COVID-19 subject HUP Q-0061

2021-05-05

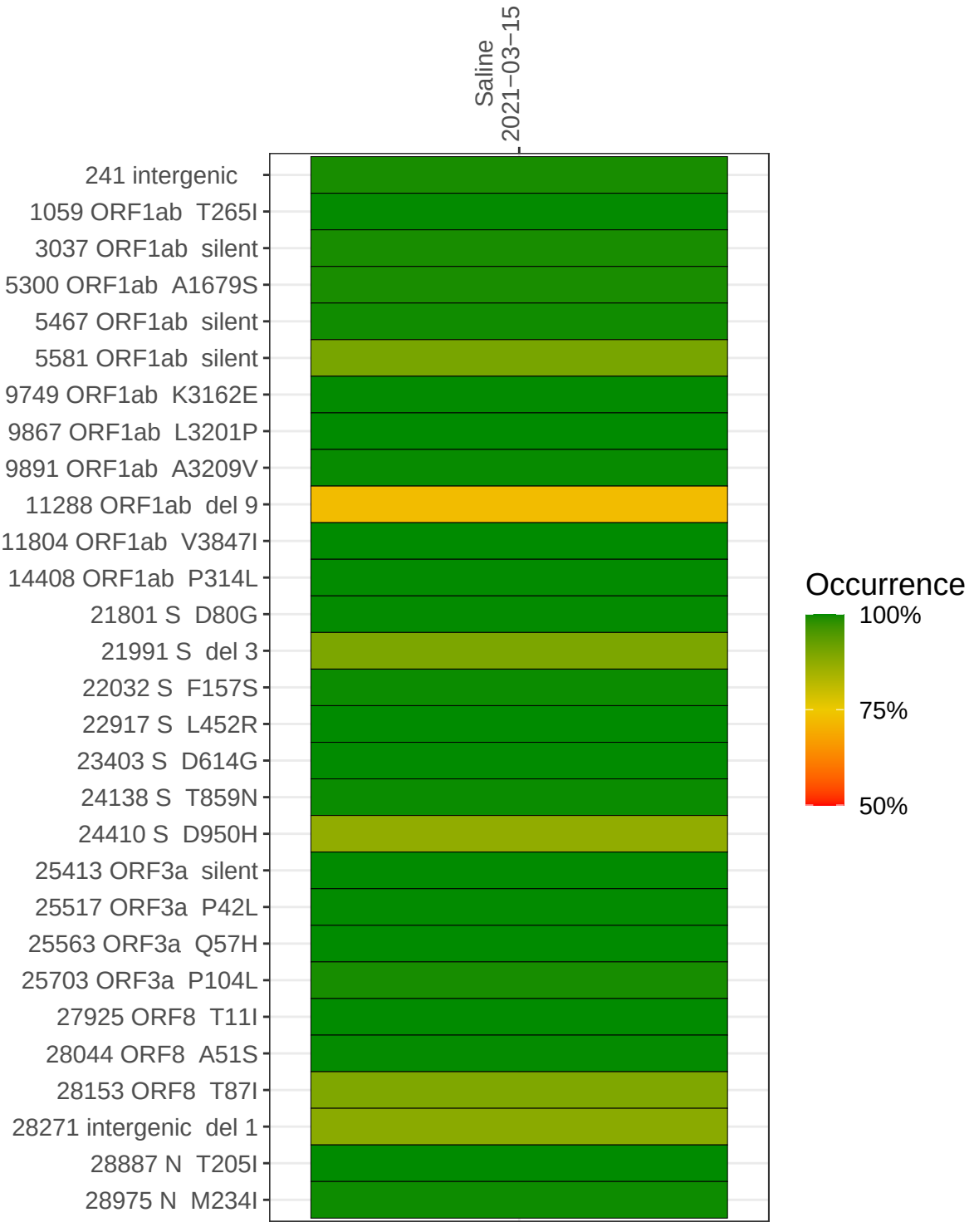
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

