COVID-19 subject HUP Q-0153

2021-05-05

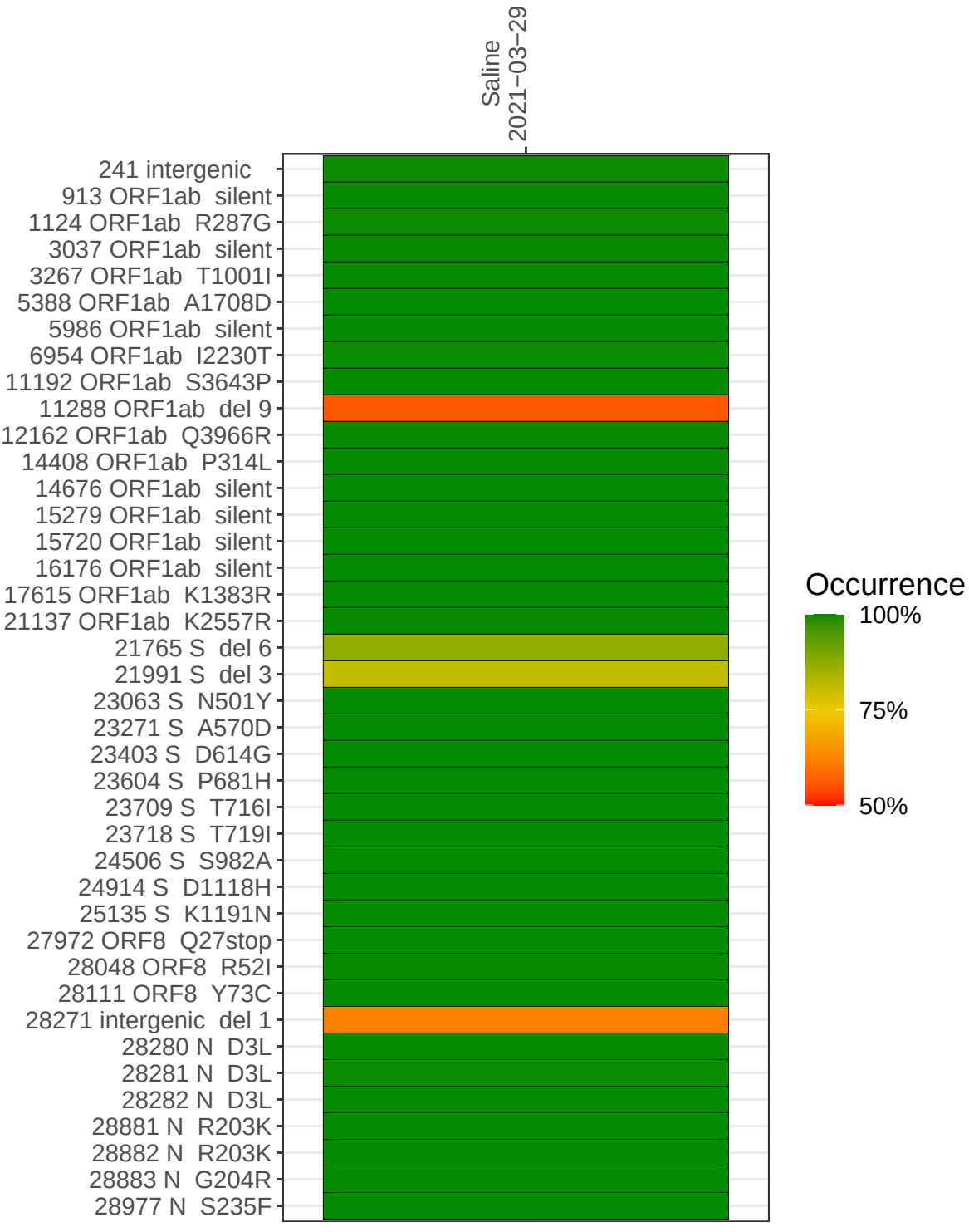
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

