COVID-19 subject HUP Q-0144

2021-05-05

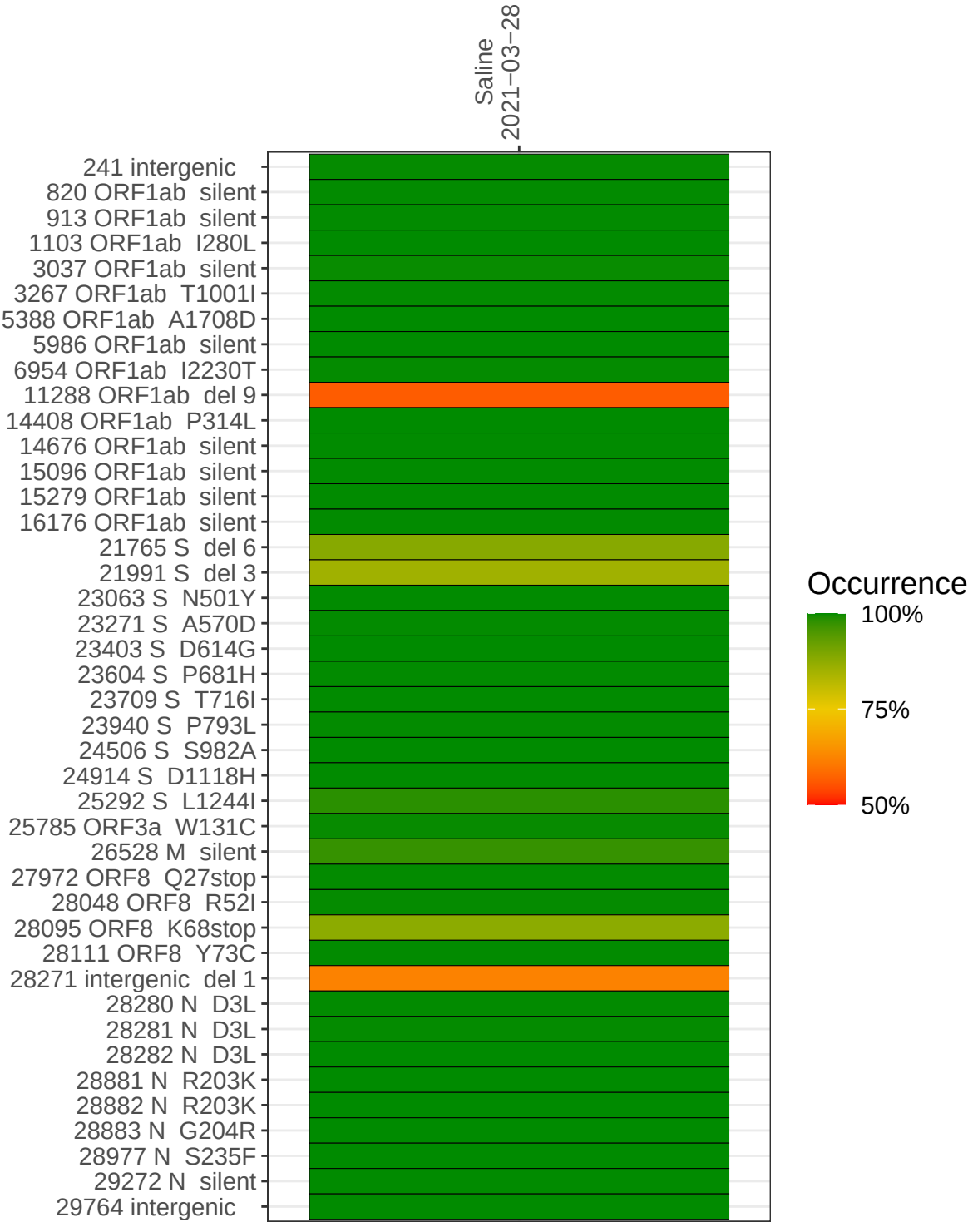
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

