COVID-19 subject HUP Q-0168

2021-05-05

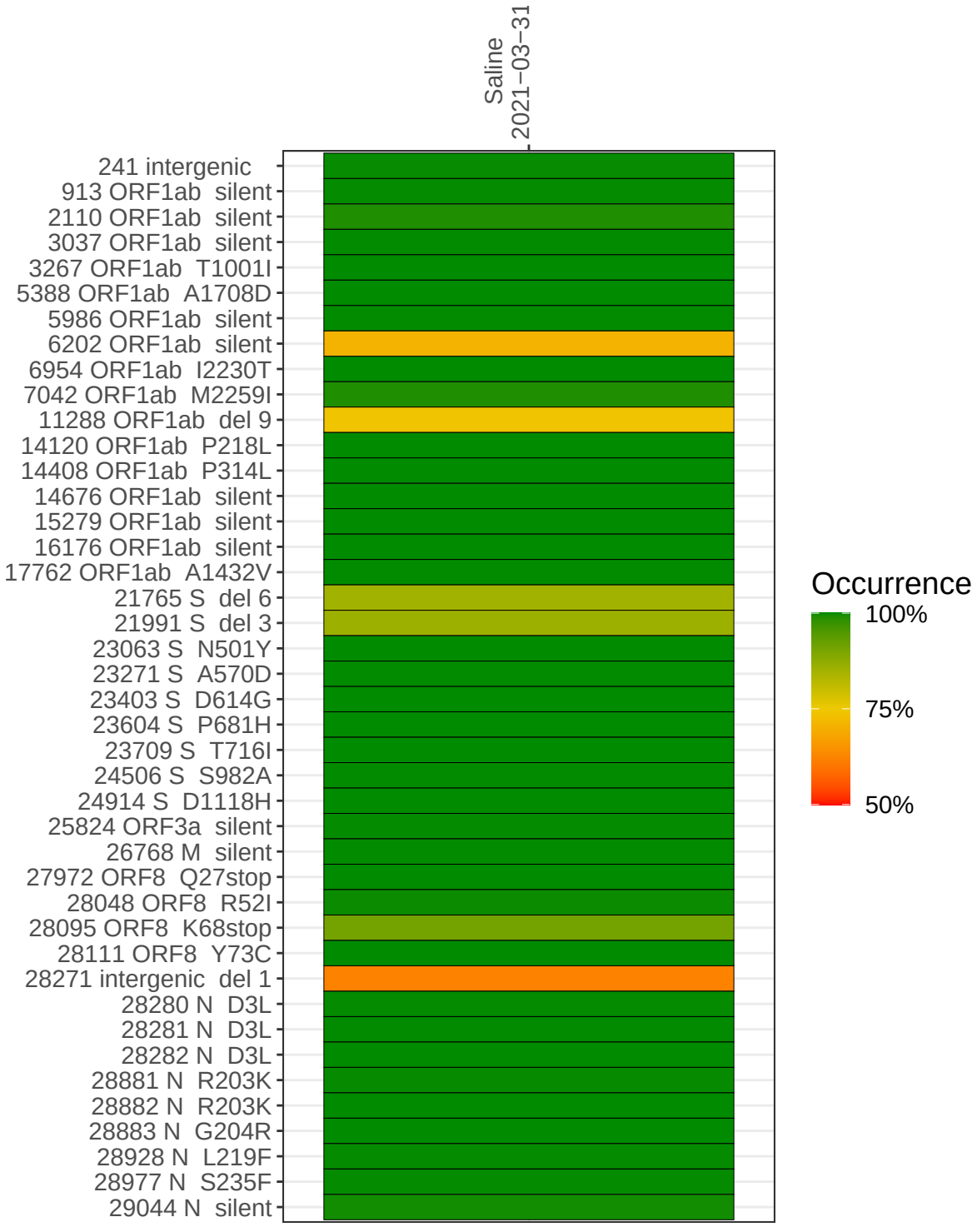
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

