COVID-19 subject HUP Q-0227

2021-05-21

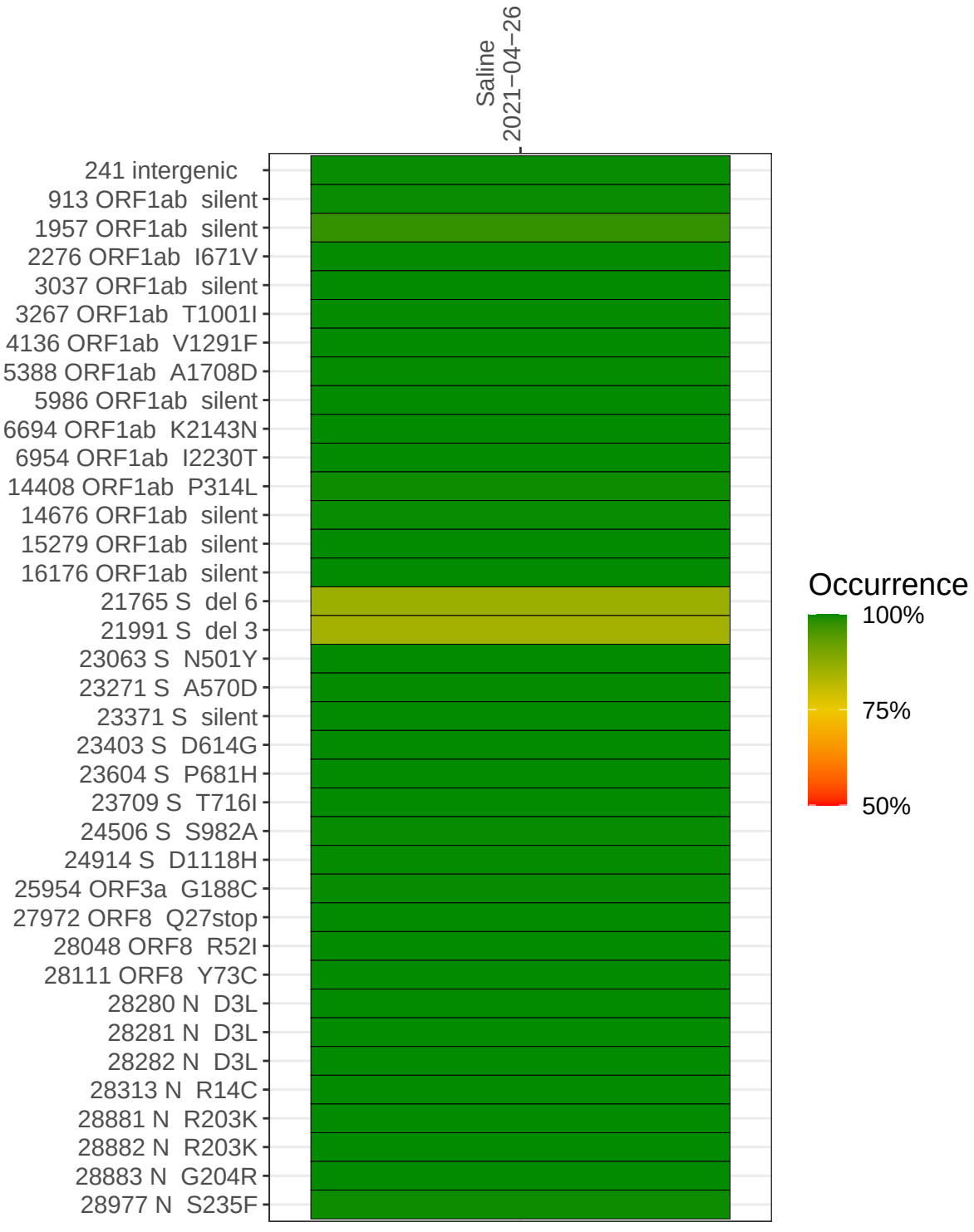
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

