COVID-19 subject HUP Q-0132

2021-06-23

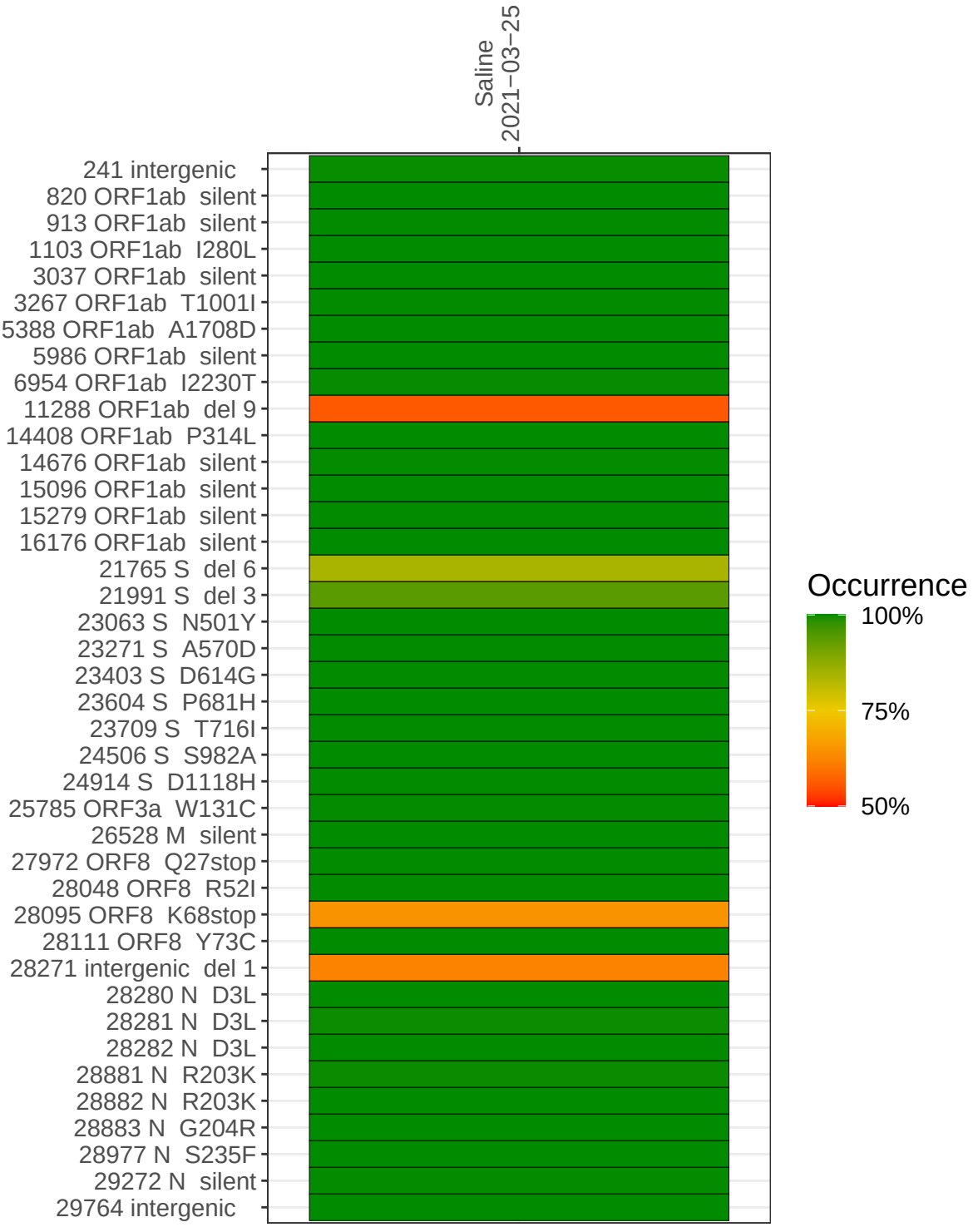
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

