COVID-19 subject UPHS-1416

2021-06-01

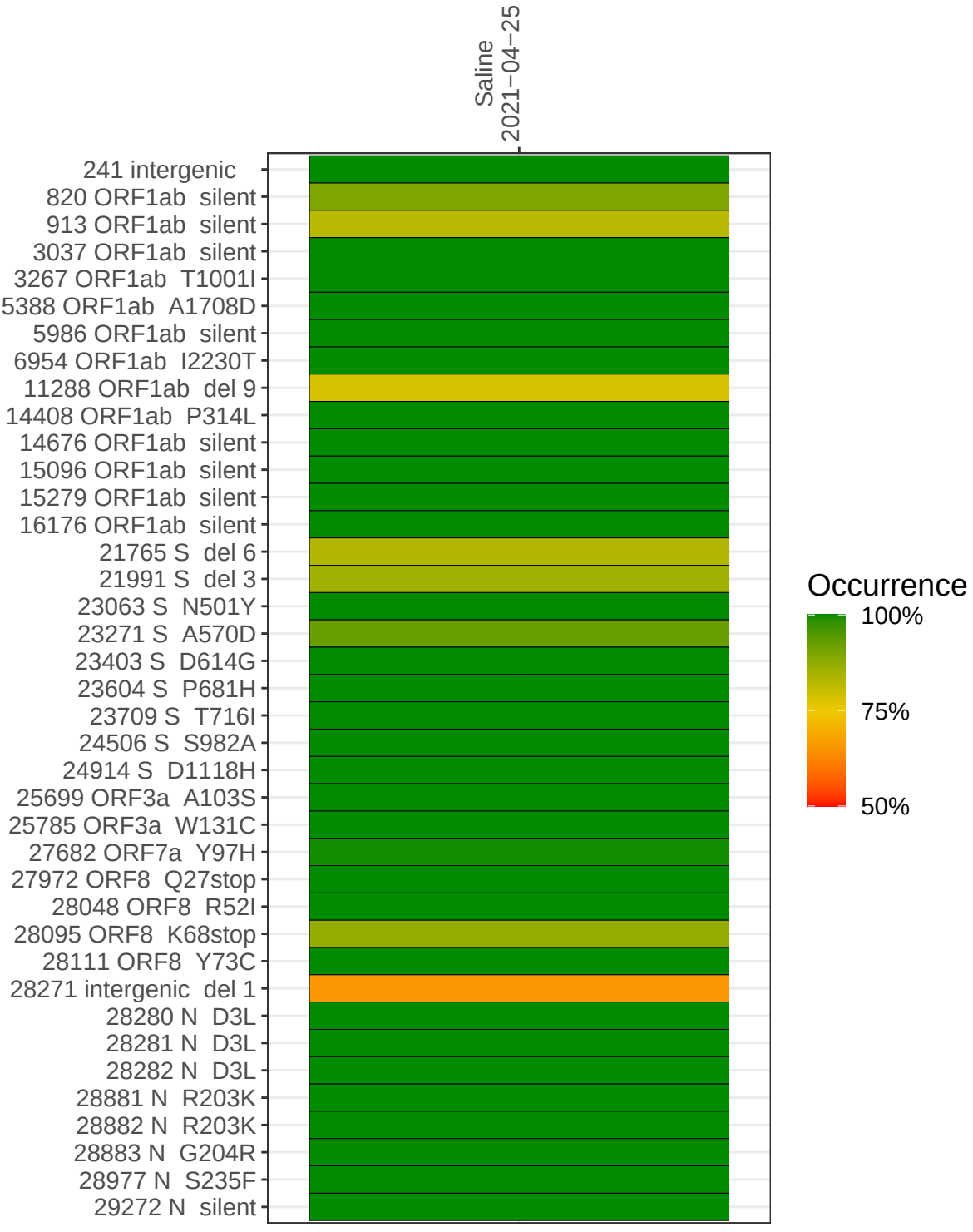
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

