COVID-19 subject HUP Q-0184

2021-05-05

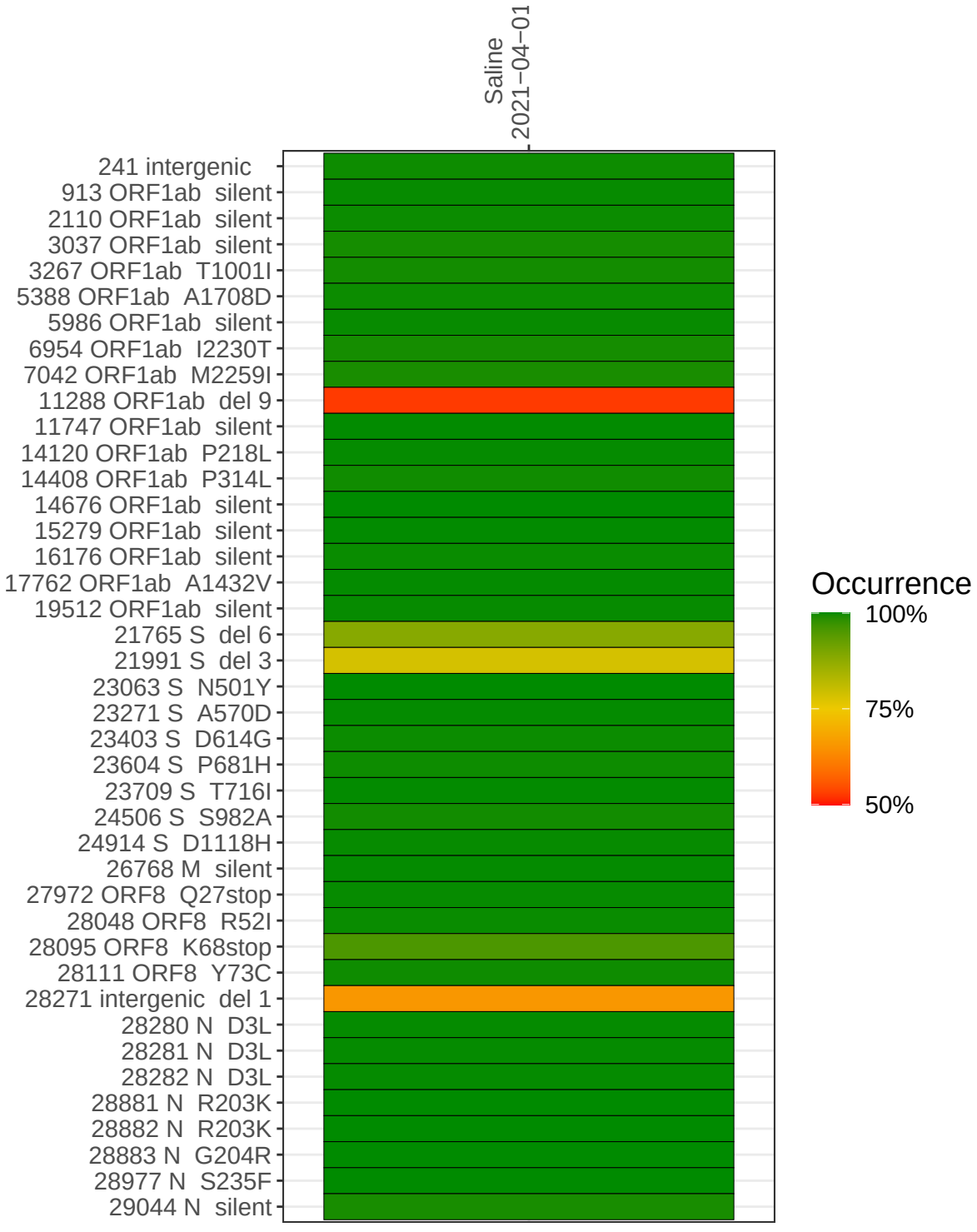
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

