COVID-19 subject HUP Q-0014

2021-05-05

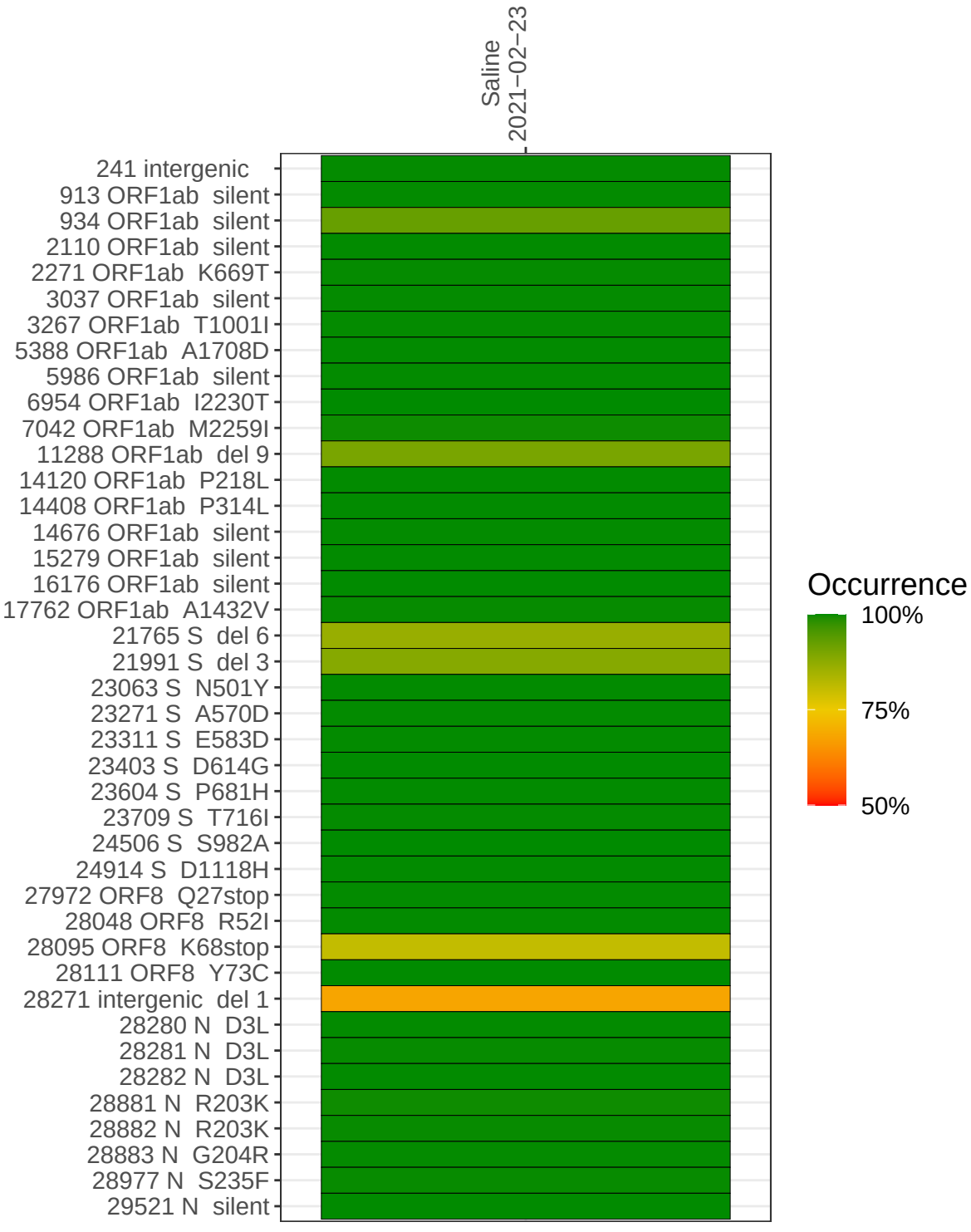
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

