COVID-19 subject HUP Q-0165

2021-05-05

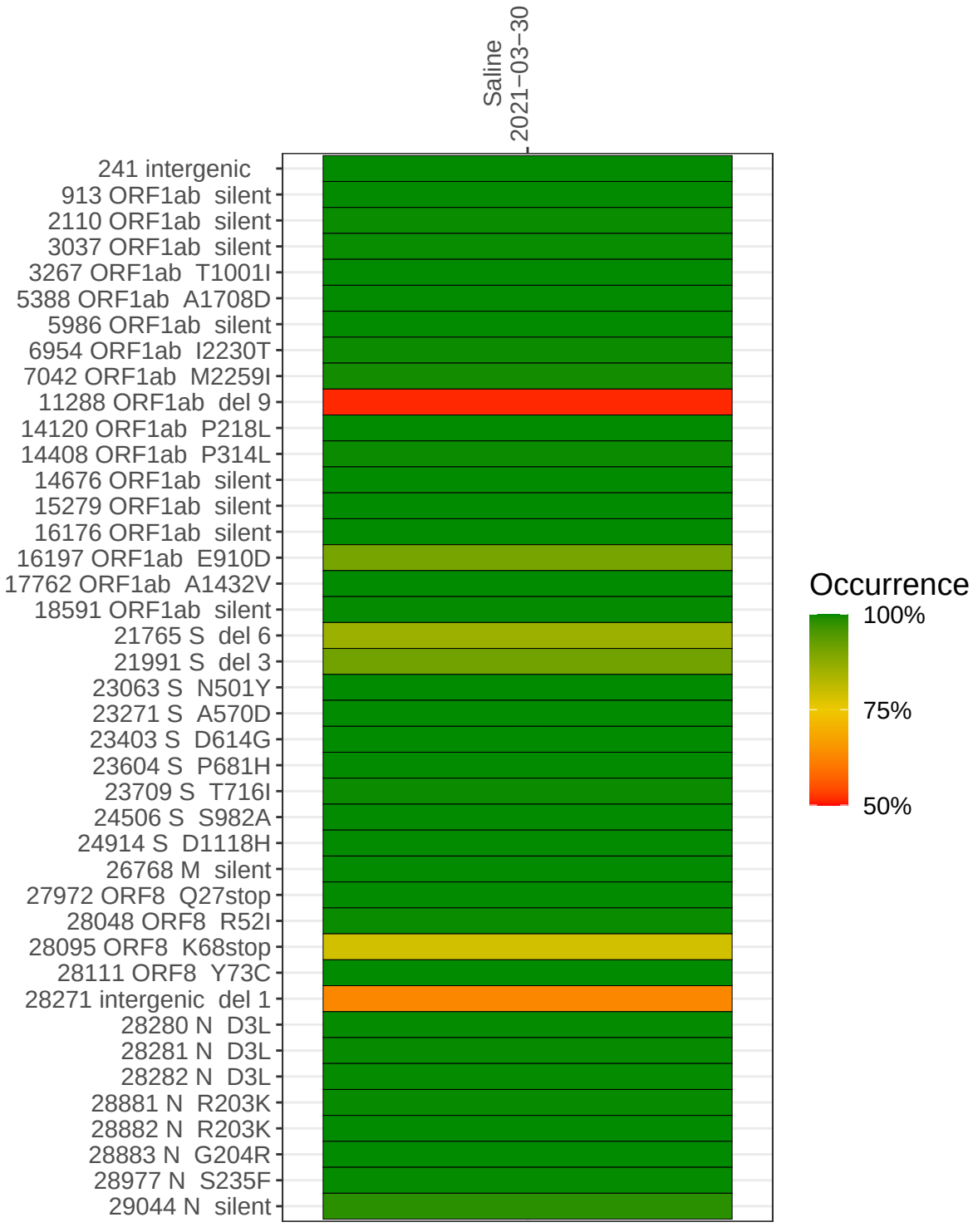
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

