COVID-19 subject HUP Q-0031

2021-04-17

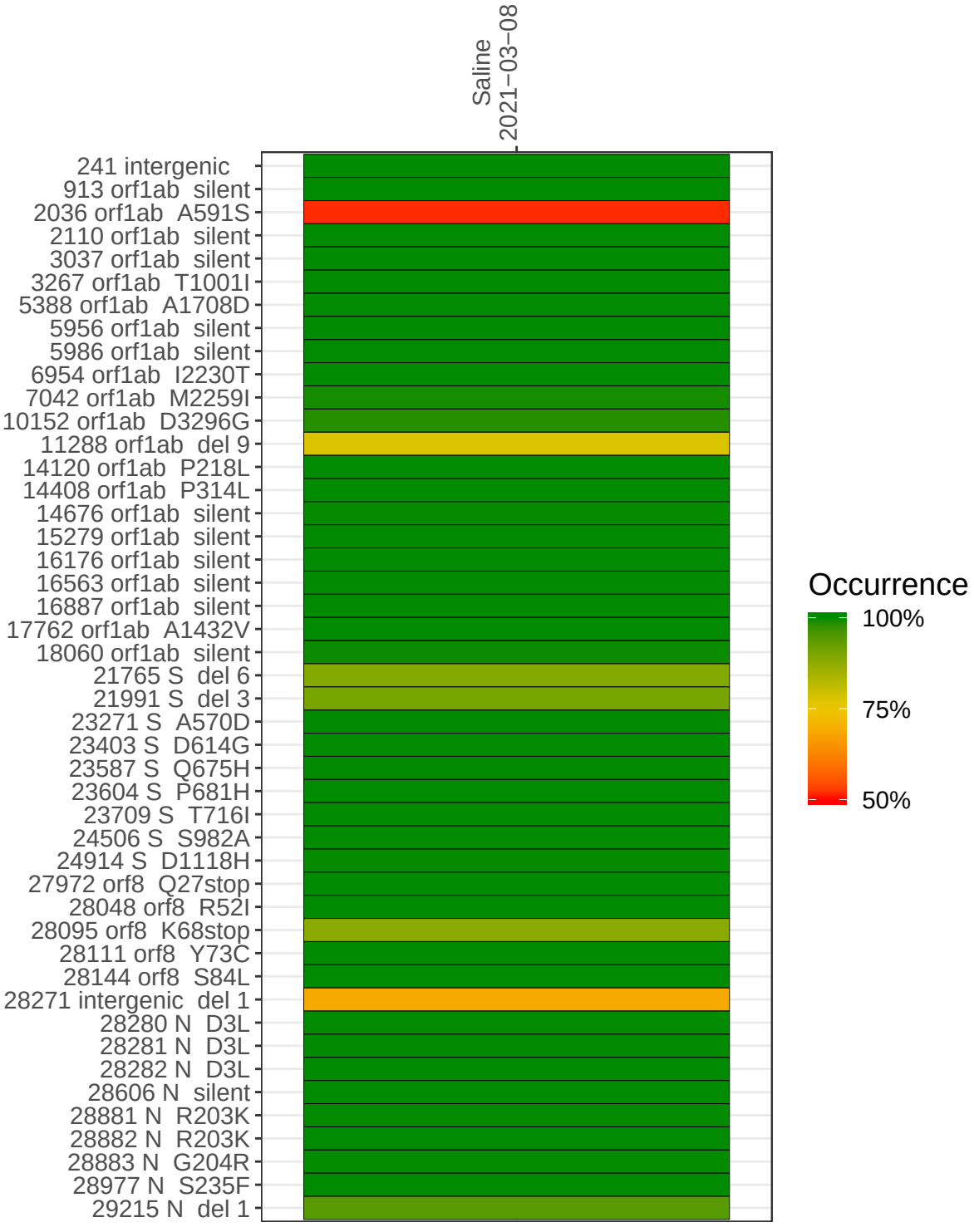
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

