COVID-19 subject UPHS-0335

2021-05-05

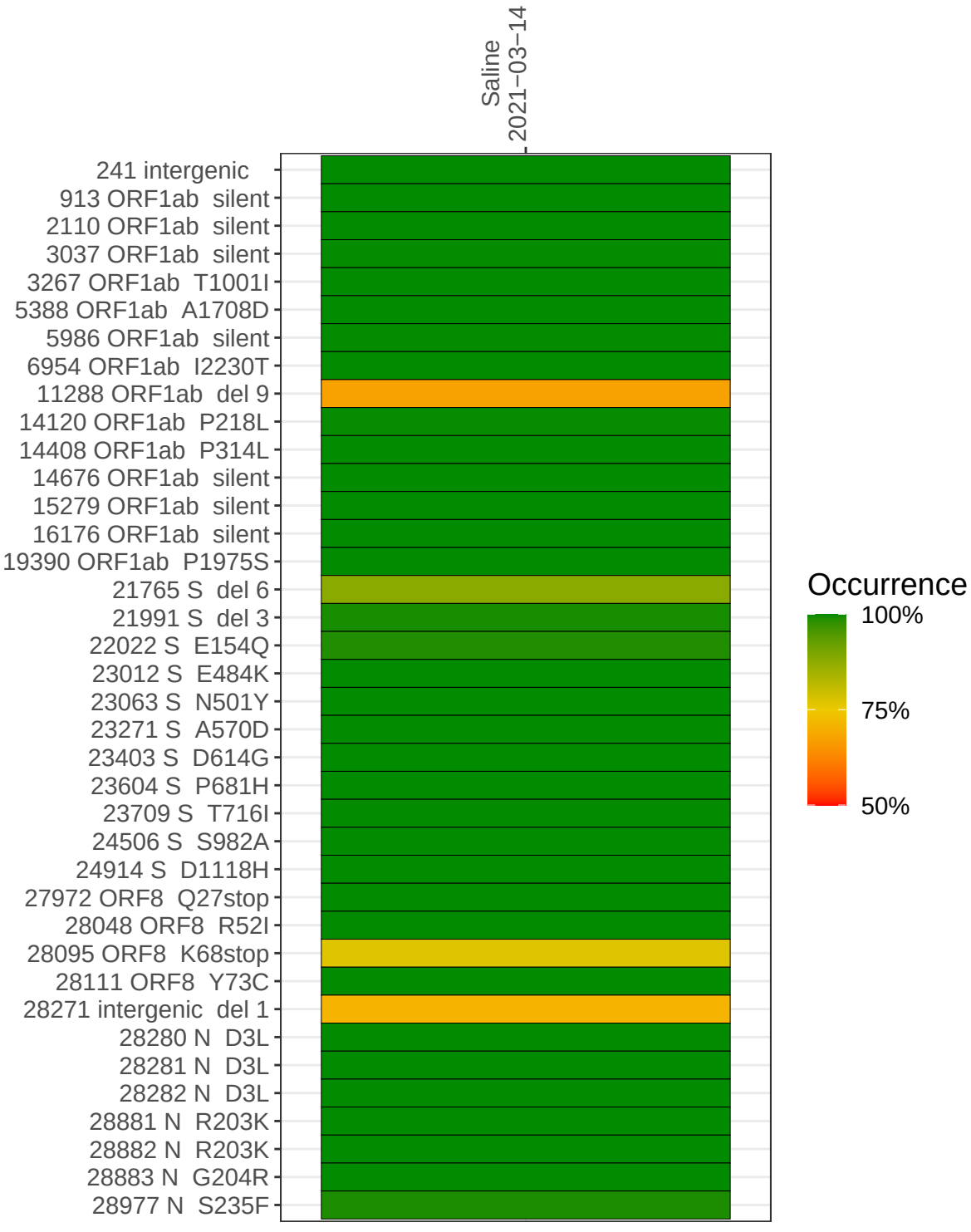
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

