COVID-19 subject HUP Q-0112

2021-05-05

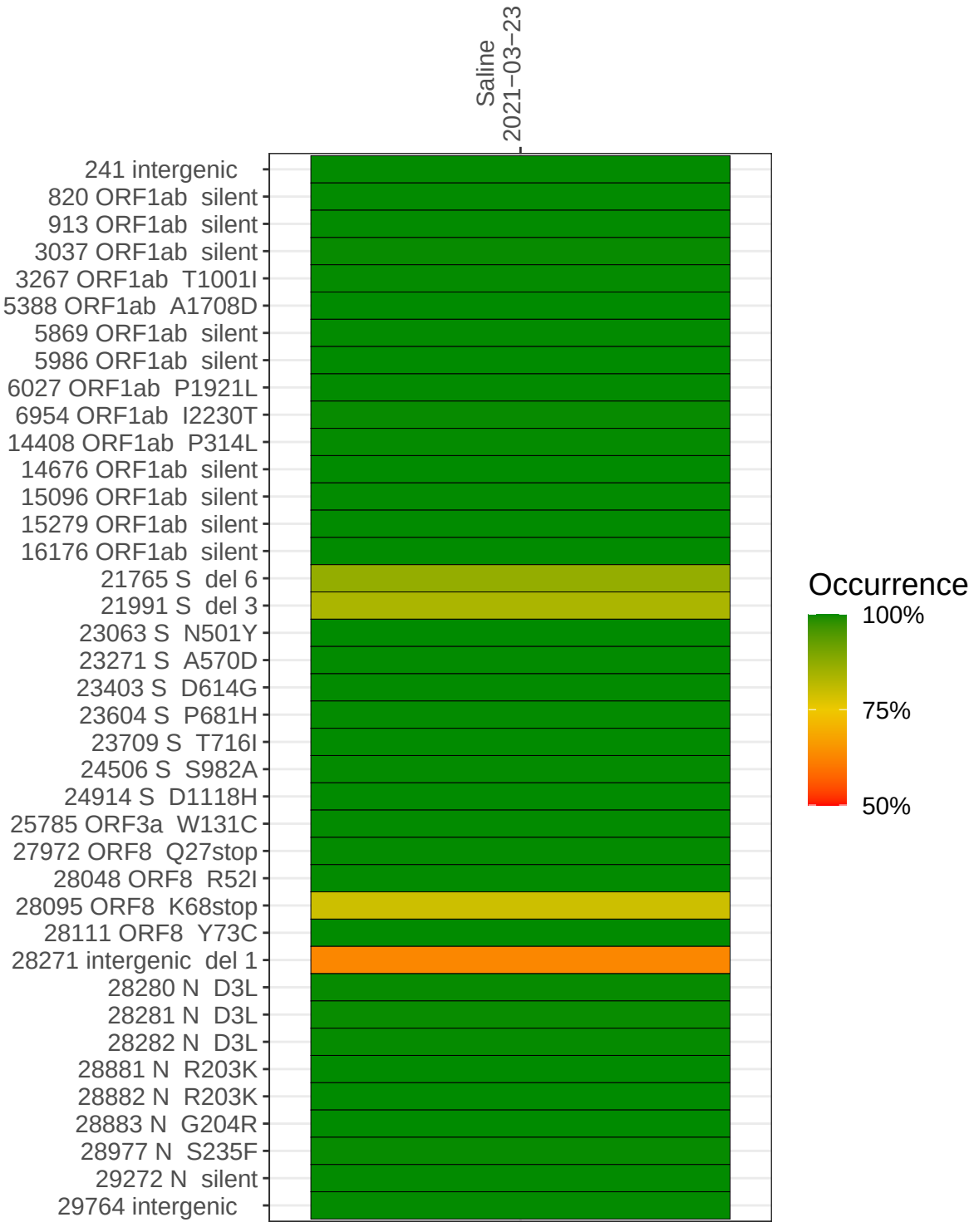
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

