COVID-19 subject HUP Q-0192

2021-05-05

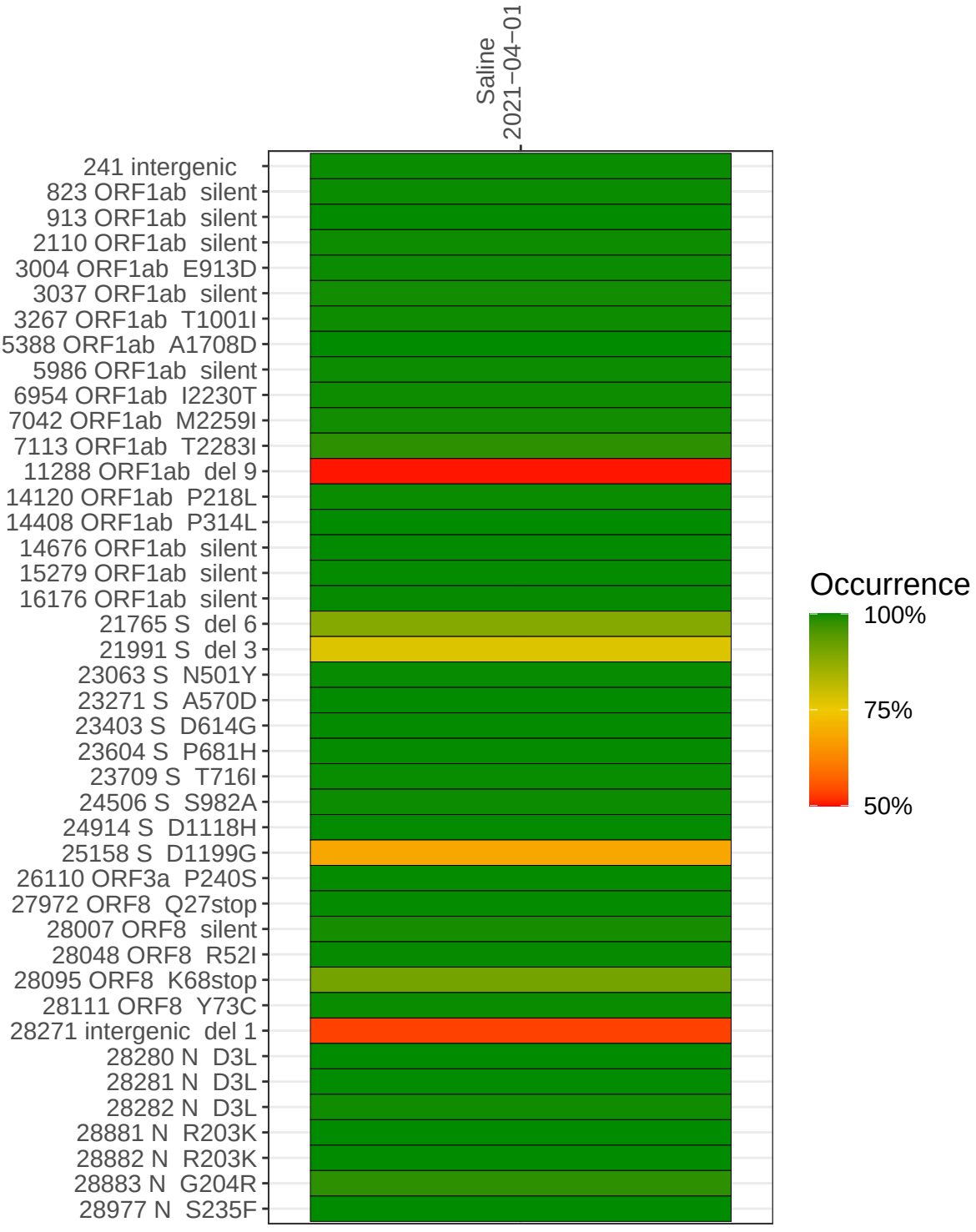
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

