COVID-19 subject UPHS-1345

2021-05-21

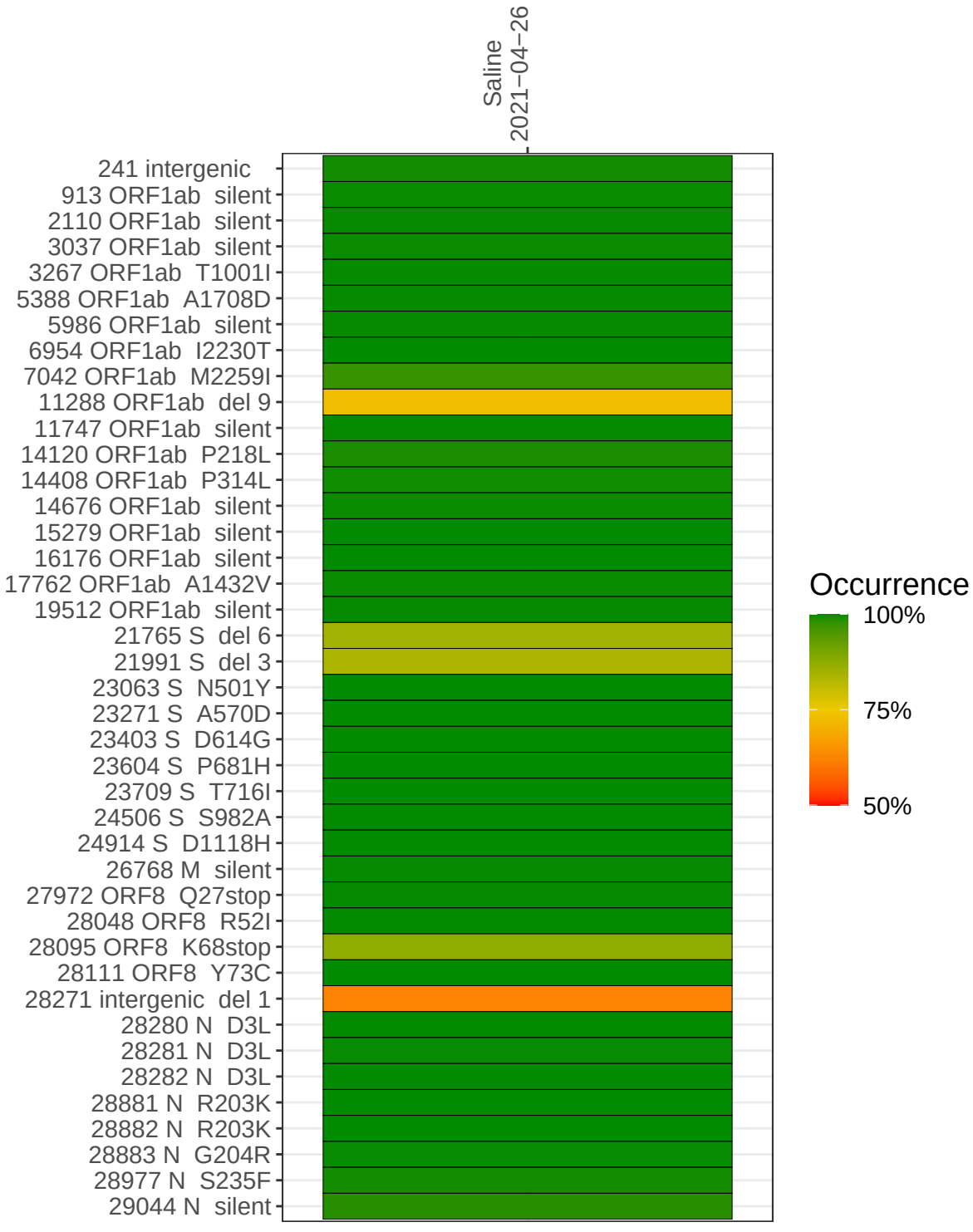
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

