COVID-19 subject HUP Q-0054

2021-05-05

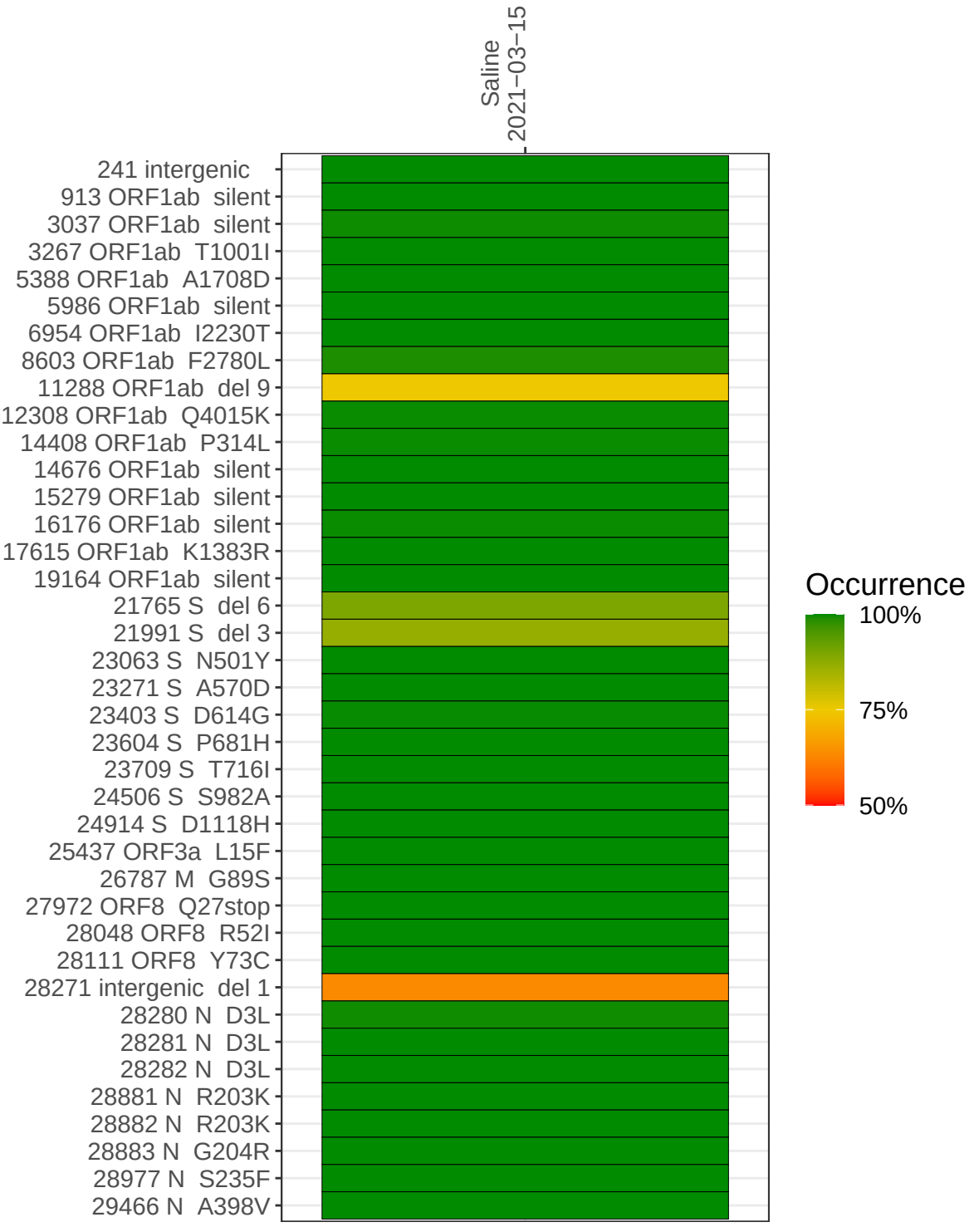
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

