COVID-19 subject UPHS-0995

2021-05-10

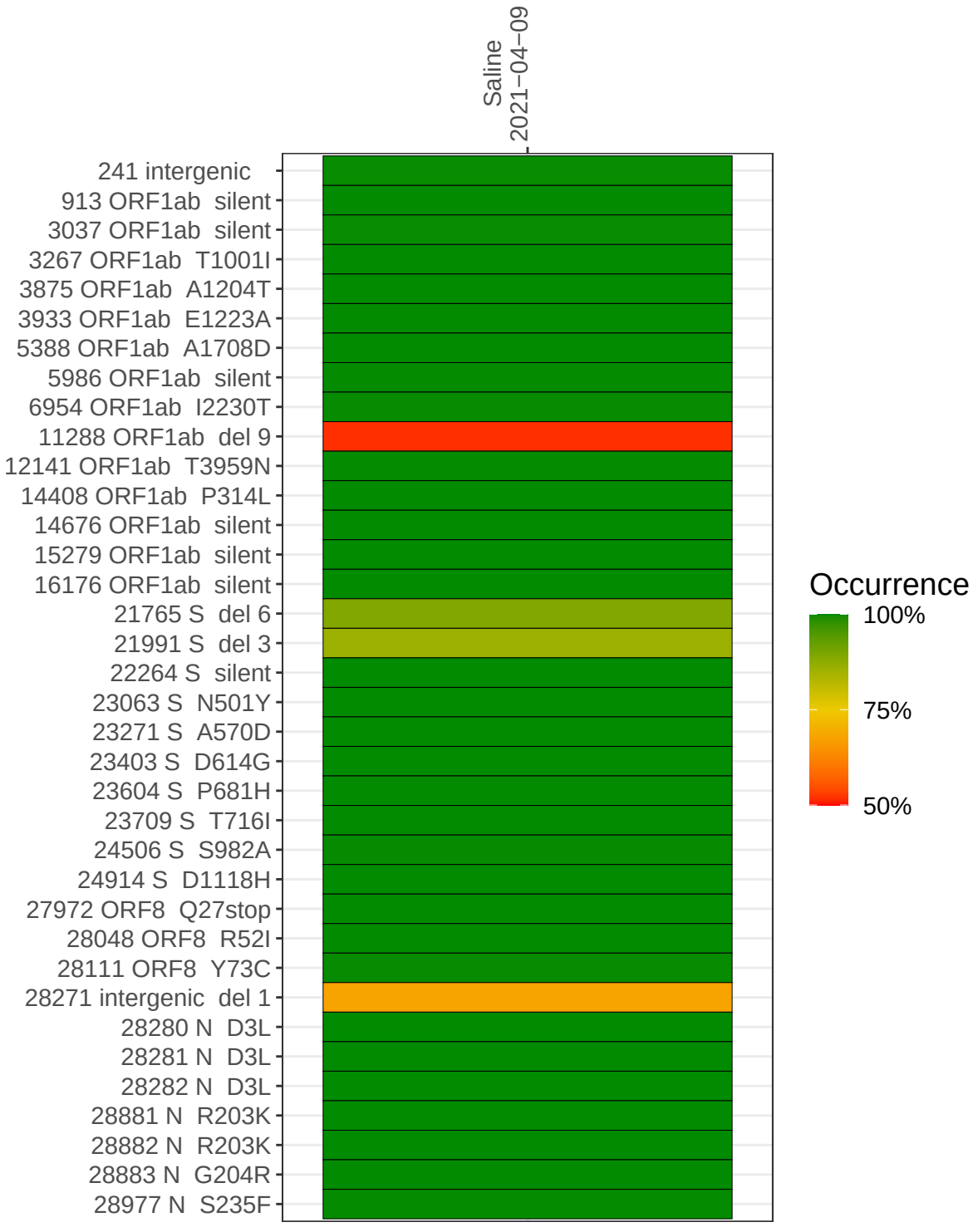
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