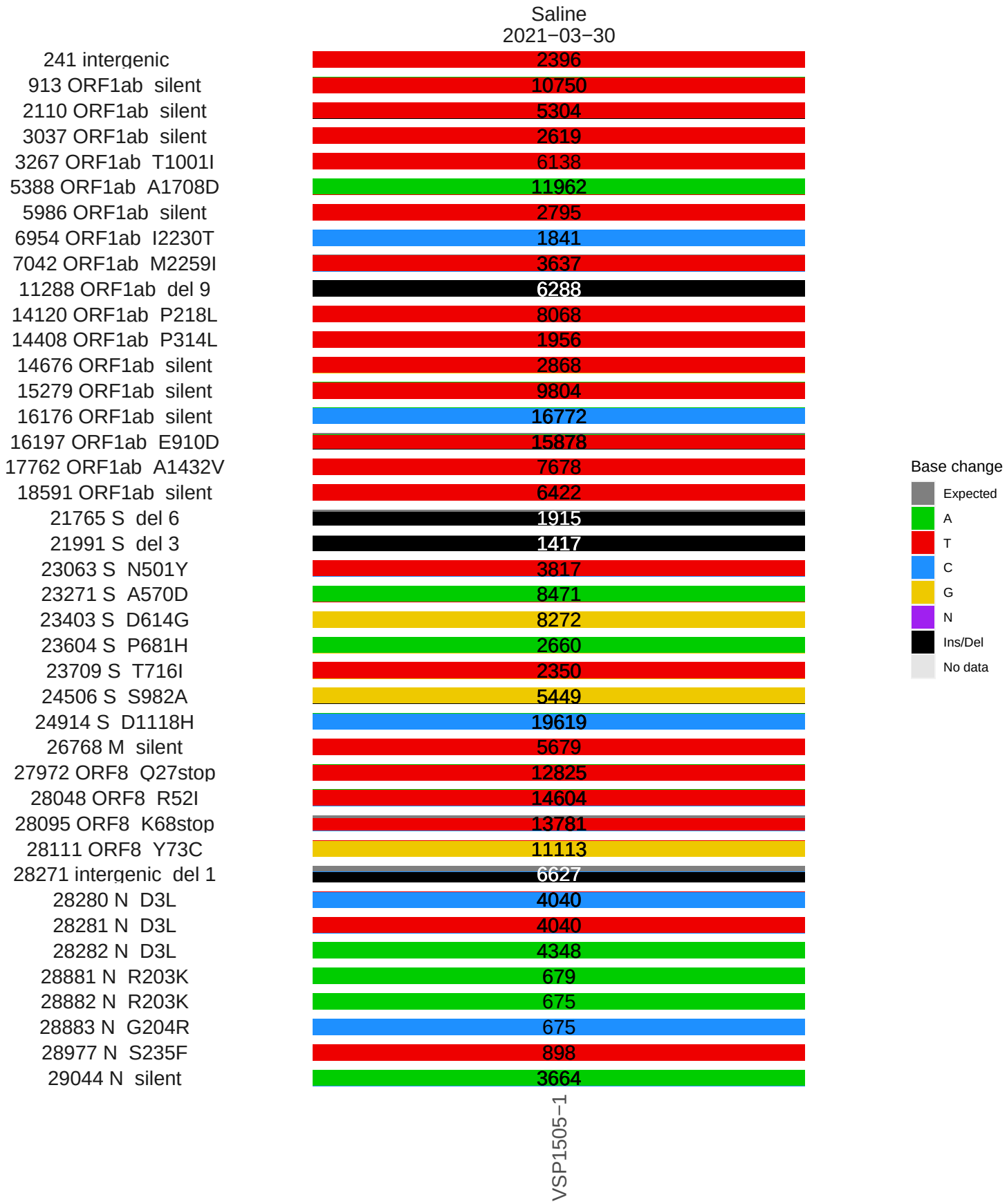
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1505-1	single experiment	NA	Saline	2021-03-30	29.95	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.

