COVID-19 subject HUP Q-0069

2021-05-05

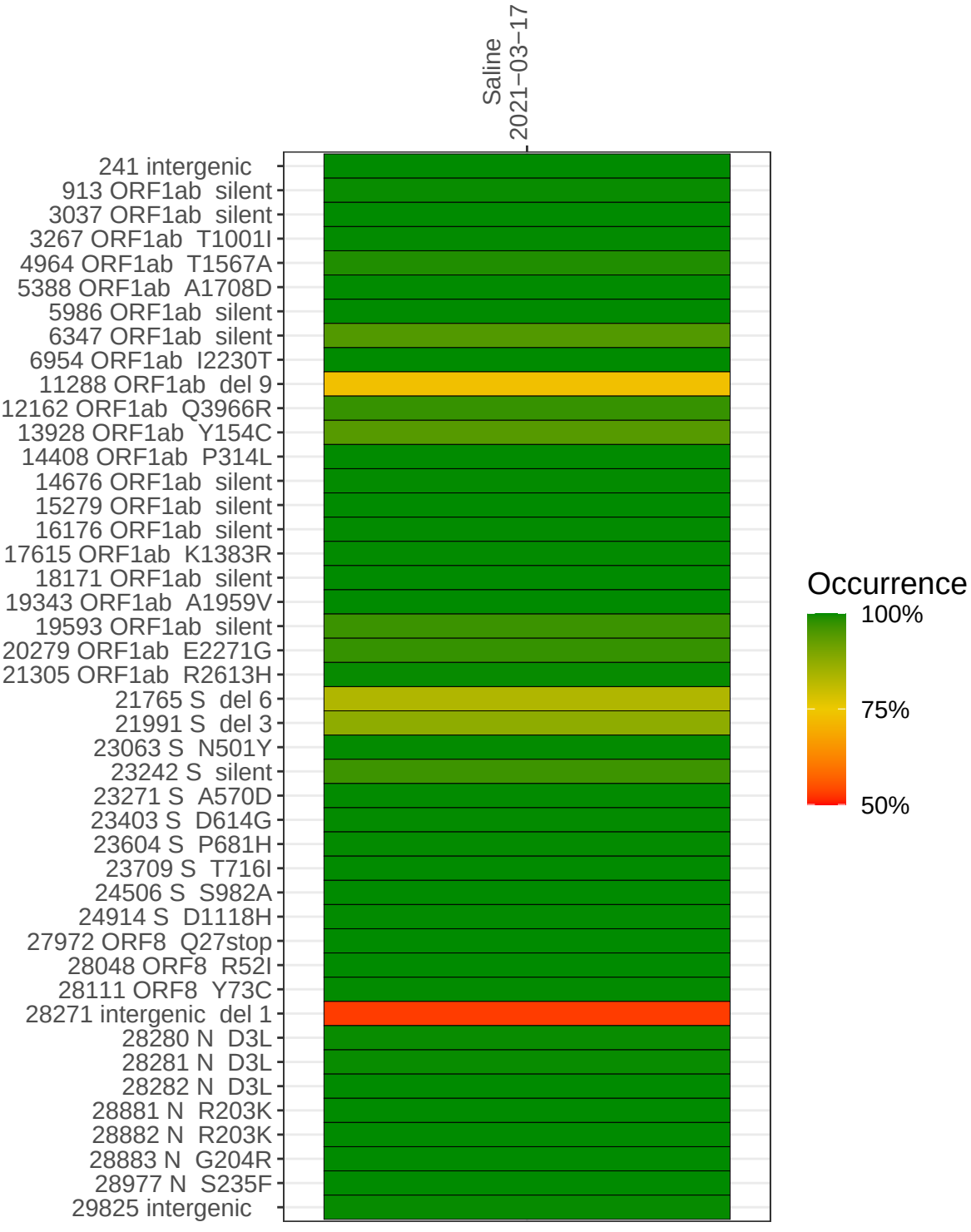
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

