COVID-19 subject HUP Q-0096

2021-05-05

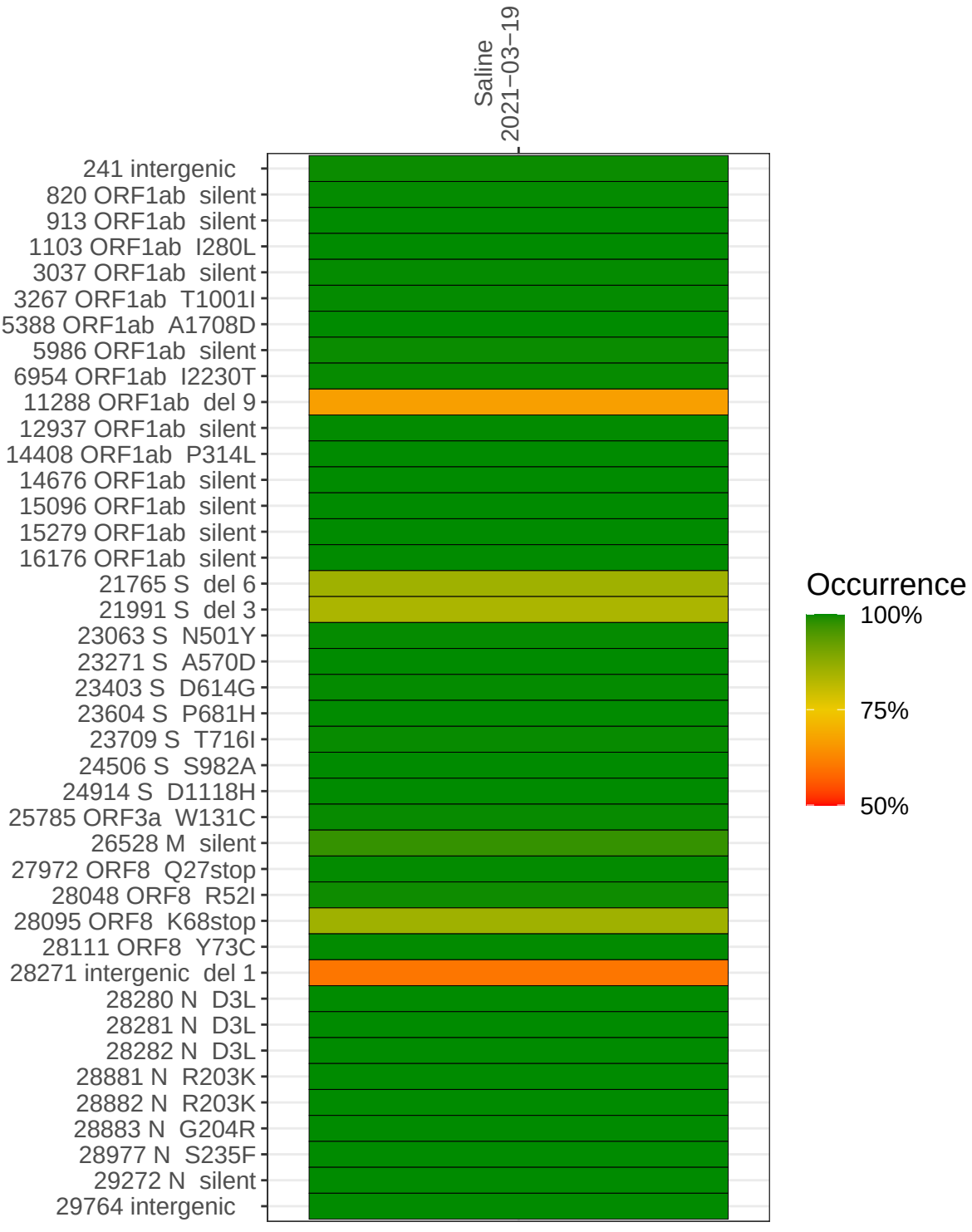
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