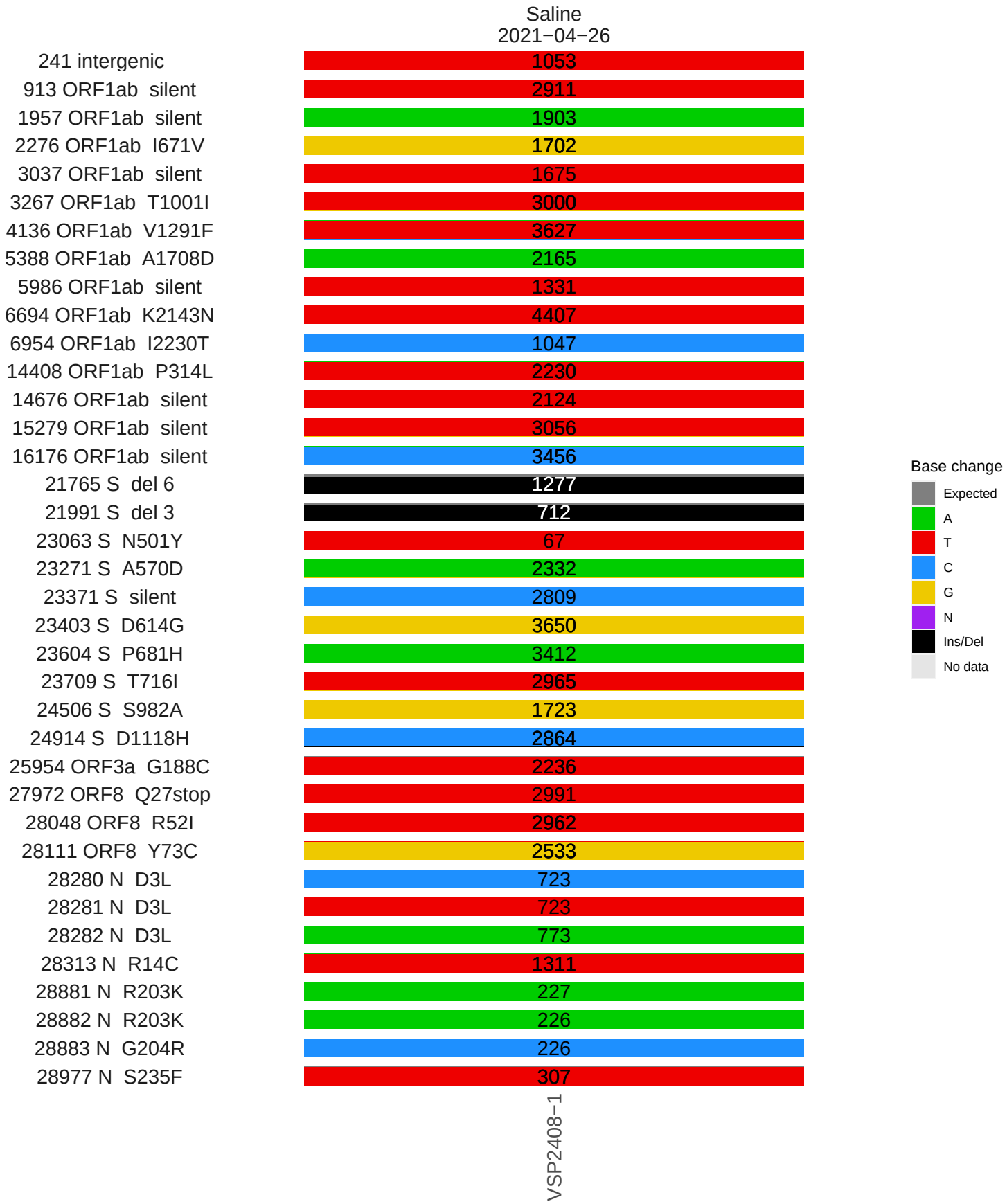
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2408-1	single experiment	NA	Saline	2021-04-26	29.81	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.