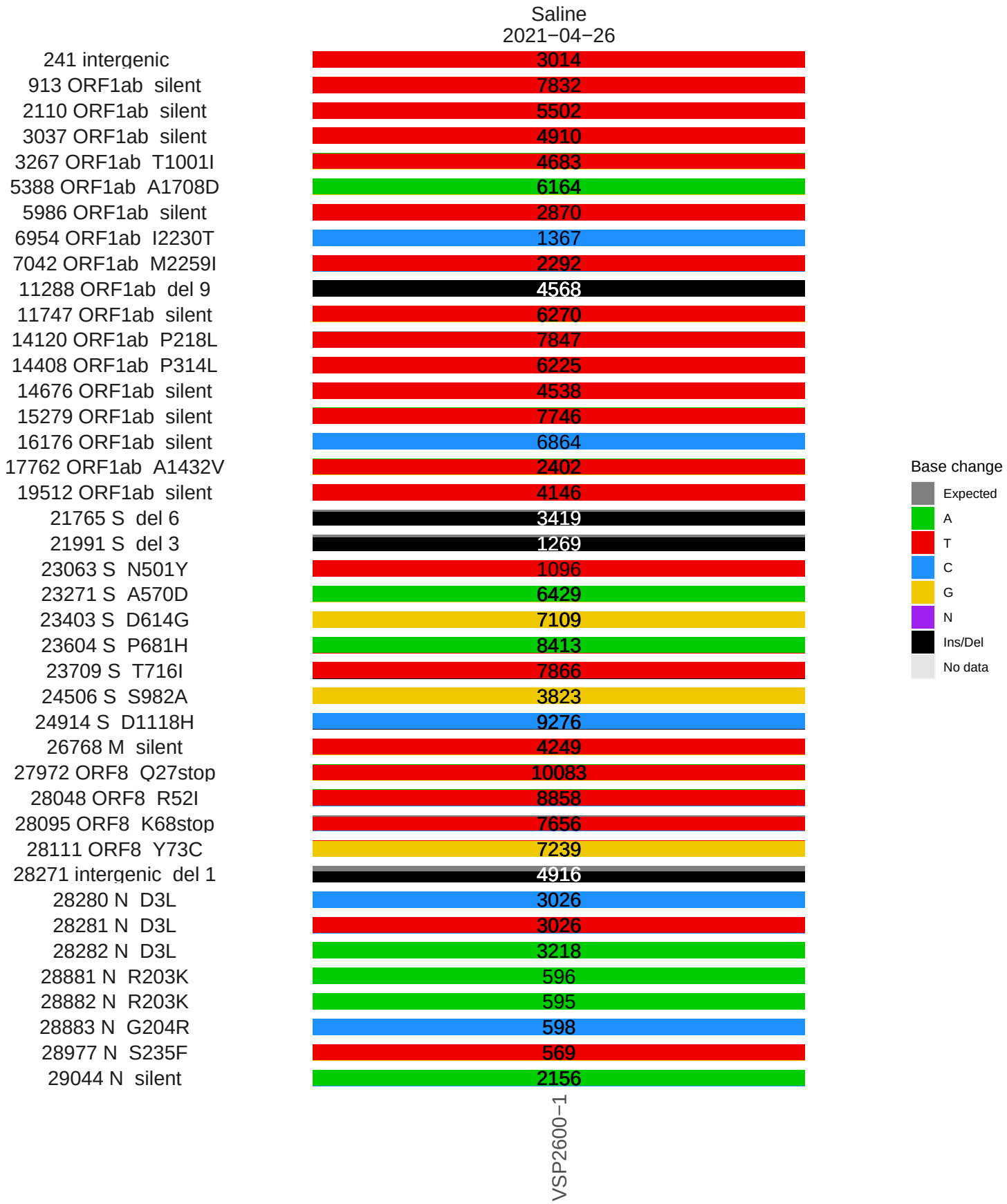
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2600-1	single experiment	NA	Saline	2021-04-26	29.89	B.1.1.7	99.8%	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.