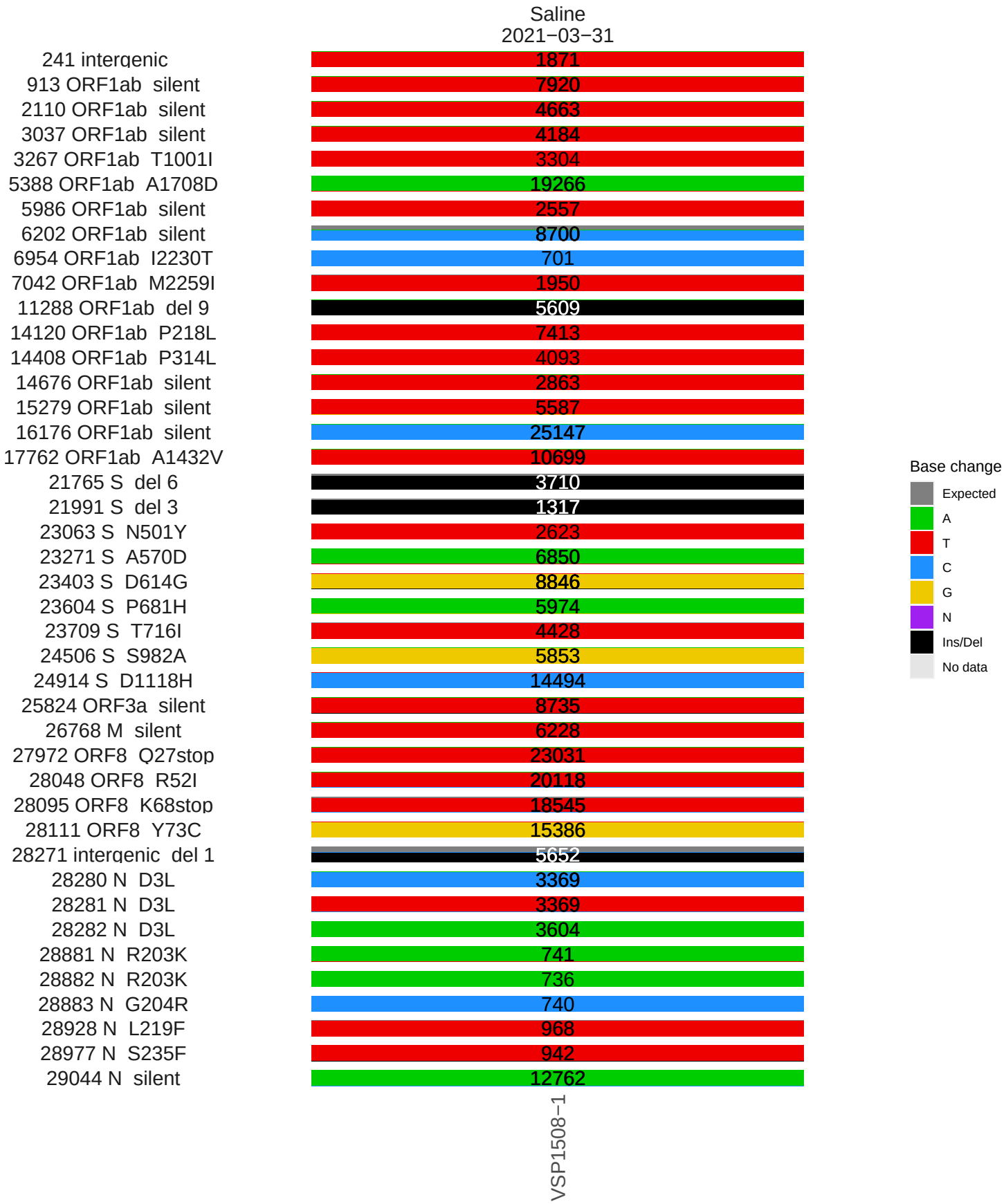
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1508-1	single experiment	NA	Saline	2021-03-31	29.81	B.1.1.7	99.9%	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.

