COVID-19 subject UPHS-1119

2021-06-23

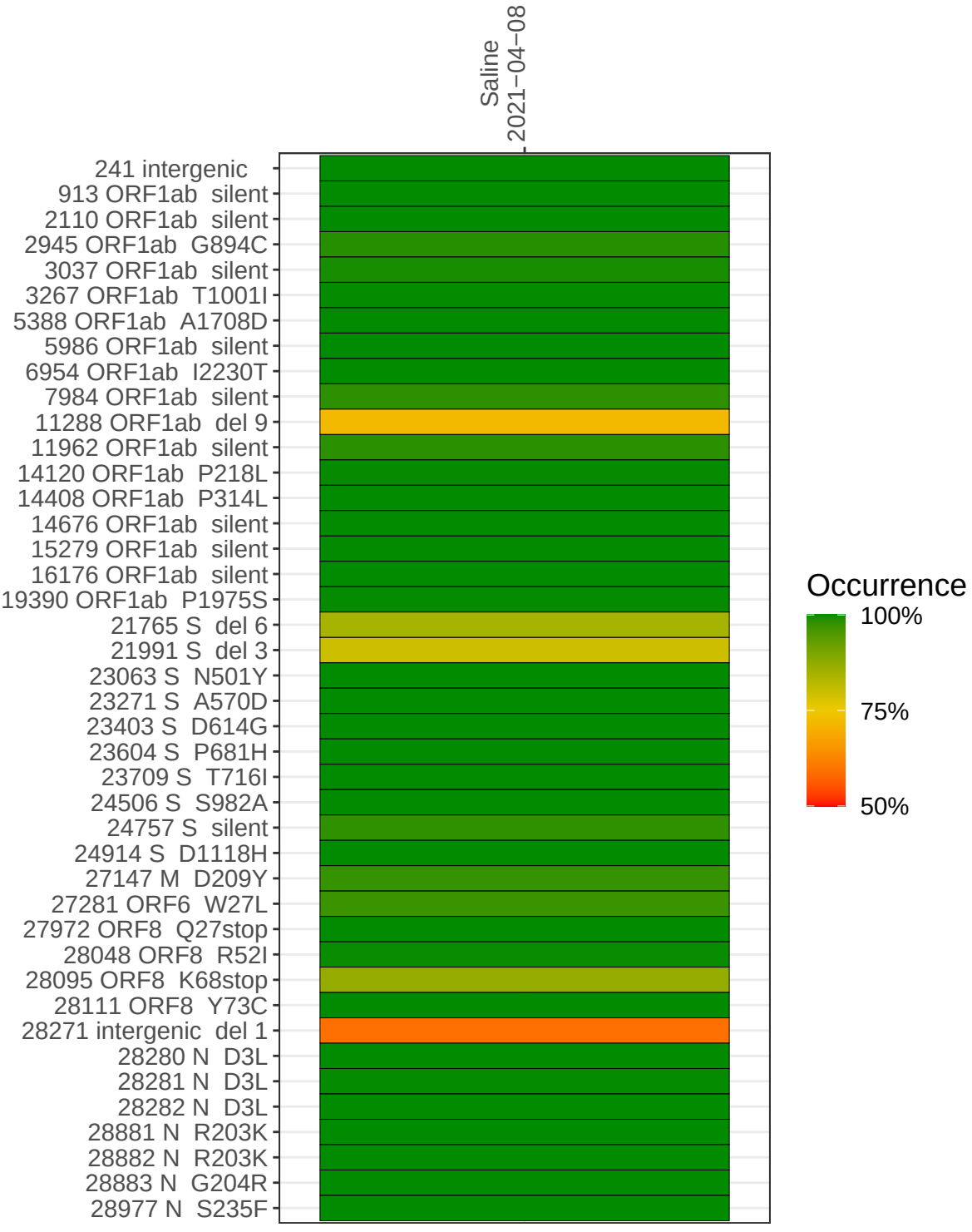
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