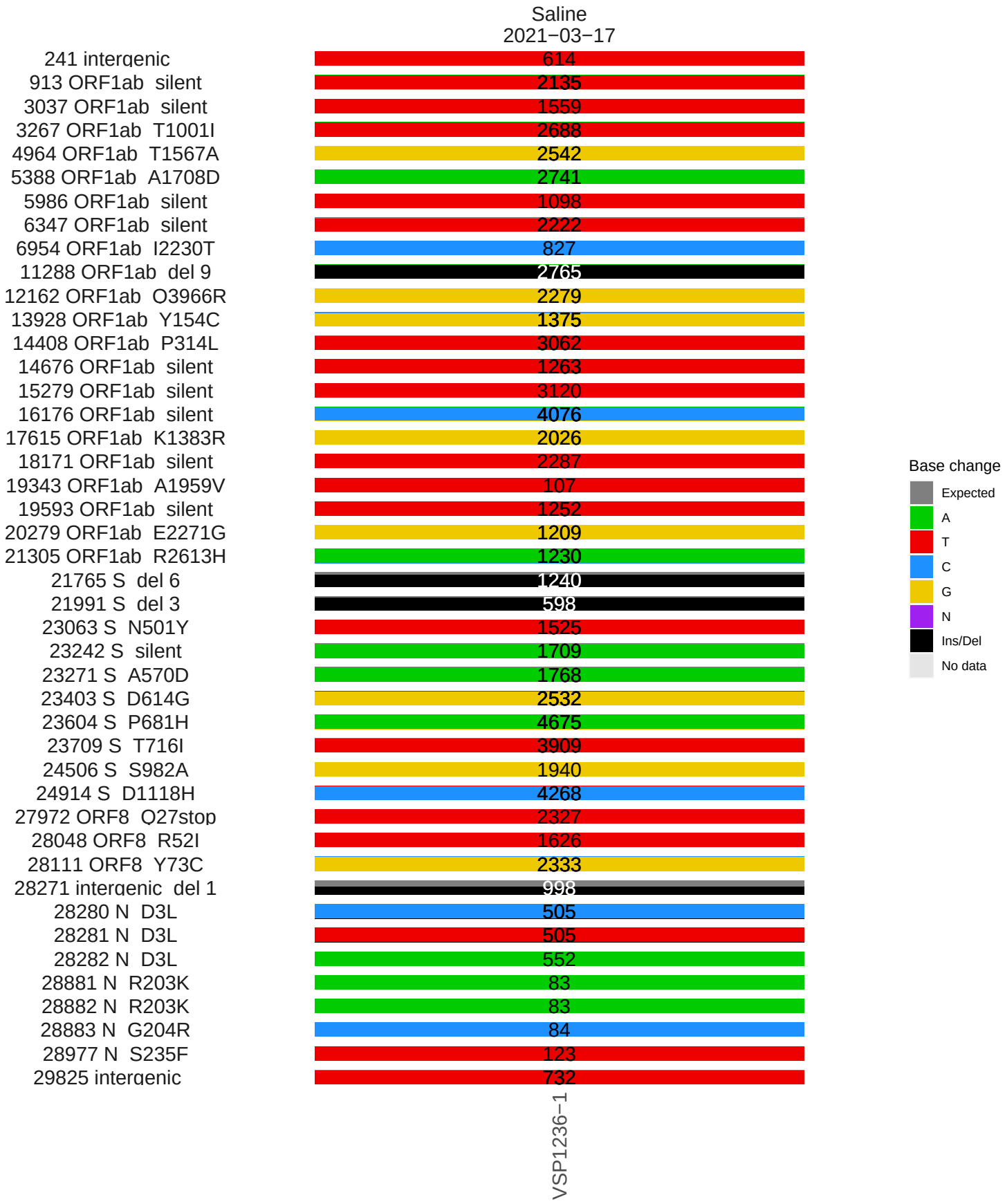
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1236-1	single experiment	NA	Saline	2021-03-17	29.91	B.1.1.7	99.8%	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.