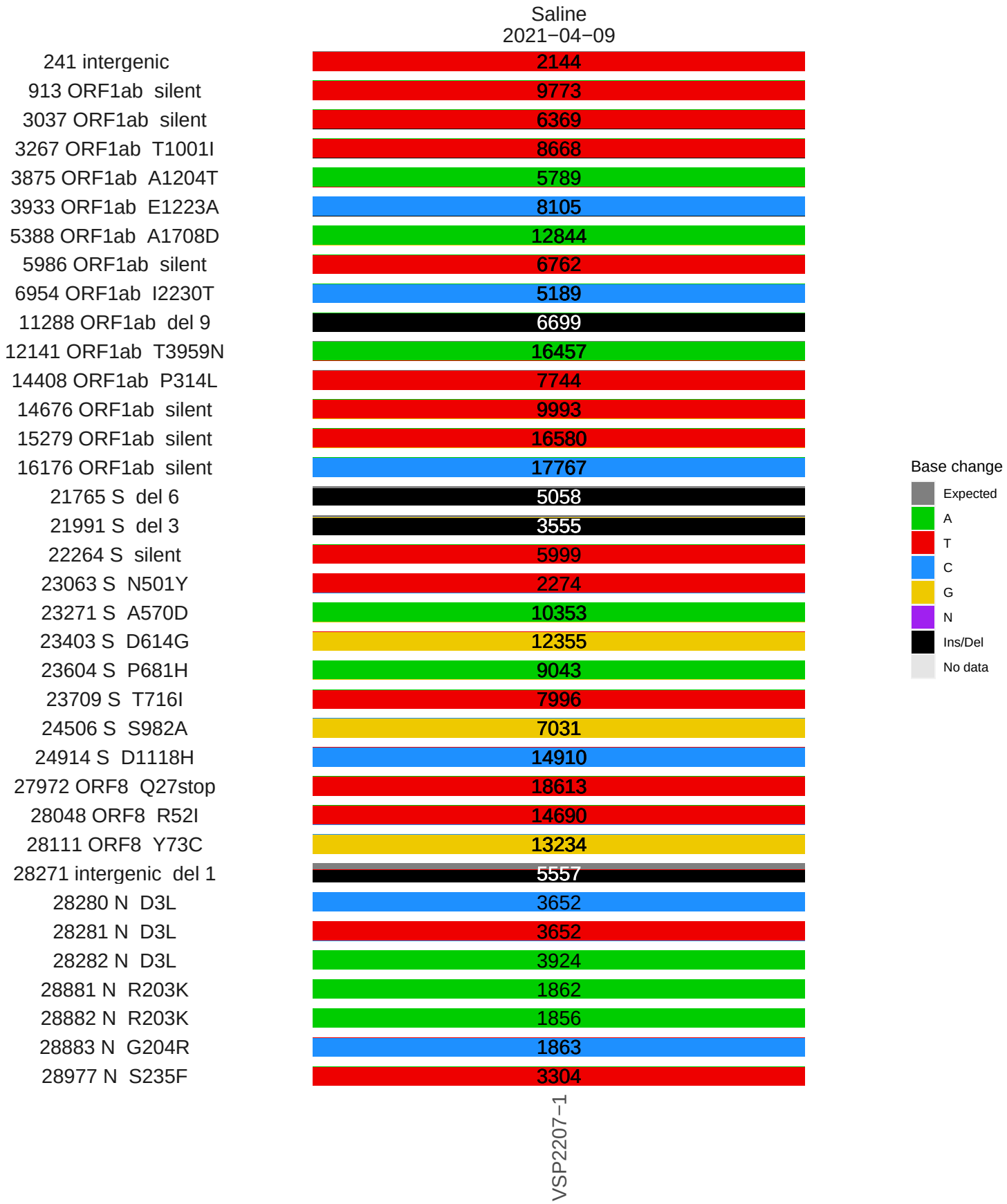
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2207-1	single experiment	NA	Saline	2021-04-09	29.80	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.