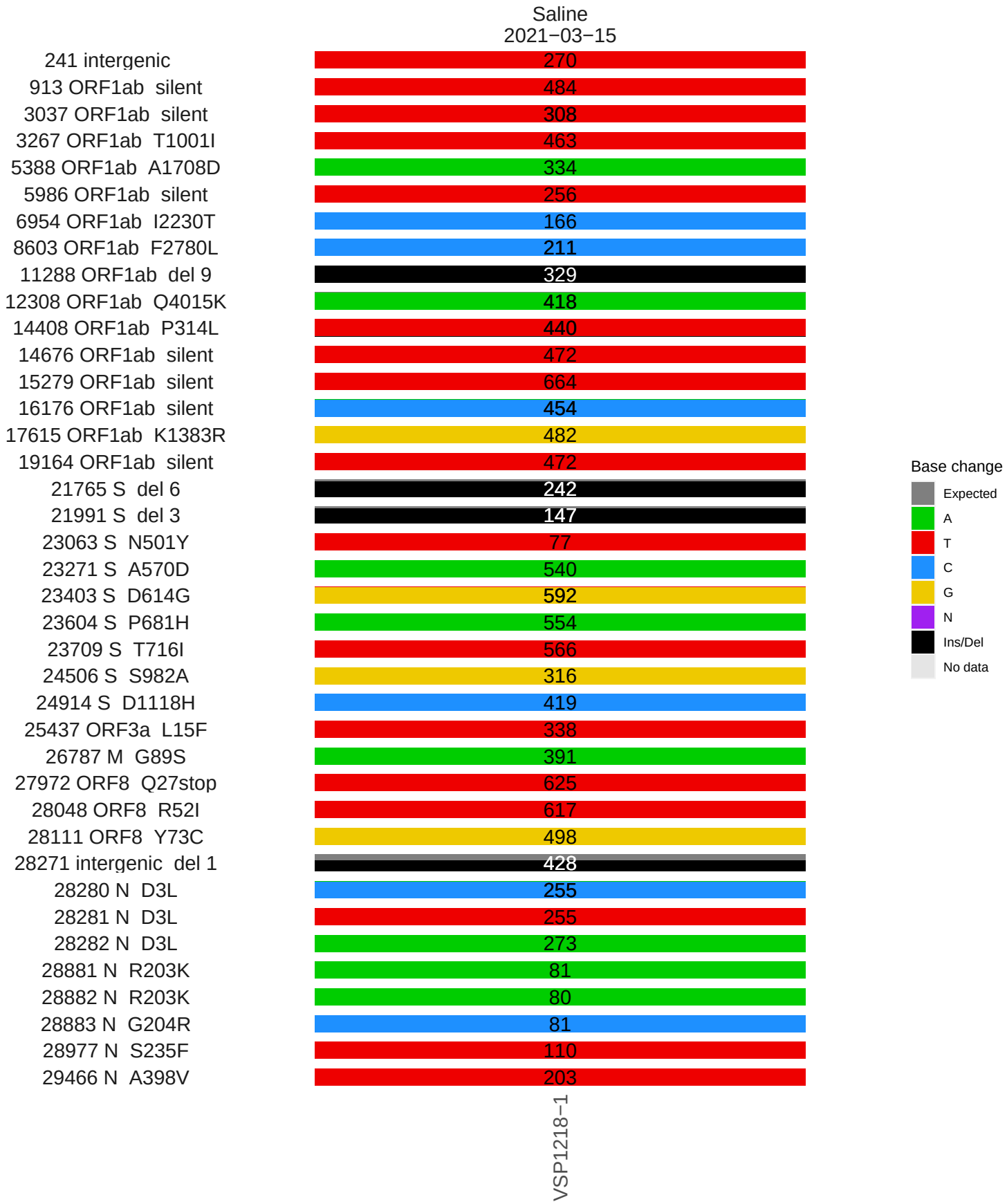
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1218-1	single experiment	NA	Saline	2021-03-15	29.79	B.1.1.7	99.7%	99.6%

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.

