COVID-19 subject HUP Q-0204

2021-05-05

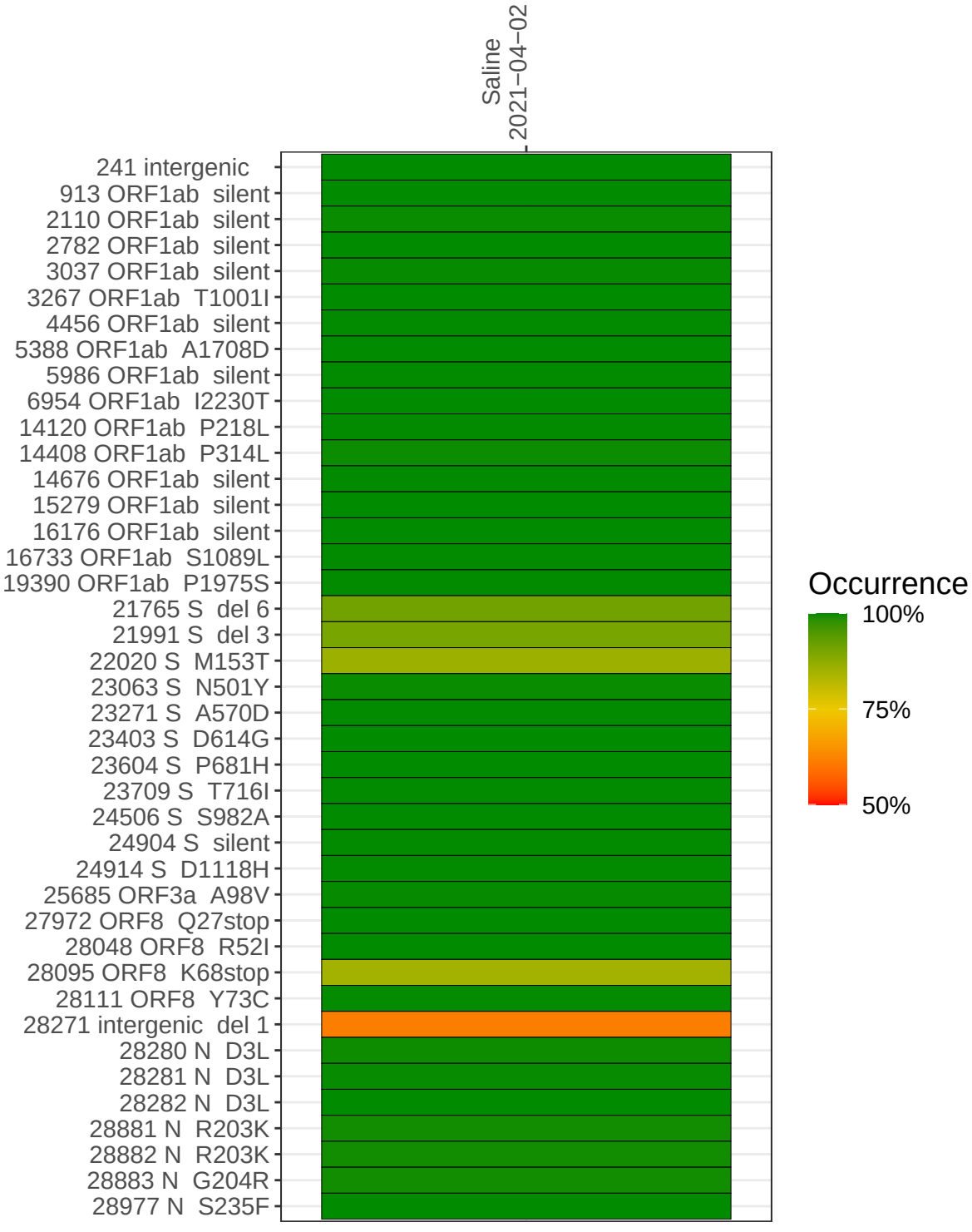
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

