COVID-19 subject HUP Q-0141

2021-06-23

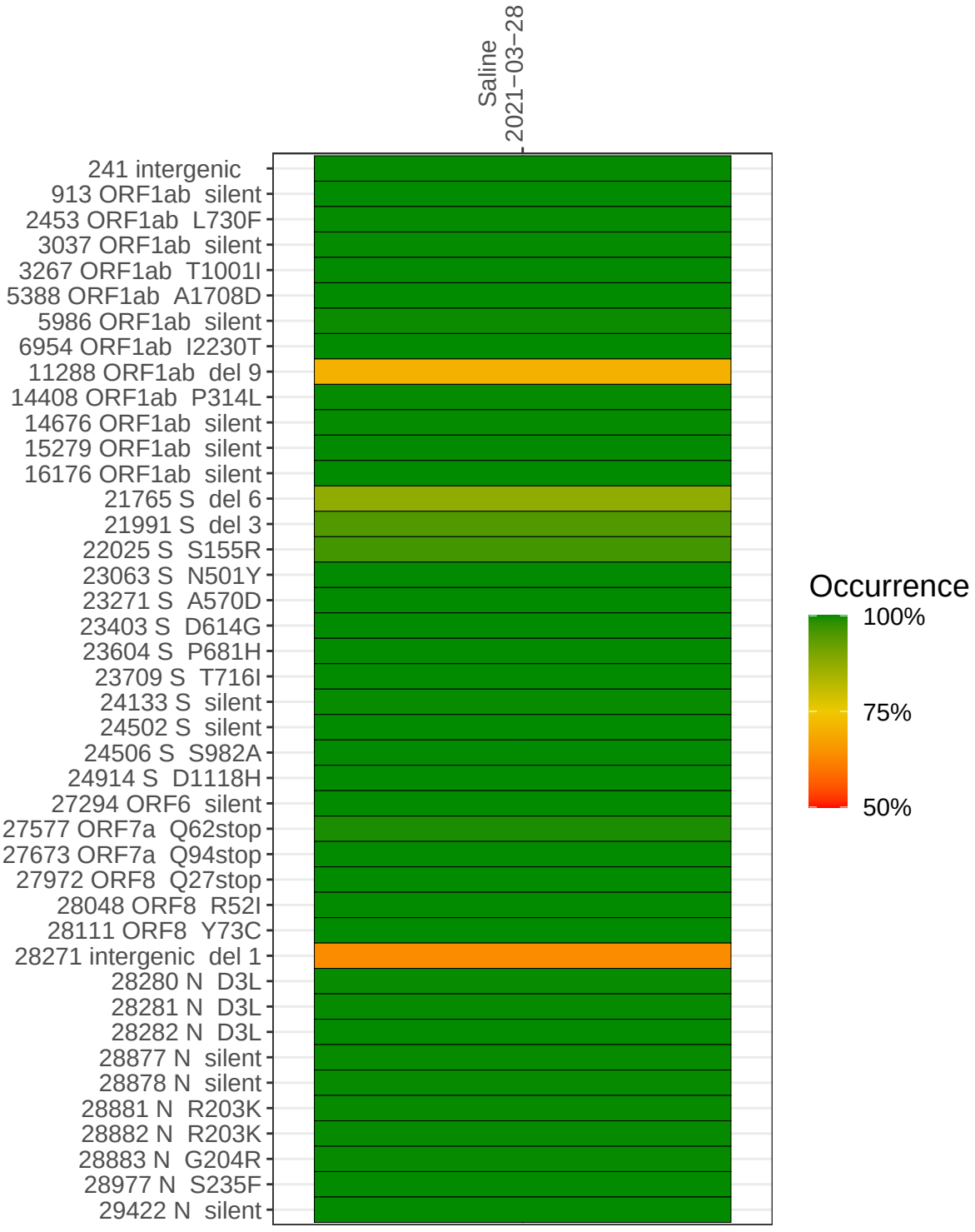
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