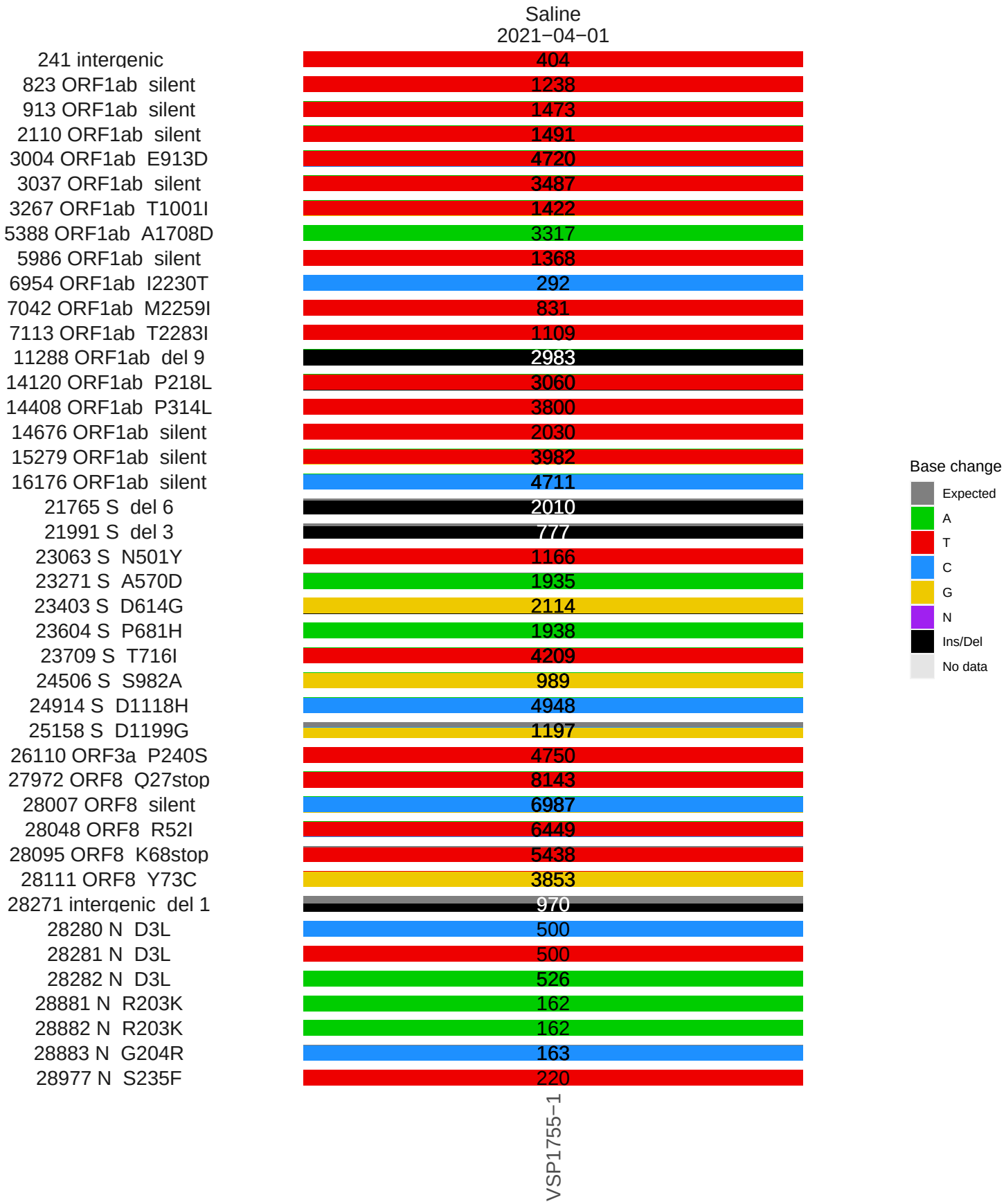
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1755-1	single experiment	NA	Saline	2021-04-01	29.85	B.1.1.7	99.7%	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.

