COVID-19 subject HUP Q-0228

2021-05-21

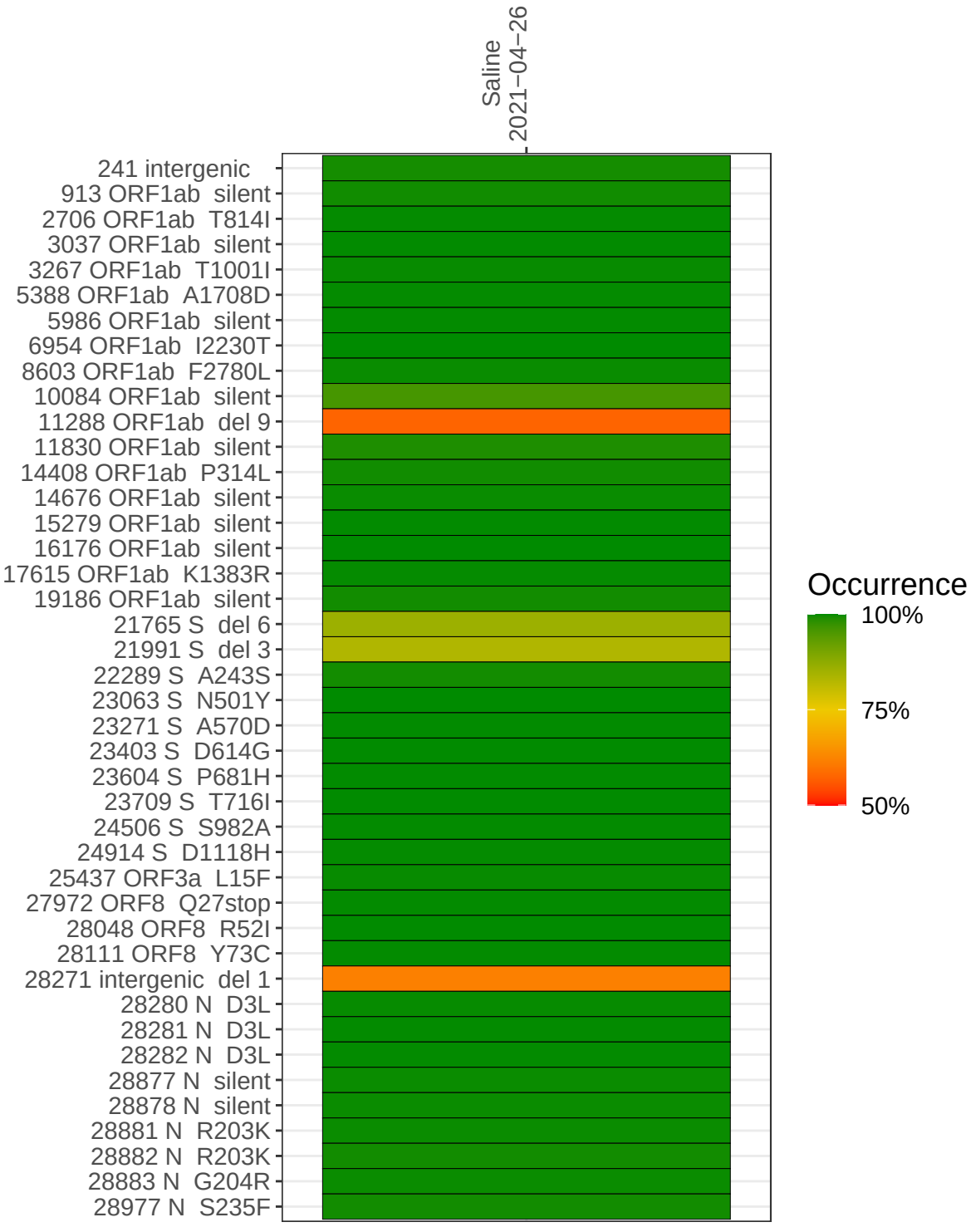
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

