COVID-19 subject HUP Q-0166

2021-05-05

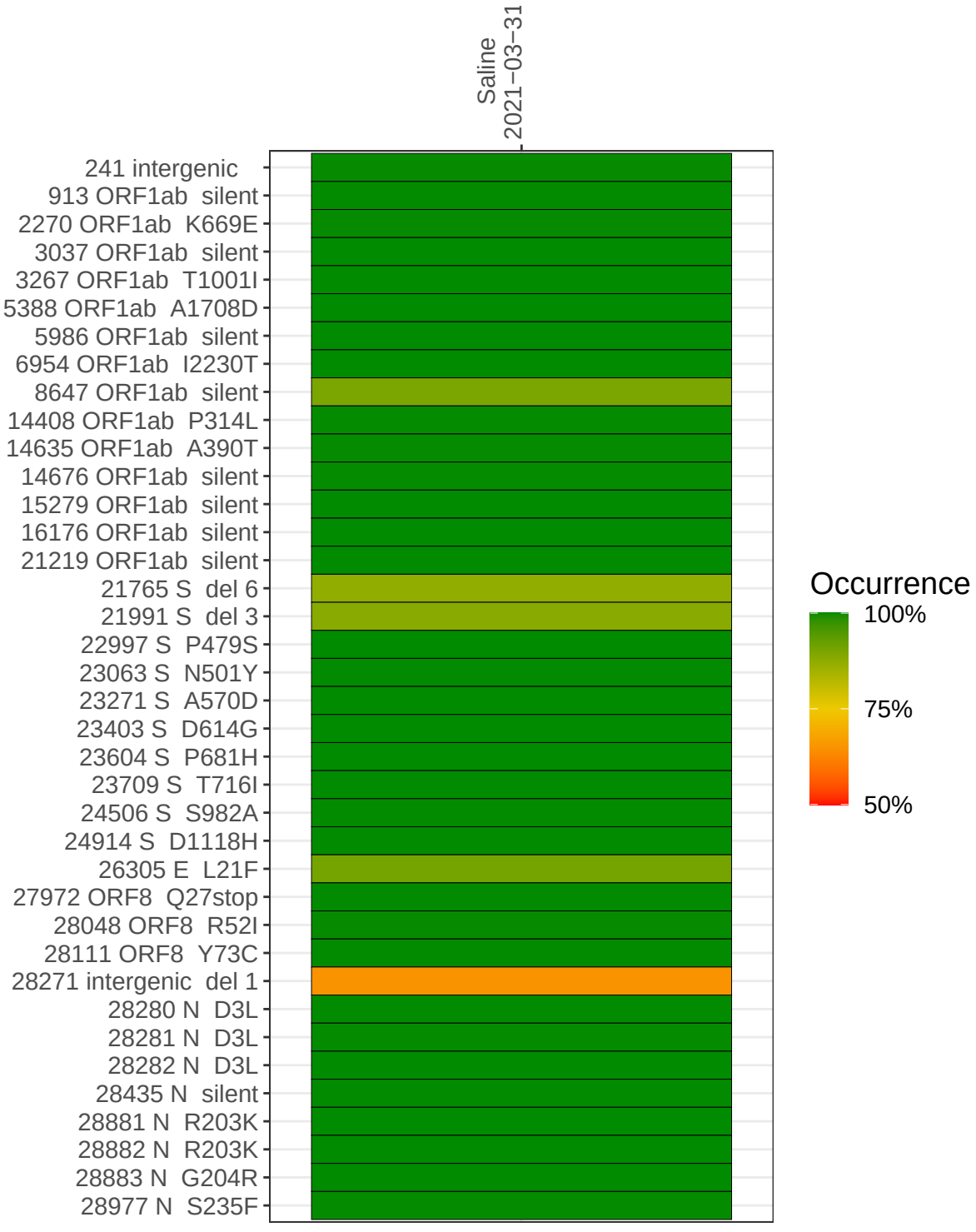
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

