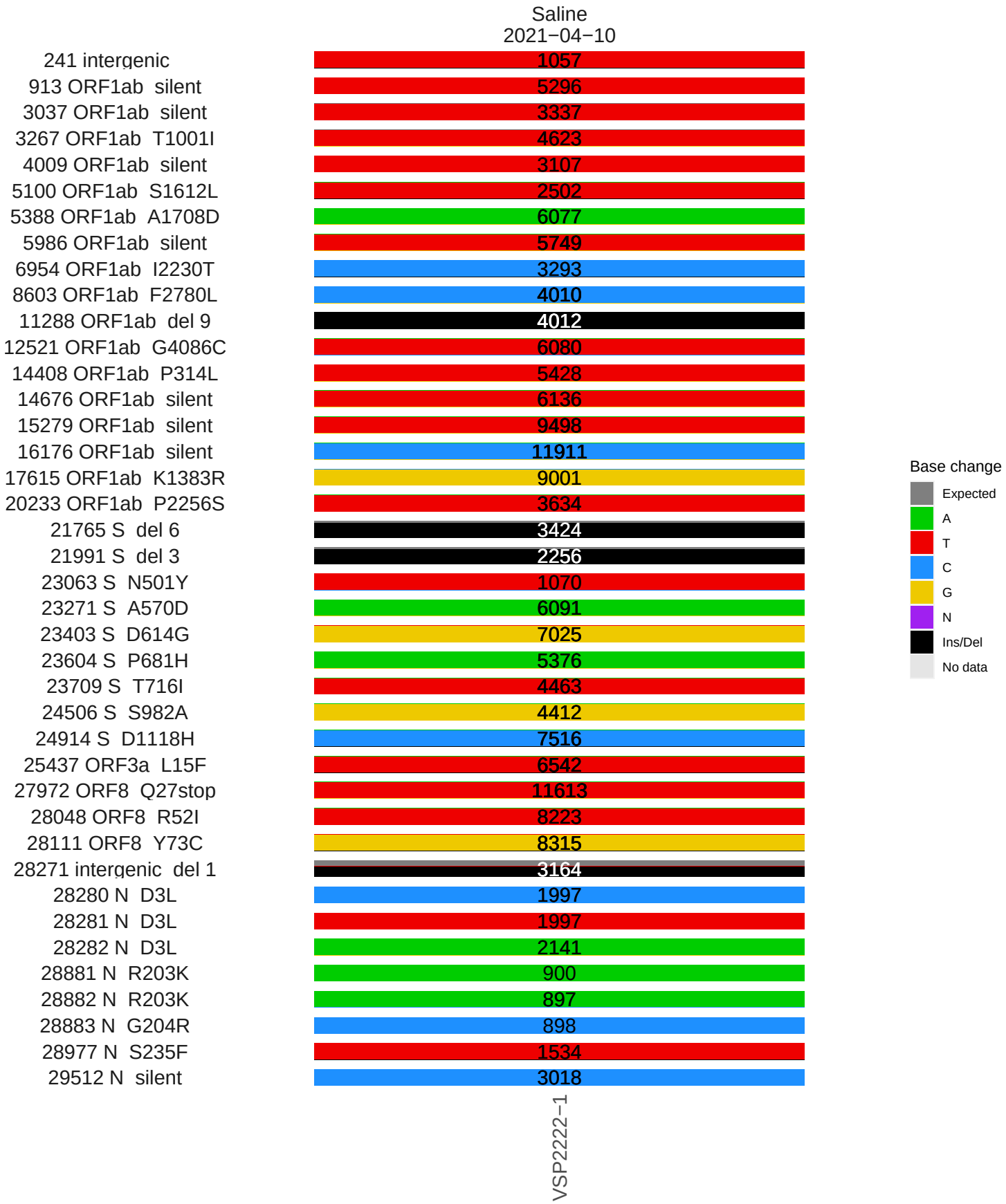
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2222-1	single experiment	NA	Saline	2021-04-10	29.83	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