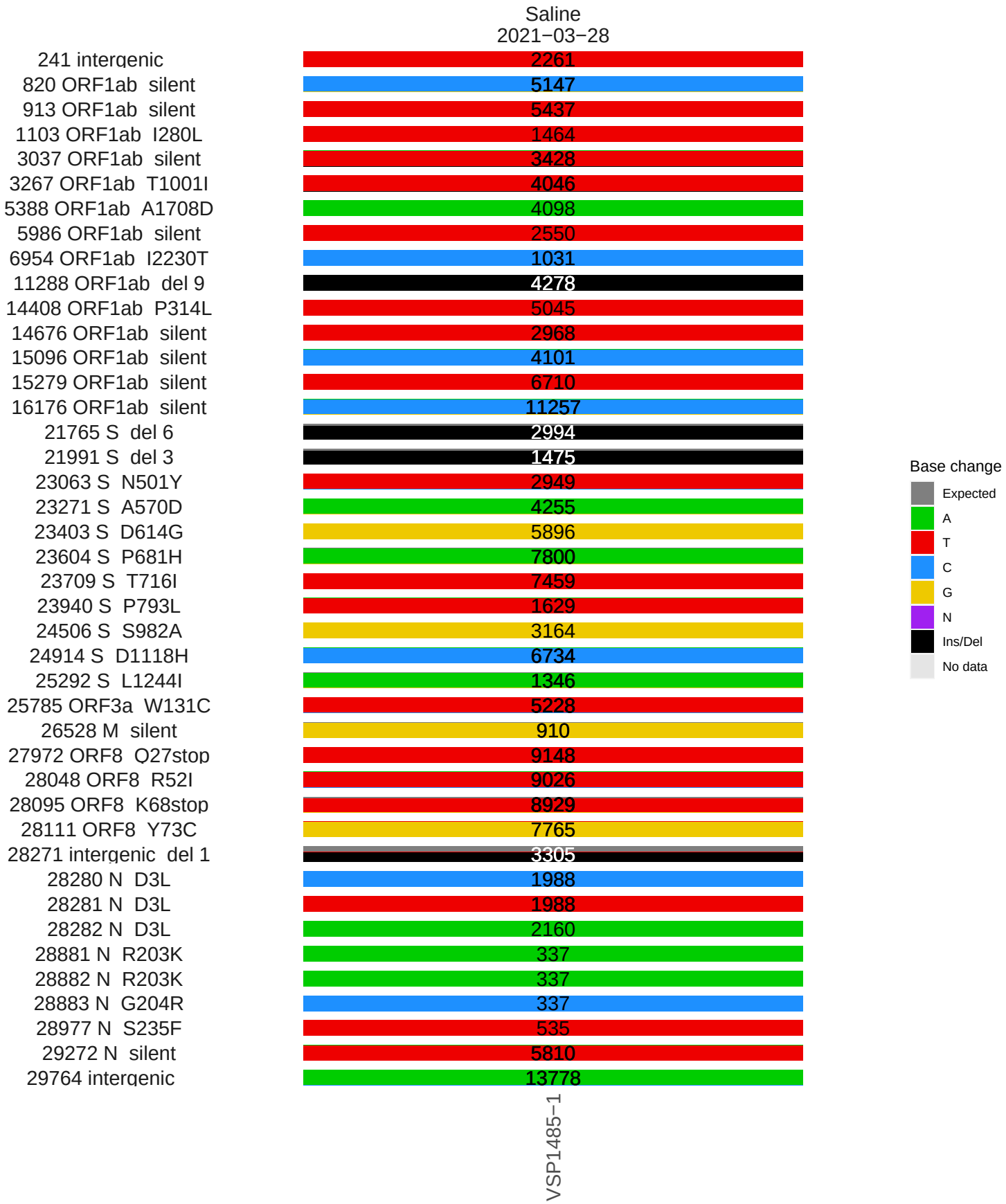
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1485-1	single experiment	NA	Saline	2021-03-28	29.86	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.