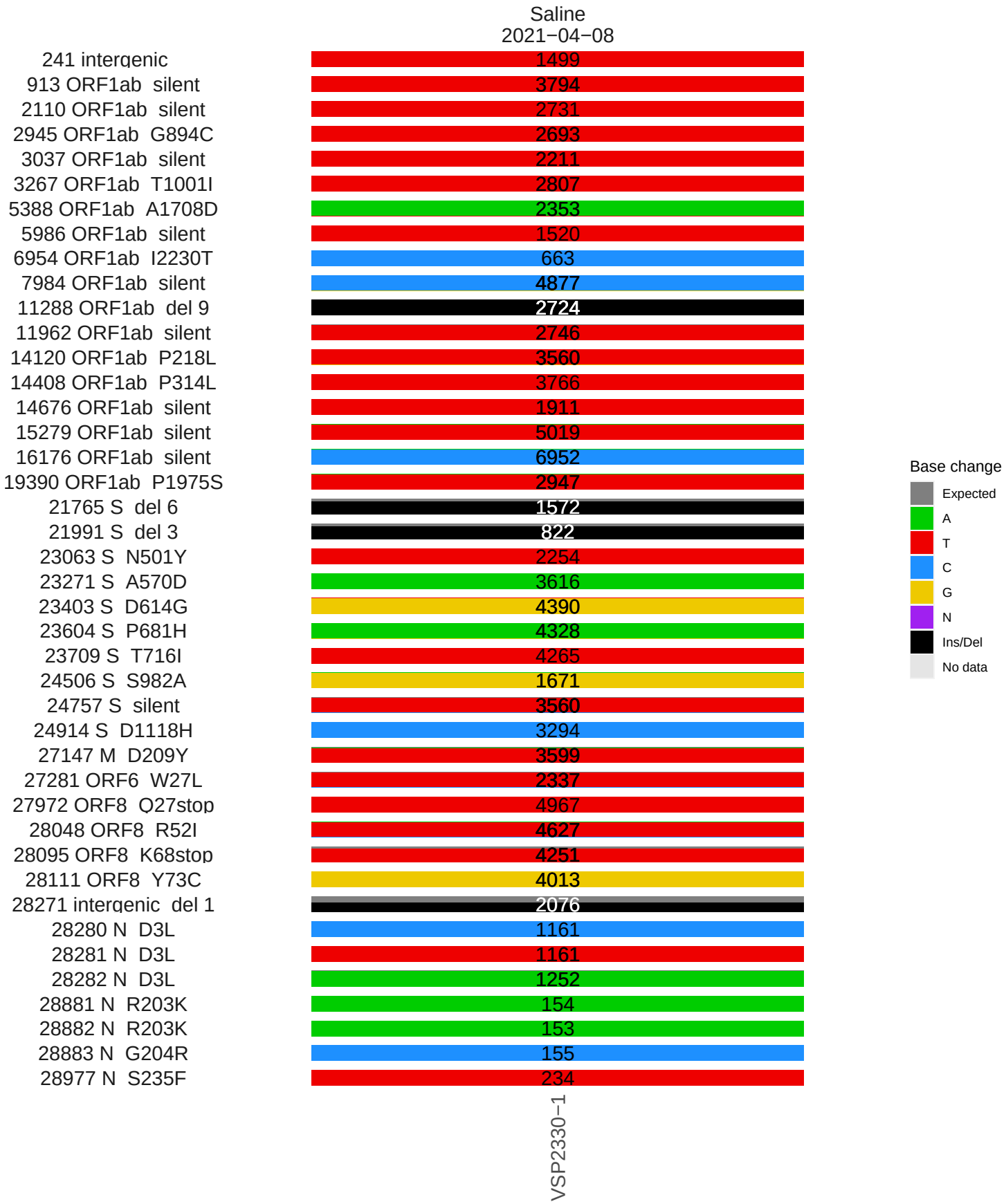
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2330-1	single experiment	NA	Saline	2021-04-08	29.83	B.1.1.7	99.7%	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.