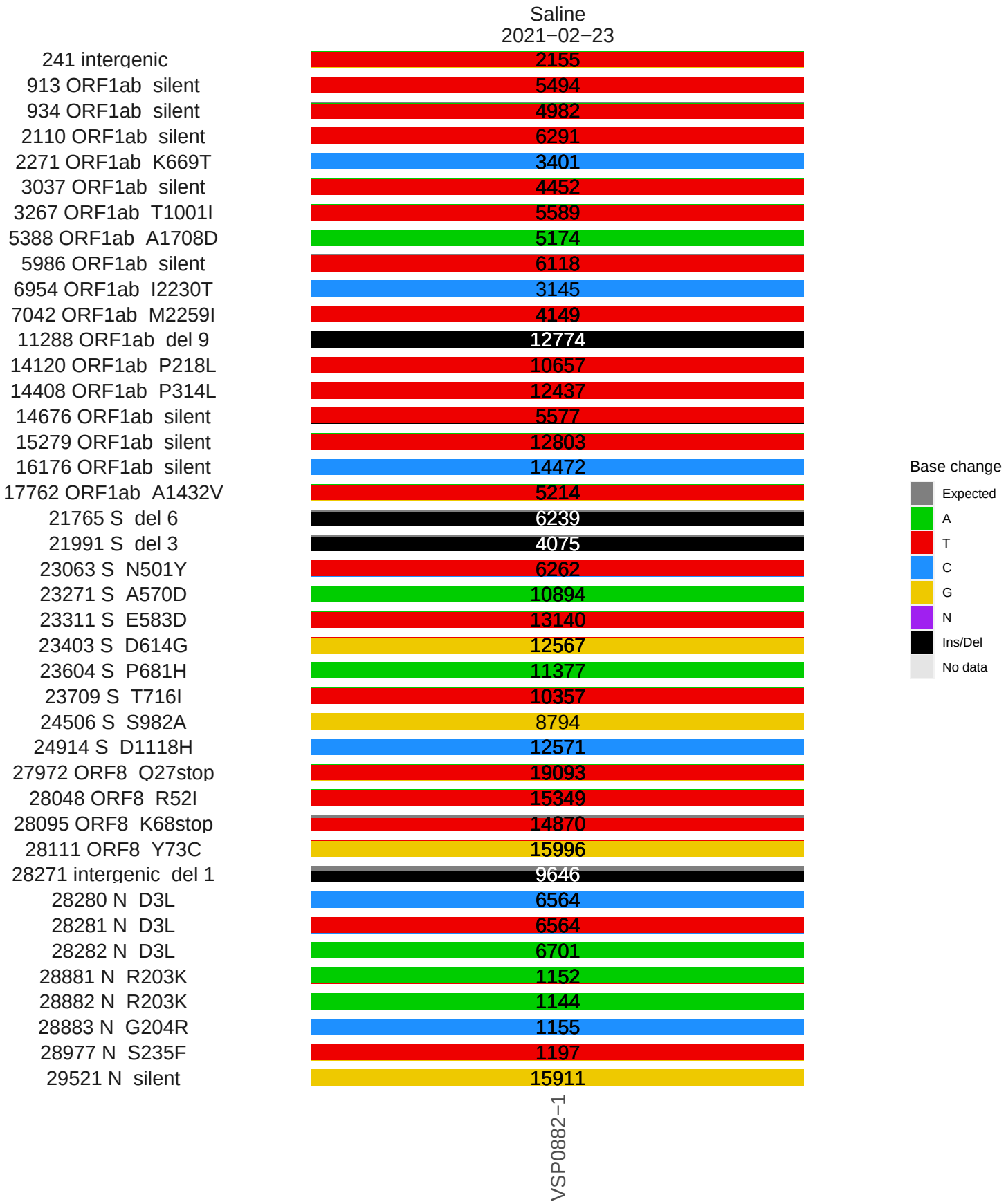
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0882-1	single experiment	NA	Saline	2021-02-23	29.81	B.1.1.7	99.9%	99.8%

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.

