COVID-19 subject HUP PH-0029

2021-05-05

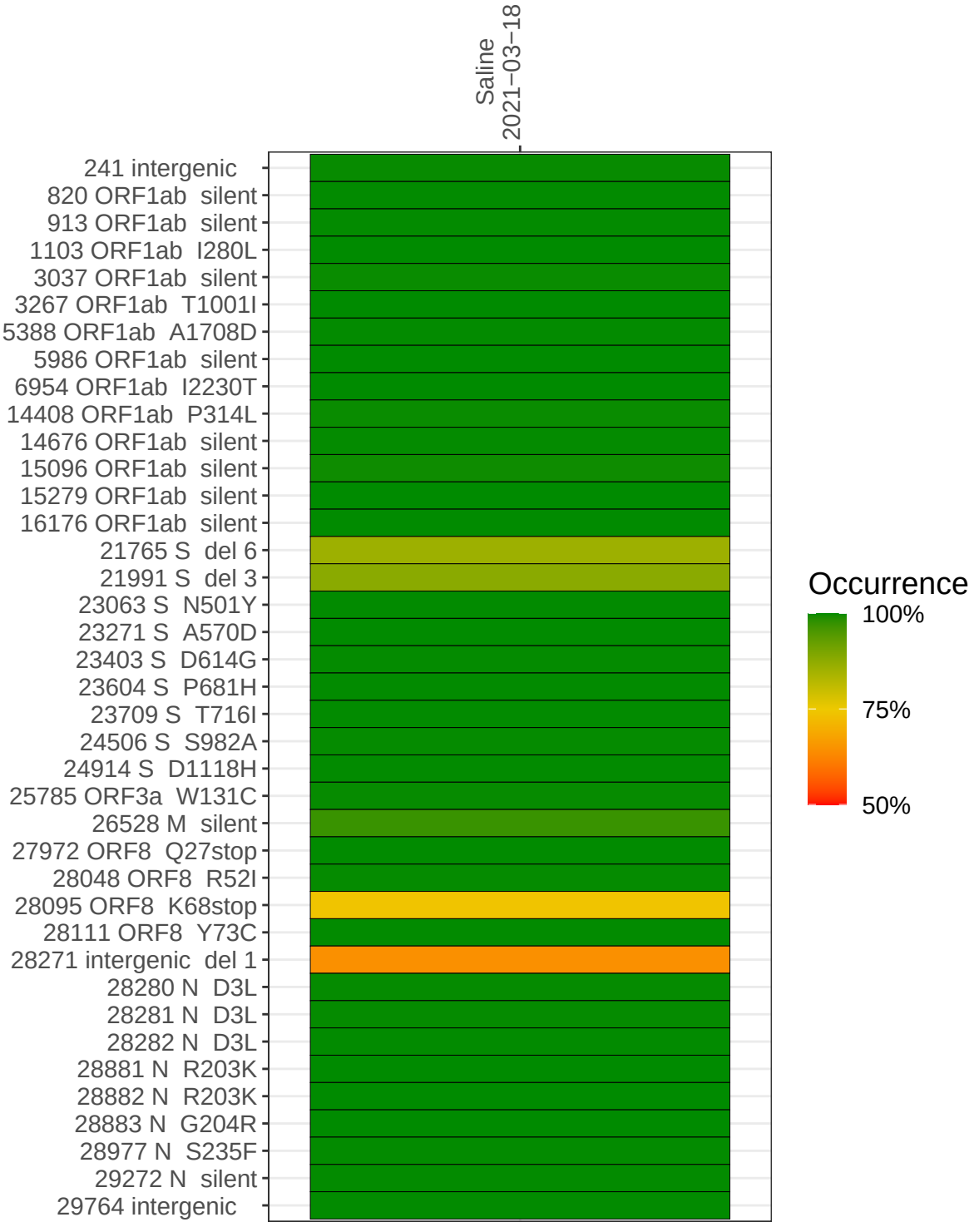
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

