COVID-19 subject HUP Q-0056

2021-05-05

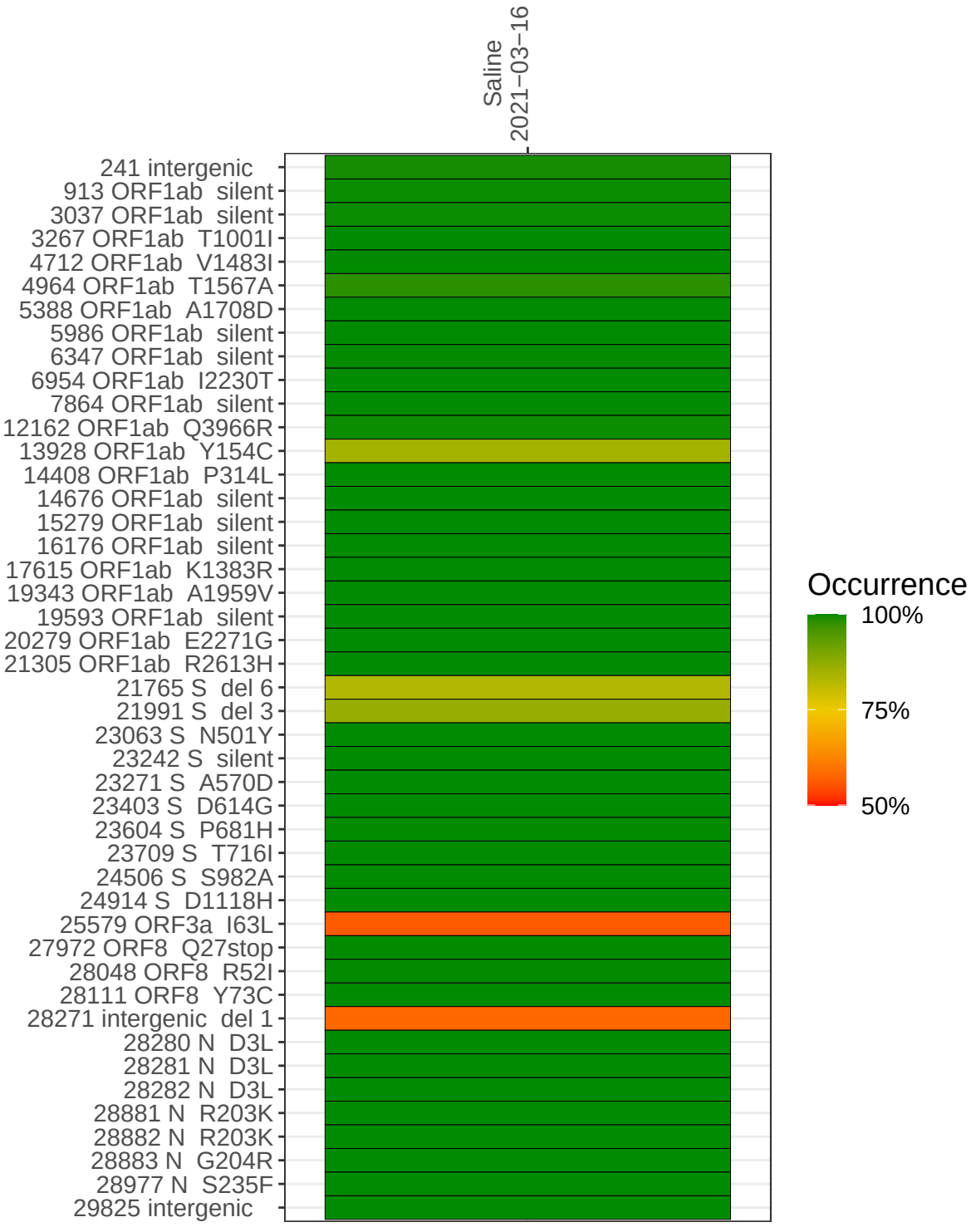
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