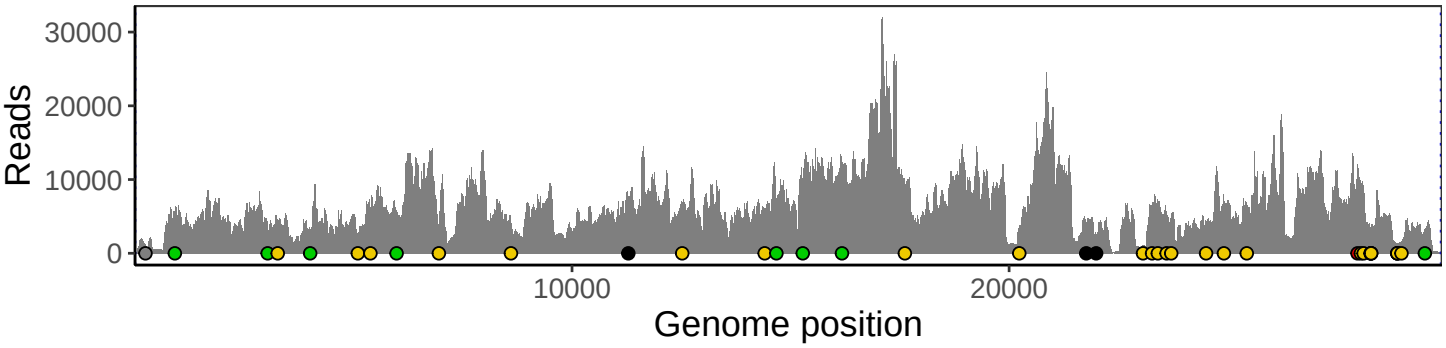



Saline
2021−04−10
241 intergenic 1057
913 ORF1ab silent 5296
3037 ORF1ab silent 3337
3267 ORF1ab T1001I 4623
4009 ORF1ab silent 3107
5100 ORF1ab S1612L 2502
5388 ORF1ab A1708D 6077
5986 ORF1ab silent 5749
6954 ORF1ab I2230T 3293
8603 ORF1ab F2780L 4010
11288 ORF1ab del 9 4012
12521 ORF1ab G4086C 6080
14408 ORF1ab P314L 5428
14676 ORF1ab silent 6136
15279 ORF1ab silent 9498
16176 ORF1ab silent 11911
17615 ORF1ab K1383R 9001
20233 ORF1ab P2256S 3634
21765 S del 6 3424
21991 S del 3 2256
23063 S N501Y 1070
23271 S A570D 6091
23403 S D614G 7025
23604 S P681H 5376
23709 S T716I 4463
24506 S S982A 4412
24914 S D1118H 7516
25437 ORF3a L15F 6542
27972 ORF8 Q27stop 11613
28048 ORF8 R52I 8223
28111 ORF8 Y73C 8315
28271 intergenic del 1 3164
28280 N D3L 1997
28281 N D3L 1997
28282 N D3L 2141
28881 N R203K 900
28882 N R203K 897
28883 N G204R 898
28977 N S235F 1534
29512 N silent 3018
VSP2222−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

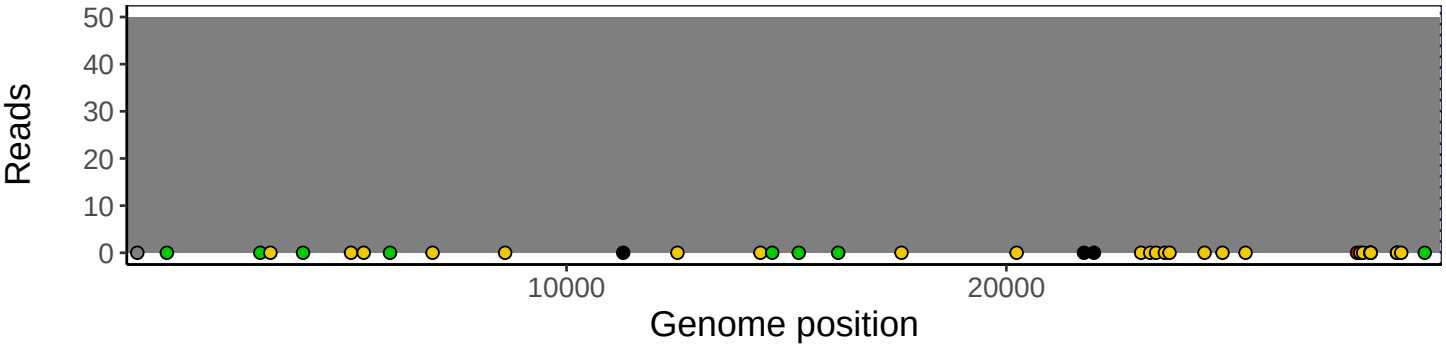
Analyses of individual experiments and composite results

VSP2222-1 | 2021-04-10 | Saline | UPHS-1010 | genomes | single experiment

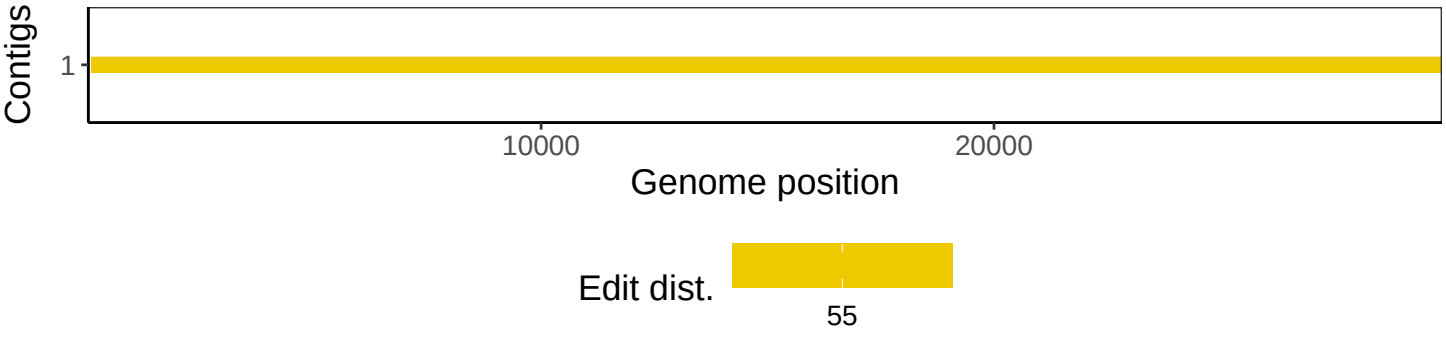
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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