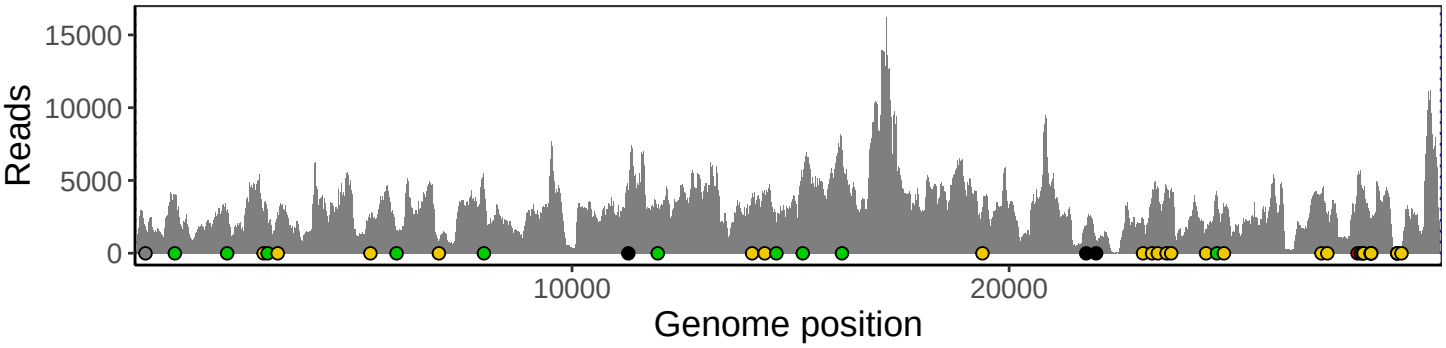



Saline
2021−04−08
241 intergenic 1499
913 ORF1ab silent 3794
2110 ORF1ab silent 2731
2945 ORF1ab G894C 2693
3037 ORF1ab silent 2211
3267 ORF1ab T1001I 2807
5388 ORF1ab A1708D 2353
5986 ORF1ab silent 1520
6954 ORF1ab I2230T 663
7984 ORF1ab silent 4877
11288 ORF1ab del 9 2724
11962 ORF1ab silent 2746
14120 ORF1ab P218L 3560
14408 ORF1ab P314L 3766
14676 ORF1ab silent 1911
15279 ORF1ab silent 5019
16176 ORF1ab silent 6952
19390 ORF1ab P1975S 2947
21765 S del 6 1572
21991 S del 3 822
23063 S N501Y 2254
23271 S A570D 3616
23403 S D614G 4390
23604 S P681H 4328
23709 S T716I 4265
24506 S S982A 1671
24757 S silent 3560
24914 S D1118H 3294
27147 M D209Y 3599
27281 ORF6 W27L 2337
27972 ORF8 Q27stop 4967
28048 ORF8 R52I 4627
28095 ORF8 K68stop 4251
28111 ORF8 Y73C 4013
28271 intergenic del 1 2076
28280 N D3L 1161
28281 N D3L 1161
28282 N D3L 1252
28881 N R203K 154
28882 N R203K 153
28883 N G204R 155
28977 N S235F 234
VSP2330−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

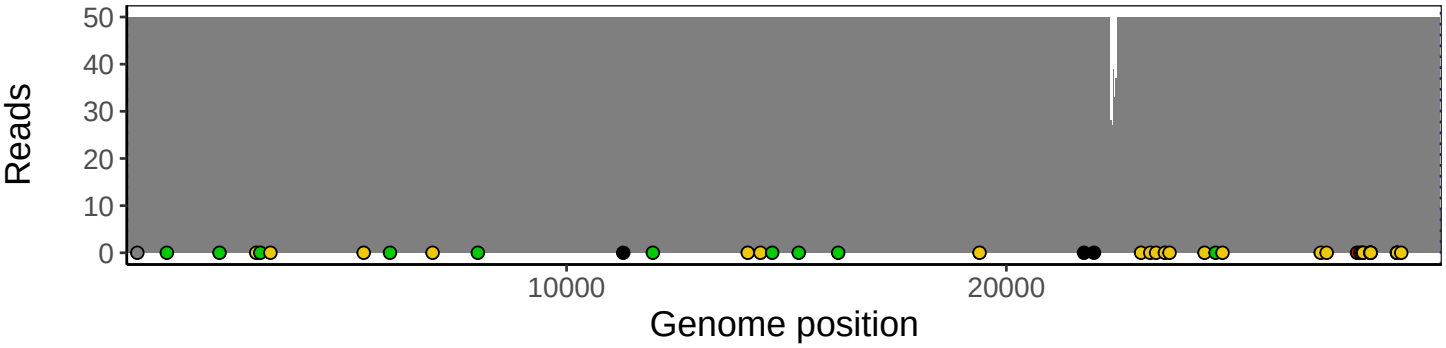
Analyses of individual experiments and composite results

VSP2330-1 | 2021-04-08 | Saline | UPHS-1119 | genomes | single experiment

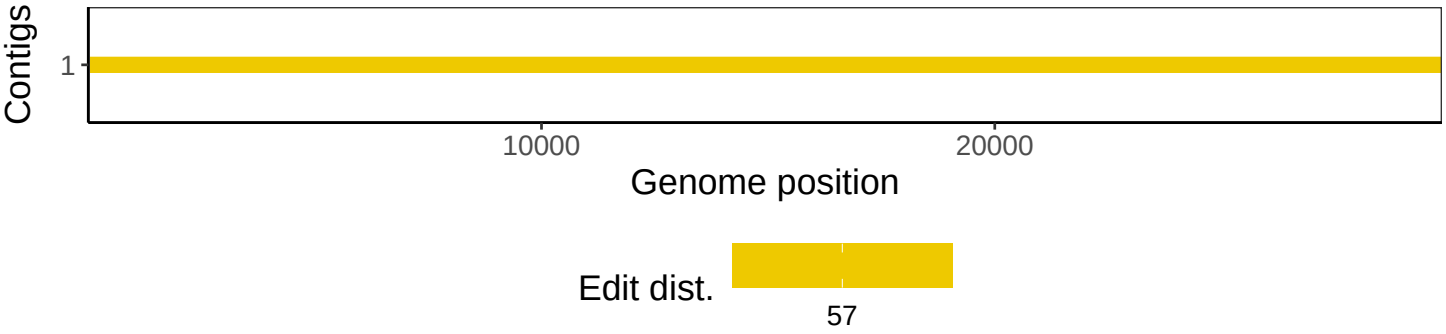
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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