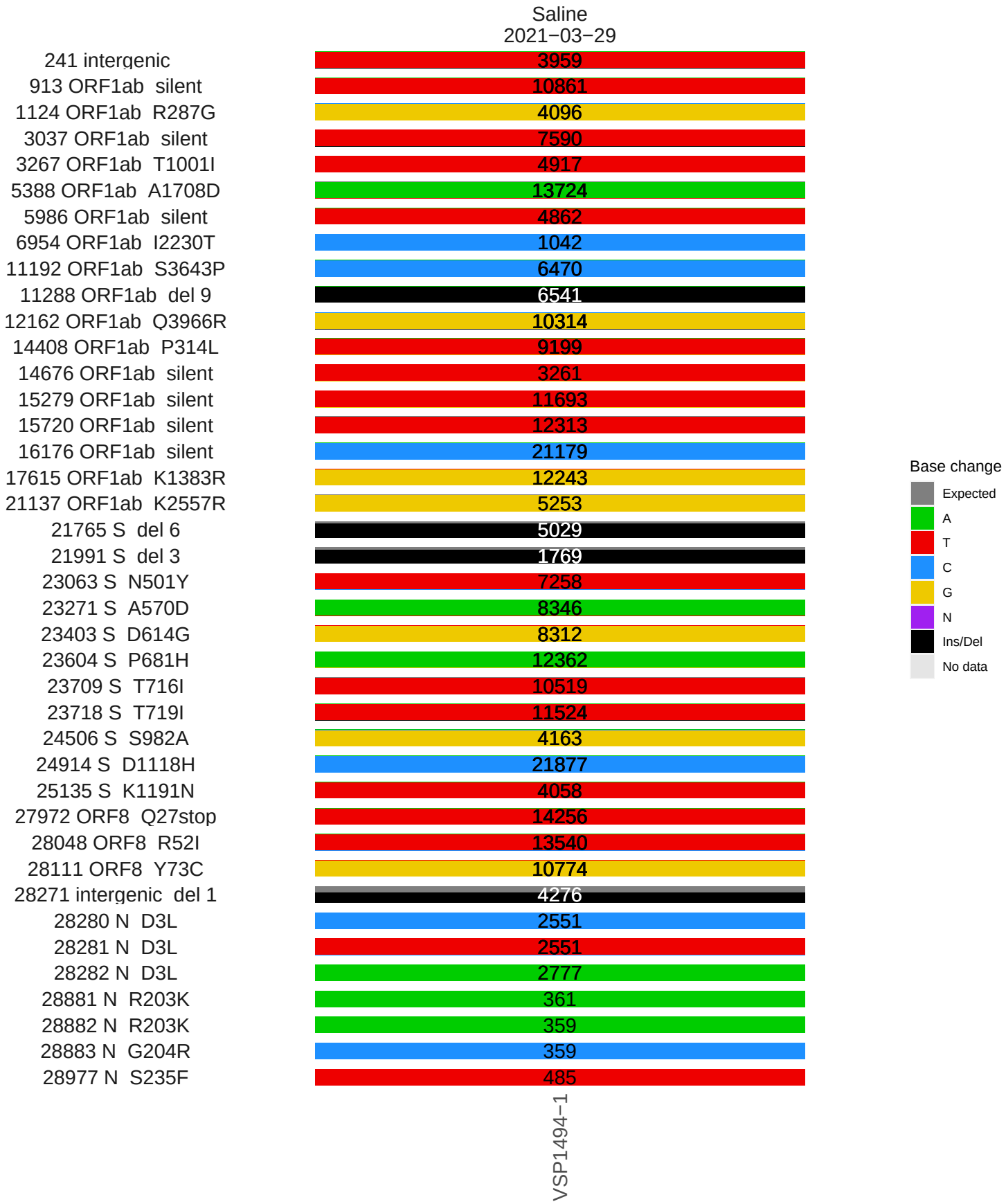
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1494-1	single experiment	NA	Saline	2021-03-29	29.90	B.1.1.7	99.9%	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.