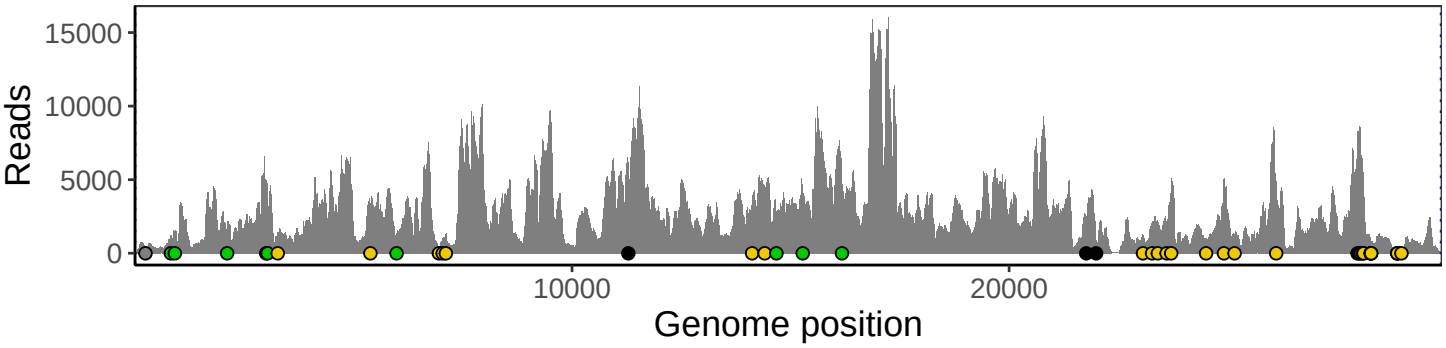



Saline
2021−04−01
241 intergenic 404
823 ORF1ab silent 1238
913 ORF1ab silent 1473
2110 ORF1ab silent 1491
3004 ORF1ab E913D 4720
3037 ORF1ab silent 3487
3267 ORF1ab T1001I 1422
5388 ORF1ab A1708D 3317
5986 ORF1ab silent 1368
6954 ORF1ab I2230T 292
7042 ORF1ab M2259I 831
7113 ORF1ab T2283I 1109
11288 ORF1ab del 9 2983
14120 ORF1ab P218L 3060
14408 ORF1ab P314L 3800
14676 ORF1ab silent 2030
15279 ORF1ab silent 3982
16176 ORF1ab silent 4711
21765 S del 6 2010
21991 S del 3 777
23063 S N501Y 1166
23271 S A570D 1935
23403 S D614G 2114
23604 S P681H 1938
23709 S T716I 4209
24506 S S982A 989
24914 S D1118H 4948
25158 S D1199G 1197
26110 ORF3a P240S 4750
27972 ORF8 Q27stop 8143
28007 ORF8 silent 6987
28048 ORF8 R52I 6449
28095 ORF8 K68stop 5438
28111 ORF8 Y73C 3853
28271 intergenic del 1 970
28280 N D3L 500
28281 N D3L 500
28282 N D3L 526
28881 N R203K 162
28882 N R203K 162
28883 N G204R 163
28977 N S235F 220
VSP1755−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

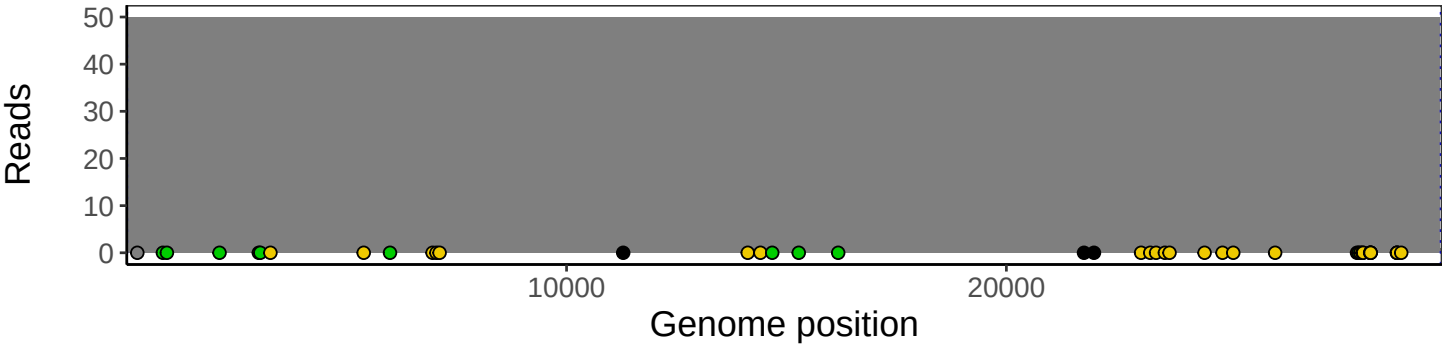
Analyses of individual experiments and composite results

VSP1755-1 | 2021-04-01 | Saline | HUP Q-0192 | genomes | single experiment

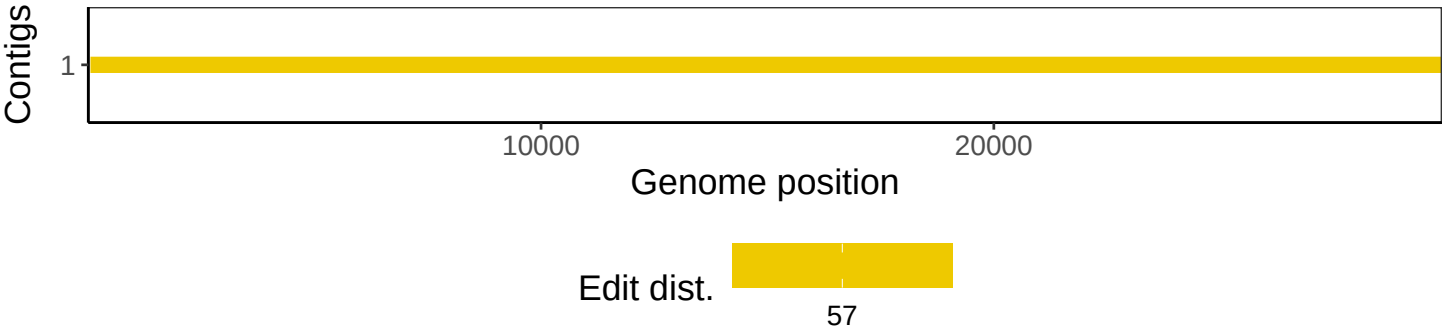
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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