COVID-19 subject HUP Q-0229

2021-06-23

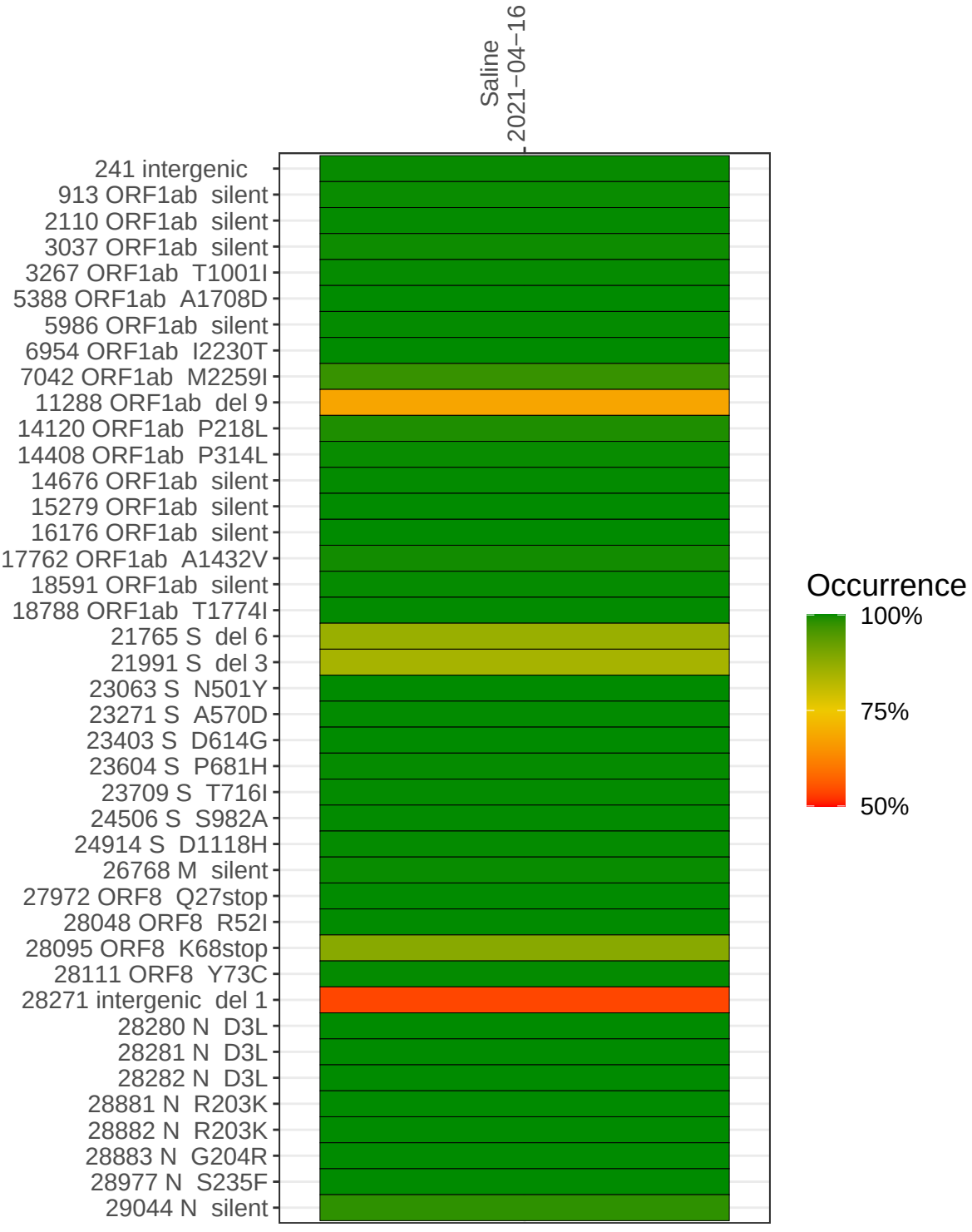
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

