COVID-19 subject HUP Q-0206

2021-06-23

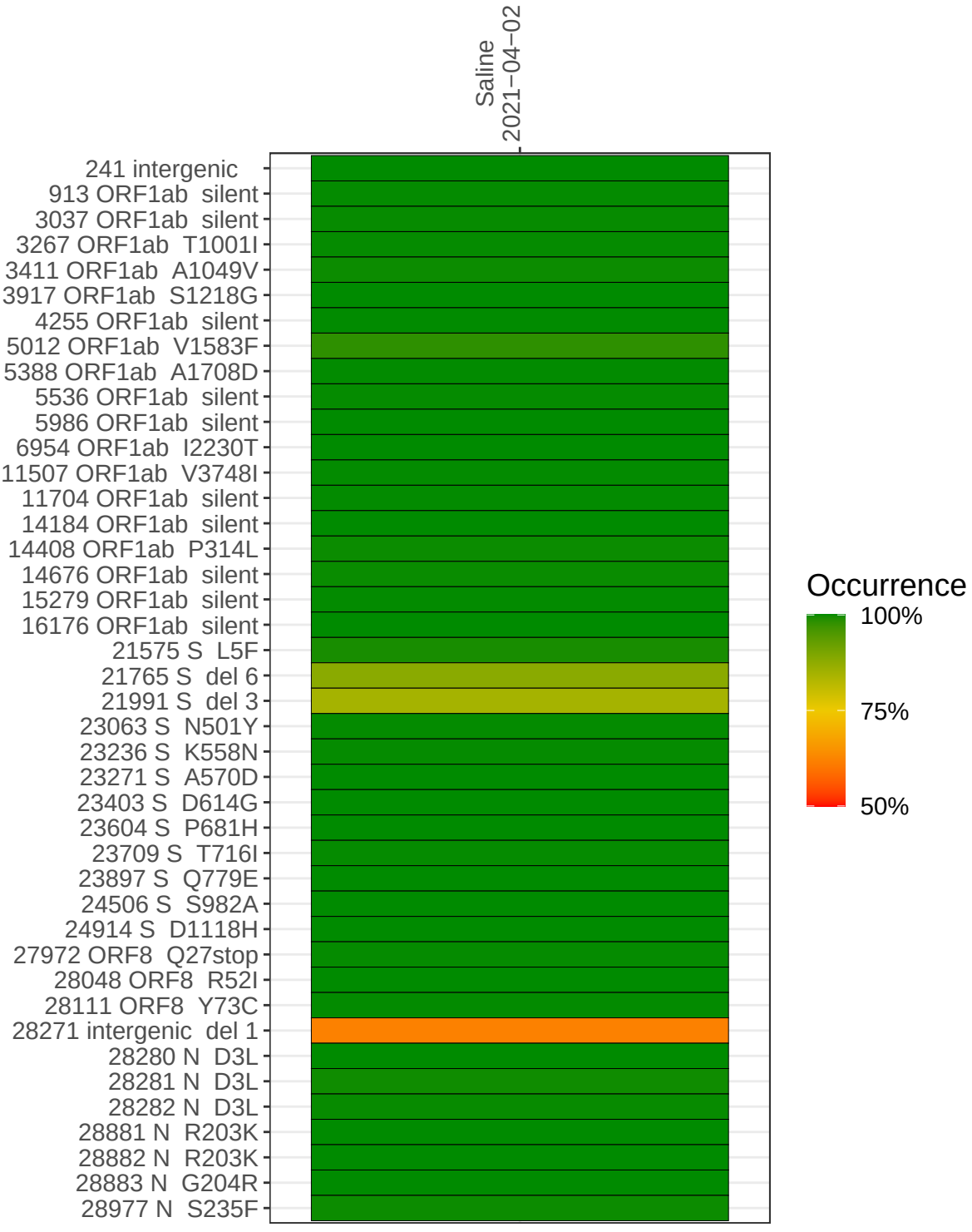
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

