COVID-19 subject UPHS-1046

2021-05-10

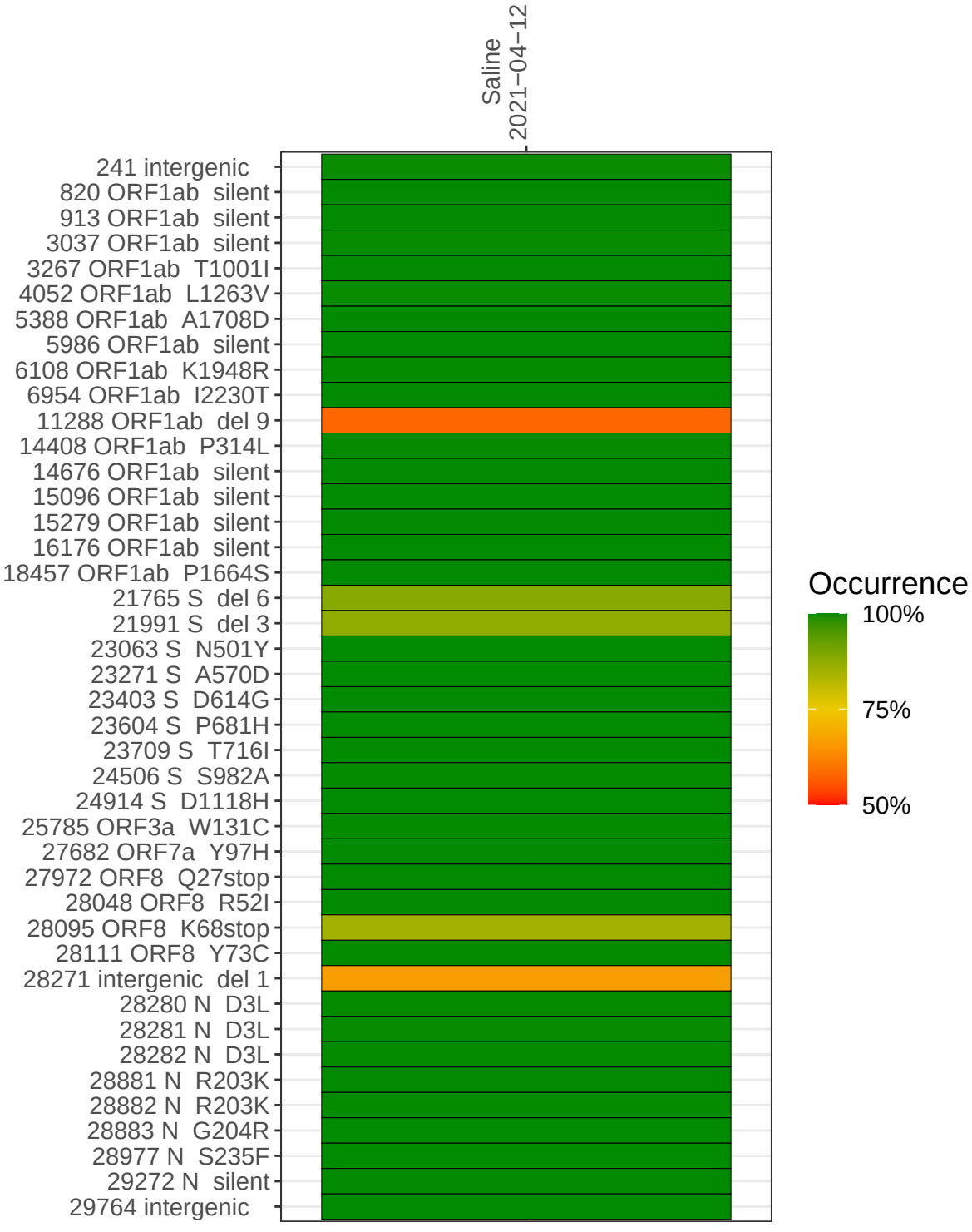
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