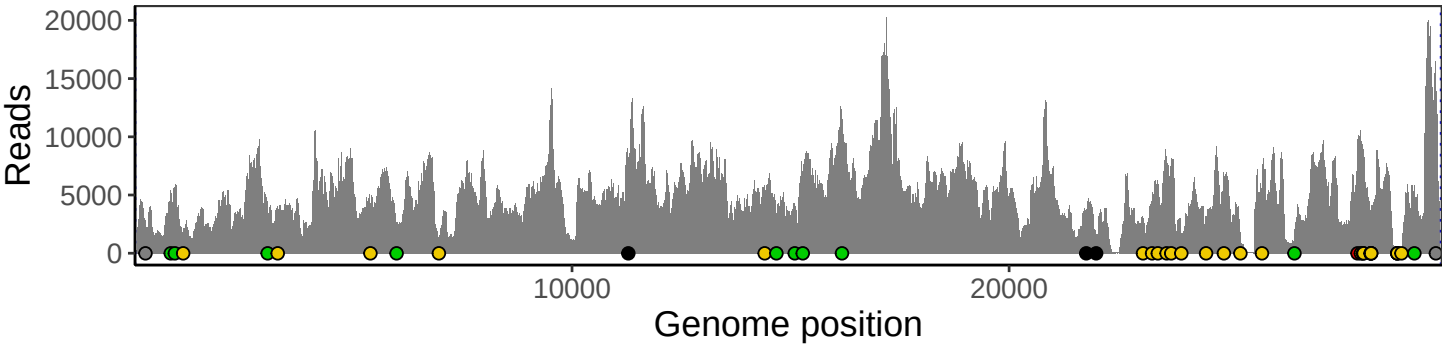



Saline
2021−03−28
241 intergenic 2261
820 ORF1ab silent 5147
913 ORF1ab silent 5437
1103 ORF1ab I280L 1464
3037 ORF1ab silent 3428
3267 ORF1ab T1001I 4046
5388 ORF1ab A1708D 4098
5986 ORF1ab silent 2550
6954 ORF1ab I2230T 1031
11288 ORF1ab del 9 4278
14408 ORF1ab P314L 5045
14676 ORF1ab silent 2968
15096 ORF1ab silent 4101
15279 ORF1ab silent 6710
16176 ORF1ab silent 11257
21765 S del 6 2994
21991 S del 3 1475
23063 S N501Y 2949
23271 S A570D 4255
23403 S D614G 5896
23604 S P681H 7800
23709 S T716I 7459
23940 S P793L 1629
24506 S S982A 3164
24914 S D1118H 6734
25292 S L1244I 1346
25785 ORF3a W131C 5228
26528 M silent 910
27972 ORF8 Q27stop 9148
28048 ORF8 R52I 9026
28095 ORF8 K68stop 8929
28111 ORF8 Y73C 7765
28271 intergenic del 1 3305
28280 N D3L 1988
28281 N D3L 1988
28282 N D3L 2160
28881 N R203K 337
28882 N R203K 337
28883 N G204R 337
28977 N S235F 535
29272 N silent 5810
29764 intergenic 13778
VSP1485−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

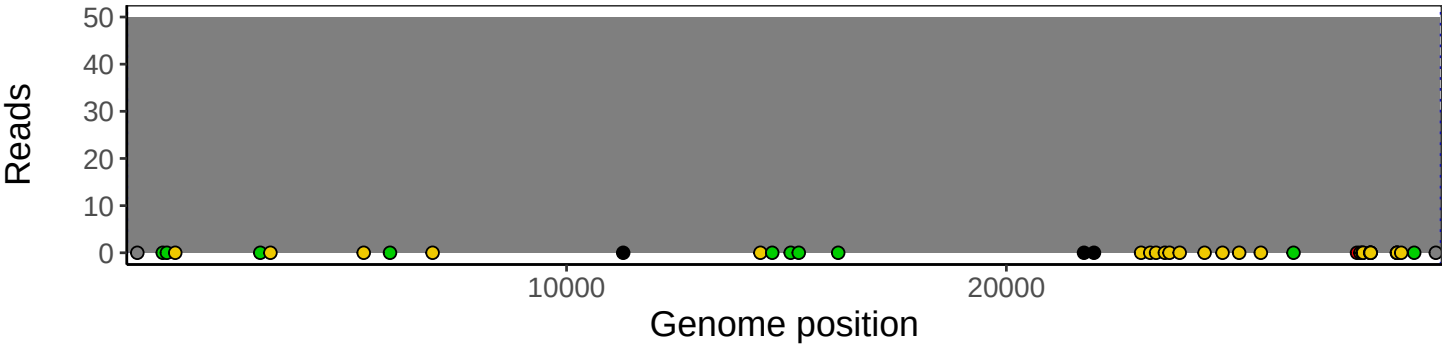
Analyses of individual experiments and composite results

VSP1485-1 | 2021-03-28 | Saline | HUP Q-0144 | genomes | single experiment

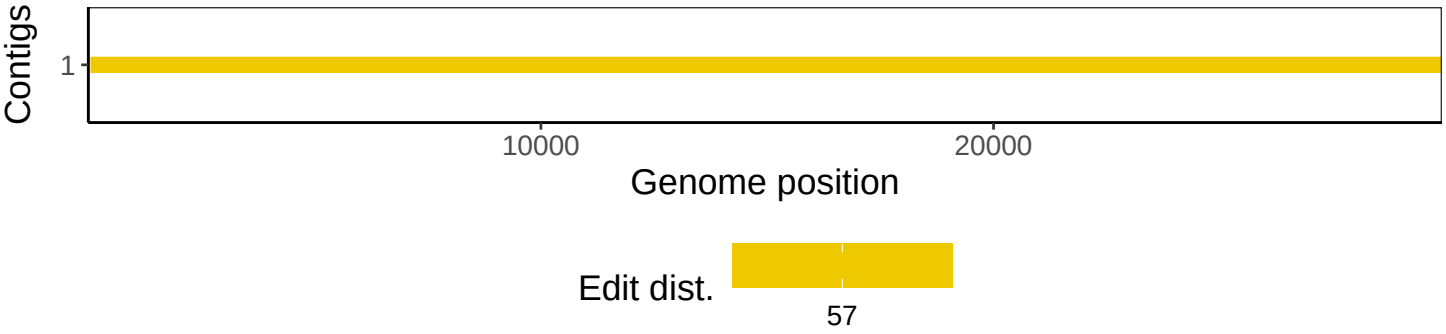
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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