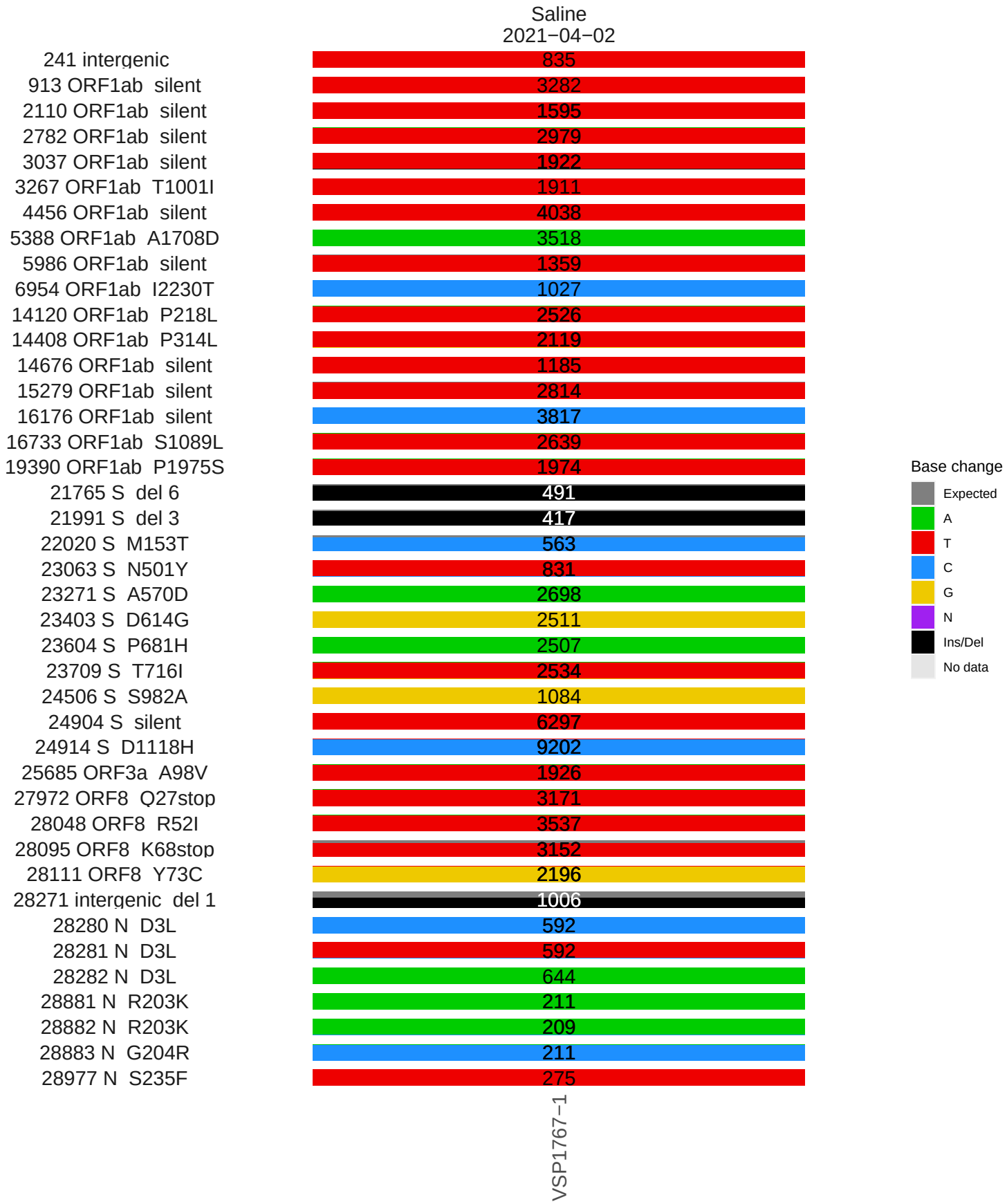
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1767-1	single experiment	NA	Saline	2021-04-02	29.80	B.1.1.7	99.8%	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.