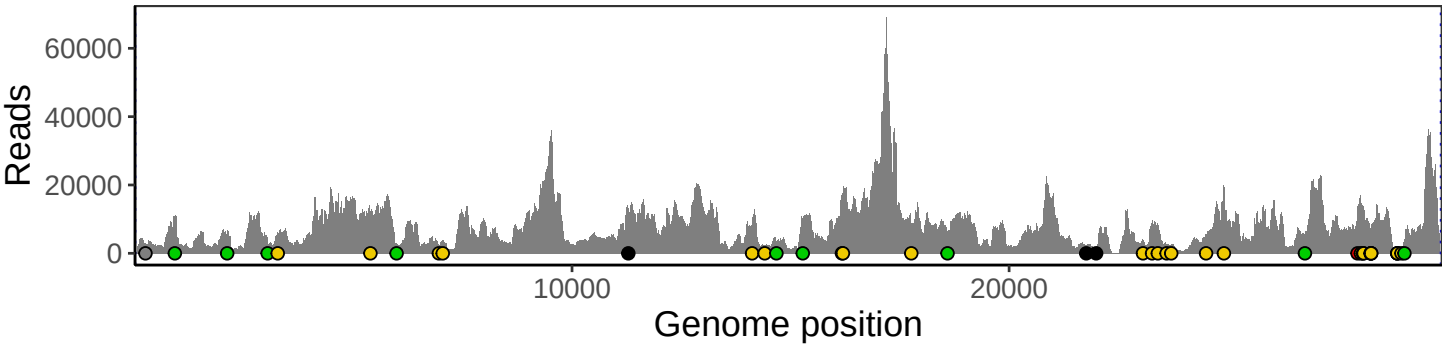



Saline
2021−03−30
241 intergenic 2396
913 ORF1ab silent 10750
2110 ORF1ab silent 5304
3037 ORF1ab silent 2619
3267 ORF1ab T1001I 6138
5388 ORF1ab A1708D 11962
5986 ORF1ab silent 2795
6954 ORF1ab I2230T 1841
7042 ORF1ab M2259I 3637
11288 ORF1ab del 9 6288
14120 ORF1ab P218L 8068
14408 ORF1ab P314L 1956
14676 ORF1ab silent 2868
15279 ORF1ab silent 9804
16176 ORF1ab silent 16772
16197 ORF1ab E910D 15878
17762 ORF1ab A1432V 7678
18591 ORF1ab silent 6422
21765 S del 6 1915
21991 S del 3 1417
23063 S N501Y 3817
23271 S A570D 8471
23403 S D614G 8272
23604 S P681H 2660
23709 S T716I 2350
24506 S S982A 5449
24914 S D1118H 19619
26768 M silent 5679
27972 ORF8 Q27stop 12825
28048 ORF8 R52I 14604
28095 ORF8 K68stop 13781
28111 ORF8 Y73C 11113
28271 intergenic del 1 6627
28280 N D3L 4040
28281 N D3L 4040
28282 N D3L 4348
28881 N R203K 679
28882 N R203K 675
28883 N G204R 675
28977 N S235F 898
29044 N silent 3664
VSP1505−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

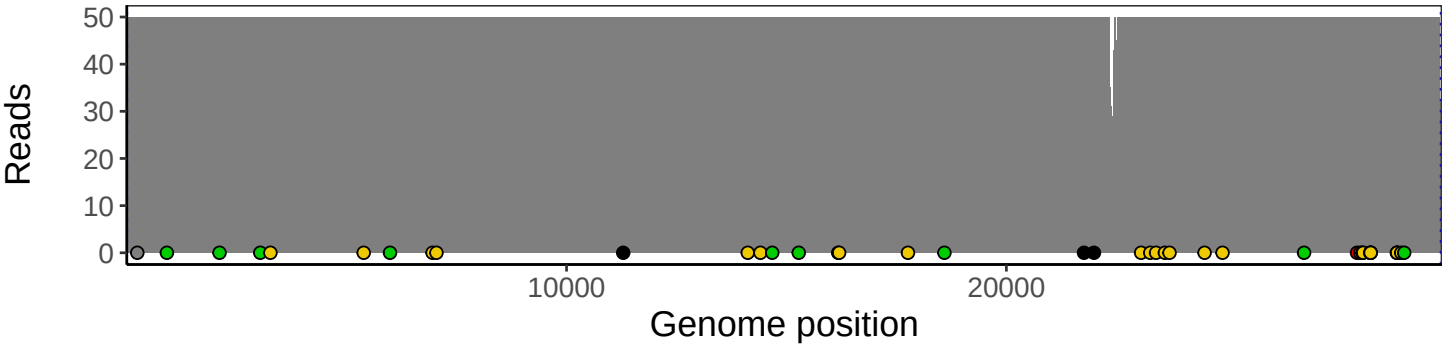
Analyses of individual experiments and composite results

VSP1505-1 | 2021-03-30 | Saline | HUP Q-0165 | genomes | single experiment

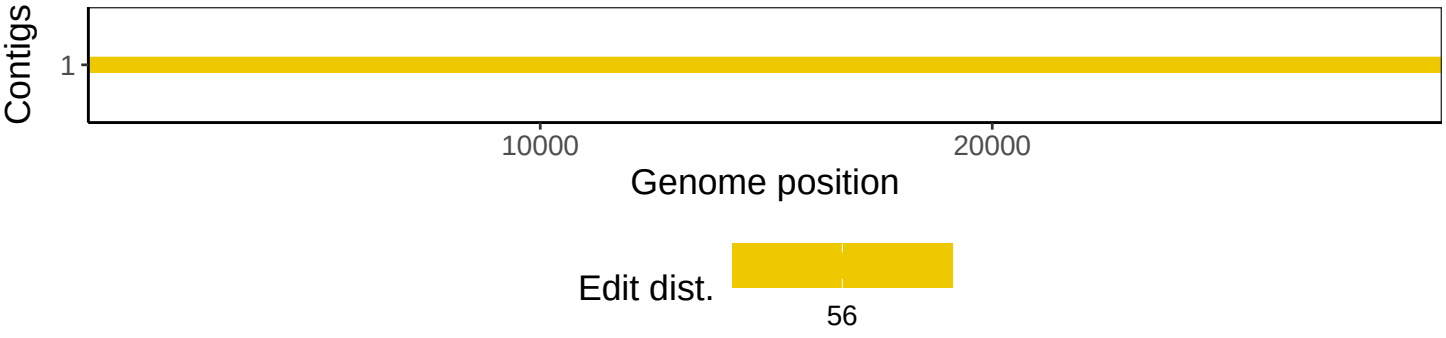
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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