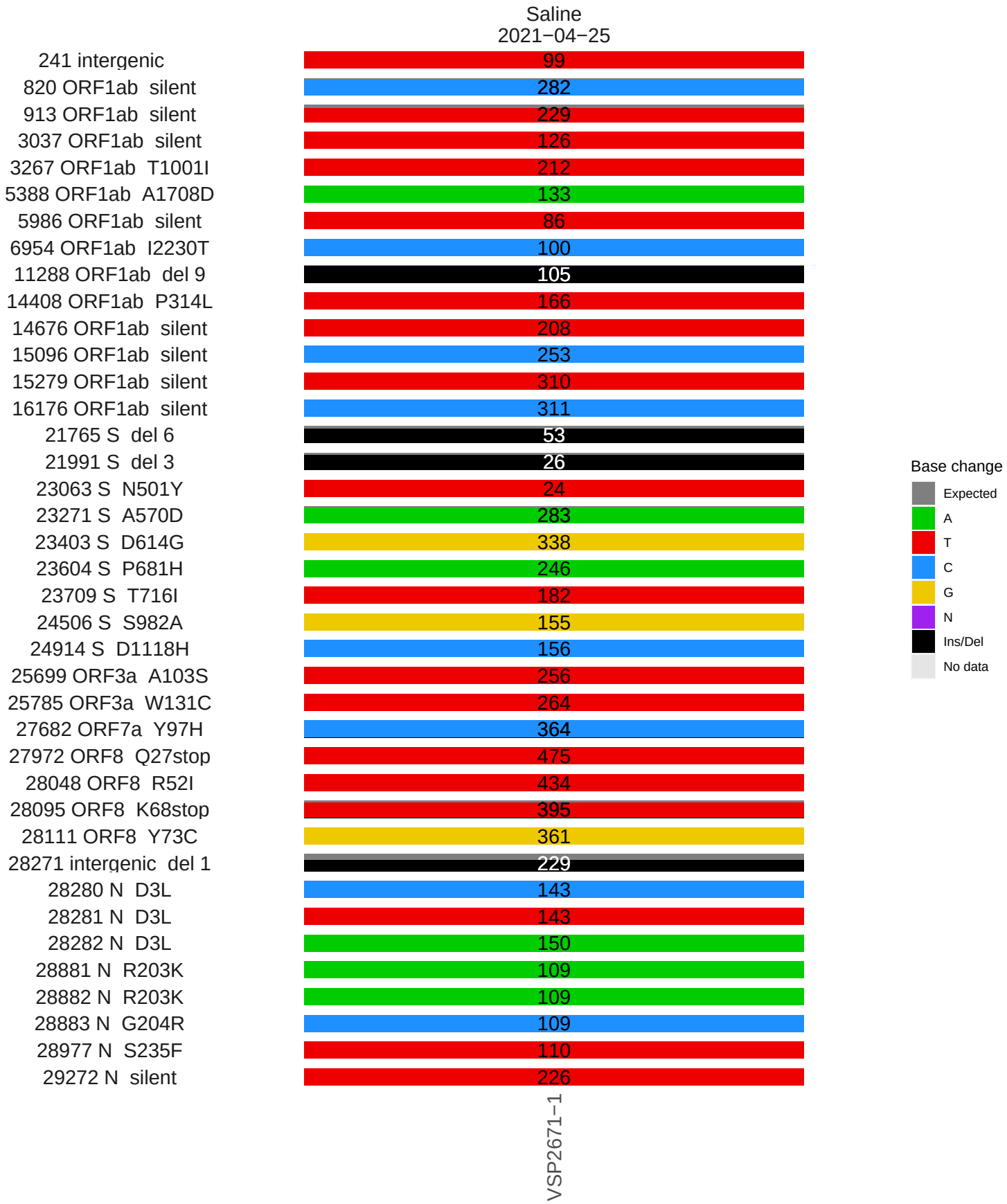
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2671-1	single experiment	NA	Saline	2021-04-25	29.79	B.1.1.7	99.7%	99.2%

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.

