COVID-19 subject UPHS-1420

2021-06-23

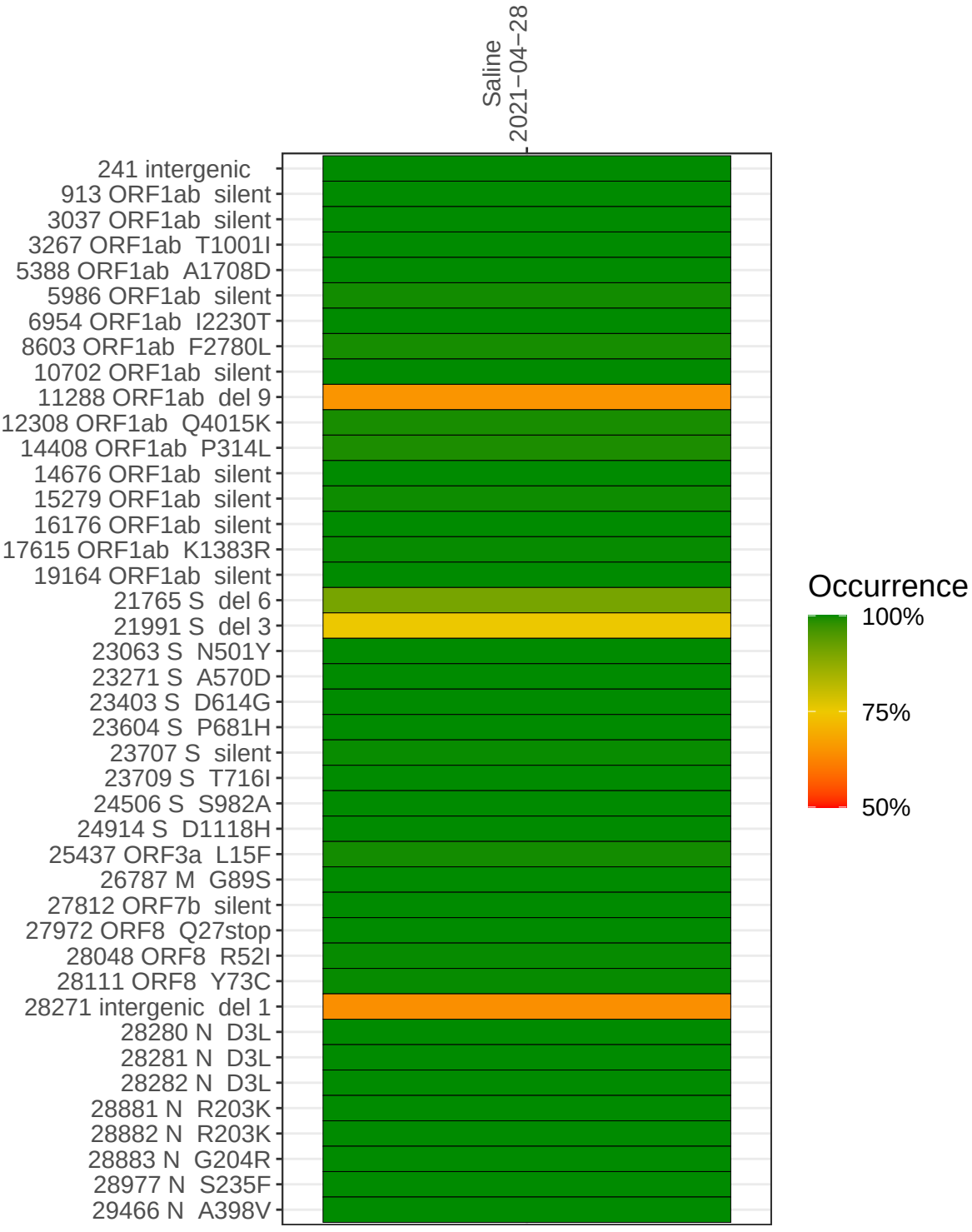
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

