COVID-19 subject UPHS-0645

2021-06-23

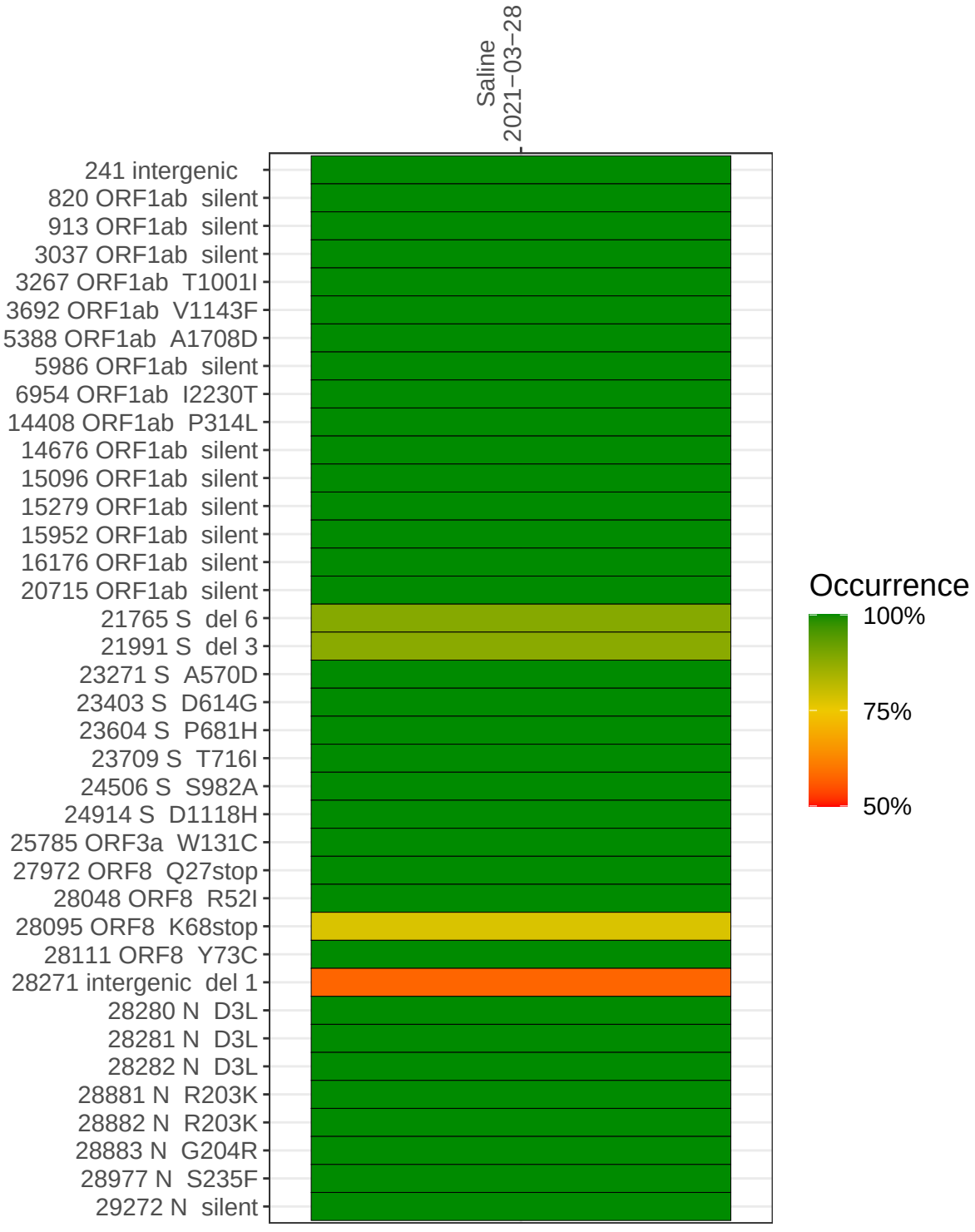
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