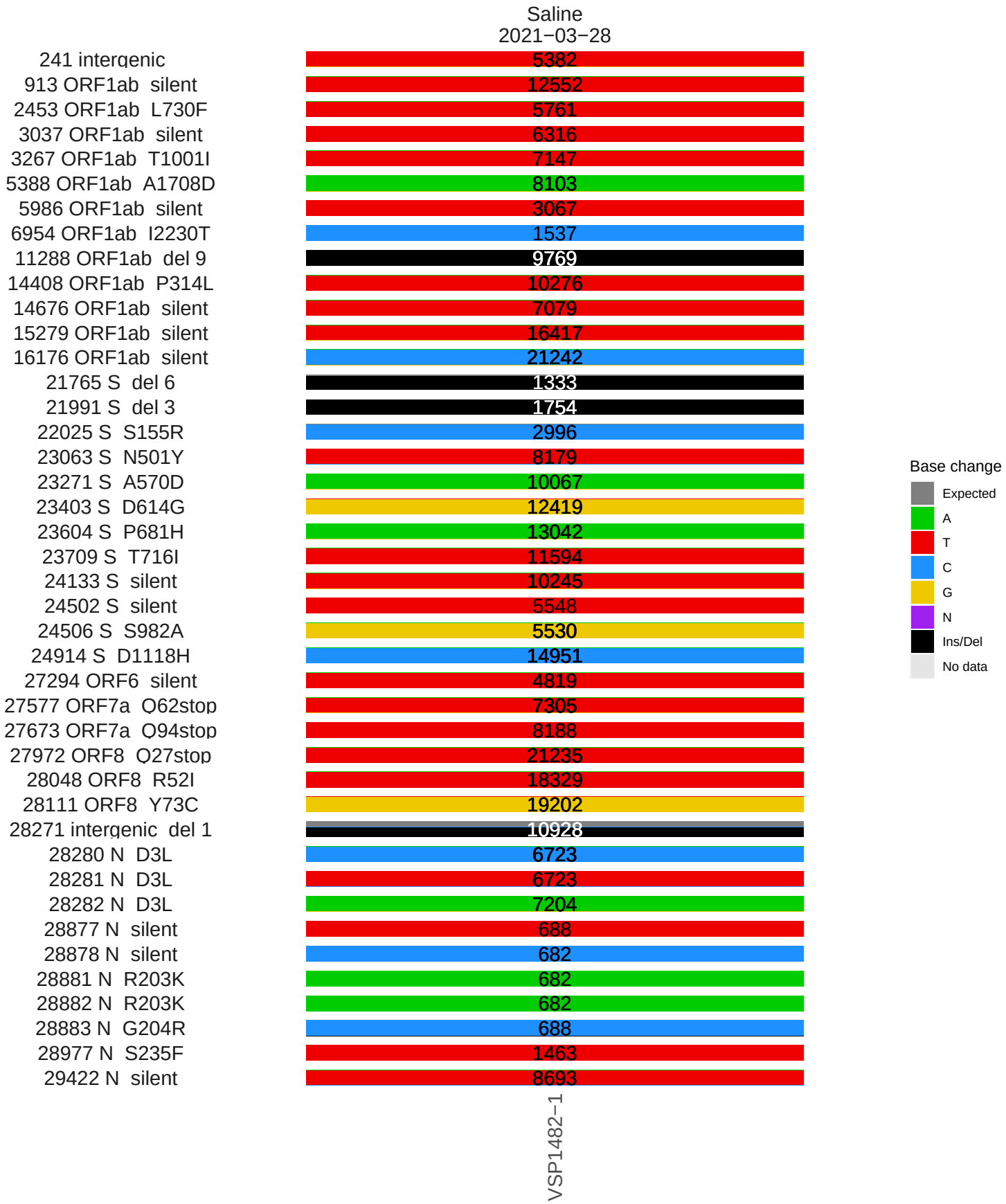
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1482-1	single experiment	NA	Saline	2021-03-28	29.80	B.1.1.7	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