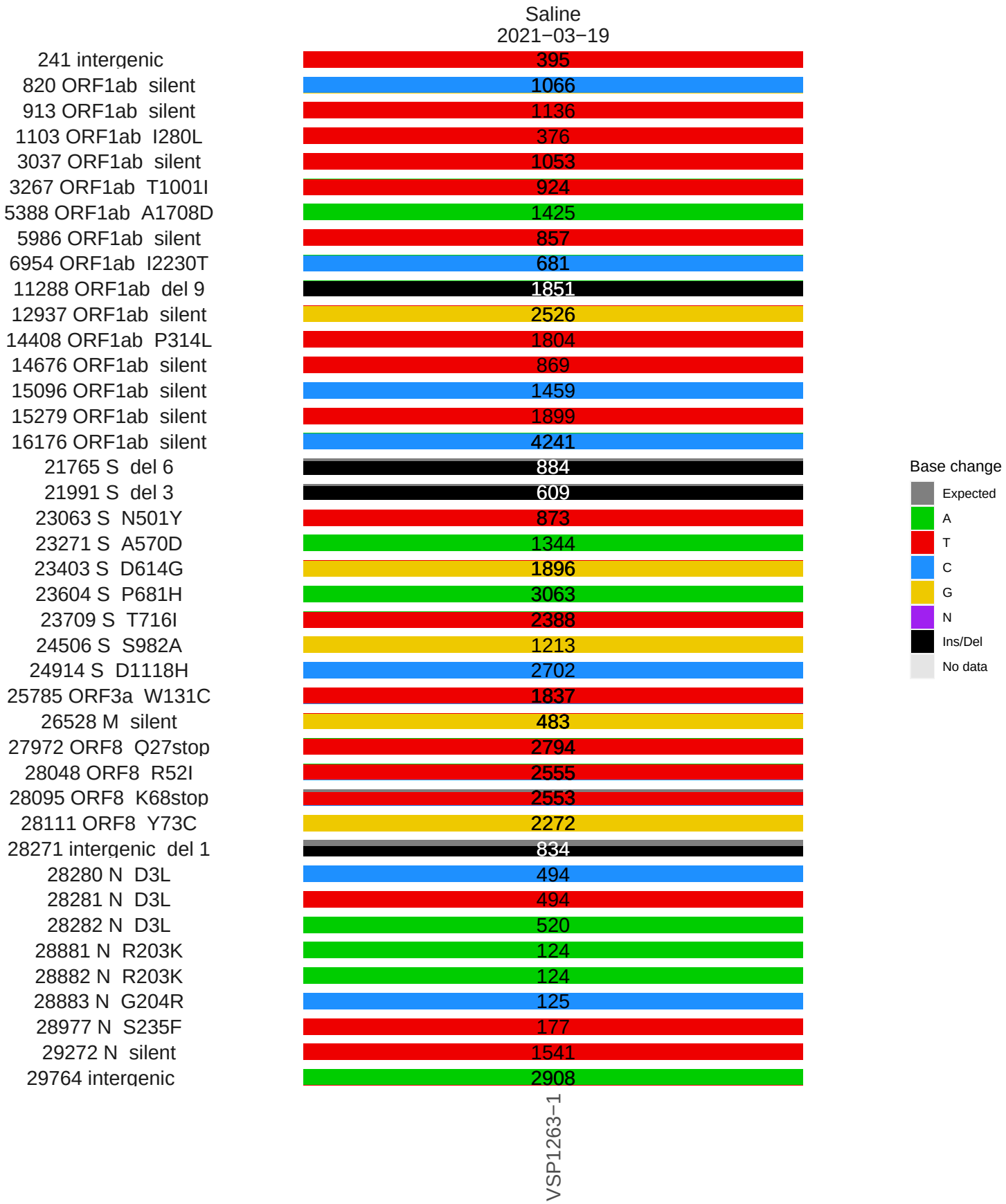
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1263-1	single experiment	NA	Saline	2021-03-19	29.84	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.