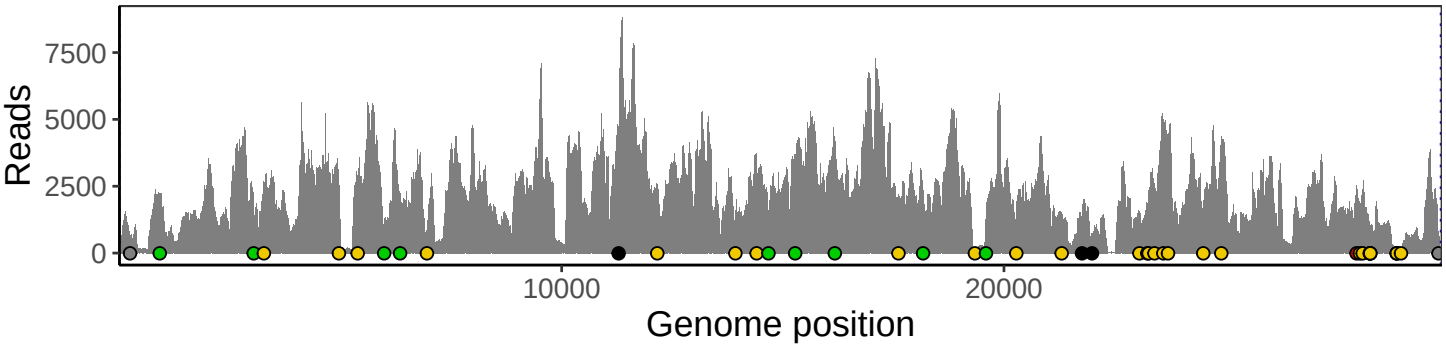



Saline
2021−03−17
241 intergenic 614
913 ORF1ab silent 2135
3037 ORF1ab silent 1559
3267 ORF1ab T1001I 2688
4964 ORF1ab T1567A 2542
5388 ORF1ab A1708D 2741
5986 ORF1ab silent 1098
6347 ORF1ab silent 2222
6954 ORF1ab I2230T 827
11288 ORF1ab del 9 2765
12162 ORF1ab O3966R 2279
13928 ORF1ab Y154C 1375
14408 ORF1ab P314L 3062
14676 ORF1ab silent 1263
15279 ORF1ab silent 3120
16176 ORF1ab silent 4076
17615 ORF1ab K1383R 2026
18171 ORF1ab silent 2287
19343 ORF1ab A1959V 107
19593 ORF1ab silent 1252
20279 ORF1ab E2271G 1209
21305 ORF1ab R2613H 1230
21765 S del 6 1240
21991 S del 3 598
23063 S N501Y 1525
23242 S silent 1709
23271 S A570D 1768
23403 S D614G 2532
23604 S P681H 4675
23709 S T716I 3909
24506 S S982A 1940
24914 S D1118H 4268
27972 ORF8 Q27stop 2327
28048 ORF8 R52I 1626
28111 ORF8 Y73C 2333
28271 intergenic del 1 998
28280 N D3L 505
28281 N D3L 505
28282 N D3L 552
28881 N R203K 83
28882 N R203K 83
28883 N G204R 84
28977 N S235F 123
29825 intergenic 732
VSP1236−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

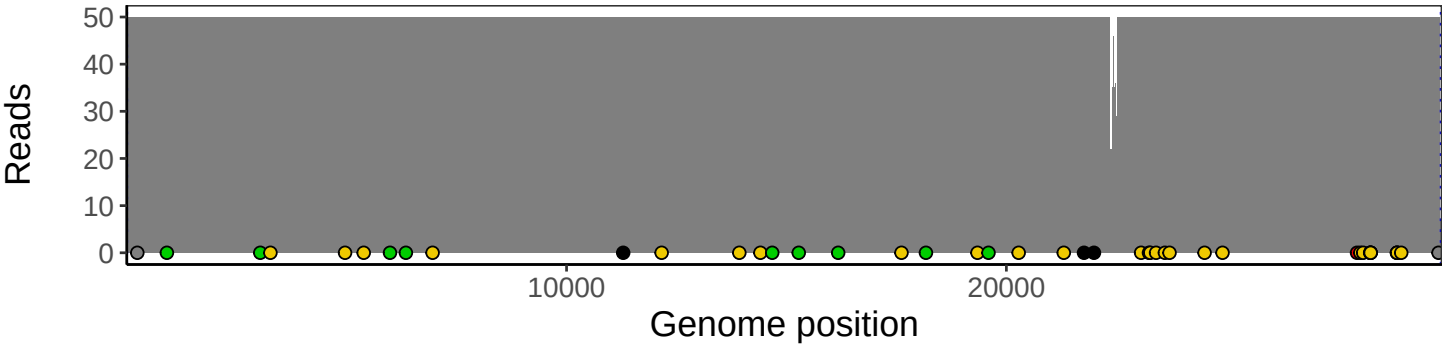
Analyses of individual experiments and composite results

VSP1236-1 | 2021-03-17 | Saline | HUP Q-0069 | genomes | single experiment

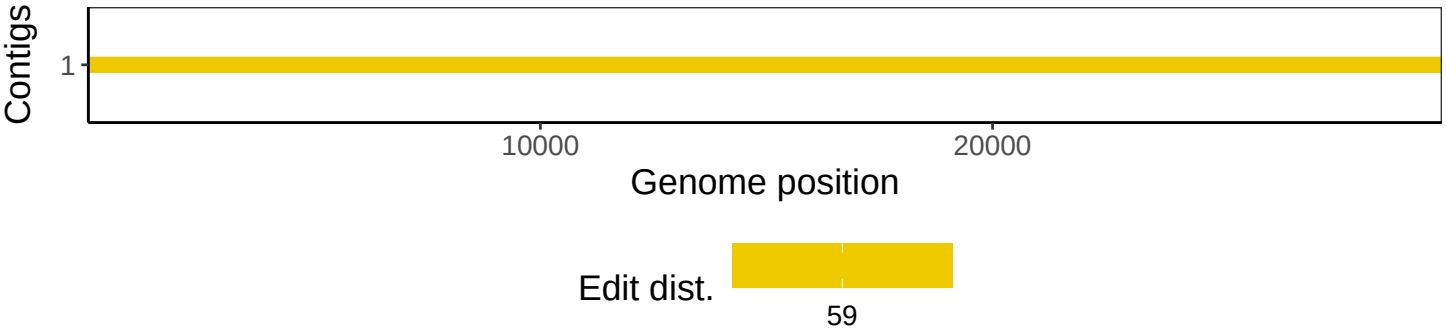
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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