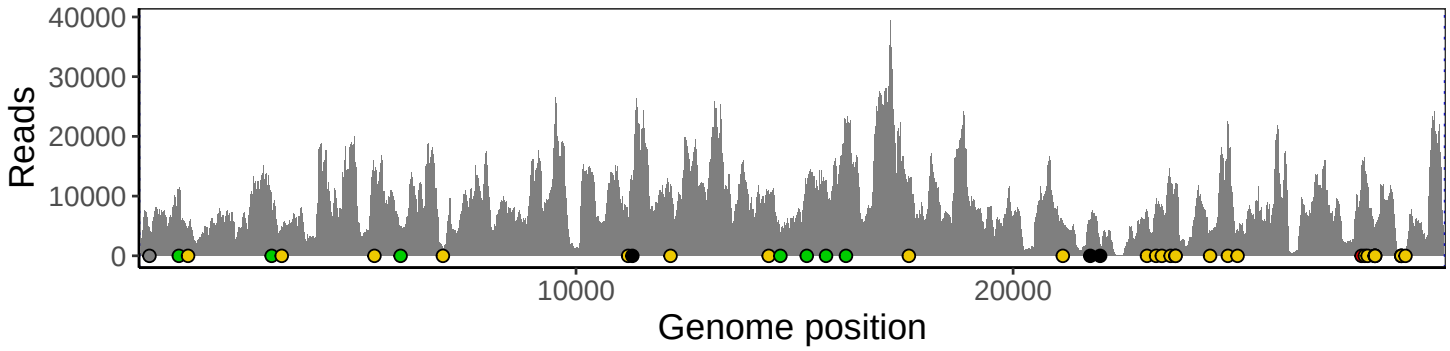



Saline
2021−03−29
241 intergenic
913 ORF1ab silent
1124 ORF1ab R287G
3037 ORF1ab silent
3267 ORF1ab T1001I
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
11192 ORF1ab S3643P
11288 ORF1ab del 9
12162 ORF1ab Q3966R
14408 ORF1ab P314L
14676 ORF1ab silent
15279 ORF1ab silent
15720 ORF1ab silent
16176 ORF1ab silent
17615 ORF1ab K1383R
21137 ORF1ab K2557R
21765 S del 6
21991 S del 3
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
23718 S T719I
24506 S S982A
24914 S D1118H
25135 S K1191N
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
3959
10861
4096
7590
4917
13724
4862
1042
6470
6541
10314
9199
3261
11693
12313
21179
12243
5253
5029
1769
7258
8346
8312
12362
10519
11524
4163
21877
4058
14256
13540
10774
4276
2551
2551
2777
361
359
359
485
VSP1494−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

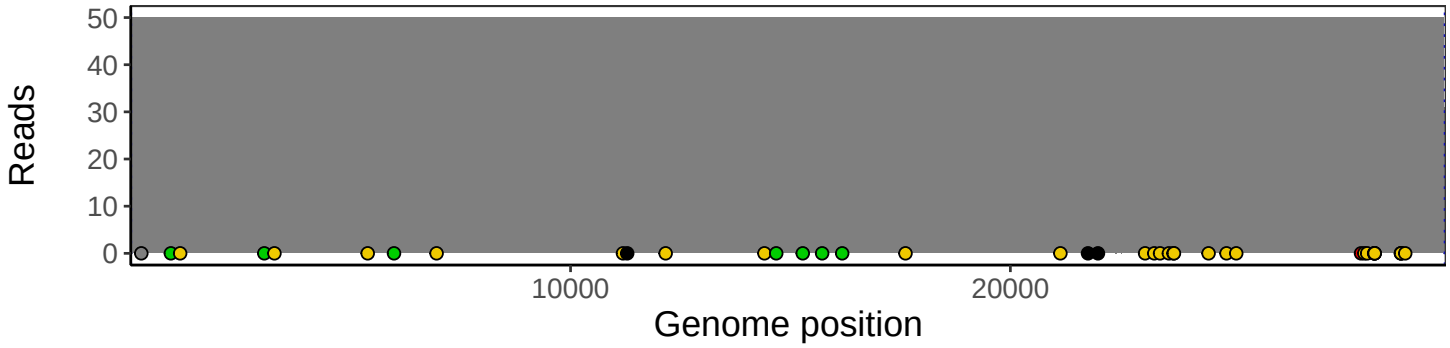
Analyses of individual experiments and composite results

VSP1494-1 | 2021-03-29 | Saline | HUP Q-0153 | genomes | single experiment

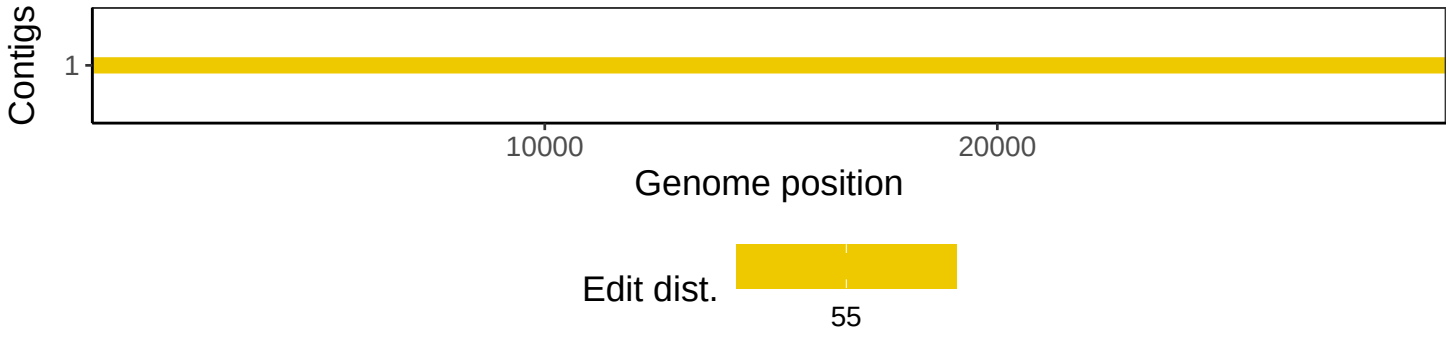
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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