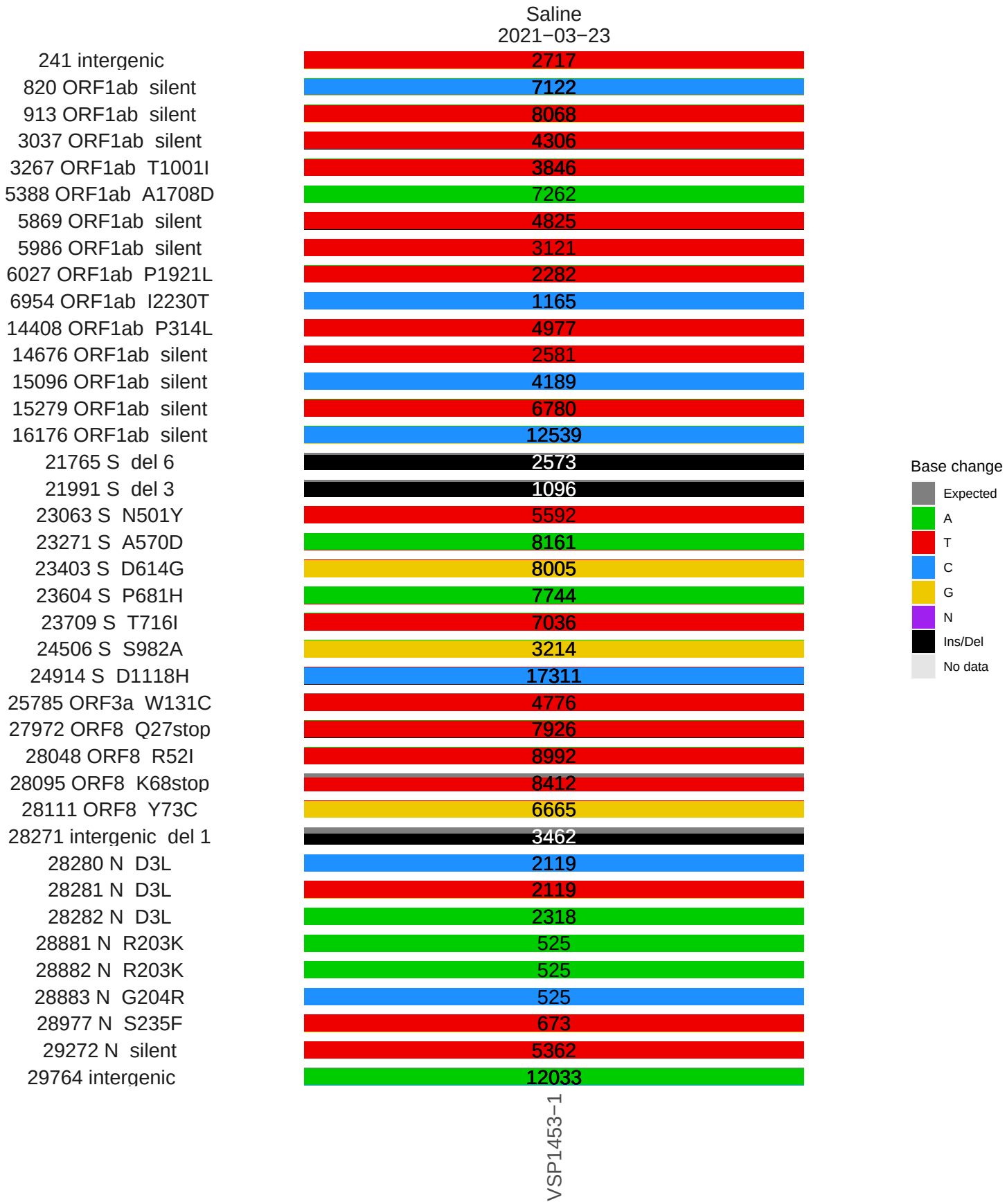
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1453-1	single experiment	NA	Saline	2021-03-23	29.90	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.