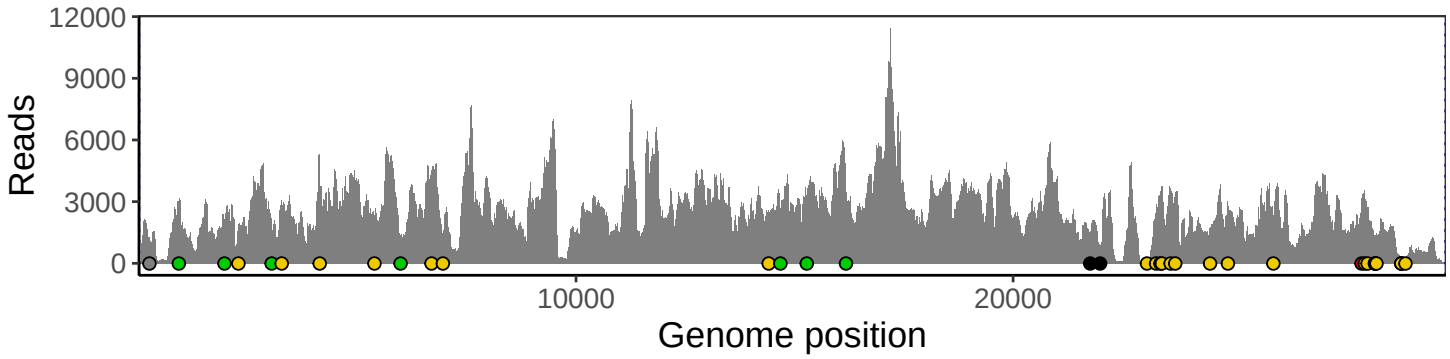



Saline
2021−04−26
241 intergenic
913 ORF1ab silent
1957 ORF1ab silent
2276 ORF1ab I671V
3037 ORF1ab silent
3267 ORF1ab T1001I
4136 ORF1ab V1291F
5388 ORF1ab A1708D
5986 ORF1ab silent
6694 ORF1ab K2143N
6954 ORF1ab I2230T
14408 ORF1ab P314L
14676 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
21765 S del 6
21991 S del 3
23063 S N501Y
23271 S A570D
23371 S silent
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
25954 ORF3a G188C
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28280 N D3L
28281 N D3L
28282 N D3L
28313 N R14C
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
1053
2911
1903
1702
1675
3000
3627
2165
1331
4407
1047
2230
2124
3056
3456
1277
712
67
2332
2809
3650
3412
2965
1723
2864
2236
2991
2962
2533
723
723
773
1311
227
226
226
307
VSP2408−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

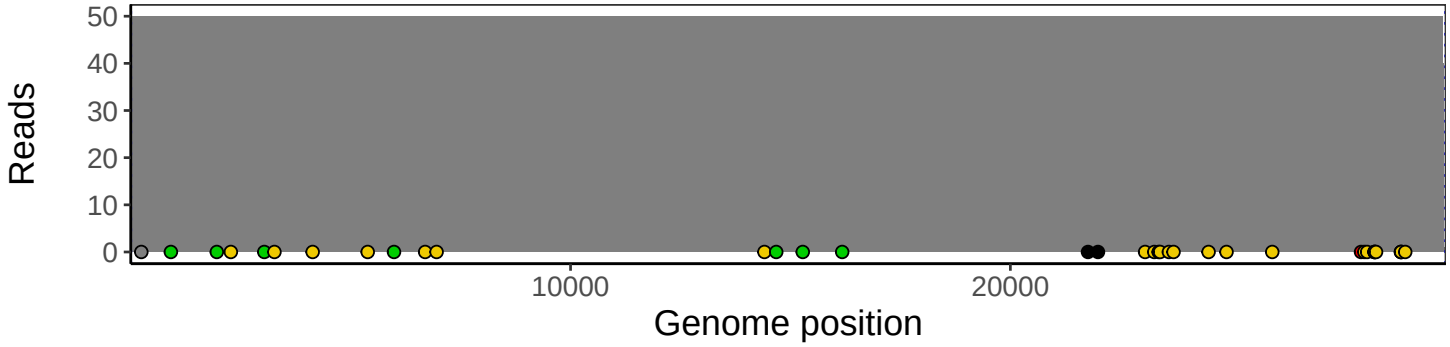
Analyses of individual experiments and composite results

VSP2408-1 | 2021-04-26 | Saline | HUP Q-0227 | genomes | single experiment

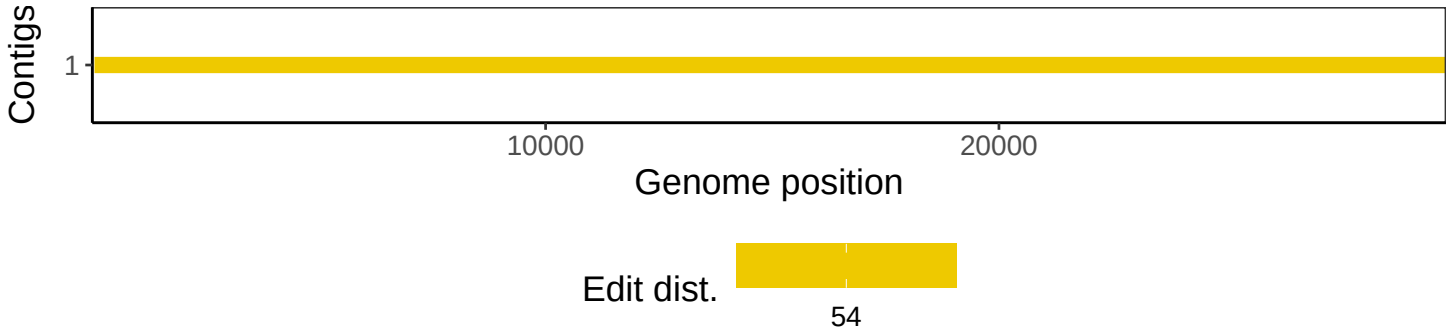
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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