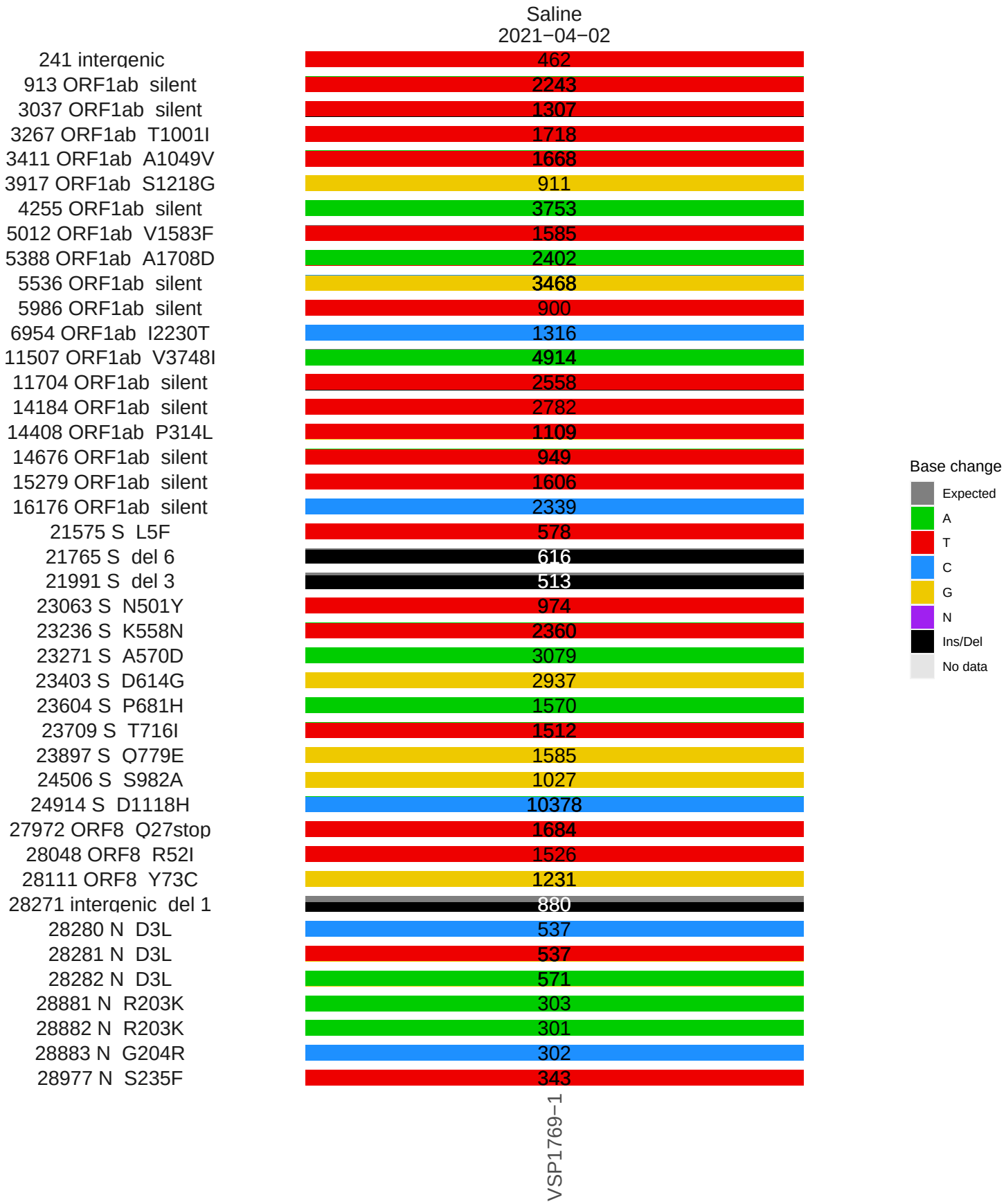
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1769-1	single experiment	NA	Saline	2021-04-02	29.82	B.1.1.7	99.8%	99.8%

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.