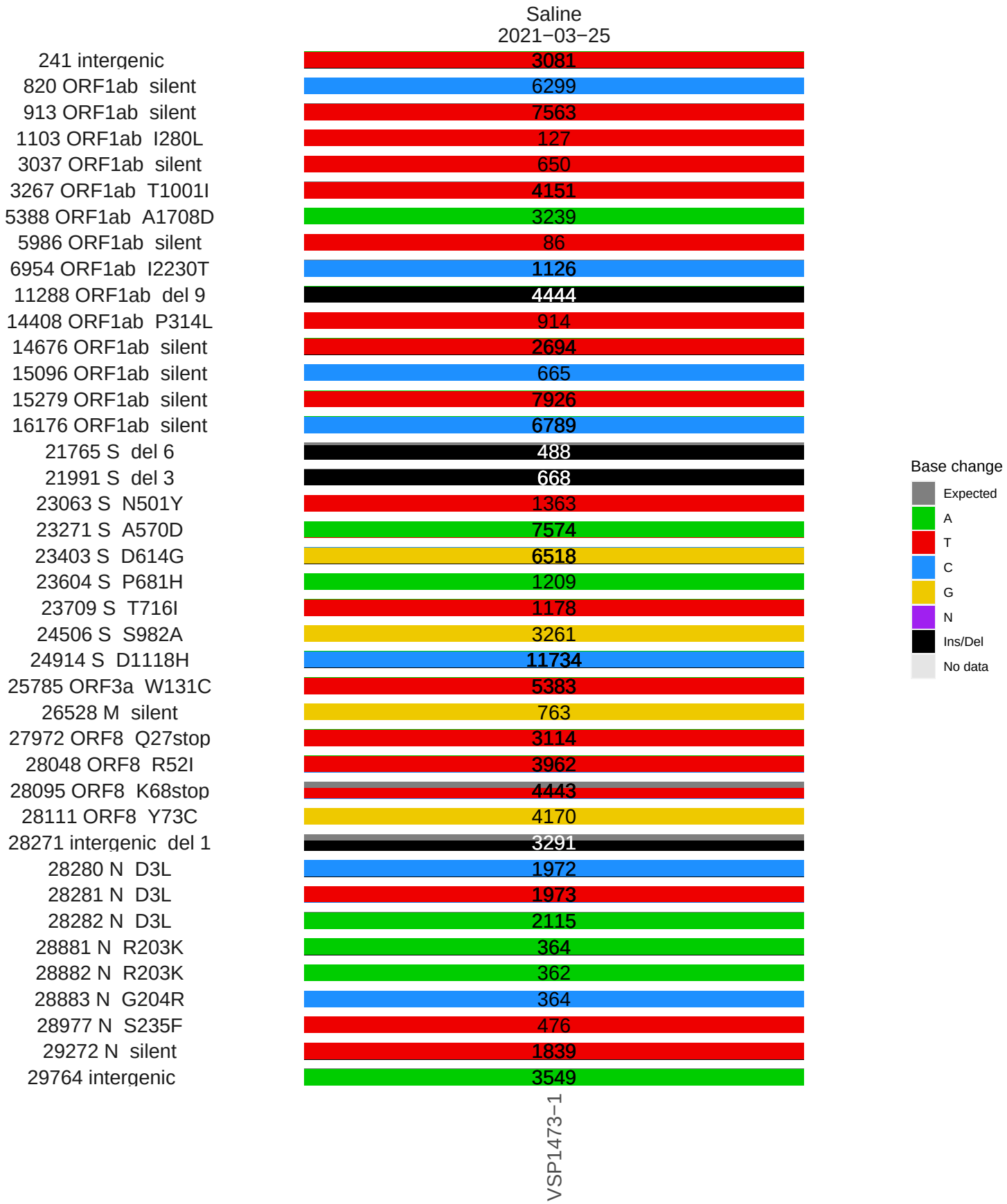
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1473-1	single experiment	NA	Saline	2021-03-25	22.29	B.1.1.7	99.6%	99.1%

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.