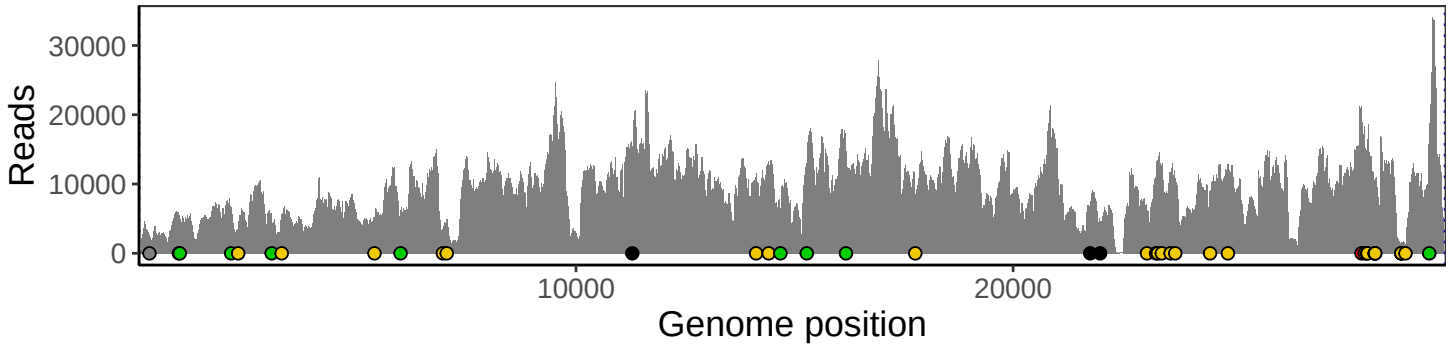



Saline
2021−02−23
241 intergenic 2155
913 ORF1ab silent 5494
934 ORF1ab silent 4982
2110 ORF1ab silent 6291
2271 ORF1ab K669T 3401
3037 ORF1ab silent 4452
3267 ORF1ab T1001I 5589
5388 ORF1ab A1708D 5174
5986 ORF1ab silent 6118
6954 ORF1ab I2230T 3145
7042 ORF1ab M2259I 4149
11288 ORF1ab del 9 12774
14120 ORF1ab P218L 10657
14408 ORF1ab P314L 12437
14676 ORF1ab silent 5577
15279 ORF1ab silent 12803
16176 ORF1ab silent 14472
17762 ORF1ab A1432V 5214
21765 S del 6 6239
21991 S del 3 4075
23063 S N501Y 6262
23271 S A570D 10894
23311 S E583D 13140
23403 S D614G 12567
23604 S P681H 11377
23709 S T716I 10357
24506 S S982A 8794
24914 S D1118H 12571
27972 ORF8 Q27stop 19093
28048 ORF8 R52I 15349
28095 ORF8 K68stop 14870
28111 ORF8 Y73C 15996
28271 intergenic del 1 9646
28280 N D3L 6564
28281 N D3L 6564
28282 N D3L 6701
28881 N R203K 1152
28882 N R203K 1144
28883 N G204R 1155
28977 N S235F 1197
29521 N silent 15911
VSP0882−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

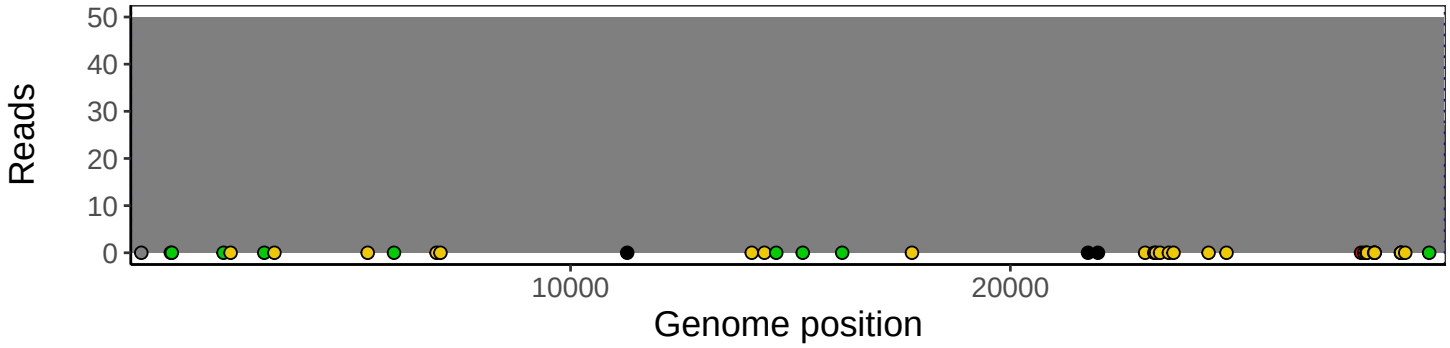
Analyses of individual experiments and composite results

VSP0882-1 | 2021-02-23 | Saline | HUP Q-0014 | genomes | single experiment

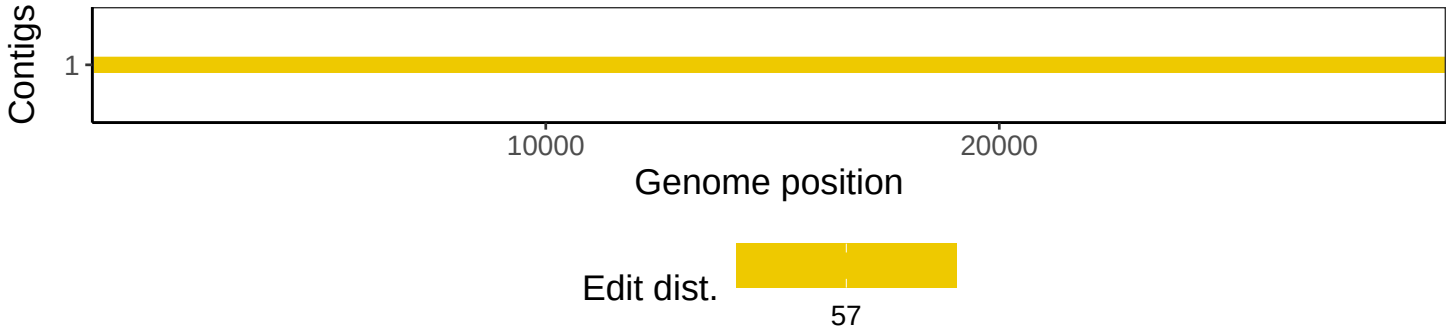
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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