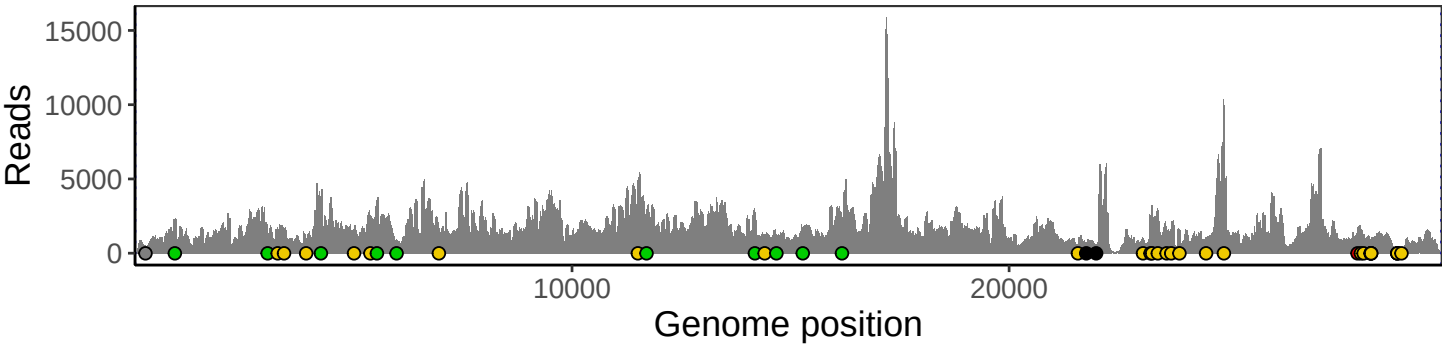



Saline
2021−04−02
241 intergenic 462
913 ORF1ab silent 2243
3037 ORF1ab silent 1307
3267 ORF1ab T1001I 1718
3411 ORF1ab A1049V 1668
3917 ORF1ab S1218G 911
4255 ORF1ab silent 3753
5012 ORF1ab V1583F 1585
5388 ORF1ab A1708D 2402
5536 ORF1ab silent 3468
5986 ORF1ab silent 900
6954 ORF1ab I2230T 1316
11507 ORF1ab V3748I 4914
11704 ORF1ab silent 2558
14184 ORF1ab silent 2782
14408 ORF1ab P314L 1109
14676 ORF1ab silent 949
15279 ORF1ab silent 1606
16176 ORF1ab silent 2339
21575 S L5F 578
21765 S del 6 616
21991 S del 3 513
23063 S N501Y 974
23236 S K558N 2360
23271 S A570D 3079
23403 S D614G 2937
23604 S P681H 1570
23709 S T716I 1512
23897 S Q779E 1585
24506 S S982A 1027
24914 S D1118H 10378
27972 ORF8 Q27stop 1684
28048 ORF8 R52I 1526
28111 ORF8 Y73C 1231
28271 intergenic del 1 880
28280 N D3L 537
28281 N D3L 537
28282 N D3L 571
28881 N R203K 303
28882 N R203K 301
28883 N G204R 302
28977 N S235F 343
VSP1769−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

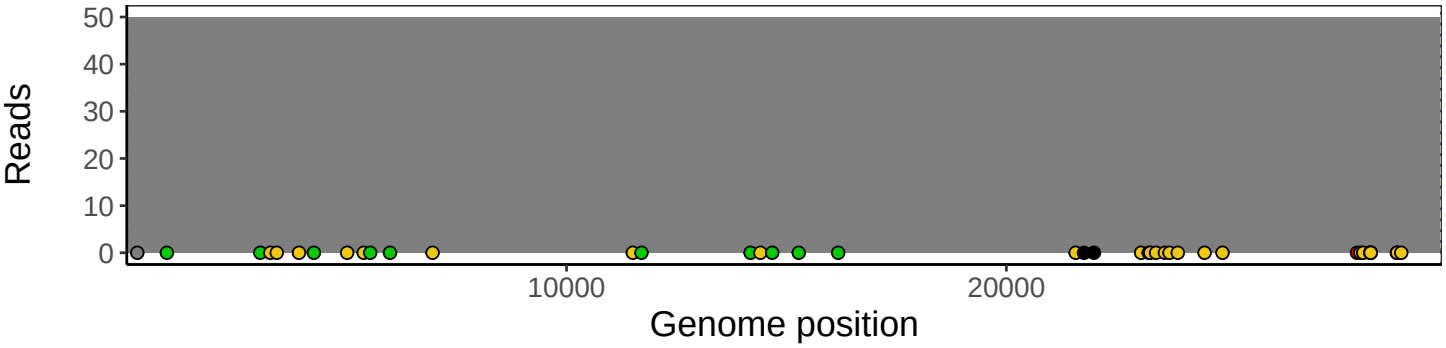
Analyses of individual experiments and composite results

VSP1769-1 | 2021-04-02 | Saline | HUP Q-0206 | genomes | single experiment

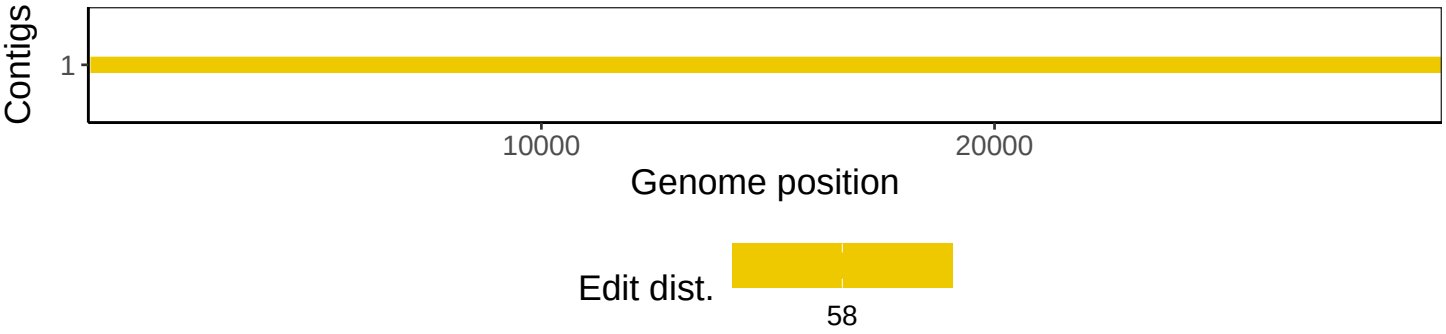
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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