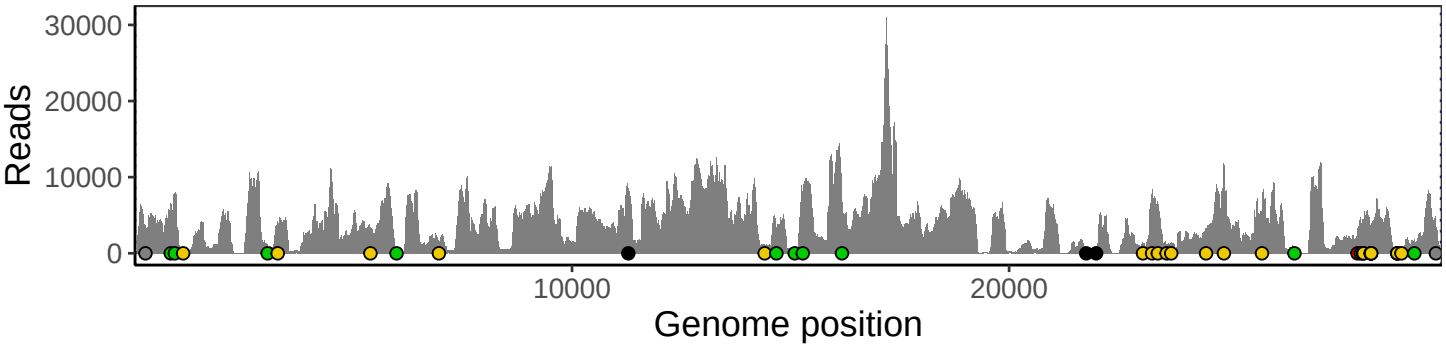



Saline
2021−03−25
241 intergenic 3081
820 ORF1ab silent 6299
913 ORF1ab silent 7563
1103 ORF1ab I280L 127
3037 ORF1ab silent 650
3267 ORF1ab T1001I 4151
5388 ORF1ab A1708D 3239
5986 ORF1ab silent 86
6954 ORF1ab I2230T 1126
11288 ORF1ab del 9 4444
14408 ORF1ab P314L 914
14676 ORF1ab silent 2694
15096 ORF1ab silent 665
15279 ORF1ab silent 7926
16176 ORF1ab silent 6789
21765 S del 6 488
21991 S del 3 668
23063 S N501Y 1363
23271 S A570D 7574
23403 S D614G 6518
23604 S P681H 1209
23709 S T716I 1178
24506 S S982A 3261
24914 S D1118H 11734
25785 ORF3a W131C 5383
26528 M silent 763
27972 ORF8 Q27stop 3114
28048 ORF8 R52I 3962
28095 ORF8 K68stop 4443
28111 ORF8 Y73C 4170
28271 intergenic del 1 3291
28280 N D3L 1972
28281 N D3L 1973
28282 N D3L 2115
28881 N R203K 364
28882 N R203K 362
28883 N G204R 364
28977 N S235F 476
29272 N silent 1839
29764 intergenic 3549
VSP1473−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

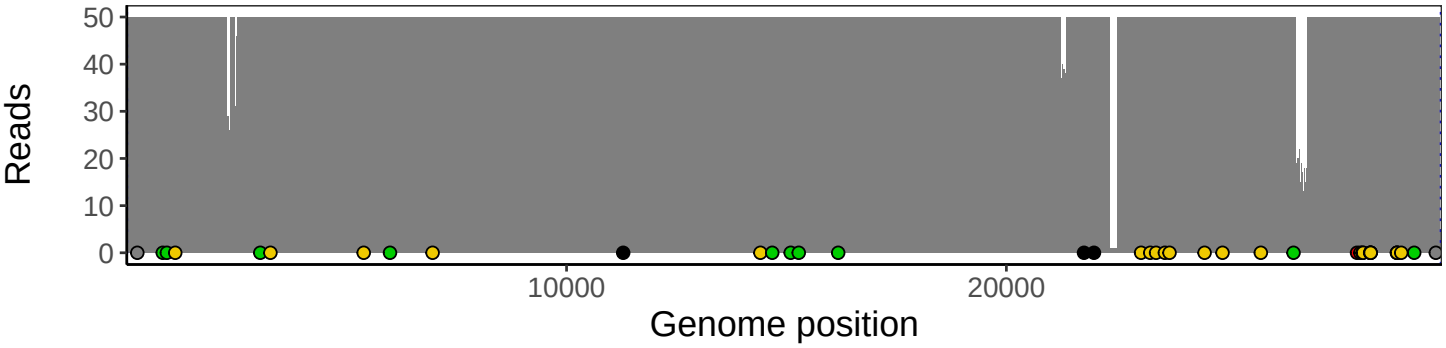
Analyses of individual experiments and composite results

VSP1473-1 | 2021-03-25 | Saline | HUP Q-0132 | genomes | single experiment

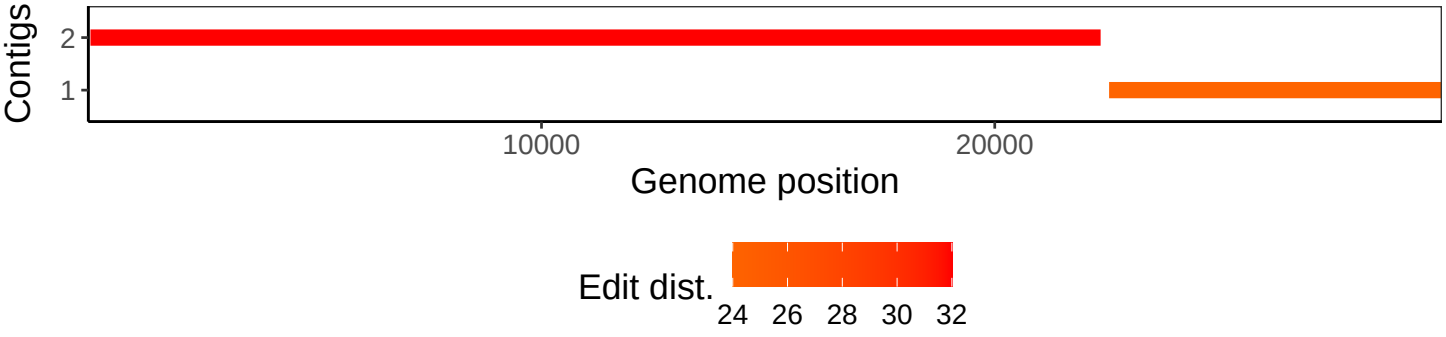
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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