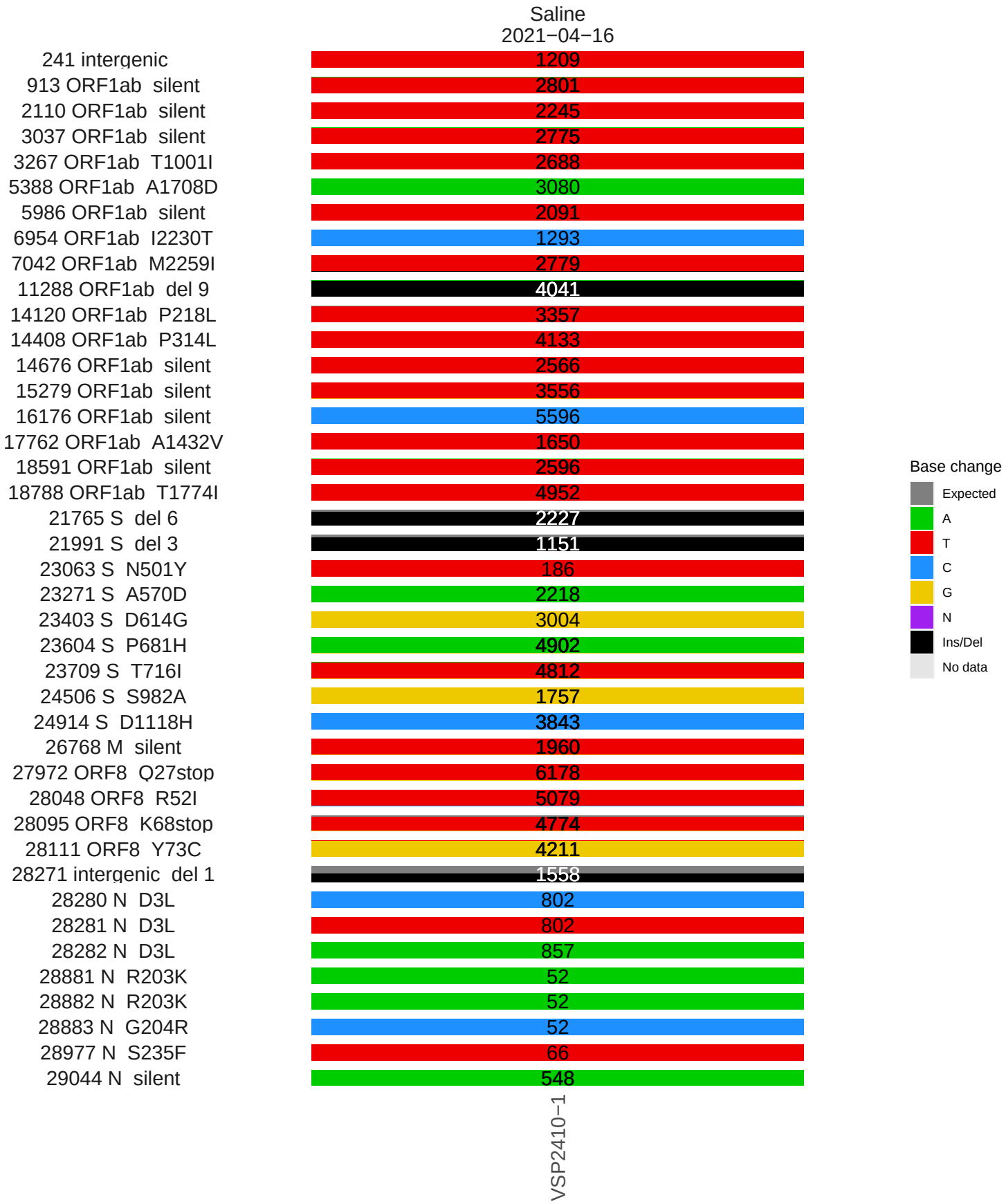
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2410-1	single experiment	NA	Saline	2021-04-16	29.82	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