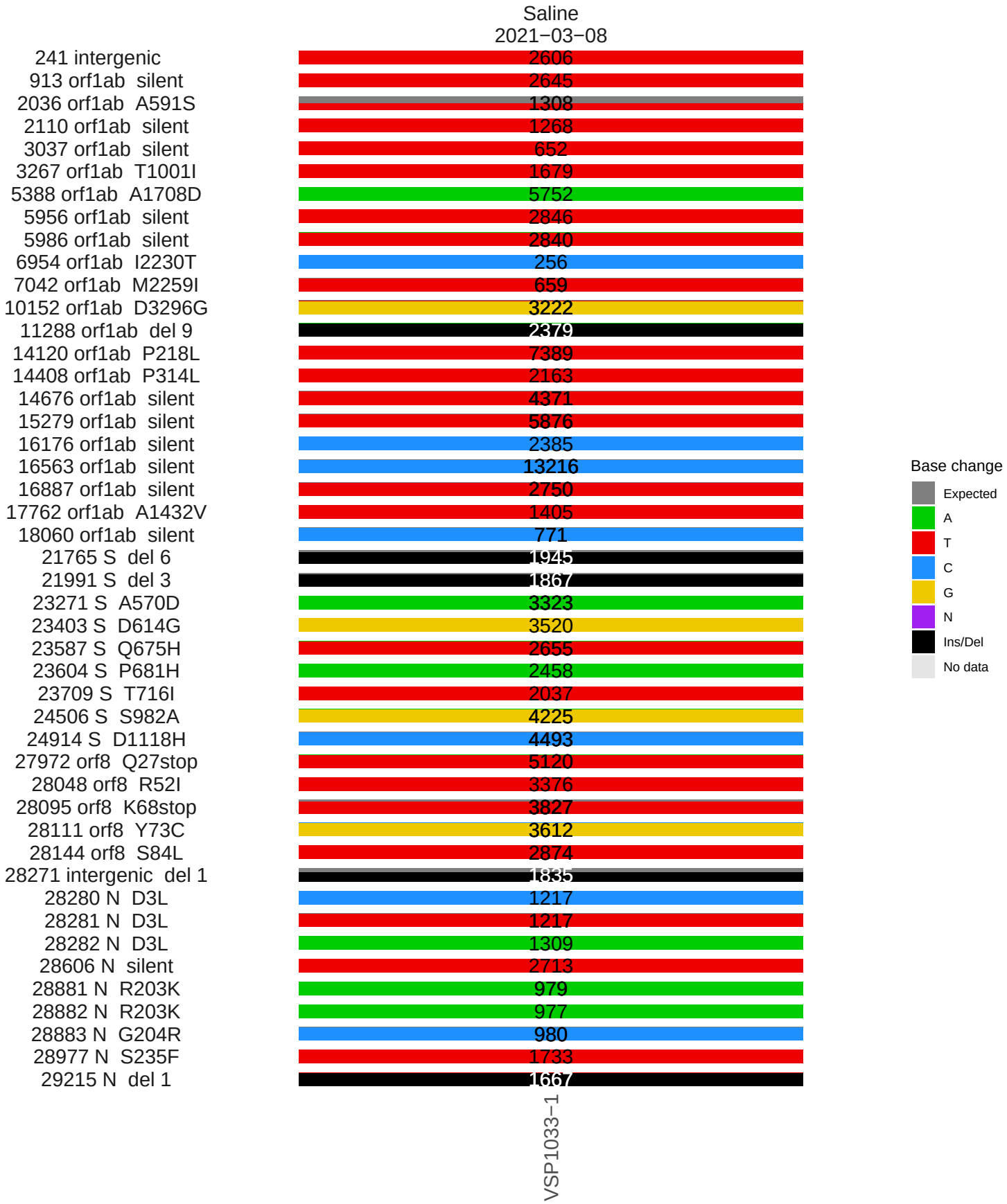
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1033-1	single experiment	NA	Saline	2021-03-08	7.13	B.1.1.7	95.3%	95.3%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