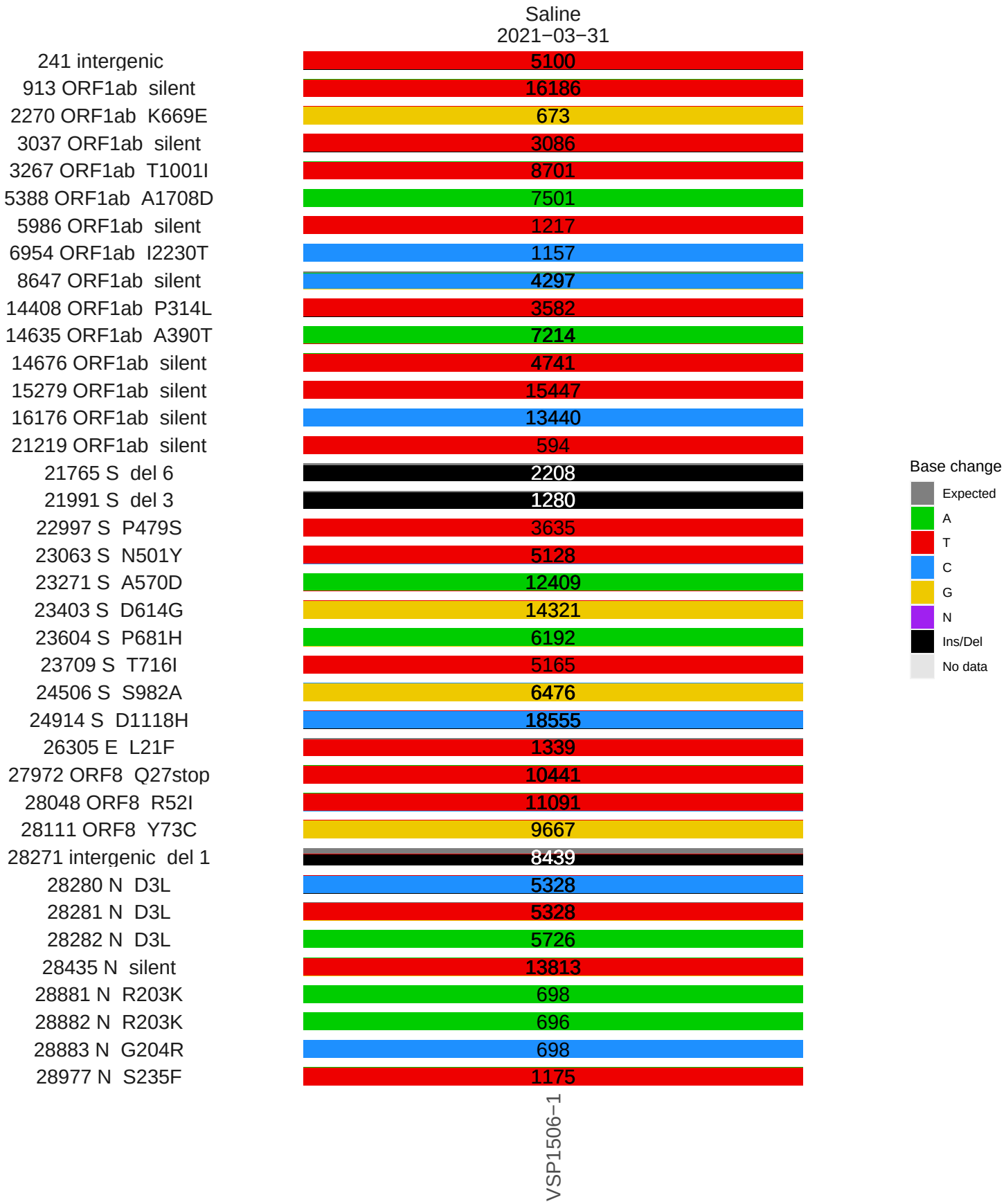
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1506-1	single experiment	NA	Saline	2021-03-31	29.82	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.