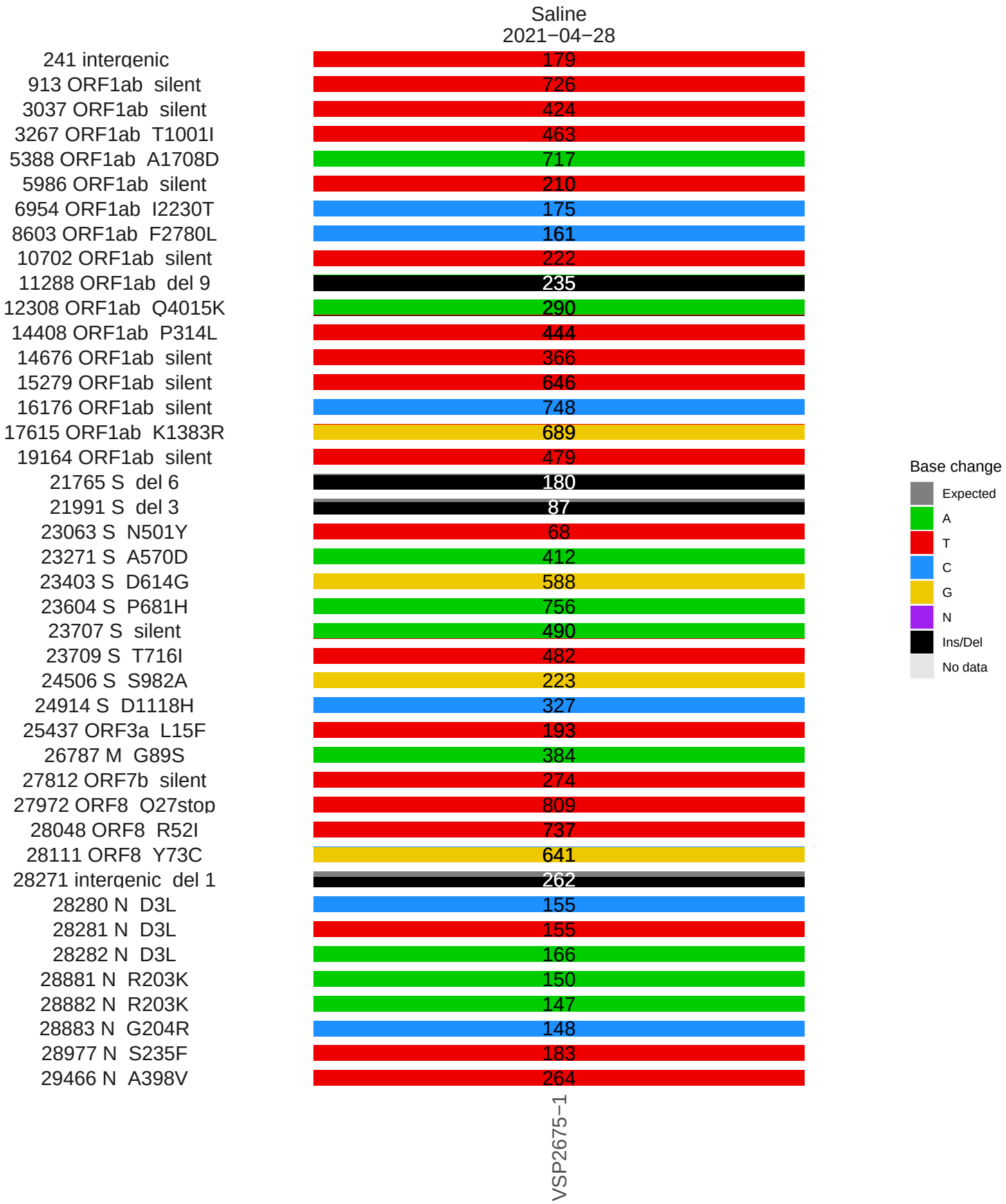
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2675-1	single experiment	NA	Saline	2021-04-28	29.79	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