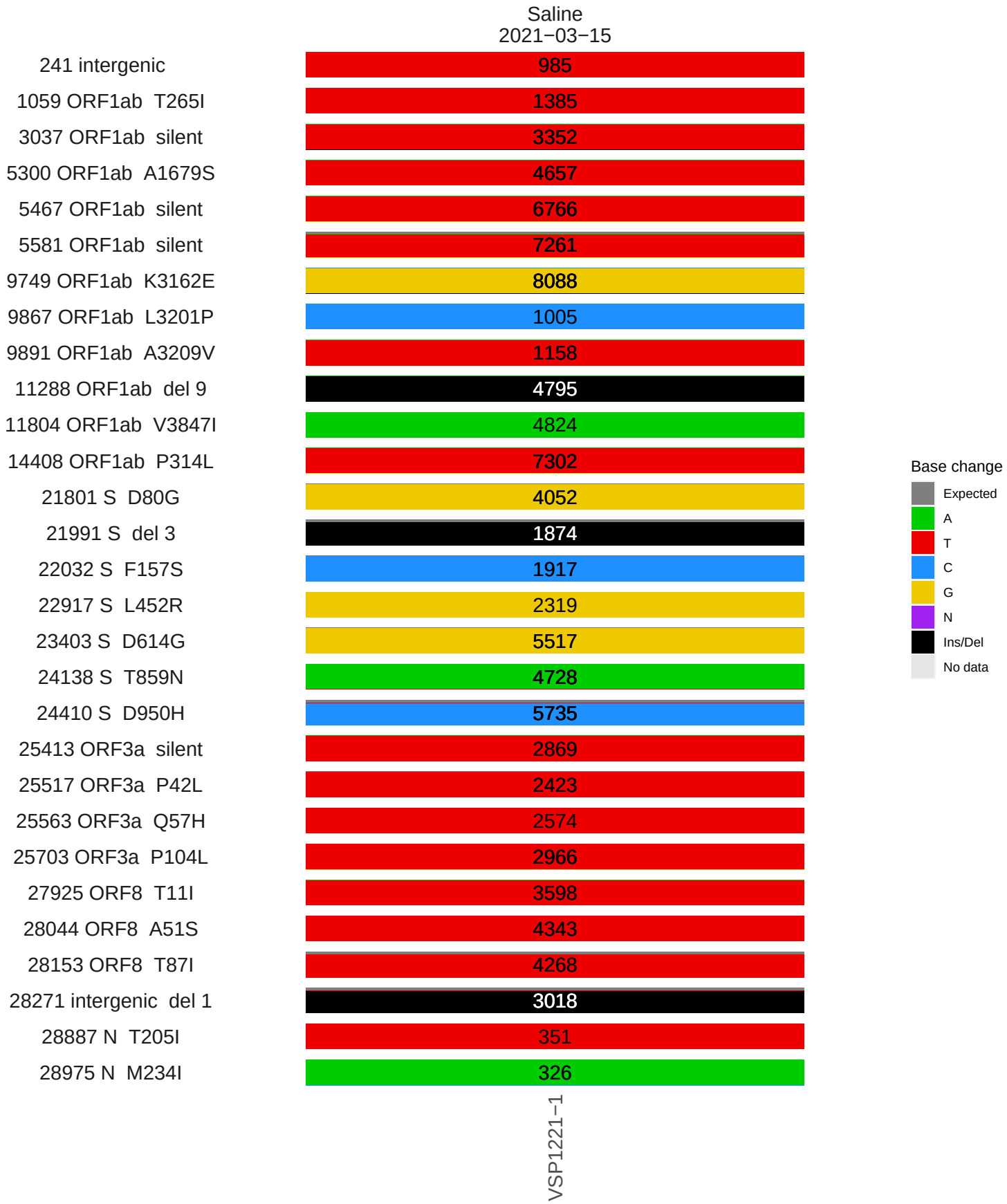
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1221-1	single experiment	NA	Saline	2021-03-15	29.91	B.1.526.1	99.9%	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.