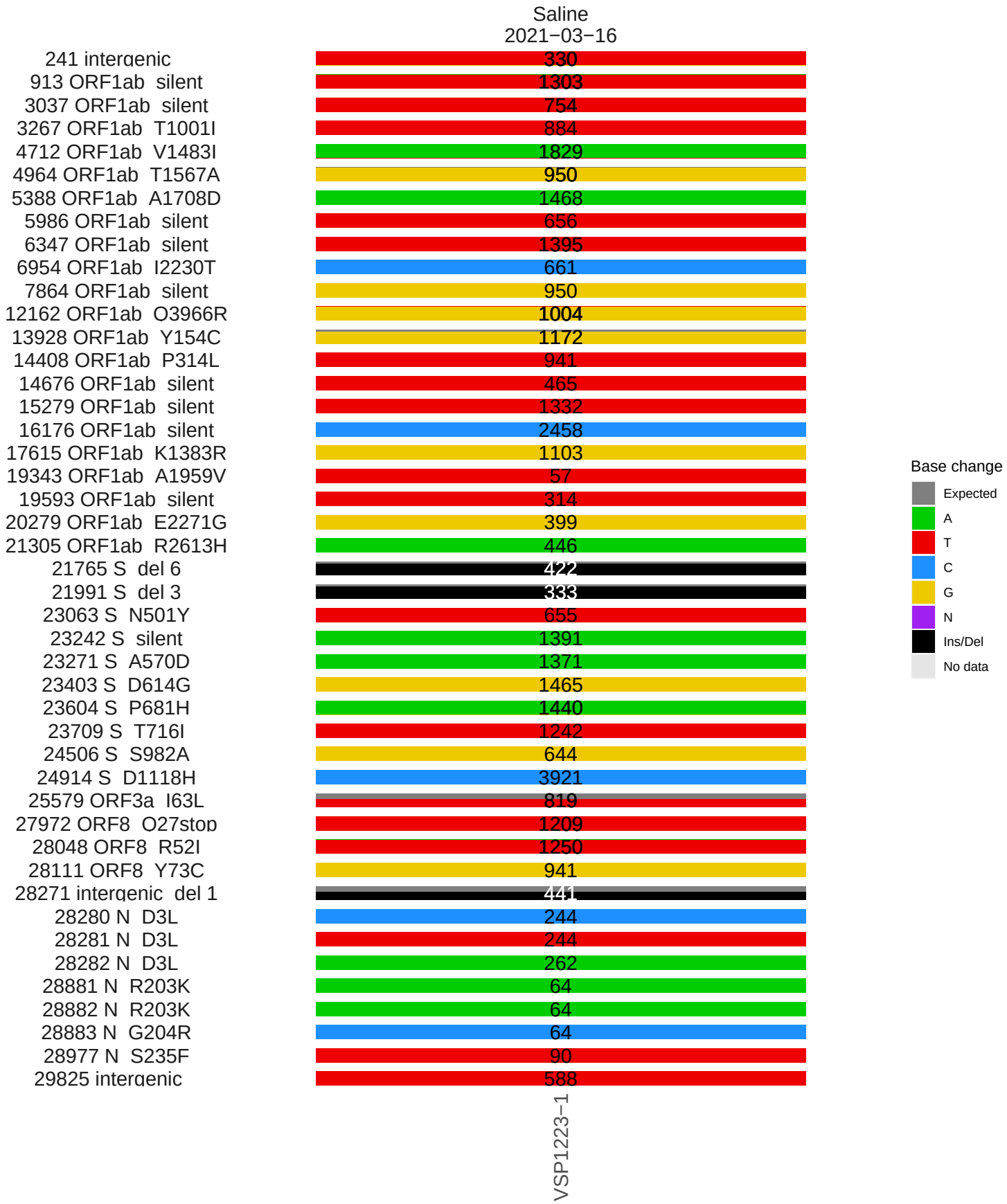
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1223-1	single experiment	NA	Saline	2021-03-16	29.86	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.