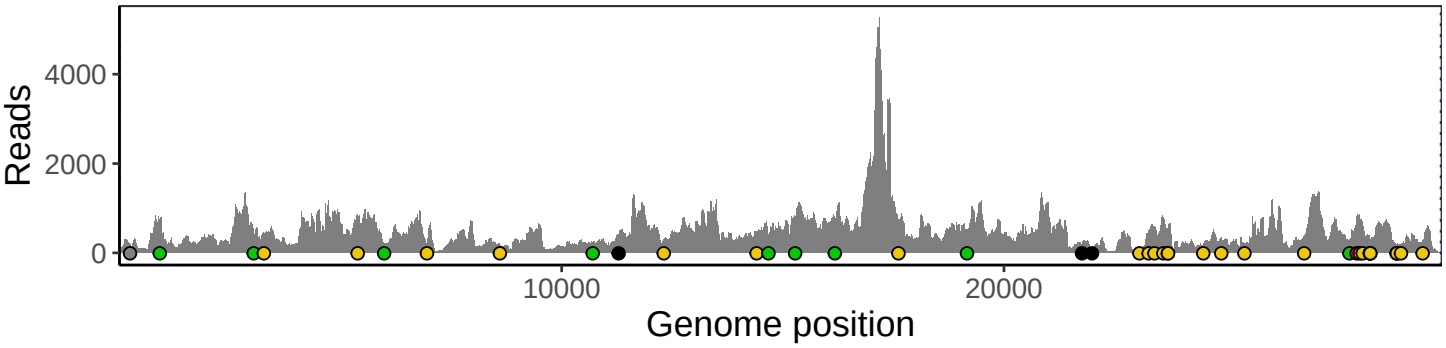



Saline
2021−04−28
241 intergenic 179
913 ORF1ab silent 726
3037 ORF1ab silent 424
3267 ORF1ab T1001I 463
5388 ORF1ab A1708D 717
5986 ORF1ab silent 210
6954 ORF1ab I2230T 175
8603 ORF1ab F2780L 161
10702 ORF1ab silent 222
11288 ORF1ab del 9 235
12308 ORF1ab Q4015K 290
14408 ORF1ab P314L 444
14676 ORF1ab silent 366
15279 ORF1ab silent 646
16176 ORF1ab silent 748
17615 ORF1ab K1383R 689
19164 ORF1ab silent 479
21765 S del 6 180
21991 S del 3 87
23063 S N501Y 68
23271 S A570D 412
23403 S D614G 588
23604 S P681H 756
23707 S silent 490
23709 S T716I 482
24506 S S982A 223
24914 S D1118H 327
25437 ORF3a L15F 193
26787 M G89S 384
27812 ORF7b silent 274
27972 ORF8 Q27stop 809
28048 ORF8 R52I 737
28111 ORF8 Y73C 641
28271 intergenic del 1 262
28280 N D3L 155
28281 N D3L 155
28282 N D3L 166
28881 N R203K 150
28882 N R203K 147
28883 N G204R 148
28977 N S235F 183
29466 N A398V 264
VSP2675−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

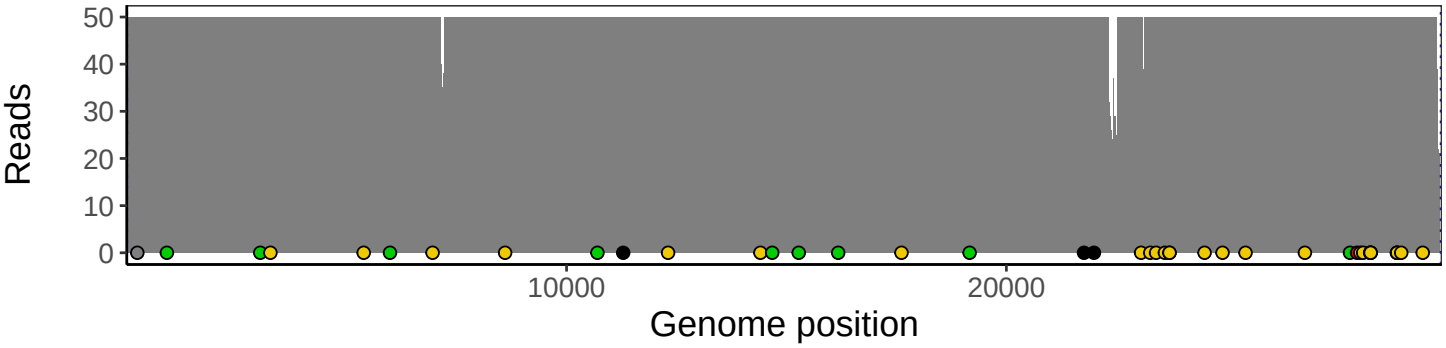
Analyses of individual experiments and composite results

VSP2675-1 | 2021-04-28 | Saline | UPHS-1420 | genomes | single experiment

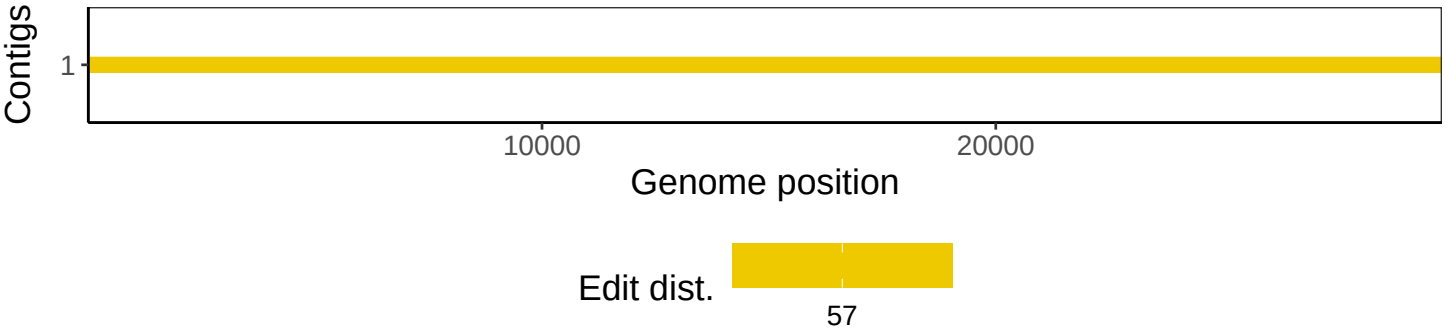
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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