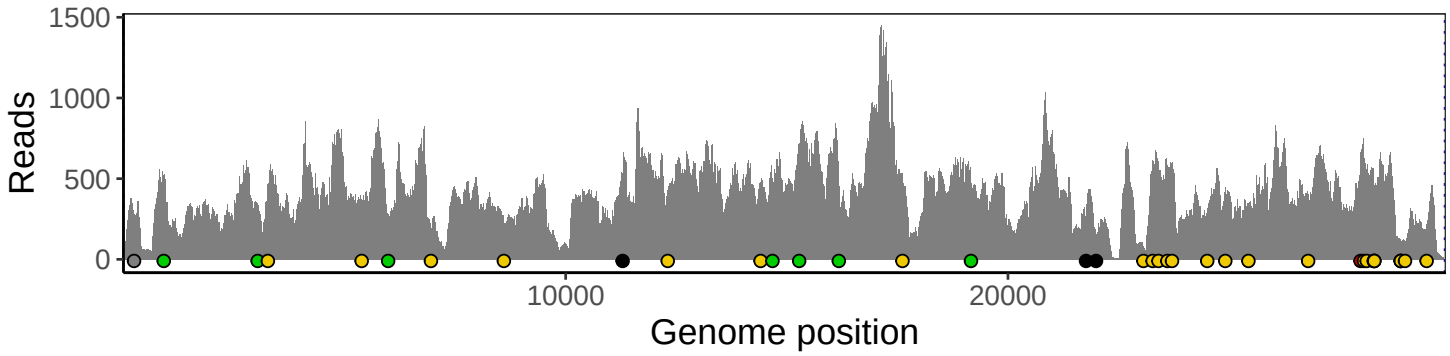



Saline
2021−03−15
241 intergenic 270
913 ORF1ab silent 484
3037 ORF1ab silent 308
3267 ORF1ab T1001I 463
5388 ORF1ab A1708D 334
5986 ORF1ab silent 256
6954 ORF1ab I2230T 166
8603 ORF1ab F2780L 211
11288 ORF1ab del 9 329
12308 ORF1ab Q4015K 418
14408 ORF1ab P314L 440
14676 ORF1ab silent 472
15279 ORF1ab silent 664
16176 ORF1ab silent 454
17615 ORF1ab K1383R 482
19164 ORF1ab silent 472
21765 S del 6 242
21991 S del 3 147
23063 S N501Y 77
23271 S A570D 540
23403 S D614G 592
23604 S P681H 554
23709 S T716I 566
24506 S S982A 316
24914 S D1118H 419
25437 ORF3a L15F 338
26787 M G89S 391
27972 ORF8 Q27stop 625
28048 ORF8 R52I 617
28111 ORF8 Y73C 498
28271 intergenic del 1 428
28280 N D3L 255
28281 N D3L 255
28282 N D3L 273
28881 N R203K 81
28882 N R203K 80
28883 N G204R 81
28977 N S235F 110
29466 N A398V 203
VSP1218−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

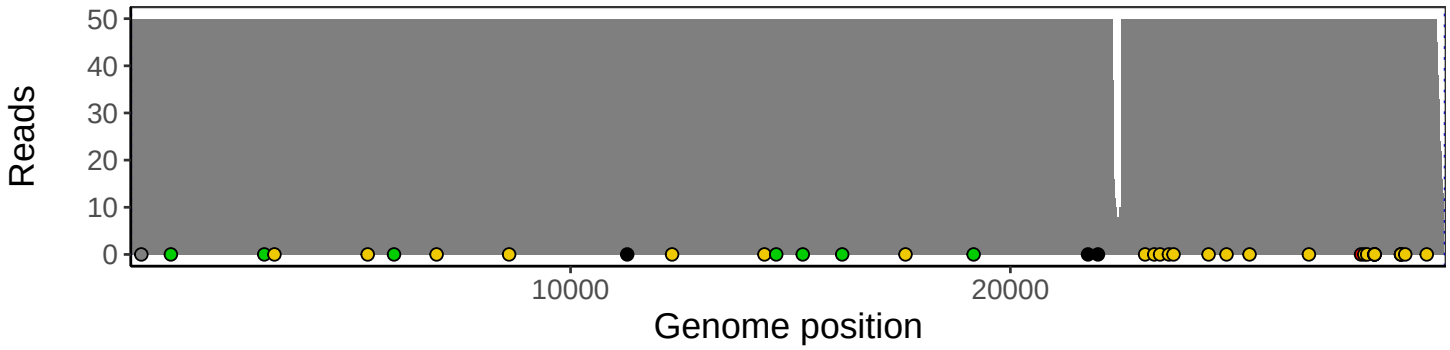
Analyses of individual experiments and composite results

VSP1218-1 | 2021-03-15 | Saline | HUP Q-0054 | genomes | single experiment

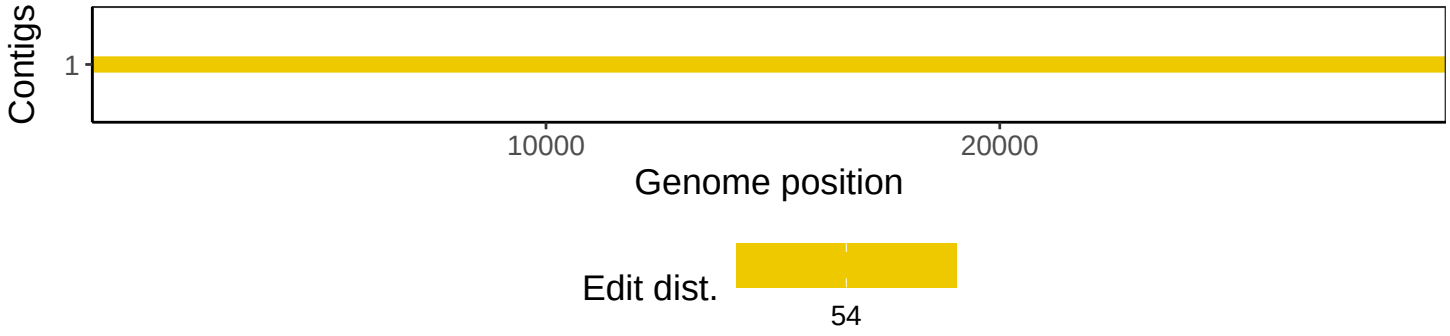
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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