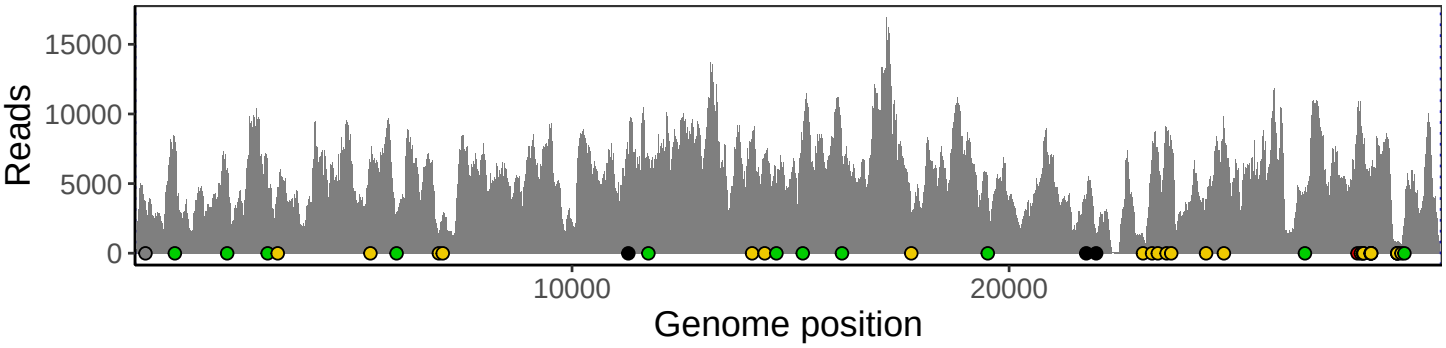



Saline
2021−04−26
241 intergenic 3014
913 ORF1ab silent 7832
2110 ORF1ab silent 5502
3037 ORF1ab silent 4910
3267 ORF1ab T1001I 4683
5388 ORF1ab A1708D 6164
5986 ORF1ab silent 2870
6954 ORF1ab I2230T 1367
7042 ORF1ab M2259I 2292
11288 ORF1ab del 9 4568
11747 ORF1ab silent 6270
14120 ORF1ab P218L 7847
14408 ORF1ab P314L 6225
14676 ORF1ab silent 4538
15279 ORF1ab silent 7746
16176 ORF1ab silent 6864
17762 ORF1ab A1432V 2402
19512 ORF1ab silent 4146
21765 S del 6 3419
21991 S del 3 1269
23063 S N501Y 1096
23271 S A570D 6429
23403 S D614G 7109
23604 S P681H 8413
23709 S T716I 7866
24506 S S982A 3823
24914 S D1118H 9276
26768 M silent 4249
27972 ORF8 Q27stop 10083
28048 ORF8 R52I 8858
28095 ORF8 K68stop 7656
28111 ORF8 Y73C 7239
28271 intergenic del 1 4916
28280 N D3L 3026
28281 N D3L 3026
28282 N D3L 3218
28881 N R203K 596
28882 N R203K 595
28883 N G204R 598
28977 N S235F 569
29044 N silent 2156
VSP2600−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

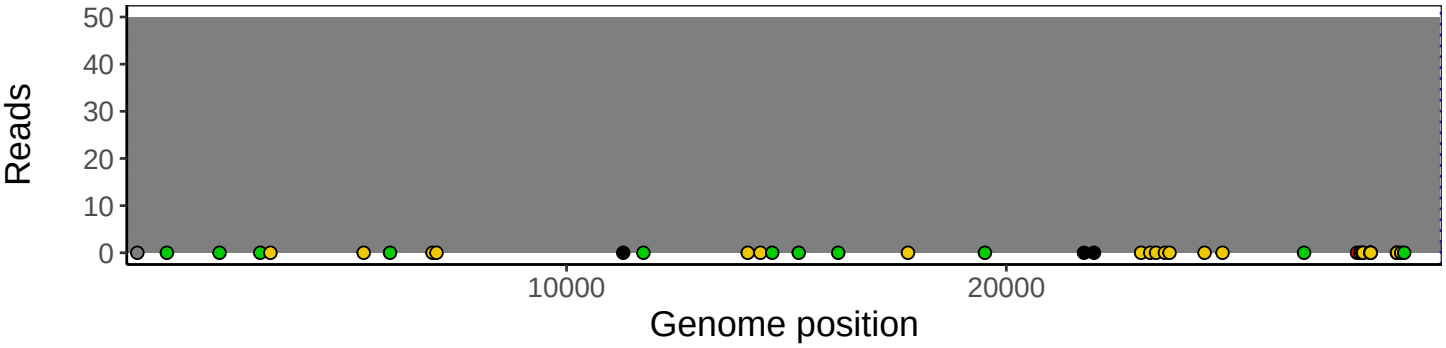
Analyses of individual experiments and composite results

VSP2600-1 | 2021-04-26 | Saline | UPHS-1345 | genomes | single experiment

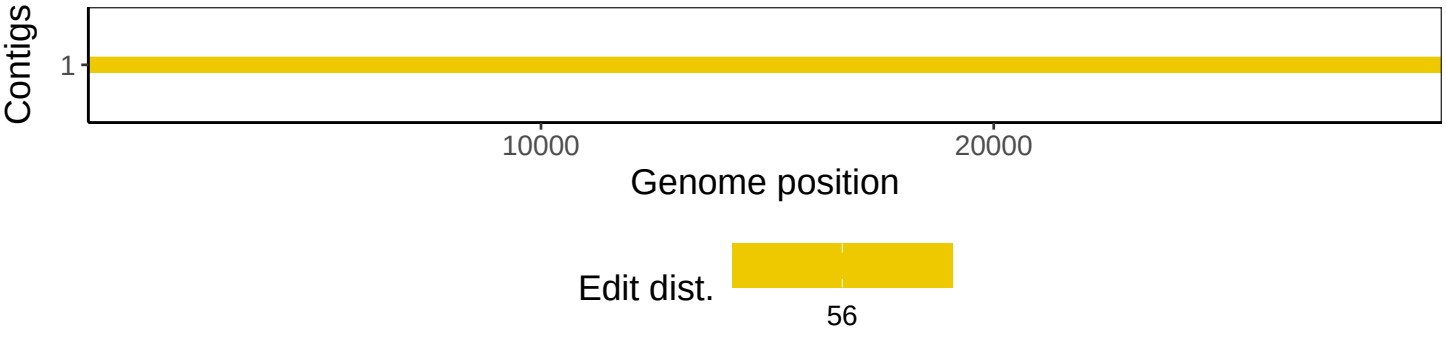
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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