COVID-19 subject HUP Q-0205

2021-05-05

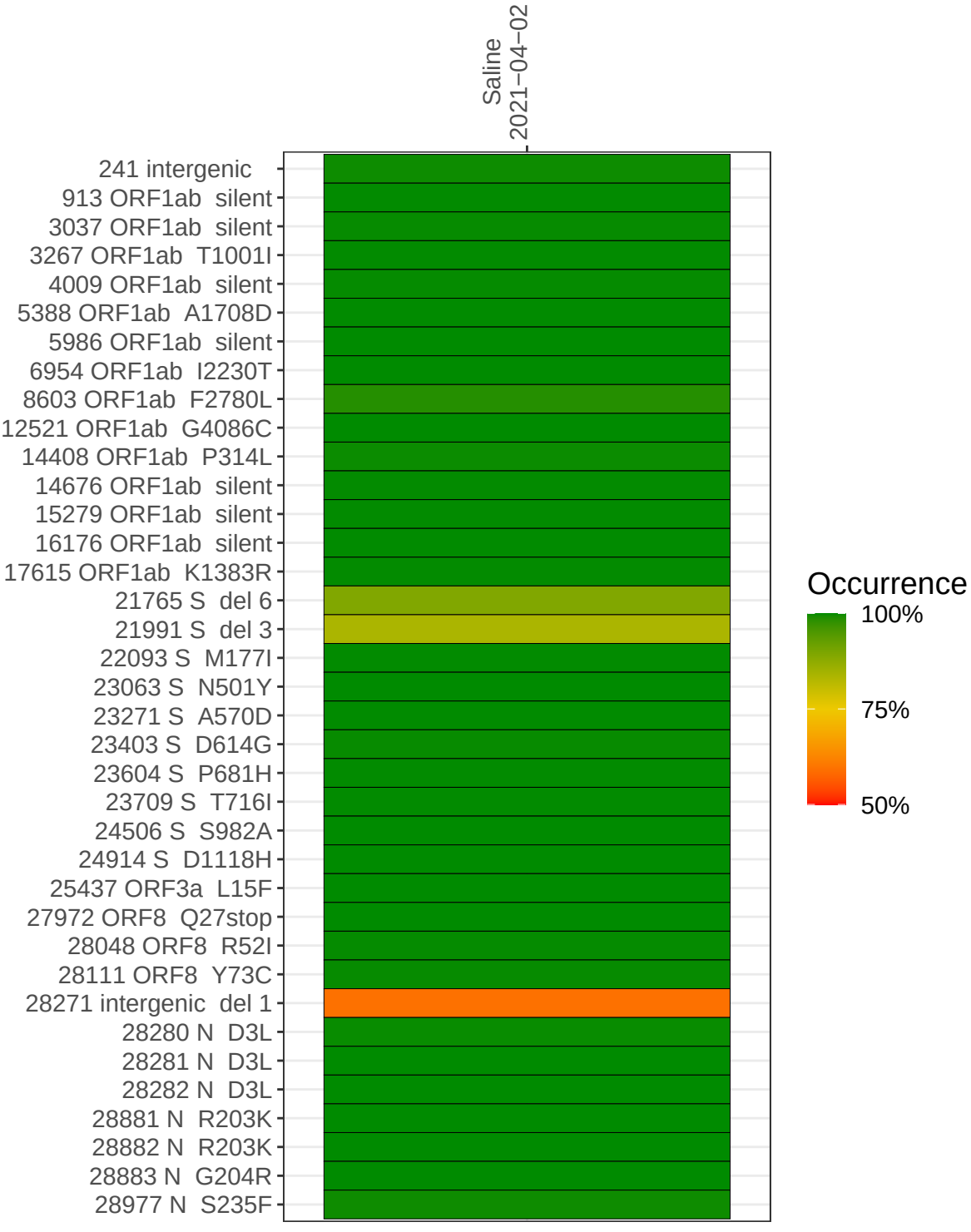
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