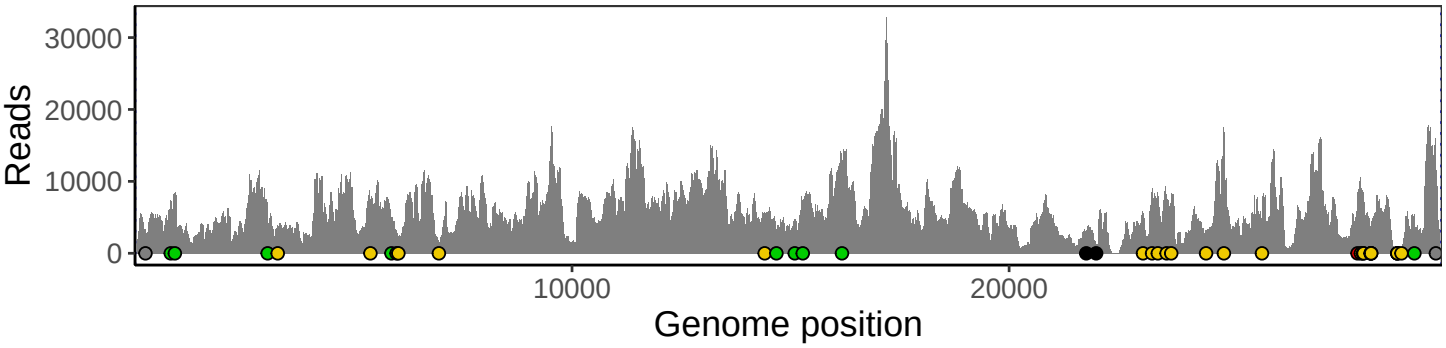



Saline
2021−03−23
241 intergenic 2717
820 ORF1ab silent 7122
913 ORF1ab silent 8068
3037 ORF1ab silent 4306
3267 ORF1ab T1001I 3846
5388 ORF1ab A1708D 7262
5869 ORF1ab silent 4825
5986 ORF1ab silent 3121
6027 ORF1ab P1921L 2282
6954 ORF1ab I2230T 1165
14408 ORF1ab P314L 4977
14676 ORF1ab silent 2581
15096 ORF1ab silent 4189
15279 ORF1ab silent 6780
16176 ORF1ab silent 12539
21765 S del 6 2573
21991 S del 3 1096
23063 S N501Y 5592
23271 S A570D 8161
23403 S D614G 8005
23604 S P681H 7744
23709 S T716I 7036
24506 S S982A 3214
24914 S D1118H 17311
25785 ORF3a W131C 4776
27972 ORF8 Q27stop 7926
28048 ORF8 R52I 8992
28095 ORF8 K68stop 8412
28111 ORF8 Y73C 6665
28271 intergenic del 1 3462
28280 N D3L 2119
28281 N D3L 2119
28282 N D3L 2318
28881 N R203K 525
28882 N R203K 525
28883 N G204R 525
28977 N S235F 673
29272 N silent 5362
29764 intergenic 12033
VSP1453−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

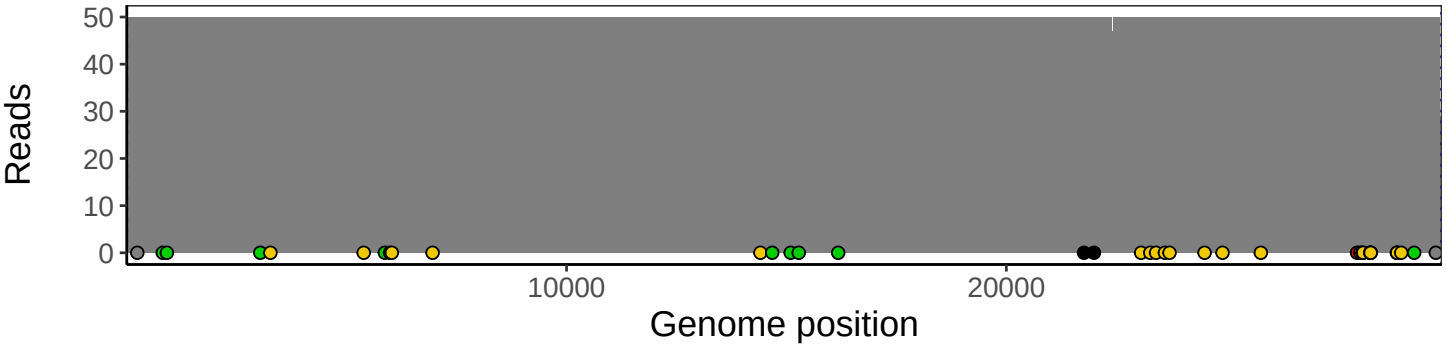
Analyses of individual experiments and composite results

VSP1453-1 | 2021-03-23 | Saline | HUP Q-0112 | genomes | single experiment

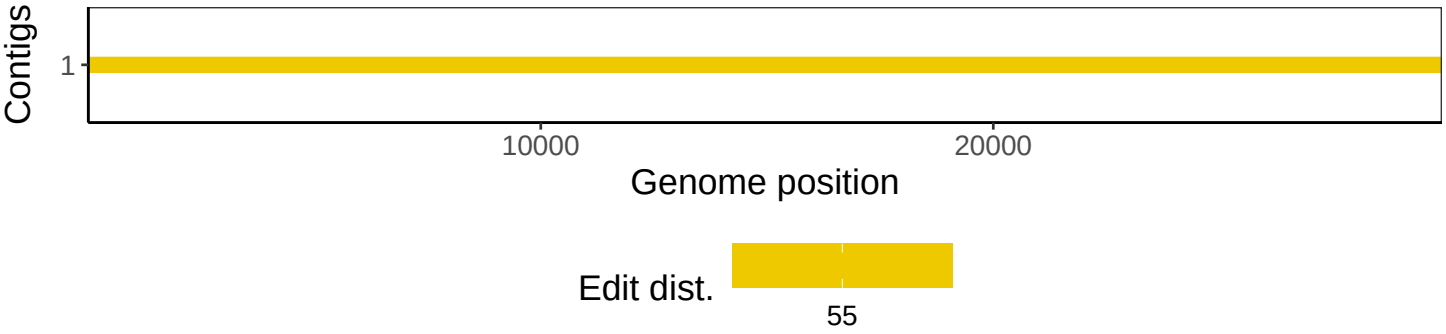
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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