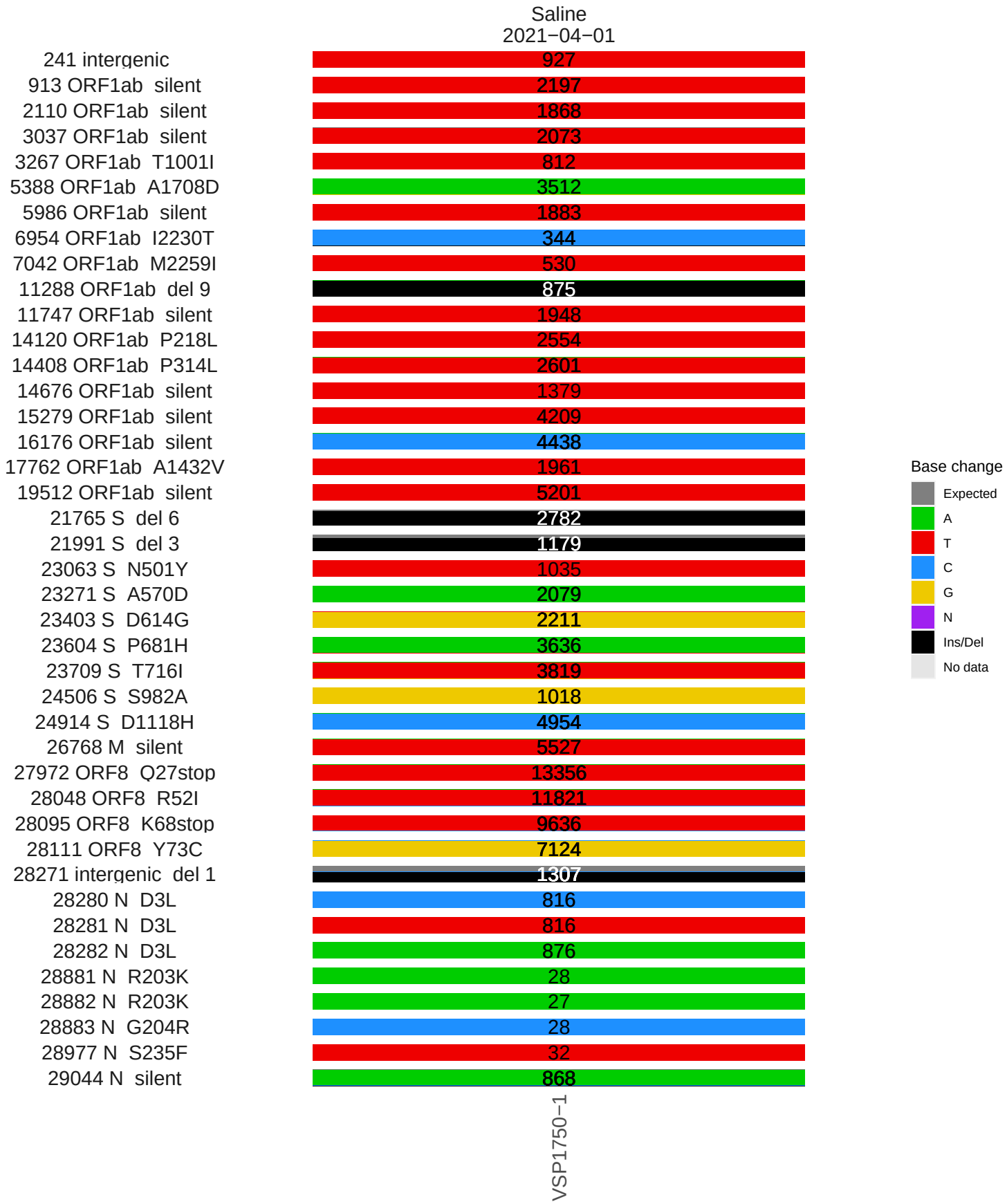
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1750-1	single experiment	NA	Saline	2021-04-01	29.84	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.