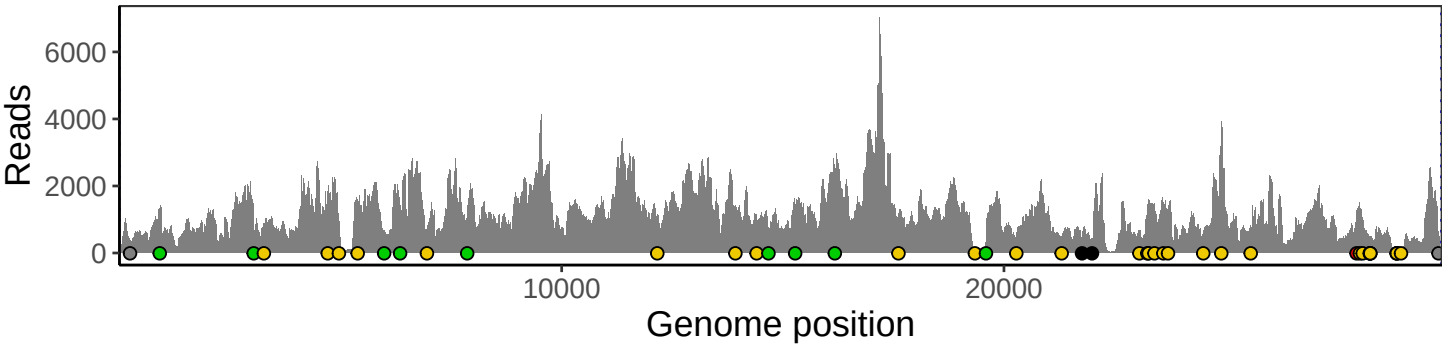



Saline
2021−03−16
241 intergenic 330
913 ORF1ab silent 1303
3037 ORF1ab silent 754
3267 ORF1ab T1001I 884
4712 ORF1ab V1483I 1829
4964 ORF1ab T1567A 950
5388 ORF1ab A1708D 1468
5986 ORF1ab silent 656
6347 ORF1ab silent 1395
6954 ORF1ab I2230T 661
7864 ORF1ab silent 950
12162 ORF1ab O3966R 1004
13928 ORF1ab Y154C 1172
14408 ORF1ab P314L 941
14676 ORF1ab silent 465
15279 ORF1ab silent 1332
16176 ORF1ab silent 2458
17615 ORF1ab K1383R 1103
19343 ORF1ab A1959V 57
19593 ORF1ab silent 314
20279 ORF1ab E2271G 399
21305 ORF1ab R2613H 446
21765 S del 6 422
21991 S del 3 333
23063 S N501Y 655
23242 S silent 1391
23271 S A570D 1371
23403 S D614G 1465
23604 S P681H 1440
23709 S T716I 1242
24506 S S982A 644
24914 S D1118H 3921
25579 ORF3a I63L 819
27972 ORF8 O27stop 1209
28048 ORF8 R52I 1250
28111 ORF8 Y73C 941
28271 intergenic del 1 441
28280 N D3L 244
28281 N D3L 244
28282 N D3L 262
28881 N R203K 64
28882 N R203K 64
28883 N G204R 64
28977 N S235F 90
29825 intergenic 588
VSP1223−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

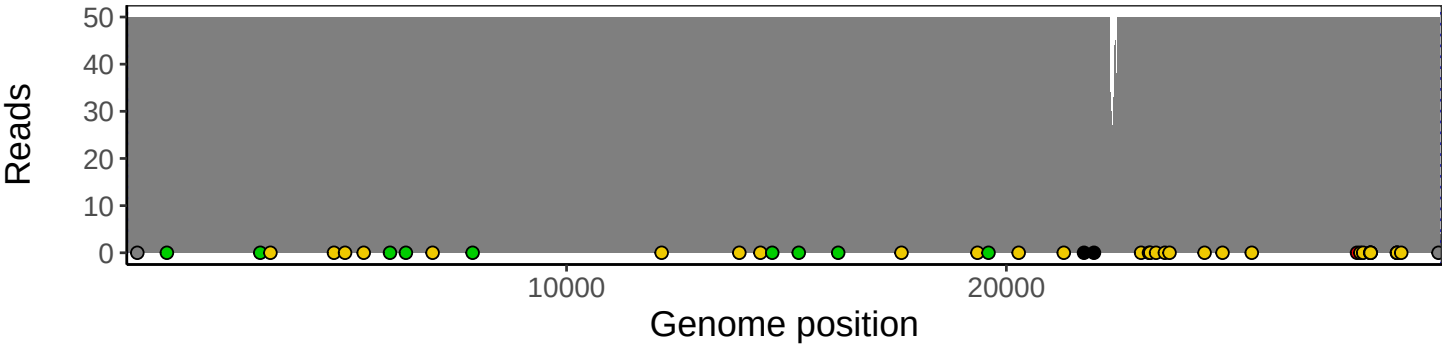
Analyses of individual experiments and composite results

VSP1223-1 | 2021-03-16 | Saline | HUP Q-0056 | genomes | single experiment

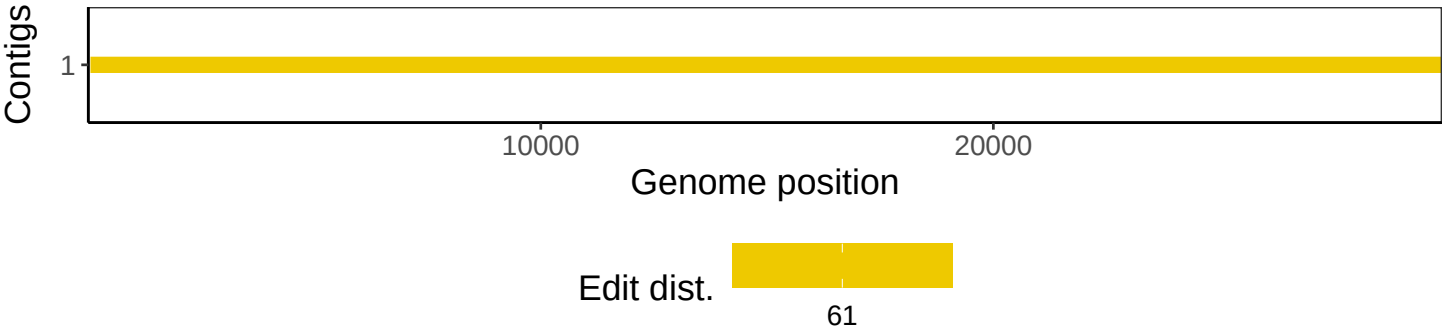
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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