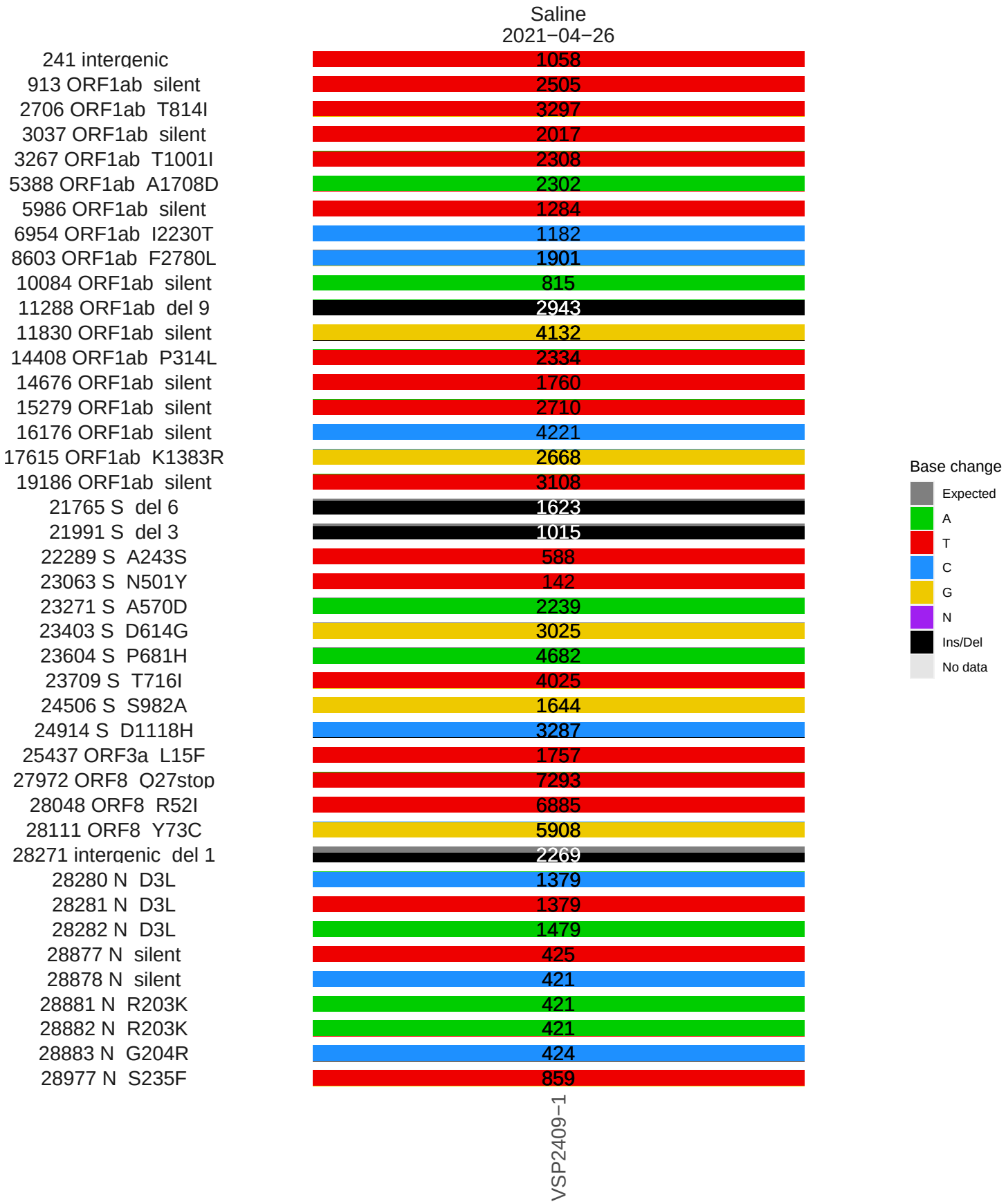
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2409-1	single experiment	NA	Saline	2021-04-26	29.81	B.1.1.7	99.8%	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.