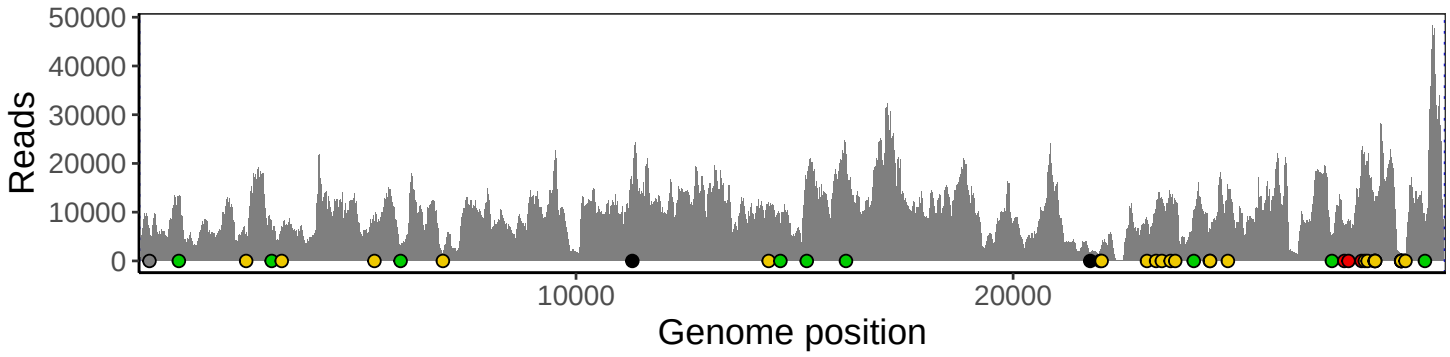



Saline
2021−03−28
241 intergenic 5382
913 ORF1ab silent 12552
2453 ORF1ab L730F 5761
3037 ORF1ab silent 6316
3267 ORF1ab T1001I 7147
5388 ORF1ab A1708D 8103
5986 ORF1ab silent 3067
6954 ORF1ab I2230T 1537
11288 ORF1ab del 9 9769
14408 ORF1ab P314L 10276
14676 ORF1ab silent 7079
15279 ORF1ab silent 16417
16176 ORF1ab silent 21242
21765 S del 6 1333
21991 S del 3 1754
22025 S S155R 2996
23063 S N501Y 8179
23271 S A570D 10067
23403 S D614G 12419
23604 S P681H 13042
23709 S T716I 11594
24133 S silent 10245
24502 S silent 5548
24506 S S982A 5530
24914 S D1118H 14951
27294 ORF6 silent 4819
27577 ORF7a Q62stop 7305
27673 ORF7a Q94stop 8188
27972 ORF8 Q27stop 21235
28048 ORF8 R52I 18329
28111 ORF8 Y73C 19202
28271 intergenic del 1 10928
28280 N D3L 6723
28281 N D3L 6723
28282 N D3L 7204
28877 N silent 688
28878 N silent 682
28881 N R203K 682
28882 N R203K 682
28883 N G204R 688
28977 N S235F 1463
29422 N silent 8693
VSP1482−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

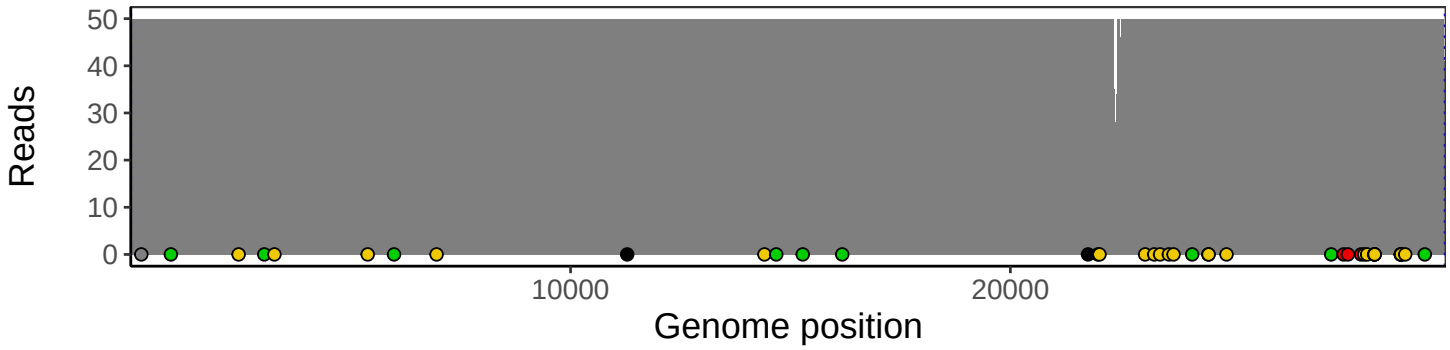
Analyses of individual experiments and composite results

VSP1482-1 | 2021-03-28 | Saline | HUP Q-0141 | genomes | single experiment

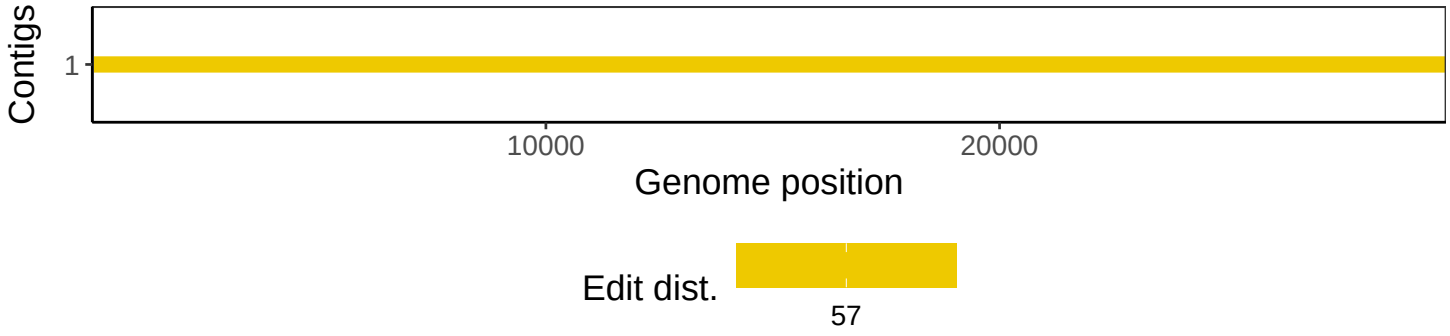
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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