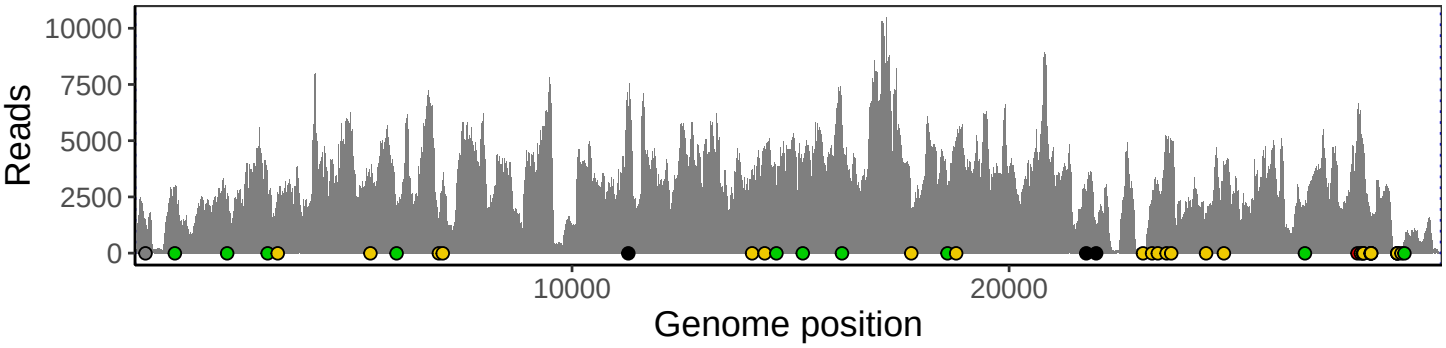



Saline
2021−04−16
241 intergenic 1209
913 ORF1ab silent 2801
2110 ORF1ab silent 2245
3037 ORF1ab silent 2775
3267 ORF1ab T1001I 2688
5388 ORF1ab A1708D 3080
5986 ORF1ab silent 2091
6954 ORF1ab I2230T 1293
7042 ORF1ab M2259I 2779
11288 ORF1ab del 9 4041
14120 ORF1ab P218L 3357
14408 ORF1ab P314L 4133
14676 ORF1ab silent 2566
15279 ORF1ab silent 3556
16176 ORF1ab silent 5596
17762 ORF1ab A1432V 1650
18591 ORF1ab silent 2596
18788 ORF1ab T1774I 4952
21765 S del 6 2227
21991 S del 3 1151
23063 S N501Y 186
23271 S A570D 2218
23403 S D614G 3004
23604 S P681H 4902
23709 S T716I 4812
24506 S S982A 1757
24914 S D1118H 3843
26768 M silent 1960
27972 ORF8 Q27stop 6178
28048 ORF8 R52I 5079
28095 ORF8 K68stop 4774
28111 ORF8 Y73C 4211
28271 intergenic del 1 1558
28280 N D3L 802
28281 N D3L 802
28282 N D3L 857
28881 N R203K 52
28882 N R203K 52
28883 N G204R 52
28977 N S235F 66
29044 N silent 548
VSP2410−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

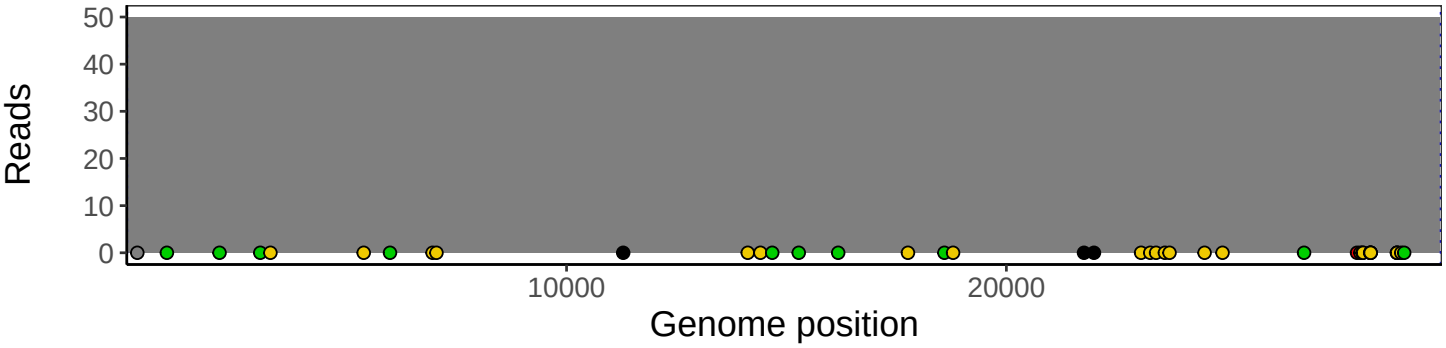
Analyses of individual experiments and composite results

VSP2410-1 | 2021-04-16 | Saline | HUP Q-0229 | genomes | single experiment

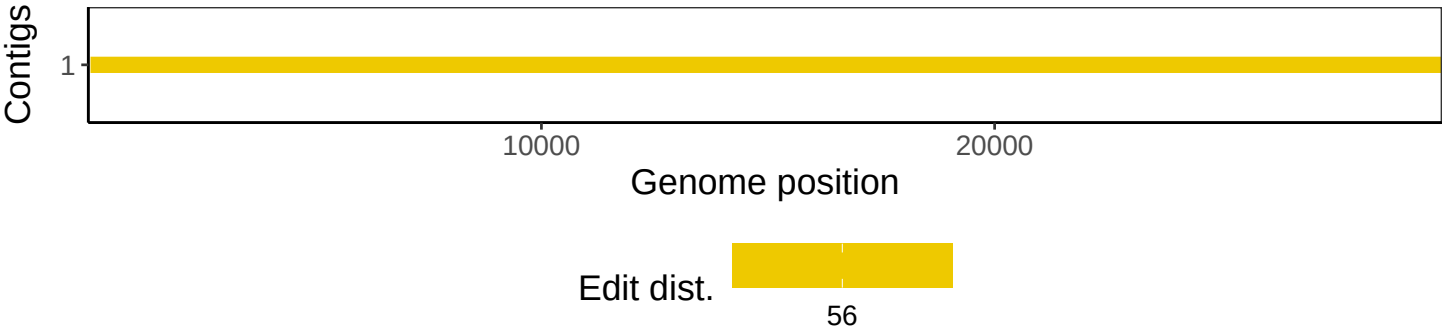
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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