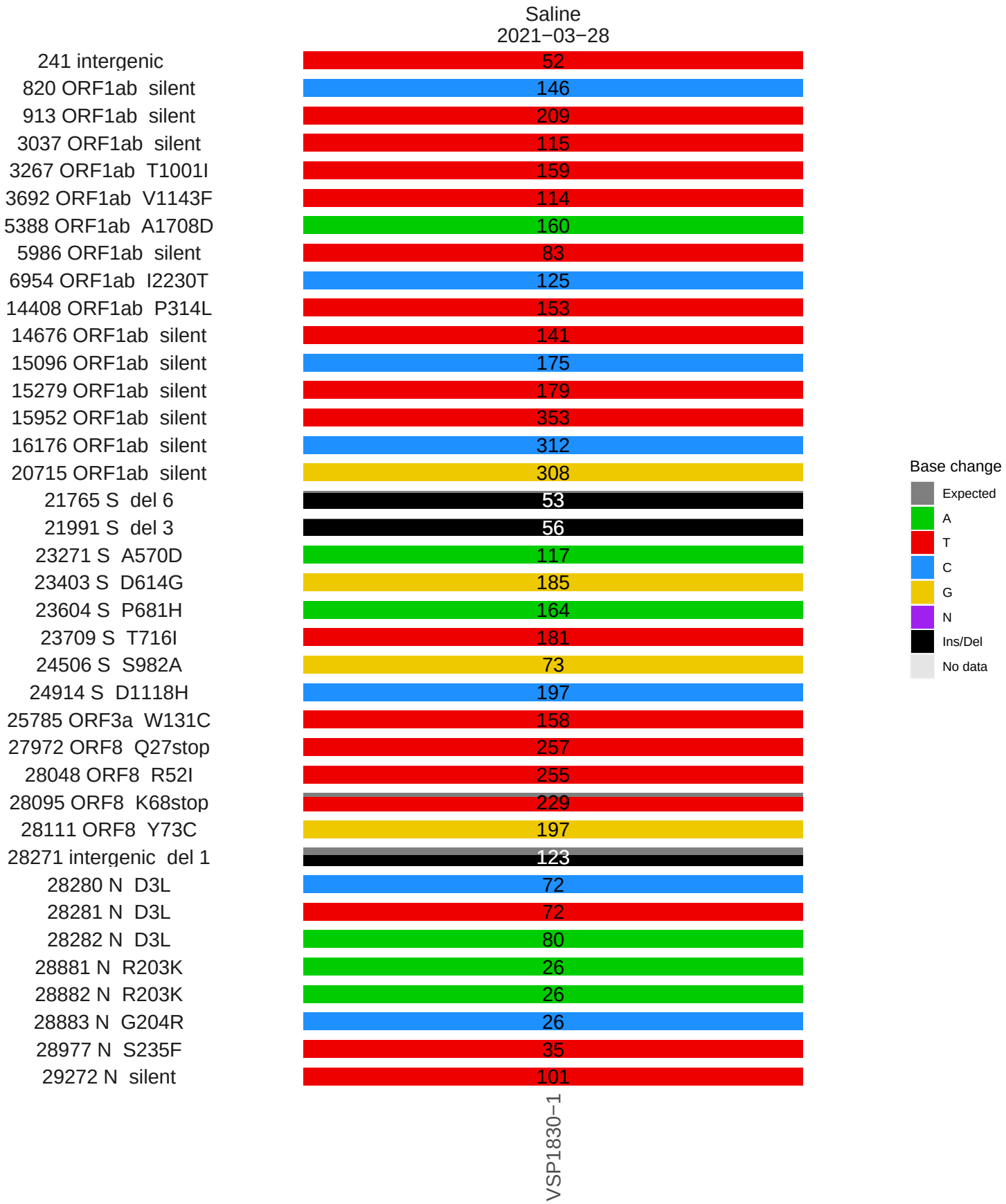
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1830-1	single experiment	NA	Saline	2021-03-28	29.78	B.1.1.7	99.8%	99.5%

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.