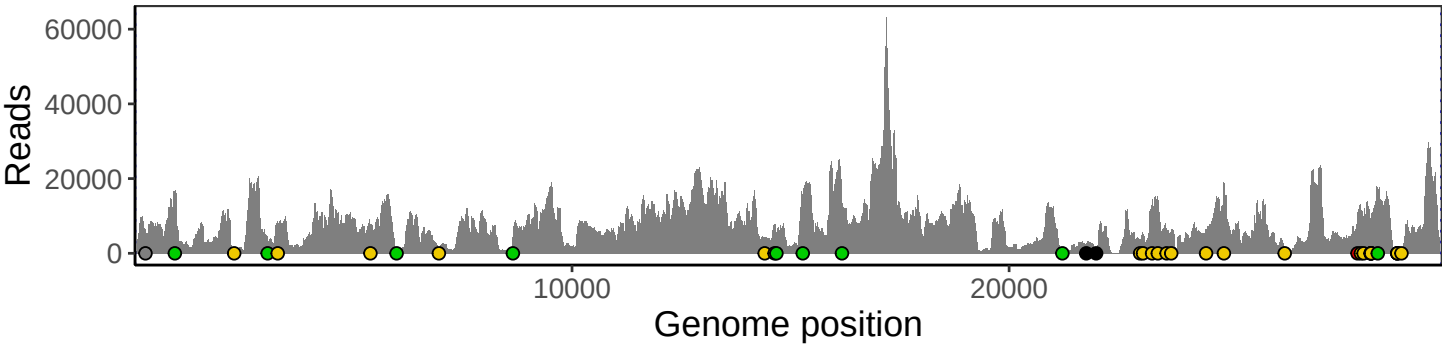



Saline
2021−03−31
241 intergenic 5100
913 ORF1ab silent 16186
2270 ORF1ab K669E 673
3037 ORF1ab silent 3086
3267 ORF1ab T1001I 8701
5388 ORF1ab A1708D 7501
5986 ORF1ab silent 1217
6954 ORF1ab I2230T 1157
8647 ORF1ab silent 4297
14408 ORF1ab P314L 3582
14635 ORF1ab A390T 7214
14676 ORF1ab silent 4741
15279 ORF1ab silent 15447
16176 ORF1ab silent 13440
21219 ORF1ab silent 594
21765 S del 6 2208
21991 S del 3 1280
22997 S P479S 3635
23063 S N501Y 5128
23271 S A570D 12409
23403 S D614G 14321
23604 S P681H 6192
23709 S T716I 5165
24506 S S982A 6476
24914 S D1118H 18555
26305 E L21F 1339
27972 ORF8 Q27stop 10441
28048 ORF8 R52I 11091
28111 ORF8 Y73C 9667
28271 intergenic del 1 8439
28280 N D3L 5328
28281 N D3L 5328
28282 N D3L 5726
28435 N silent 13813
28881 N R203K 698
28882 N R203K 696
28883 N G204R 698
28977 N S235F 1175
VSP1506−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

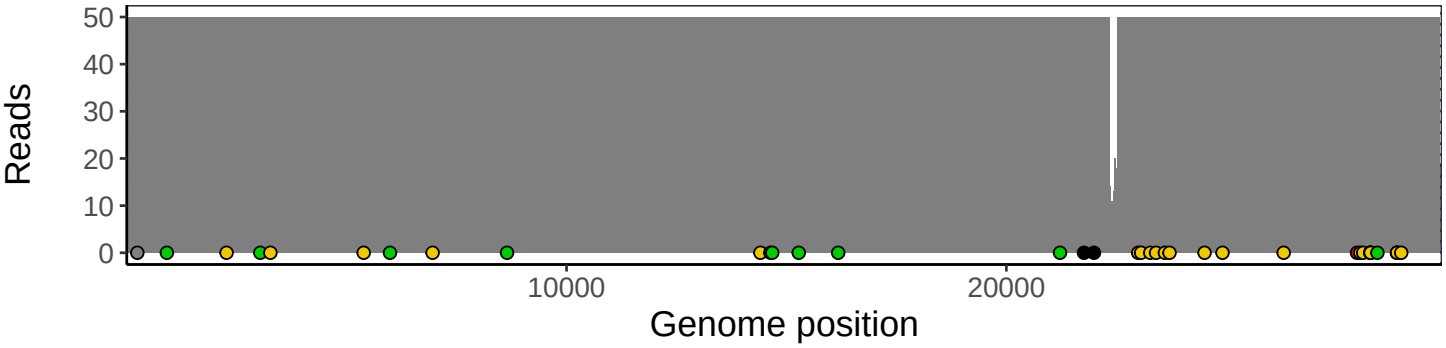
Analyses of individual experiments and composite results

VSP1506-1 | 2021-03-31 | Saline | HUP Q-0166 | genomes | single experiment

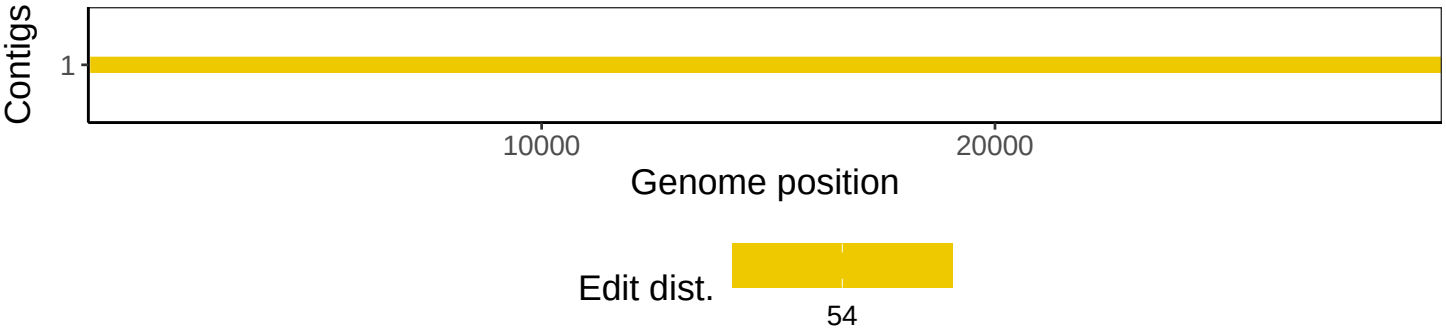
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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