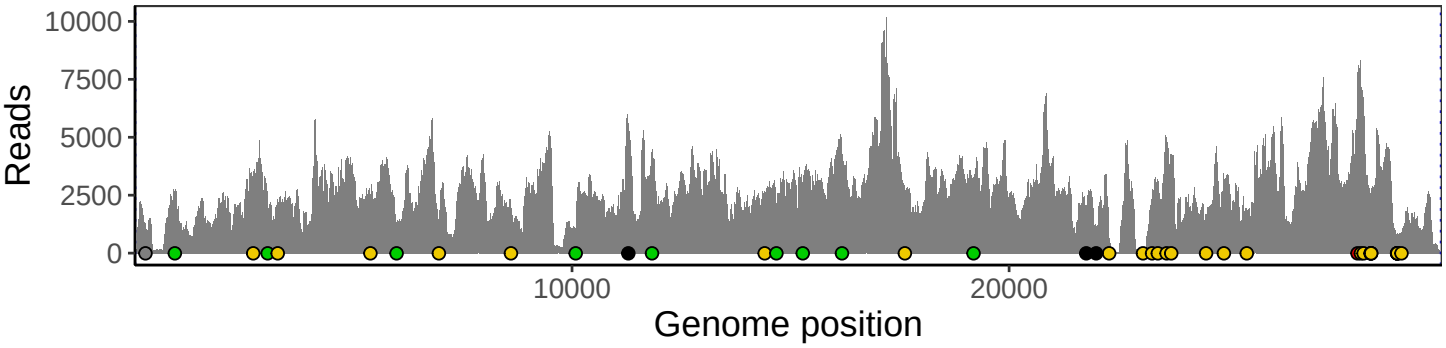



Saline
2021−04−26
241 intergenic 1058
913 ORF1ab silent 2505
2706 ORF1ab T814I 3297
3037 ORF1ab silent 2017
3267 ORF1ab T1001I 2308
5388 ORF1ab A1708D 2302
5986 ORF1ab silent 1284
6954 ORF1ab I2230T 1182
8603 ORF1ab F2780L 1901
10084 ORF1ab silent 815
11288 ORF1ab del 9 2943
11830 ORF1ab silent 4132
14408 ORF1ab P314L 2334
14676 ORF1ab silent 1760
15279 ORF1ab silent 2710
16176 ORF1ab silent 4221
17615 ORF1ab K1383R 2668
19186 ORF1ab silent 3108
21765 S del 6 1623
21991 S del 3 1015
22289 S A243S 588
23063 S N501Y 142
23271 S A570D 2239
23403 S D614G 3025
23604 S P681H 4682
23709 S T716I 4025
24506 S S982A 1644
24914 S D1118H 3287
25437 ORF3a L15F 1757
27972 ORF8 Q27stop 7293
28048 ORF8 R52I 6885
28111 ORF8 Y73C 5908
28271 intergenic del 1 2269
28280 N D3L 1379
28281 N D3L 1379
28282 N D3L 1479
28877 N silent 425
28878 N silent 421
28881 N R203K 421
28882 N R203K 421
28883 N G204R 424
28977 N S235F 859
VSP2409−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

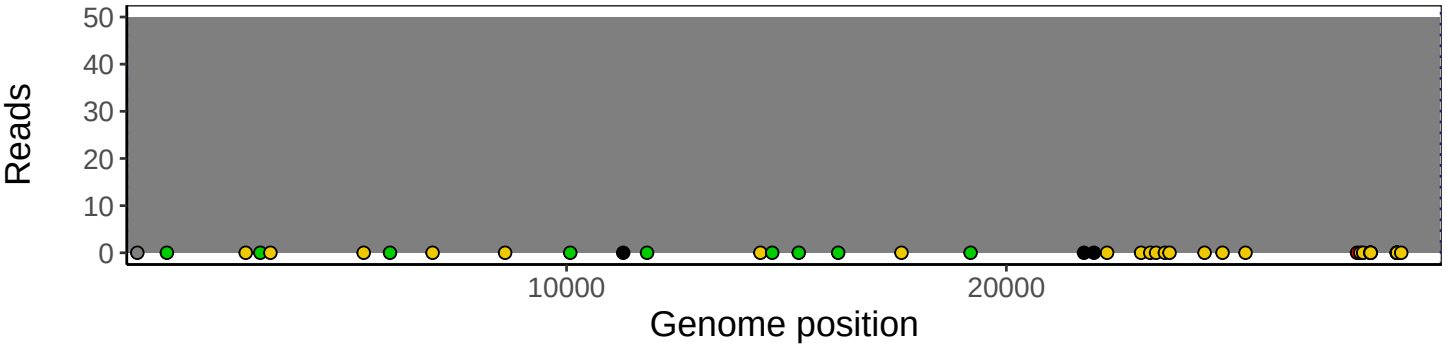
Analyses of individual experiments and composite results

VSP2409-1 | 2021-04-26 | Saline | HUP Q-0228 | genomes | single experiment

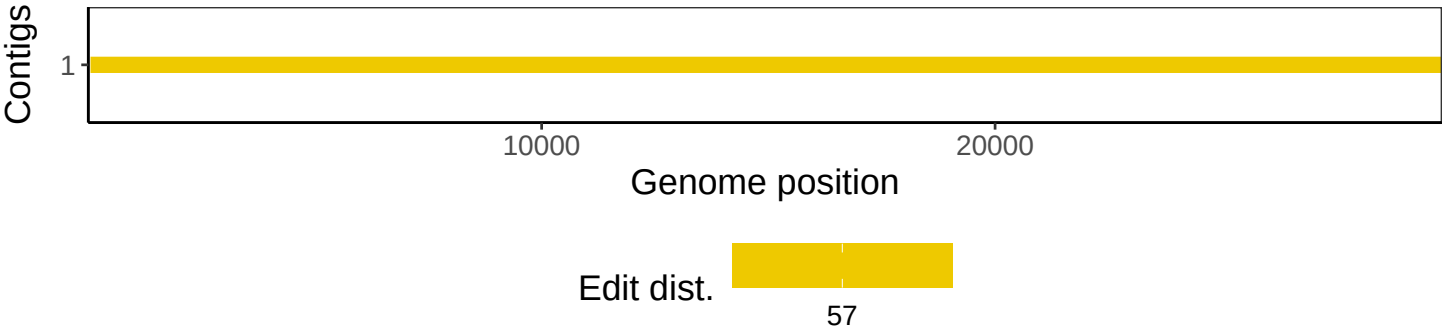
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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