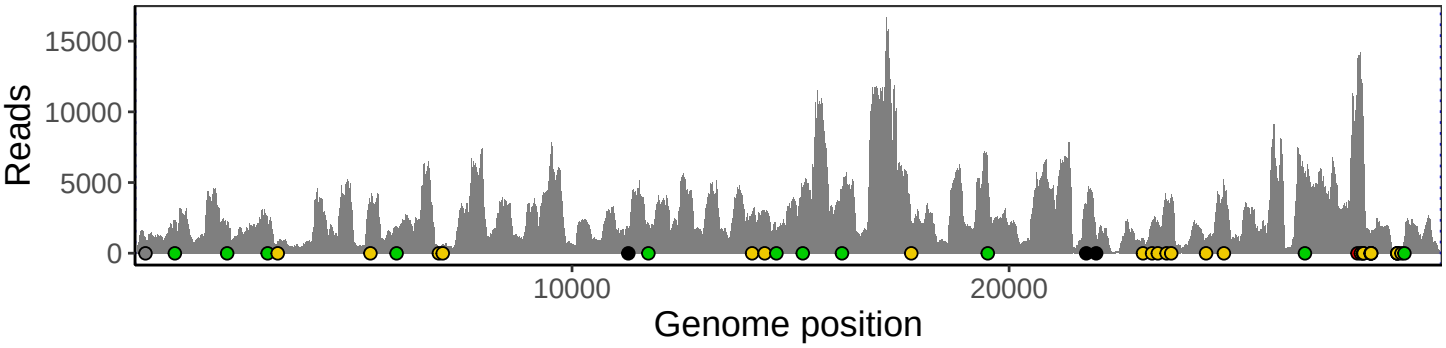



Saline
2021−04−01
241 intergenic 927
913 ORF1ab silent 2197
2110 ORF1ab silent 1868
3037 ORF1ab silent 2073
3267 ORF1ab T1001I 812
5388 ORF1ab A1708D 3512
5986 ORF1ab silent 1883
6954 ORF1ab I2230T 344
7042 ORF1ab M2259I 530
11288 ORF1ab del 9 875
11747 ORF1ab silent 1948
14120 ORF1ab P218L 2554
14408 ORF1ab P314L 2601
14676 ORF1ab silent 1379
15279 ORF1ab silent 4209
16176 ORF1ab silent 4438
17762 ORF1ab A1432V 1961
19512 ORF1ab silent 5201
21765 S del 6 2782
21991 S del 3 1179
23063 S N501Y 1035
23271 S A570D 2079
23403 S D614G 2211
23604 S P681H 3636
23709 S T716I 3819
24506 S S982A 1018
24914 S D1118H 4954
26768 M silent 5527
27972 ORF8 Q27stop 13356
28048 ORF8 R52I 11821
28095 ORF8 K68stop 9636
28111 ORF8 Y73C 7124
28271 intergenic del 1 1307
28280 N D3L 816
28281 N D3L 816
28282 N D3L 876
28881 N R203K 28
28882 N R203K 27
28883 N G204R 28
28977 N S235F 32
29044 N silent 868
VSP1750−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

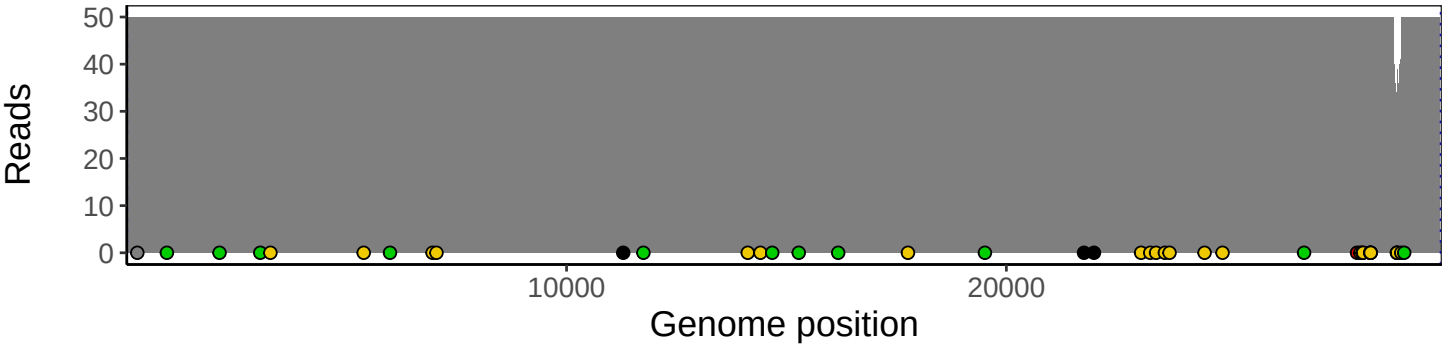
Analyses of individual experiments and composite results

VSP1750-1 | 2021-04-01 | Saline | HUP Q-0184 | genomes | single experiment

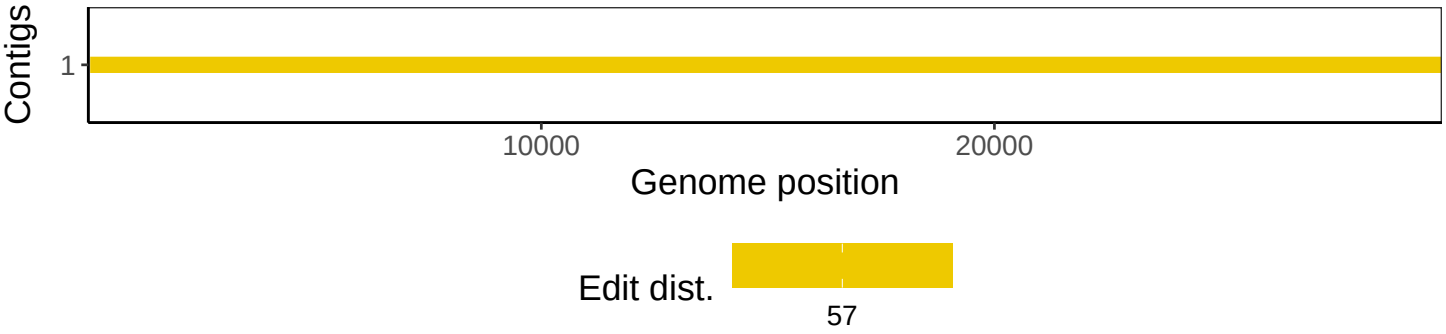
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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