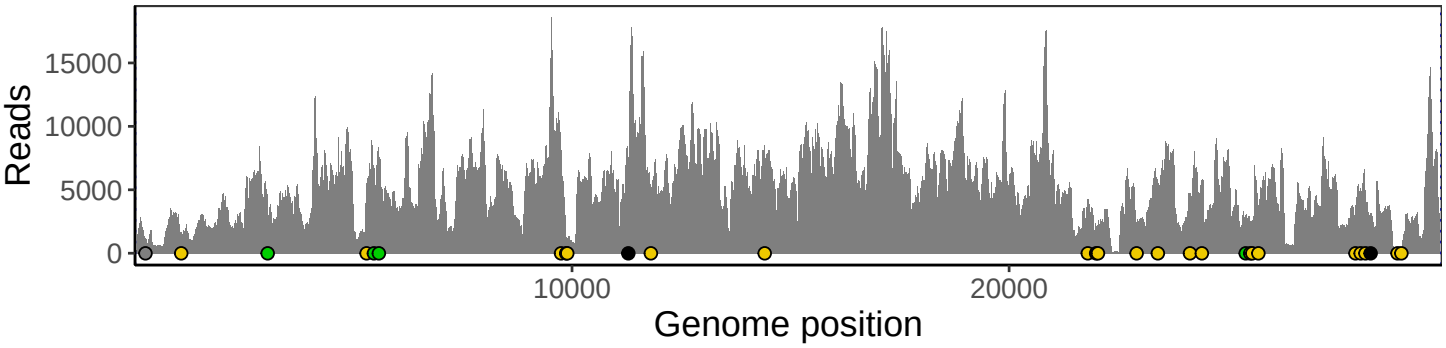



Saline
2021−03−15
241 intergenic
985
1059 ORF1ab T265I
1385
3037 ORF1ab silent
3352
5300 ORF1ab A1679S
4657
5467 ORF1ab silent
6766
5581 ORF1ab silent
7261
9749 ORF1ab K3162E
8088
9867 ORF1ab L3201P
1005
9891 ORF1ab A3209V
1158
11288 ORF1ab del 9
4795
11804 ORF1ab V3847I
4824
14408 ORF1ab P314L
7302
21801 S D80G
4052
21991 S del 3
1874
22032 S F157S
1917
22917 S L452R
2319
23403 S D614G
5517
24138 S T859N
4728
24410 S D950H
5735
25413 ORF3a silent
2869
25517 ORF3a P42L
2423
25563 ORF3a Q57H
2574
25703 ORF3a P104L
2966
27925 ORF8 T11I
3598
28044 ORF8 A51S
4343
28153 ORF8 T87I
4268
28271 intergenic del 1
3018
28887 N T205I
351
28975 N M234I
326
VSP1221−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

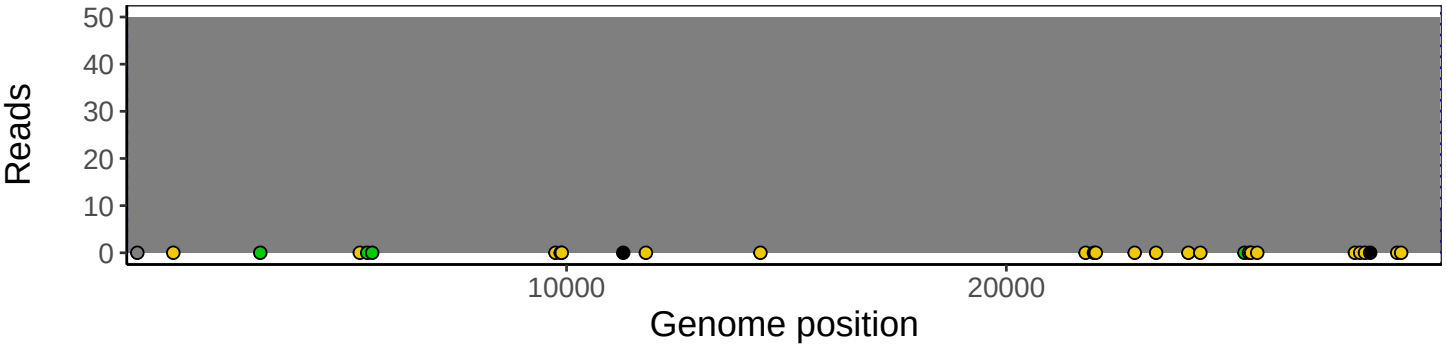
Analyses of individual experiments and composite results

VSP1221-1 | 2021-03-15 | Saline | HUP Q-0061 | genomes | single experiment

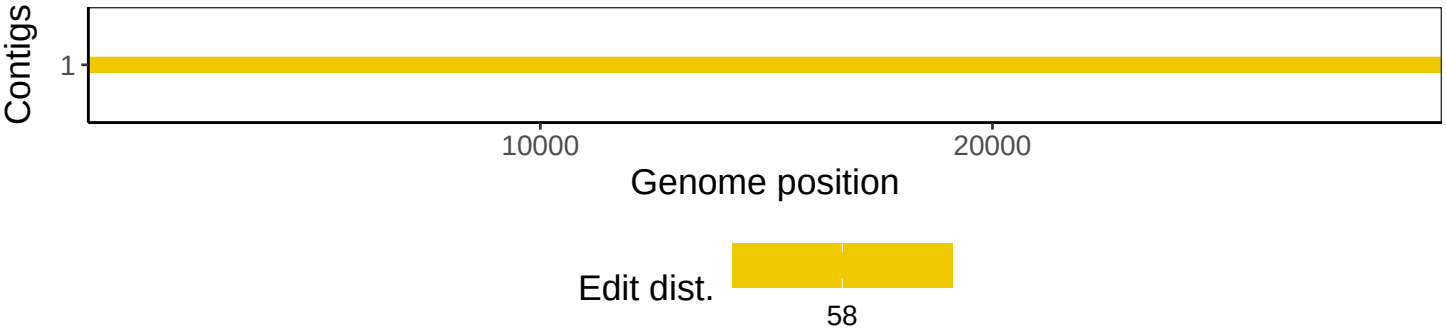
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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