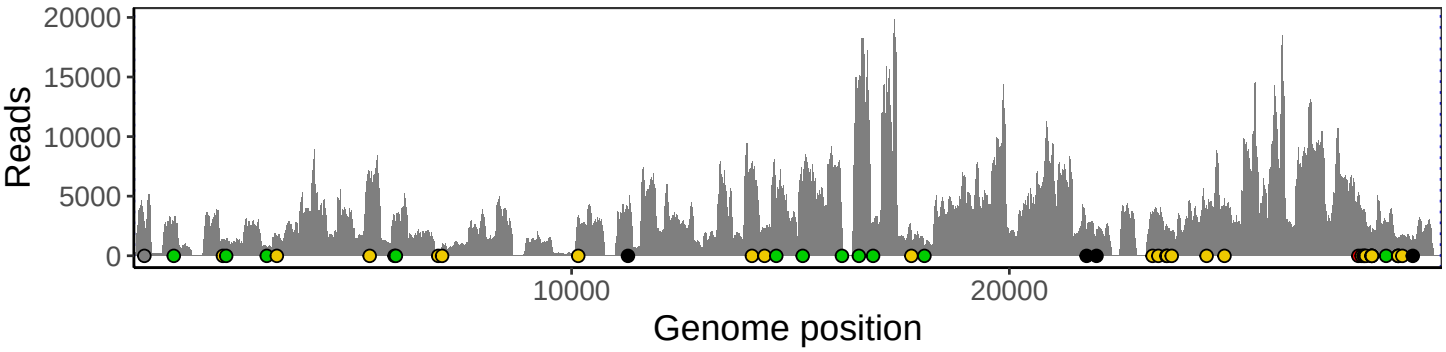



Saline
2021−03−08
241 intergenic
913 orf1ab silent
2036 orf1ab A591S
2110 orf1ab silent
3037 orf1ab silent
3267 orf1ab T1001I
5388 orf1ab A1708D
5956 orf1ab silent
5986 orf1ab silent
6954 orf1ab I2230T
7042 orf1ab M2259I
10152 orf1ab D3296G
11288 orf1ab del 9
14120 orf1ab P218L
14408 orf1ab P314L
14676 orf1ab silent
15279 orf1ab silent
16176 orf1ab silent
16563 orf1ab silent
16887 orf1ab silent
17762 orf1ab A1432V
18060 orf1ab silent
21765 S del 6
21991 S del 3
23271 S A570D
23403 S D614G
23587 S Q675H
23604 S P681H
23709 S T716I
24506 S S982A
24914 S D1118H
27972 orf8 Q27stop
28048 orf8 R52I
28095 orf8 K68stop
28111 orf8 Y73C
28144 orf8 S84L
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28606 N silent
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29215 N del 1
2606
2645
1308
1268
652
1679
5752
2846
2840
256
659
3222
2379
7389
2163
4371
5876
2385
13216
2750
1405
771
1945
1867
3323
3520
2655
2458
2037
4225
4493
5120
3376
3827
3612
2874
1835
1217
1217
1309
2713
979
977
980
1733
1667
VSP1033−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

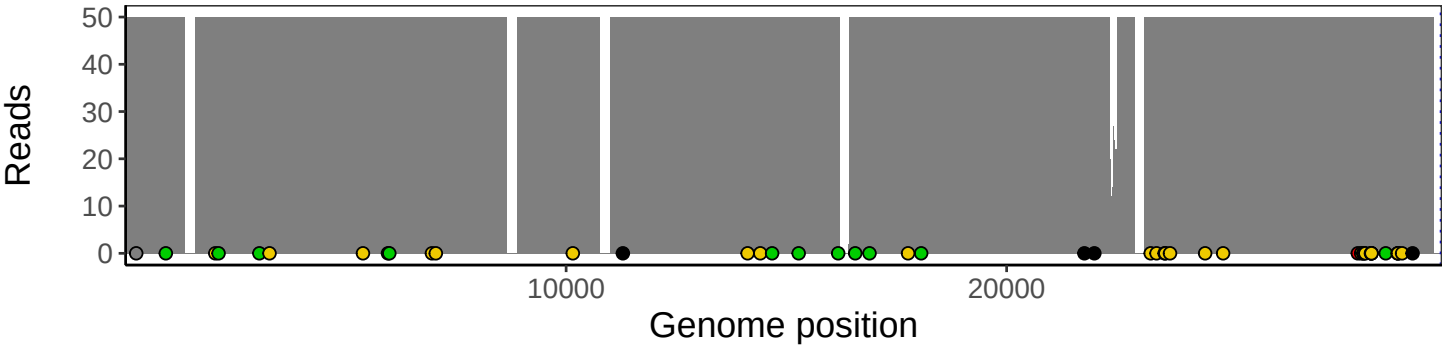
Analyses of individual experiments and composite results

VSP1033-1 | 2021-03-08 | Saline | HUP Q-0031 | genomes | single experiment

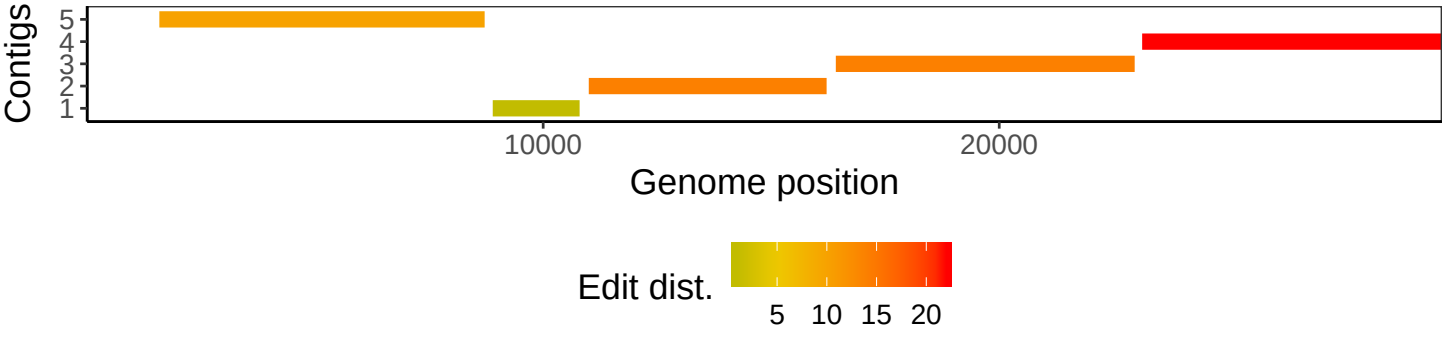
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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