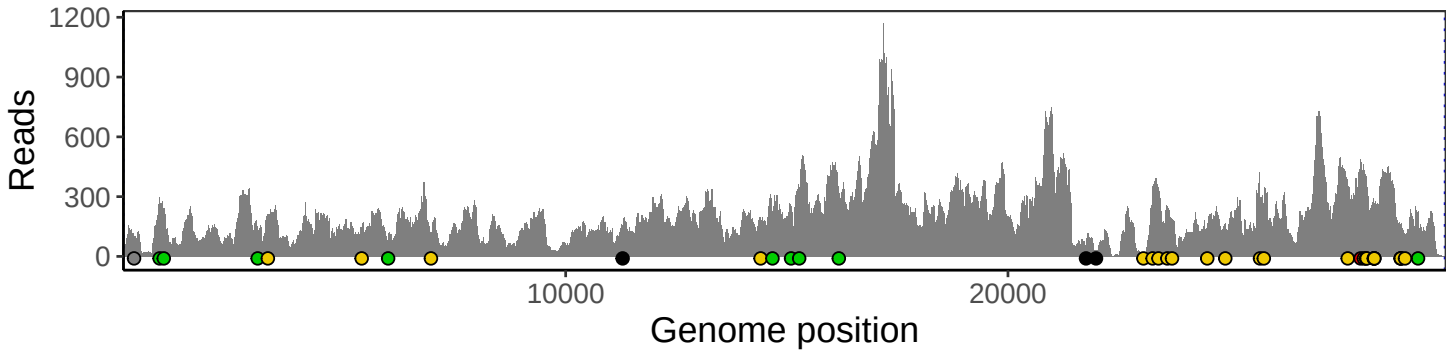



Saline
2021−04−25
241 intergenic 99
820 ORF1ab silent 282
913 ORF1ab silent 229
3037 ORF1ab silent 126
3267 ORF1ab T1001I 212
5388 ORF1ab A1708D 133
5986 ORF1ab silent 86
6954 ORF1ab I2230T 100
11288 ORF1ab del 9 105
14408 ORF1ab P314L 166
14676 ORF1ab silent 208
15096 ORF1ab silent 253
15279 ORF1ab silent 310
16176 ORF1ab silent 311
21765 S del 6 53
21991 S del 3 26
23063 S N501Y 24
23271 S A570D 283
23403 S D614G 338
23604 S P681H 246
23709 S T716I 182
24506 S S982A 155
24914 S D1118H 156
25699 ORF3a A103S 256
25785 ORF3a W131C 264
27682 ORF7a Y97H 364
27972 ORF8 Q27stop 475
28048 ORF8 R52I 434
28095 ORF8 K68stop 395
28111 ORF8 Y73C 361
28271 intergenic del 1 229
28280 N D3L 143
28281 N D3L 143
28282 N D3L 150
28881 N R203K 109
28882 N R203K 109
28883 N G204R 109
28977 N S235F 110
29272 N silent 226
VSP2671−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

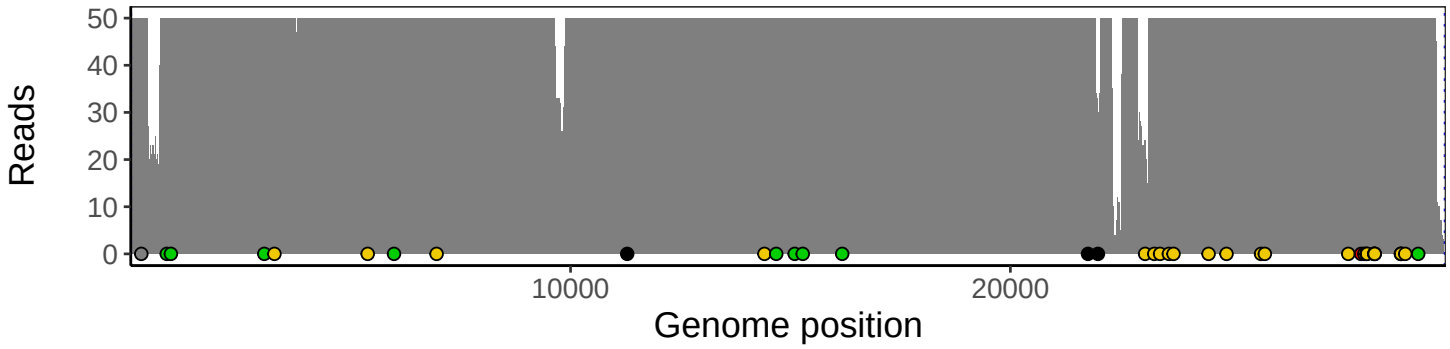
Analyses of individual experiments and composite results

VSP2671-1 | 2021-04-25 | Saline | UPHS-1416 | genomes | single experiment

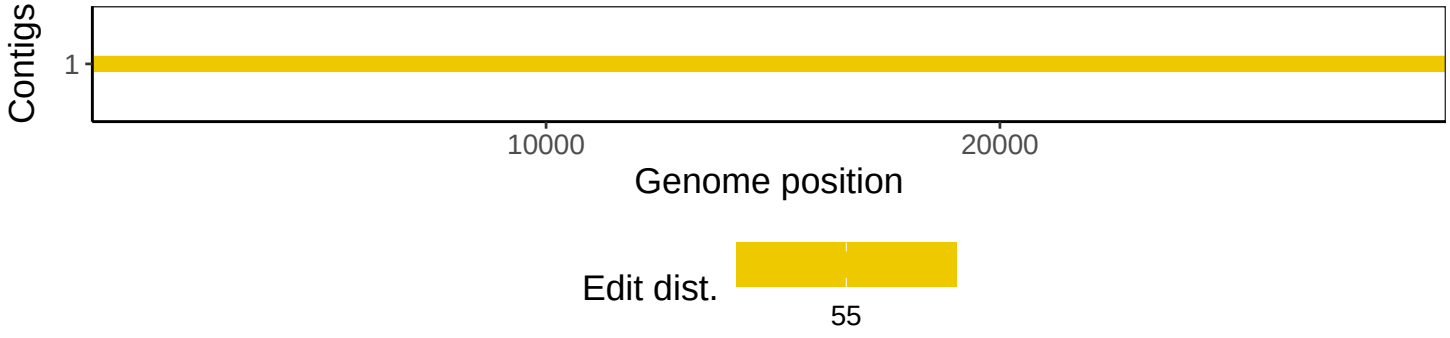
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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