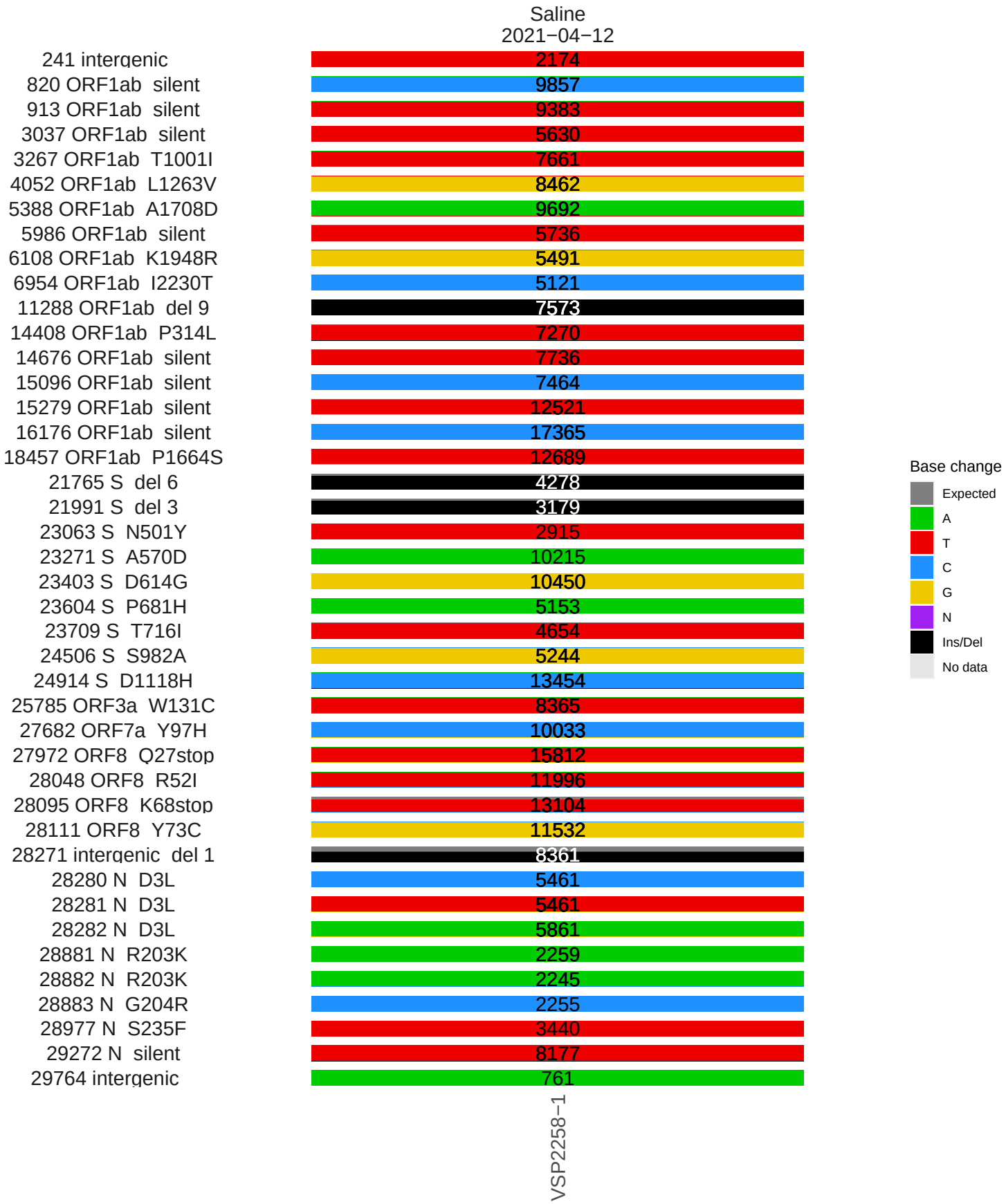
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2258-1	single experiment	NA	Saline	2021-04-12	29.85	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.