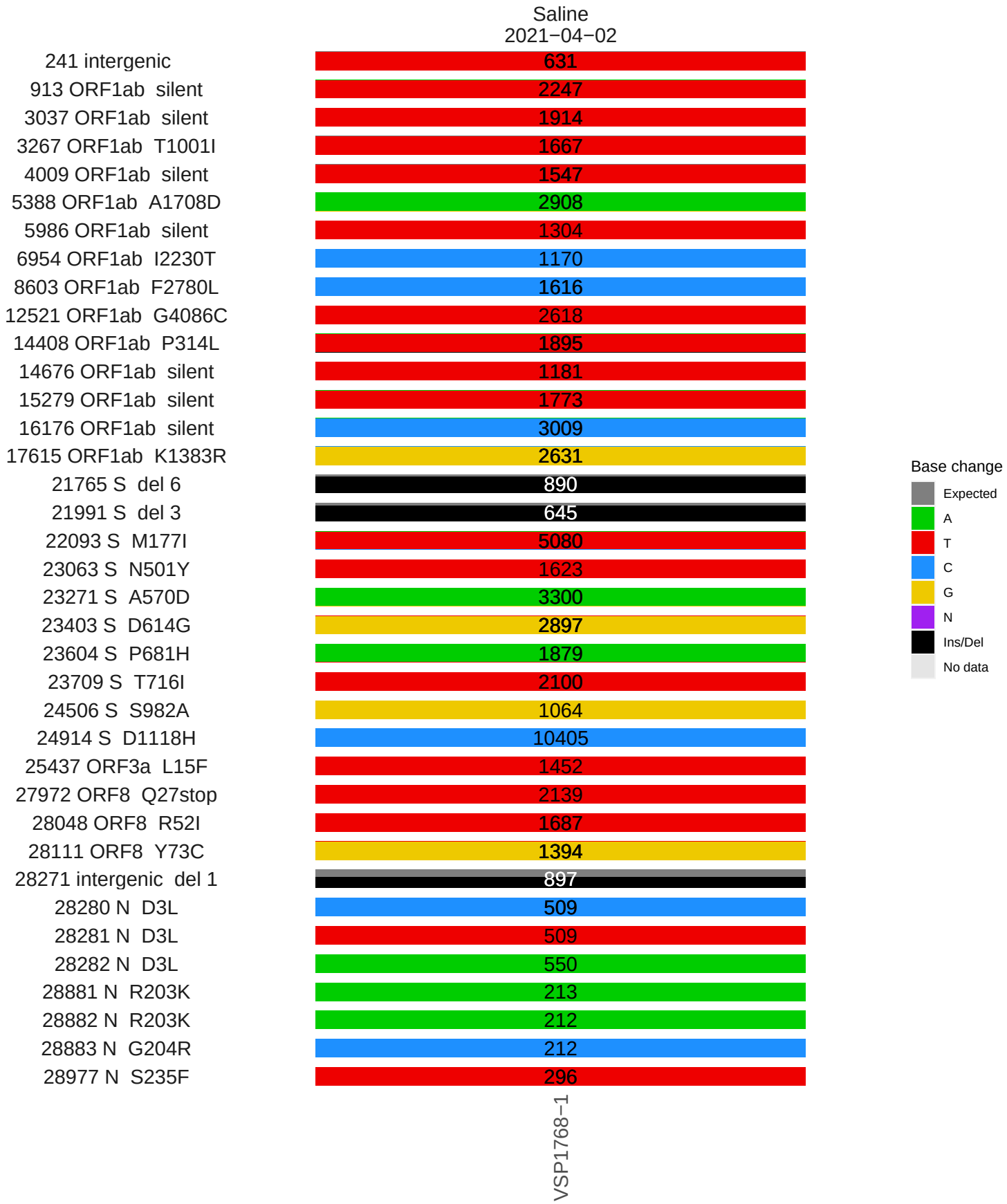
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1768-1	single experiment	NA	Saline	2021-04-02	29.83	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.