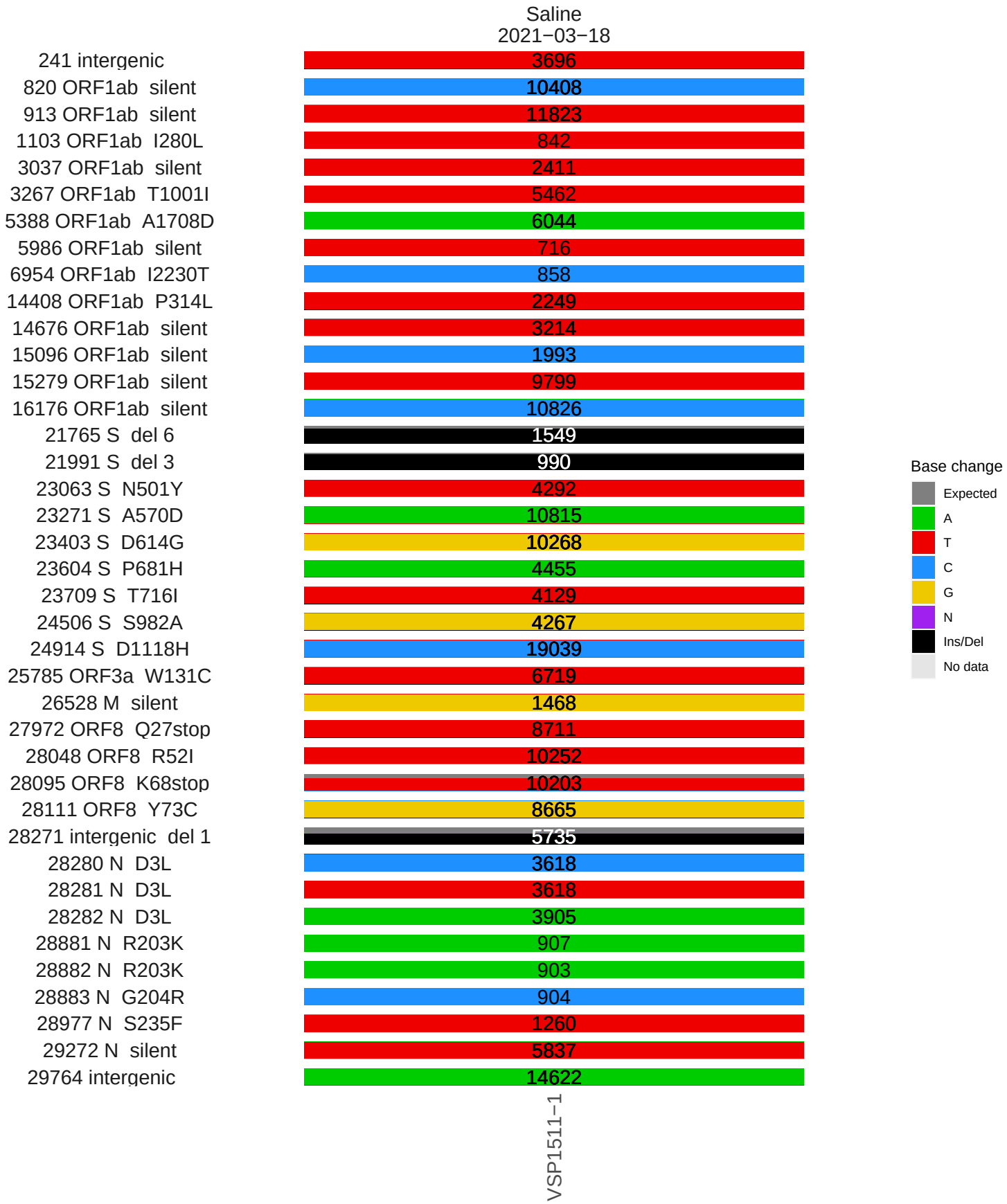
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1511-1	single experiment	NA	Saline	2021-03-18	29.80	B.1.1.7	99.9%	99.5%

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.