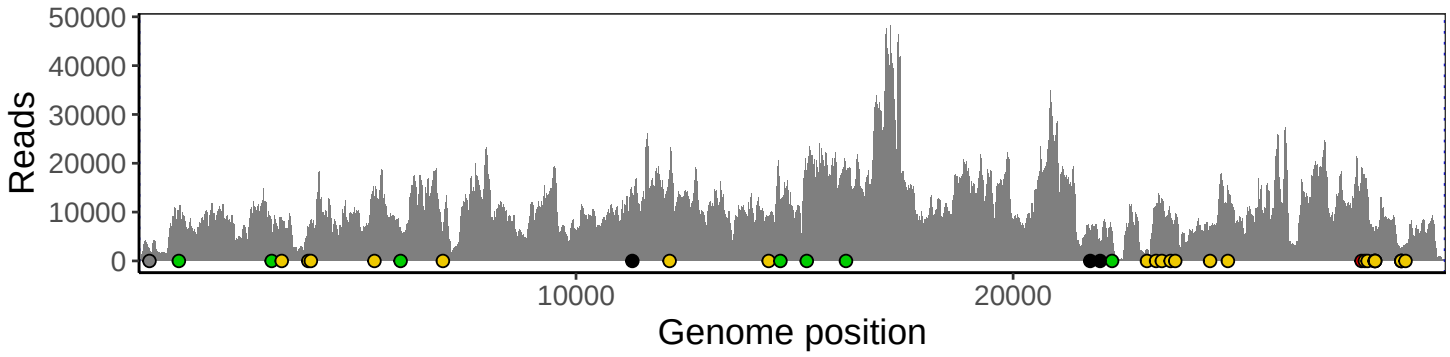



Saline
2021−04−09
241 intergenic 2144
913 ORF1ab silent 9773
3037 ORF1ab silent 6369
3267 ORF1ab T1001I 8668
3875 ORF1ab A1204T 5789
3933 ORF1ab E1223A 8105
5388 ORF1ab A1708D 12844
5986 ORF1ab silent 6762
6954 ORF1ab I2230T 5189
11288 ORF1ab del 9 6699
12141 ORF1ab T3959N 16457
14408 ORF1ab P314L 7744
14676 ORF1ab silent 9993
15279 ORF1ab silent 16580
16176 ORF1ab silent 17767
21765 S del 6 5058
21991 S del 3 3555
22264 S silent 5999
23063 S N501Y 2274
23271 S A570D 10353
23403 S D614G 12355
23604 S P681H 9043
23709 S T716I 7996
24506 S S982A 7031
24914 S D1118H 14910
27972 ORF8 Q27stop 18613
28048 ORF8 R52I 14690
28111 ORF8 Y73C 13234
28271 intergenic del 1 5557
28280 N D3L 3652
28281 N D3L 3652
28282 N D3L 3924
28881 N R203K 1862
28882 N R203K 1856
28883 N G204R 1863
28977 N S235F 3304
VSP2207−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

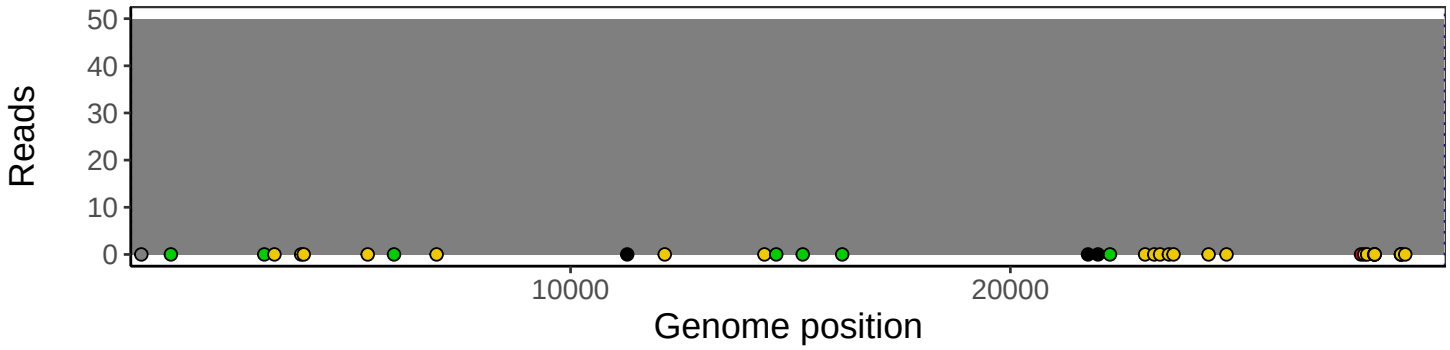
Analyses of individual experiments and composite results

VSP2207-1 | 2021-04-09 | Saline | UPHS-0995 | genomes | single experiment

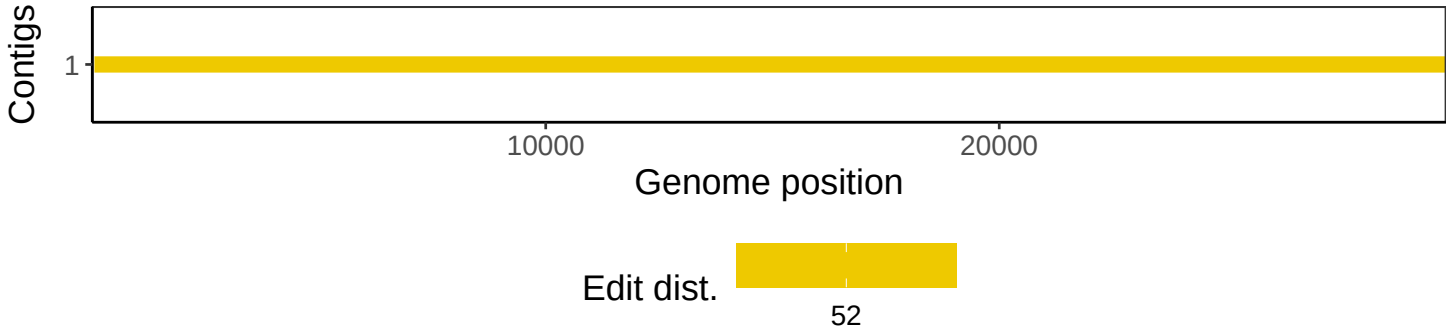
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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