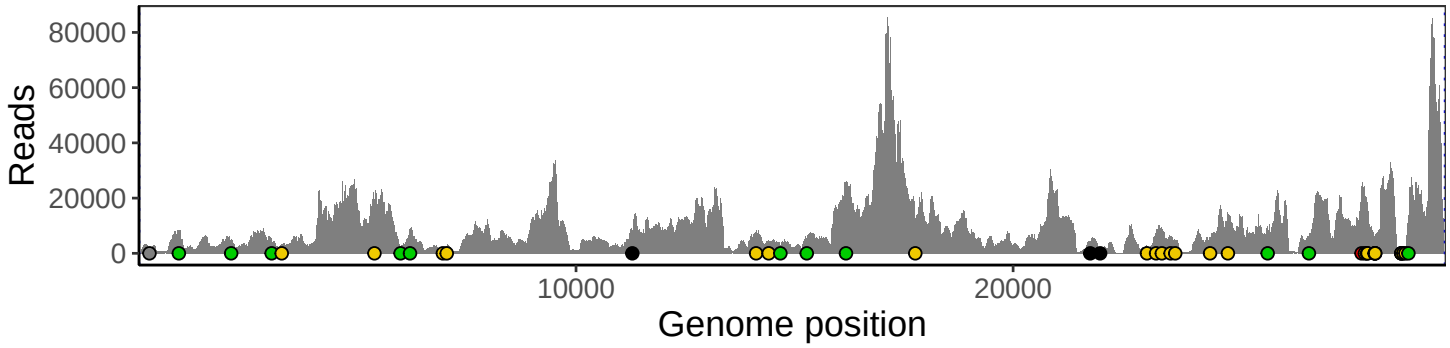



Saline
2021−03−31
241 intergenic 1871
913 ORF1ab silent 7920
2110 ORF1ab silent 4663
3037 ORF1ab silent 4184
3267 ORF1ab T1001I 3304
5388 ORF1ab A1708D 19266
5986 ORF1ab silent 2557
6202 ORF1ab silent 8700
6954 ORF1ab I2230T 701
7042 ORF1ab M2259I 1950
11288 ORF1ab del 9 5609
14120 ORF1ab P218L 7413
14408 ORF1ab P314L 4093
14676 ORF1ab silent 2863
15279 ORF1ab silent 5587
16176 ORF1ab silent 25147
17762 ORF1ab A1432V 10699
21765 S del 6 3710
21991 S del 3 1317
23063 S N501Y 2623
23271 S A570D 6850
23403 S D614G 8846
23604 S P681H 5974
23709 S T716I 4428
24506 S S982A 5853
24914 S D1118H 14494
25824 ORF3a silent 8735
26768 M silent 6228
27972 ORF8 Q27stop 23031
28048 ORF8 R52I 20118
28095 ORF8 K68stop 18545
28111 ORF8 Y73C 15386
28271 intergenic del 1 5652
28280 N D3L 3369
28281 N D3L 3369
28282 N D3L 3604
28881 N R203K 741
28882 N R203K 736
28883 N G204R 740
28928 N L219F 968
28977 N S235F 942
29044 N silent 12762
VSP1508−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

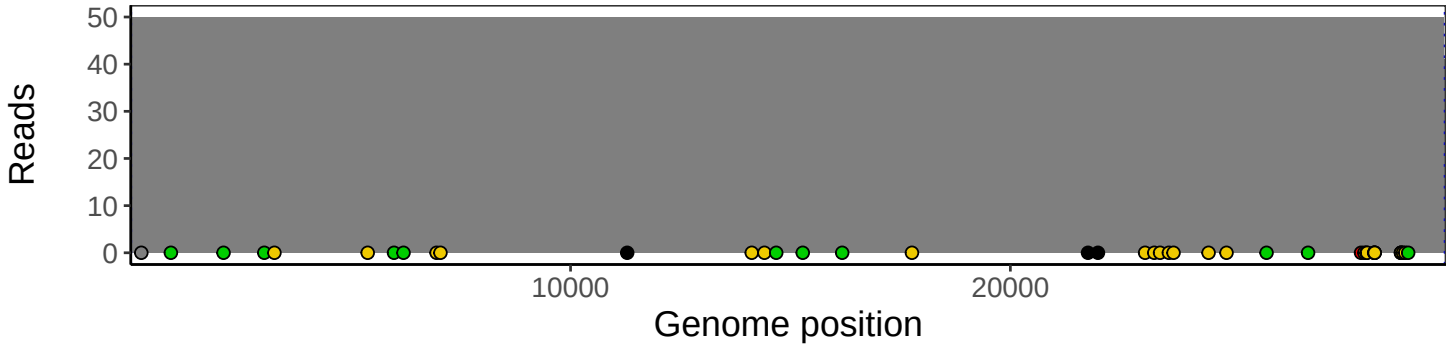
Analyses of individual experiments and composite results

VSP1508-1 | 2021-03-31 | Saline | HUP Q-0168 | genomes | single experiment

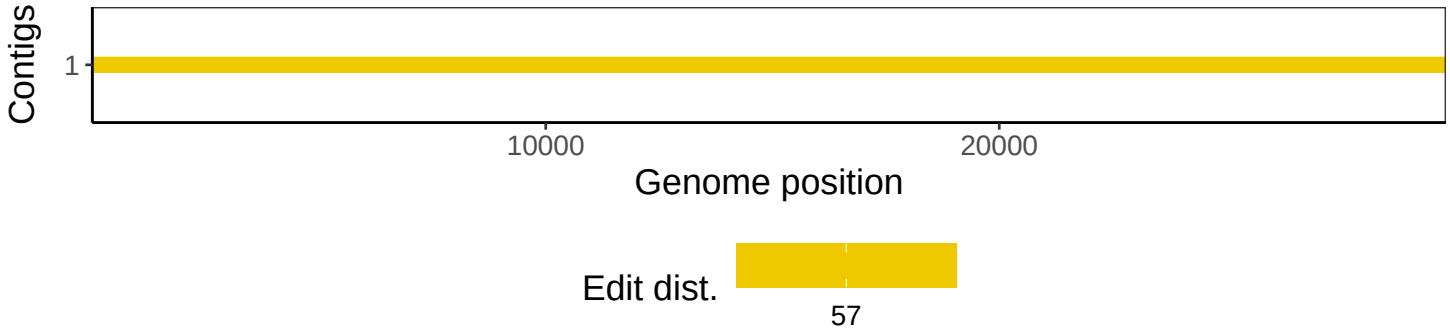
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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