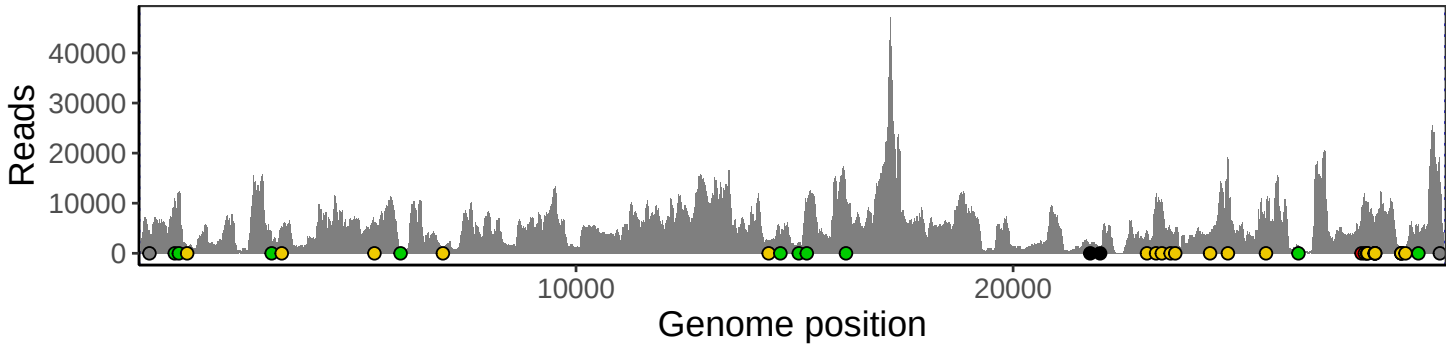



Saline
2021−03−18
241 intergenic 3696
820 ORF1ab silent 10408
913 ORF1ab silent 11823
1103 ORF1ab I280L 842
3037 ORF1ab silent 2411
3267 ORF1ab T1001I 5462
5388 ORF1ab A1708D 6044
5986 ORF1ab silent 716
6954 ORF1ab I2230T 858
14408 ORF1ab P314L 2249
14676 ORF1ab silent 3214
15096 ORF1ab silent 1993
15279 ORF1ab silent 9799
16176 ORF1ab silent 10826
21765 S del 6 1549
21991 S del 3 990
23063 S N501Y 4292
23271 S A570D 10815
23403 S D614G 10268
23604 S P681H 4455
23709 S T716I 4129
24506 S S982A 4267
24914 S D1118H 19039
25785 ORF3a W131C 6719
26528 M silent 1468
27972 ORF8 Q27stop 8711
28048 ORF8 R52I 10252
28095 ORF8 K68stop 10203
28111 ORF8 Y73C 8665
28271 intergenic del 1 5735
28280 N D3L 3618
28281 N D3L 3618
28282 N D3L 3905
28881 N R203K 907
28882 N R203K 903
28883 N G204R 904
28977 N S235F 1260
29272 N silent 5837
29764 intergenic 14622
VSP1511−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

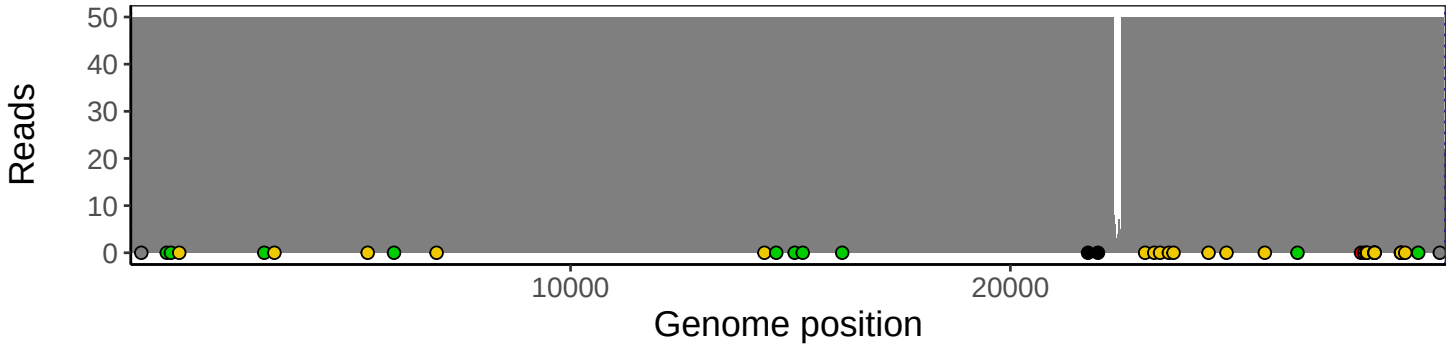
Analyses of individual experiments and composite results

VSP1511-1 | 2021-03-18 | Saline | HUP PH-0029 | genomes | single experiment

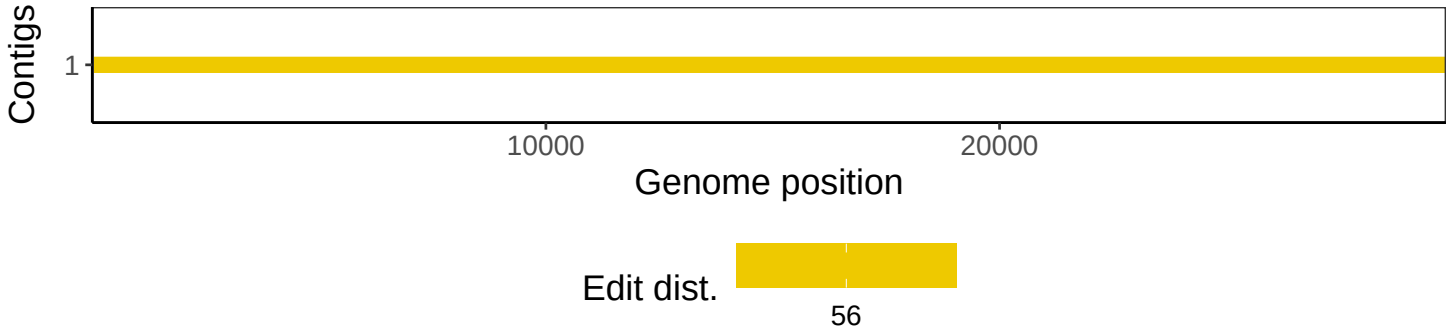
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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