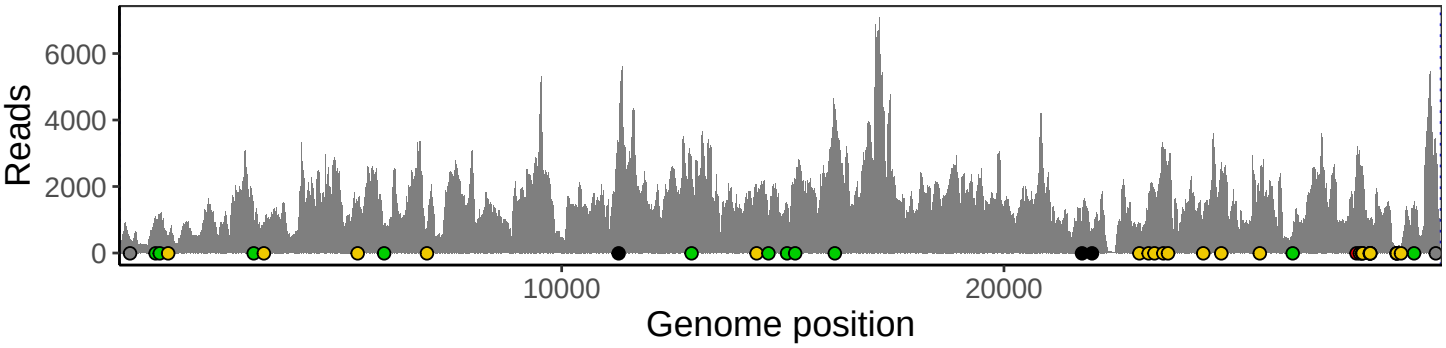



Saline
2021−03−19
241 intergenic 395
820 ORF1ab silent 1066
913 ORF1ab silent 1136
1103 ORF1ab I280L 376
3037 ORF1ab silent 1053
3267 ORF1ab T1001I 924
5388 ORF1ab A1708D 1425
5986 ORF1ab silent 857
6954 ORF1ab I2230T 681
11288 ORF1ab del 9 1851
12937 ORF1ab silent 2526
14408 ORF1ab P314L 1804
14676 ORF1ab silent 869
15096 ORF1ab silent 1459
15279 ORF1ab silent 1899
16176 ORF1ab silent 4241
21765 S del 6 884
21991 S del 3 609
23063 S N501Y 873
23271 S A570D 1344
23403 S D614G 1896
23604 S P681H 3063
23709 S T716I 2388
24506 S S982A 1213
24914 S D1118H 2702
25785 ORF3a W131C 1837
26528 M silent 483
27972 ORF8 Q27stop 2794
28048 ORF8 R52I 2555
28095 ORF8 K68stop 2553
28111 ORF8 Y73C 2272
28271 intergenic del 1 834
28280 N D3L 494
28281 N D3L 494
28282 N D3L 520
28881 N R203K 124
28882 N R203K 124
28883 N G204R 125
28977 N S235F 177
29272 N silent 1541
29764 intergenic 2908
VSP1263−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

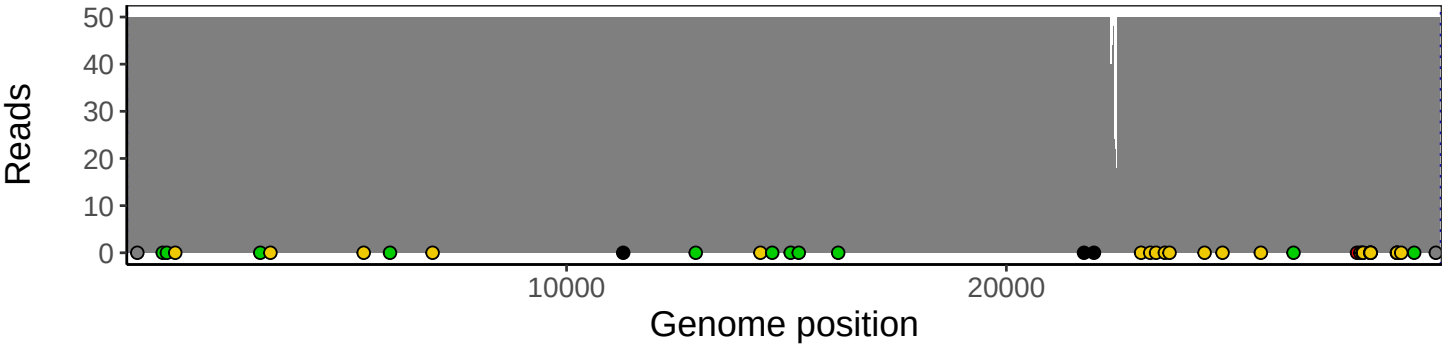
Analyses of individual experiments and composite results

VSP1263-1 | 2021-03-19 | Saline | HUP Q-0096 | genomes | single experiment

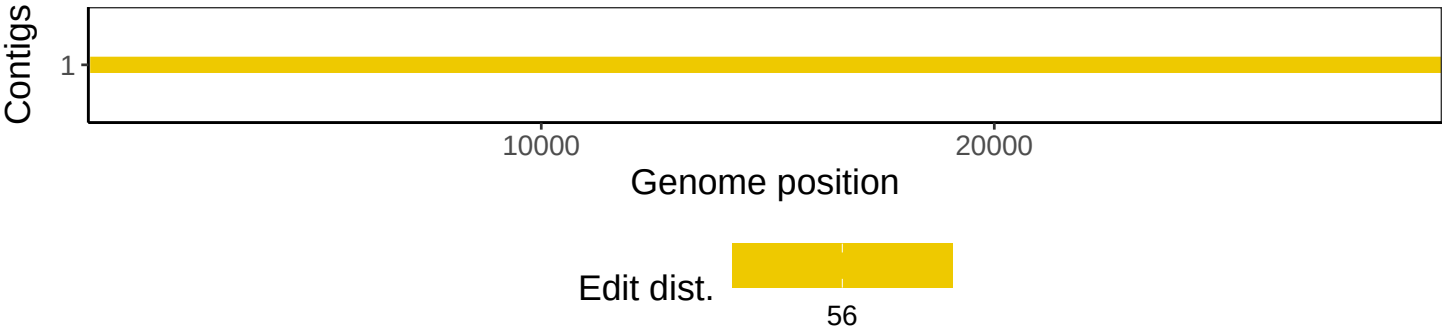
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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