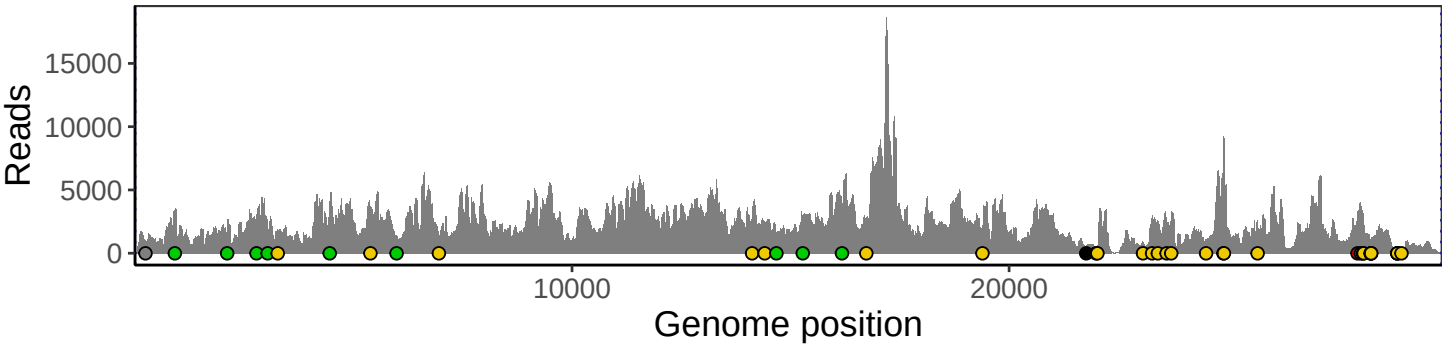



Saline
2021−04−02
241 intergenic 835
913 ORF1ab silent 3282
2110 ORF1ab silent 1595
2782 ORF1ab silent 2979
3037 ORF1ab silent 1922
3267 ORF1ab T1001I 1911
4456 ORF1ab silent 4038
5388 ORF1ab A1708D 3518
5986 ORF1ab silent 1359
6954 ORF1ab I2230T 1027
14120 ORF1ab P218L 2526
14408 ORF1ab P314L 2119
14676 ORF1ab silent 1185
15279 ORF1ab silent 2814
16176 ORF1ab silent 3817
16733 ORF1ab S1089L 2639
19390 ORF1ab P1975S 1974
21765 S del 6 491
21991 S del 3 417
22020 S M153T 563
23063 S N501Y 831
23271 S A570D 2698
23403 S D614G 2511
23604 S P681H 2507
23709 S T716I 2534
24506 S S982A 1084
24904 S silent 6297
24914 S D1118H 9202
25685 ORF3a A98V 1926
27972 ORF8 Q27stop 3171
28048 ORF8 R52I 3537
28095 ORF8 K68stop 3152
28111 ORF8 Y73C 2196
28271 intergenic del 1 1006
28280 N D3L 592
28281 N D3L 592
28282 N D3L 644
28881 N R203K 211
28882 N R203K 209
28883 N G204R 211
28977 N S235F 275
VSP1767−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

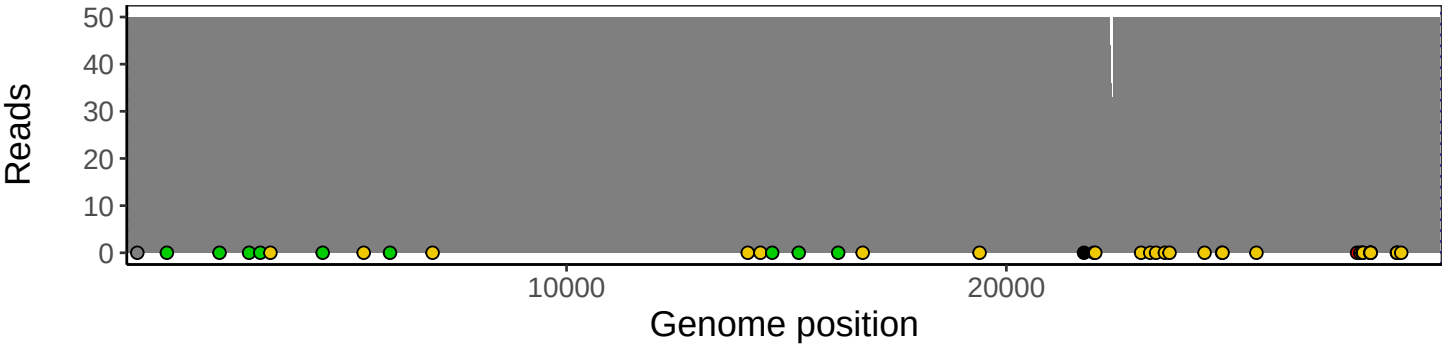
Analyses of individual experiments and composite results

VSP1767-1 | 2021-04-02 | Saline | HUP Q-0204 | genomes | single experiment

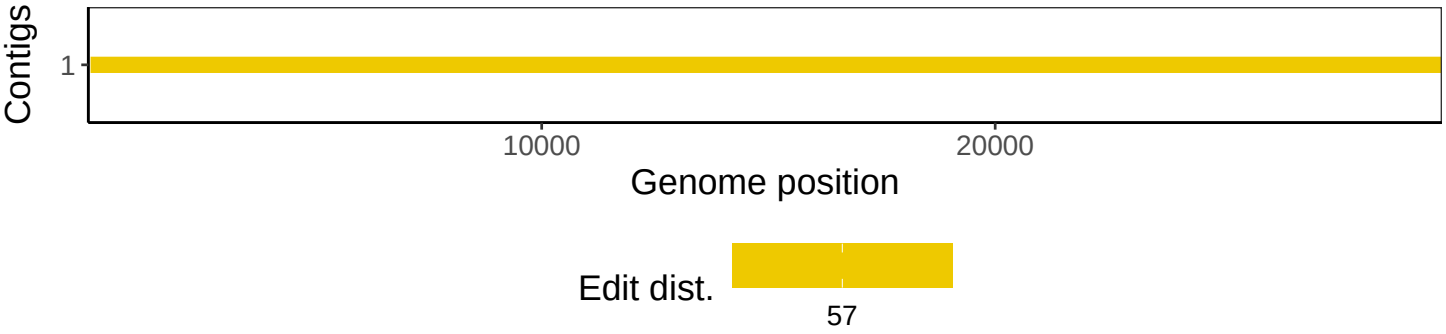
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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