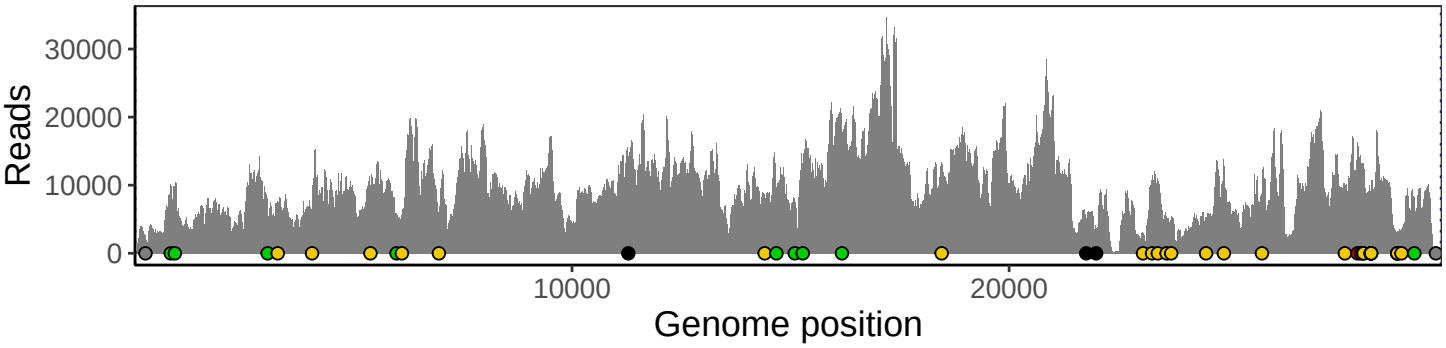



Saline
2021−04−12
241 intergenic 2174
820 ORF1ab silent 9857
913 ORF1ab silent 9383
3037 ORF1ab silent 5630
3267 ORF1ab T1001I 7661
4052 ORF1ab L1263V 8462
5388 ORF1ab A1708D 9692
5986 ORF1ab silent 5736
6108 ORF1ab K1948R 5491
6954 ORF1ab I2230T 5121
11288 ORF1ab del 9 7573
14408 ORF1ab P314L 7270
14676 ORF1ab silent 7736
15096 ORF1ab silent 7464
15279 ORF1ab silent 12521
16176 ORF1ab silent 17365
18457 ORF1ab P1664S 12689
21765 S del 6 4278
21991 S del 3 3179
23063 S N501Y 2915
23271 S A570D 10215
23403 S D614G 10450
23604 S P681H 5153
23709 S T716I 4654
24506 S S982A 5244
24914 S D1118H 13454
25785 ORF3a W131C 8365
27682 ORF7a Y97H 10033
27972 ORF8 Q27stop 15812
28048 ORF8 R52I 11996
28095 ORF8 K68stop 13104
28111 ORF8 Y73C 11532
28271 intergenic del 1 8361
28280 N D3L 5461
28281 N D3L 5461
28282 N D3L 5861
28881 N R203K 2259
28882 N R203K 2245
28883 N G204R 2255
28977 N S235F 3440
29272 N silent 8177
29764 intergenic 761
VSP2258−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

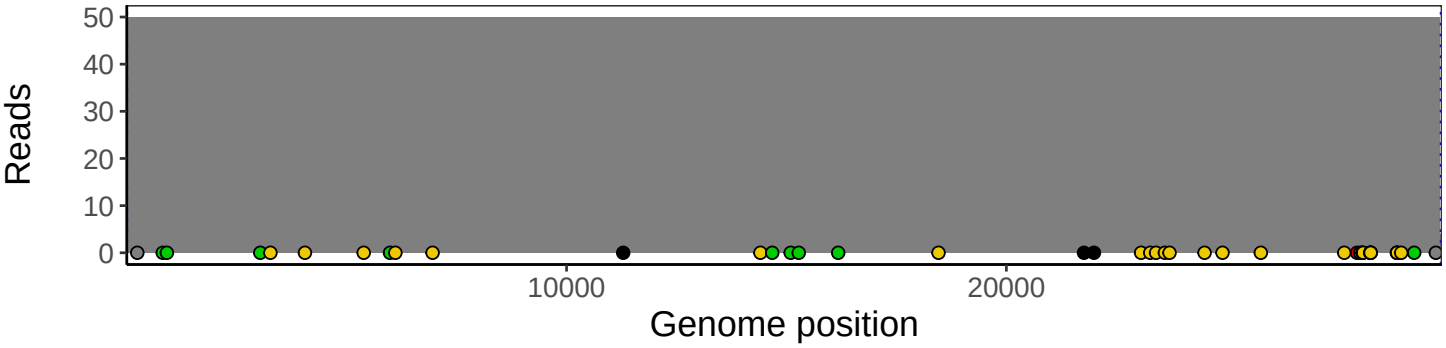
Analyses of individual experiments and composite results

VSP2258-1 | 2021-04-12 | Saline | UPHS-1046 | genomes | single experiment

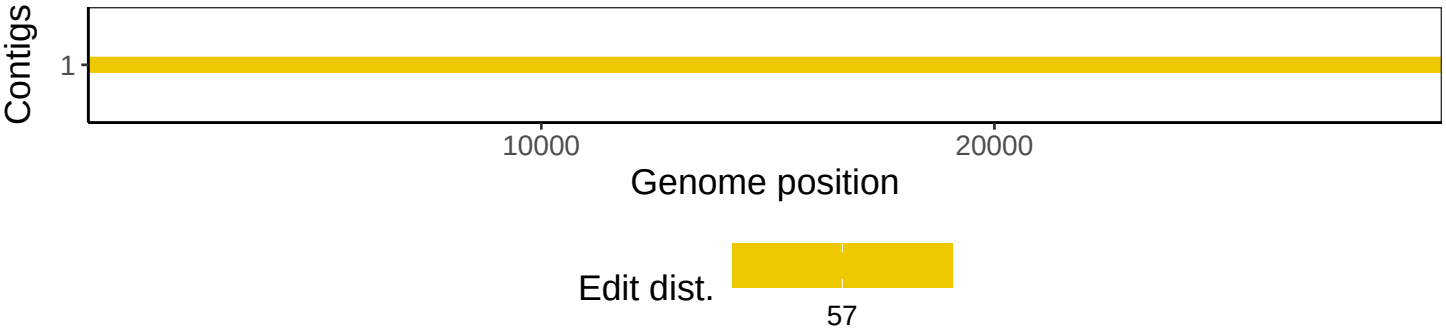
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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