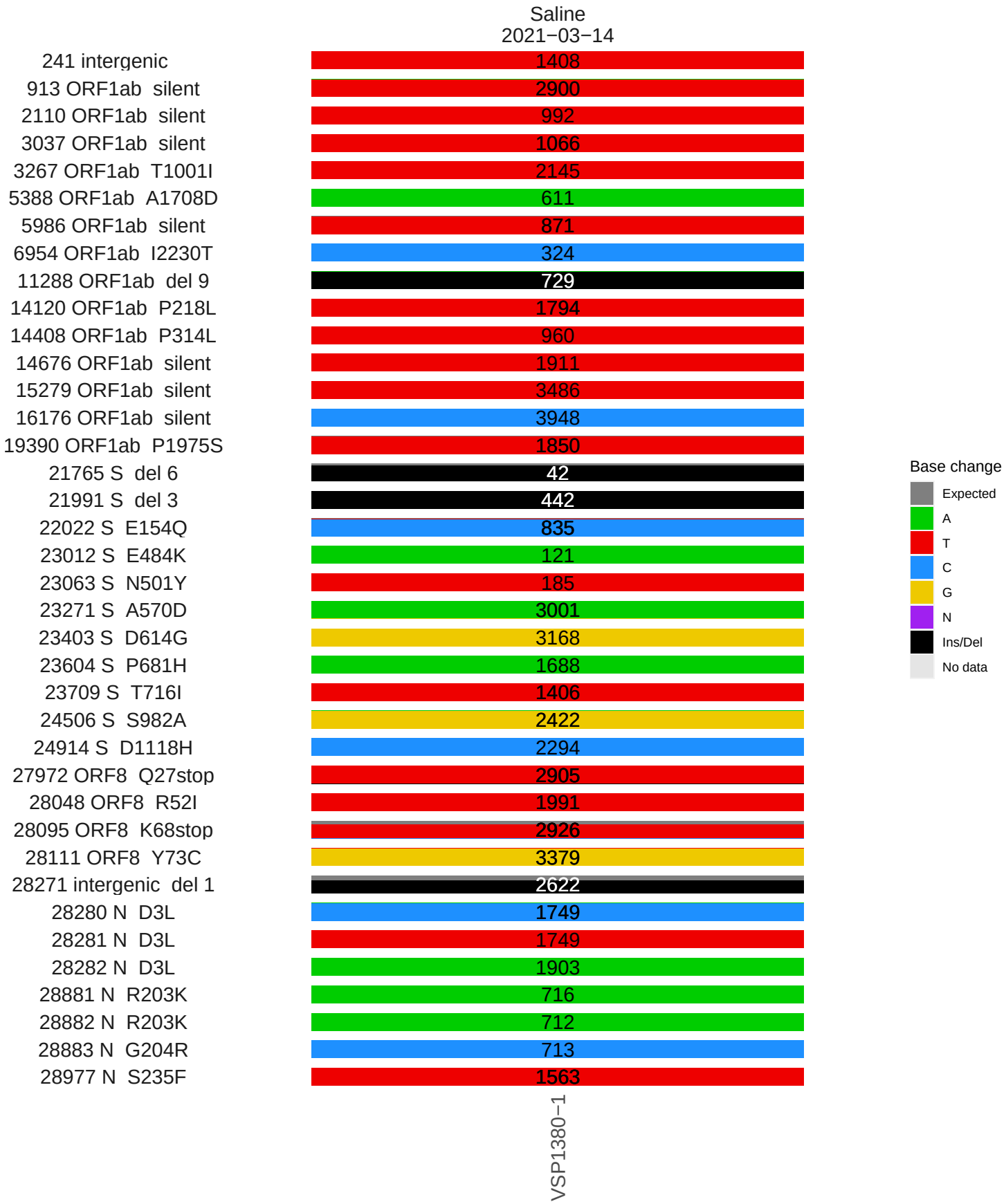
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1380-1	single experiment	NA	Saline	2021-03-14	29.80	B.1.1.7	99.8%	99.8%

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.