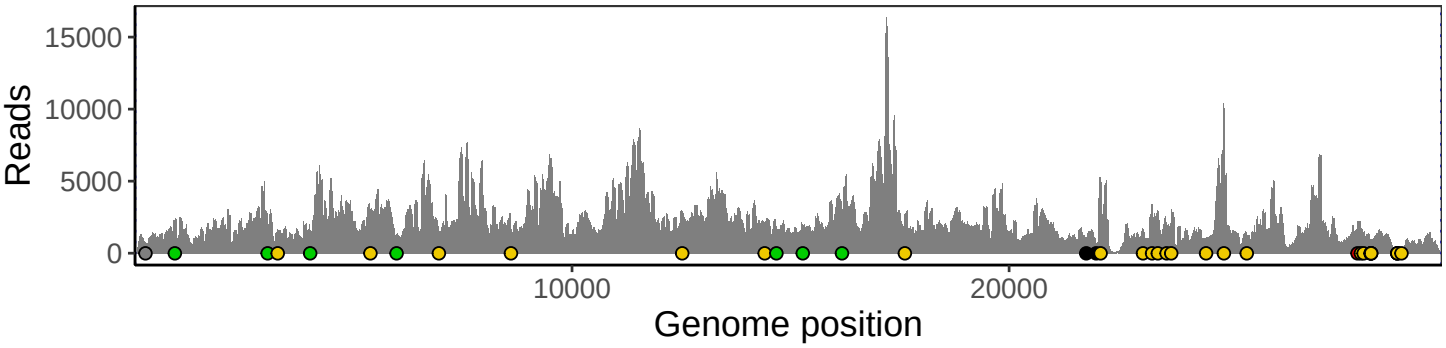



Saline
2021−04−02
241 intergenic
913 ORF1ab silent
3037 ORF1ab silent
3267 ORF1ab T1001I
4009 ORF1ab silent
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
8603 ORF1ab F2780L
12521 ORF1ab G4086C
14408 ORF1ab P314L
14676 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
17615 ORF1ab K1383R
21765 S del 6
21991 S del 3
22093 S M177I
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
25437 ORF3a L15F
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
631
2247
1914
1667
1547
2908
1304
1170
1616
2618
1895
1181
1773
3009
2631
890
645
5080
1623
3300
2897
1879
2100
1064
10405
1452
2139
1687
1394
897
509
509
550
213
212
212
296
VSP1768−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

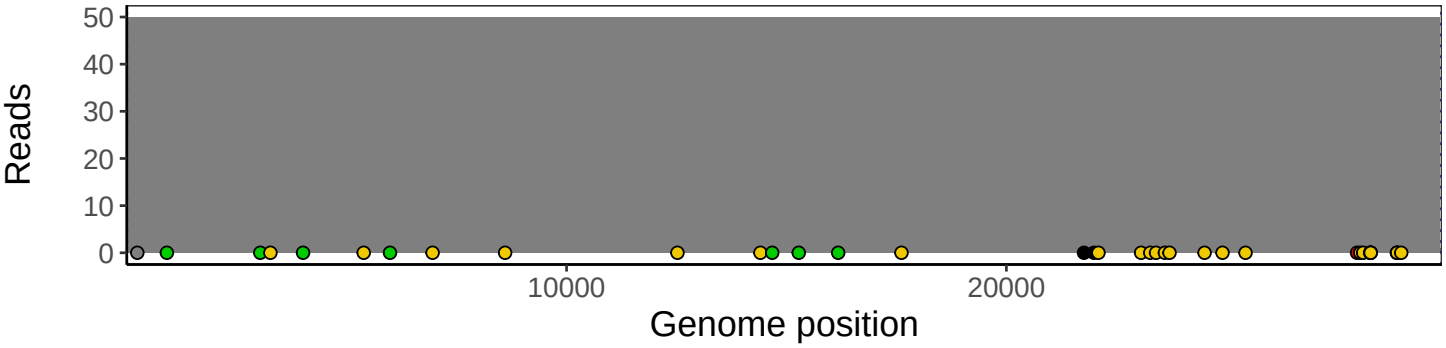
Analyses of individual experiments and composite results

VSP1768-1 | 2021-04-02 | Saline | HUP Q-0205 | genomes | single experiment

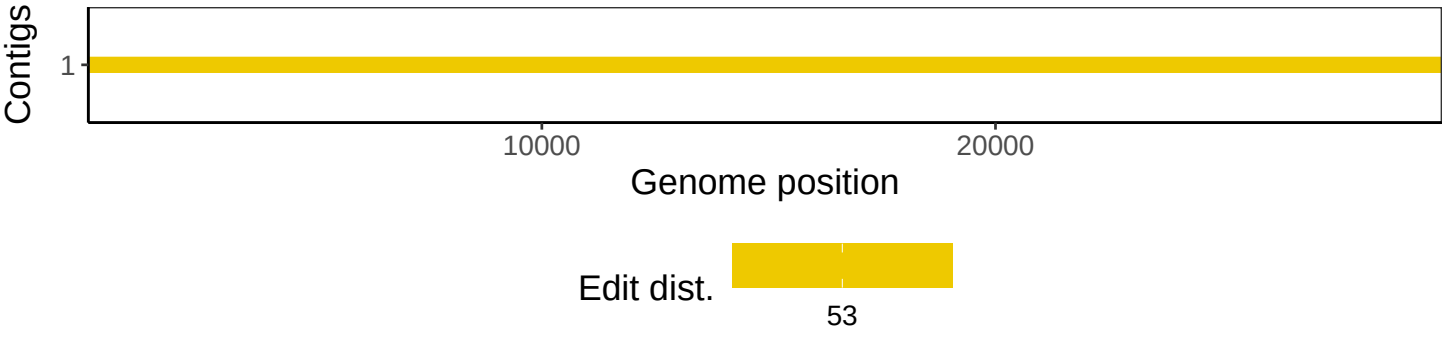
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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