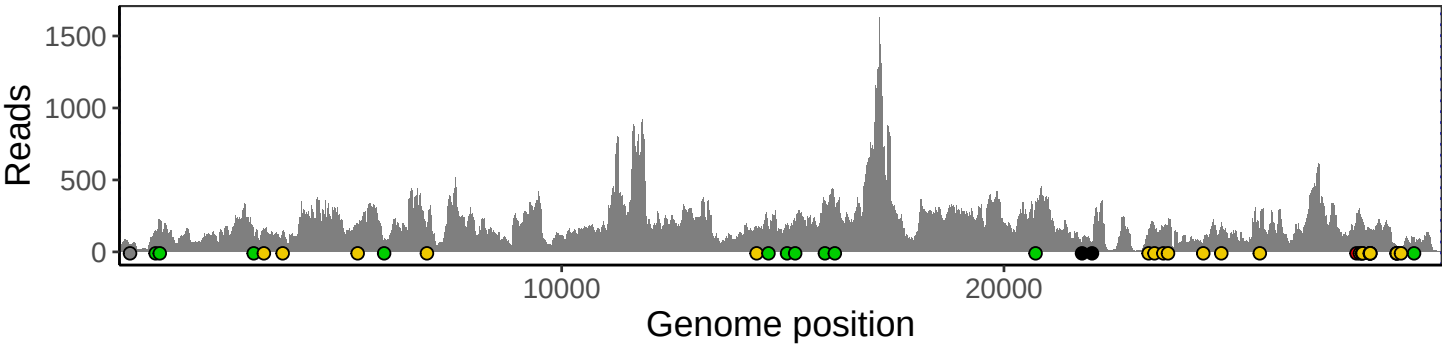



Saline
2021−03−28
241 intergenic 52
820 ORF1ab silent 146
913 ORF1ab silent 209
3037 ORF1ab silent 115
3267 ORF1ab T1001I 159
3692 ORF1ab V1143F 114
5388 ORF1ab A1708D 160
5986 ORF1ab silent 83
6954 ORF1ab I2230T 125
14408 ORF1ab P314L 153
14676 ORF1ab silent 141
15096 ORF1ab silent 175
15279 ORF1ab silent 179
15952 ORF1ab silent 353
16176 ORF1ab silent 312
20715 ORF1ab silent 308
21765 S del 6 53
21991 S del 3 56
23271 S A570D 117
23403 S D614G 185
23604 S P681H 164
23709 S T716I 181
24506 S S982A 73
24914 S D1118H 197
25785 ORF3a W131C 158
27972 ORF8 Q27stop 257
28048 ORF8 R52I 255
28095 ORF8 K68stop 229
28111 ORF8 Y73C 197
28271 intergenic del 1 123
28280 N D3L 72
28281 N D3L 72
28282 N D3L 80
28881 N R203K 26
28882 N R203K 26
28883 N G204R 26
28977 N S235F 35
29272 N silent 101
VSP1830−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

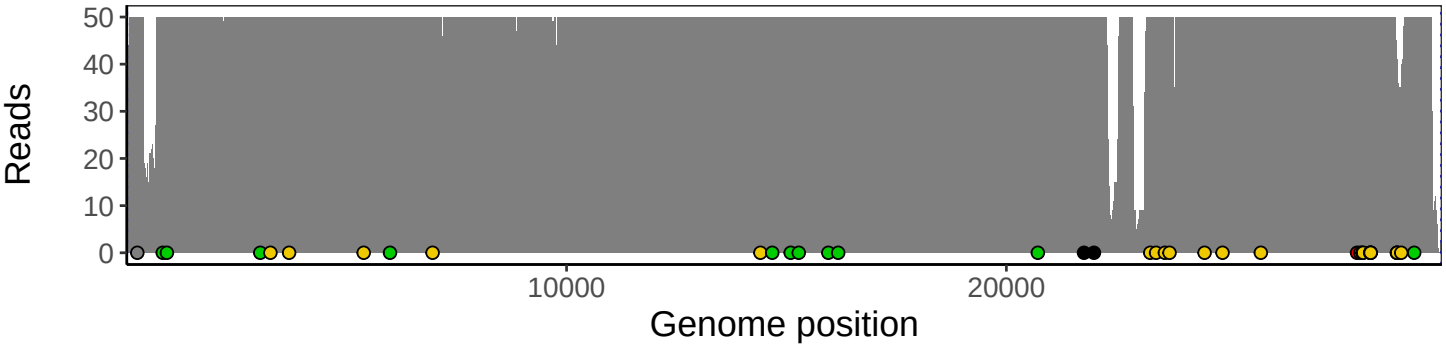
Analyses of individual experiments and composite results

VSP1830-1 | 2021-03-28 | Saline | UPHS-0645 | genomes | single experiment

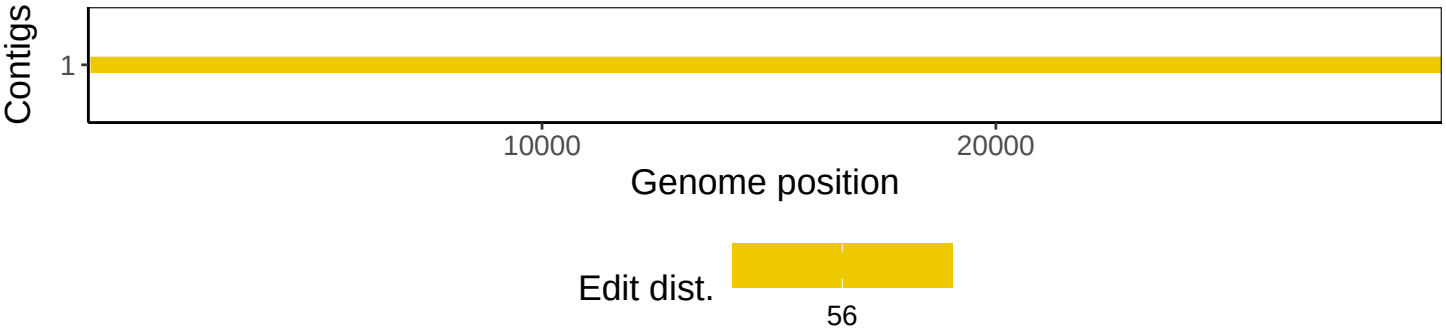
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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