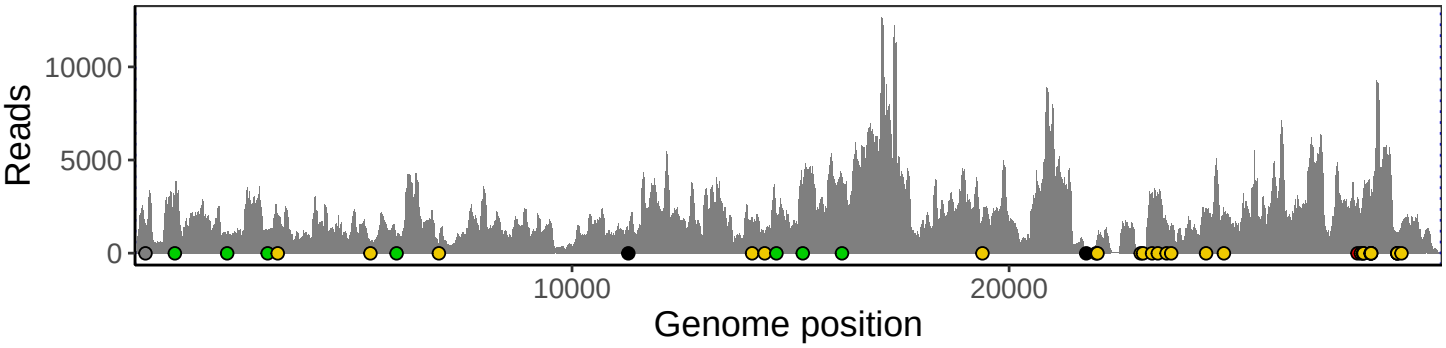



Saline
2021−03−14
241 intergenic 1408
913 ORF1ab silent 2900
2110 ORF1ab silent 992
3037 ORF1ab silent 1066
3267 ORF1ab T1001I 2145
5388 ORF1ab A1708D 611
5986 ORF1ab silent 871
6954 ORF1ab I2230T 324
11288 ORF1ab del 9 729
14120 ORF1ab P218L 1794
14408 ORF1ab P314L 960
14676 ORF1ab silent 1911
15279 ORF1ab silent 3486
16176 ORF1ab silent 3948
19390 ORF1ab P1975S 1850
21765 S del 6 42
21991 S del 3 442
22022 S E154Q 835
23012 S E484K 121
23063 S N501Y 185
23271 S A570D 3001
23403 S D614G 3168
23604 S P681H 1688
23709 S T716I 1406
24506 S S982A 2422
24914 S D1118H 2294
27972 ORF8 Q27stop 2905
28048 ORF8 R52I 1991
28095 ORF8 K68stop 2926
28111 ORF8 Y73C 3379
28271 intergenic del 1 2622
28280 N D3L 1749
28281 N D3L 1749
28282 N D3L 1903
28881 N R203K 716
28882 N R203K 712
28883 N G204R 713
28977 N S235F 1563
VSP1380−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

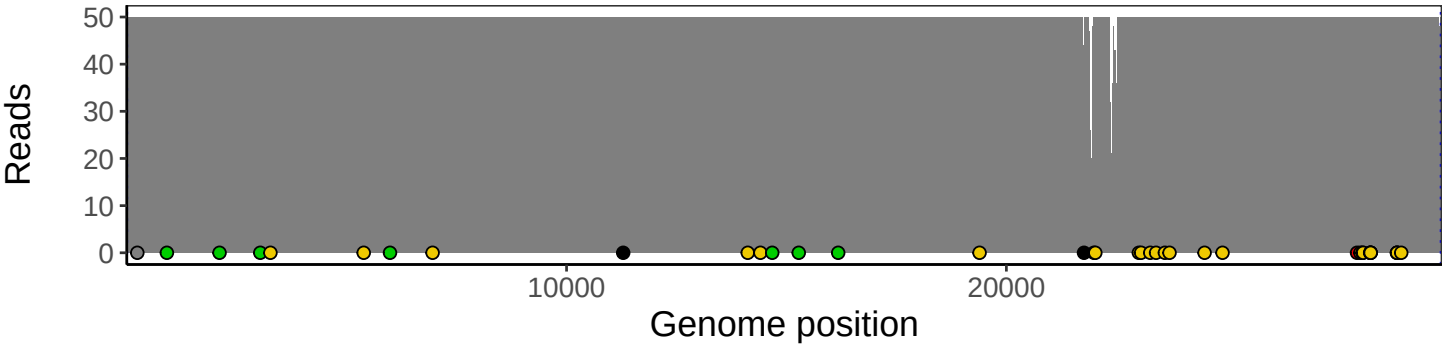
Analyses of individual experiments and composite results

VSP1380-1 | 2021-03-14 | Saline | UPHS-0335 | genomes | single experiment

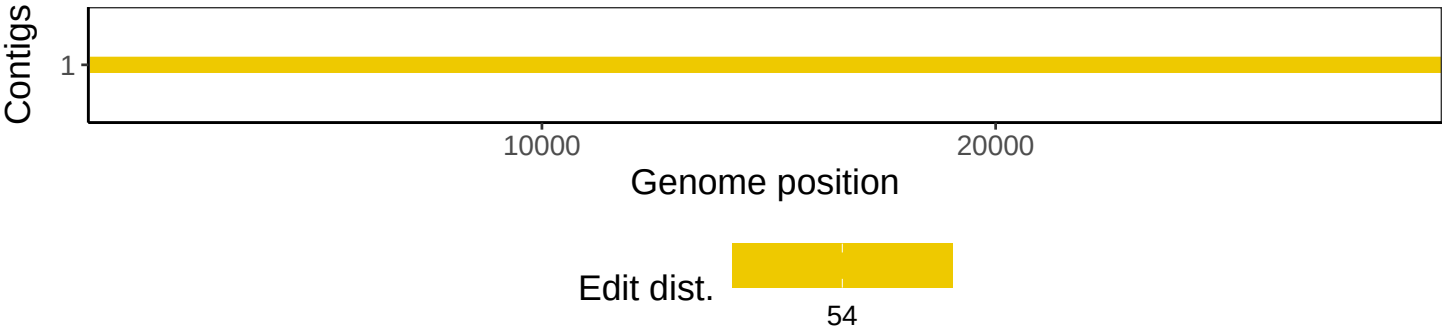
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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