COVID-19 subject UPHS-1334

2021-06-23

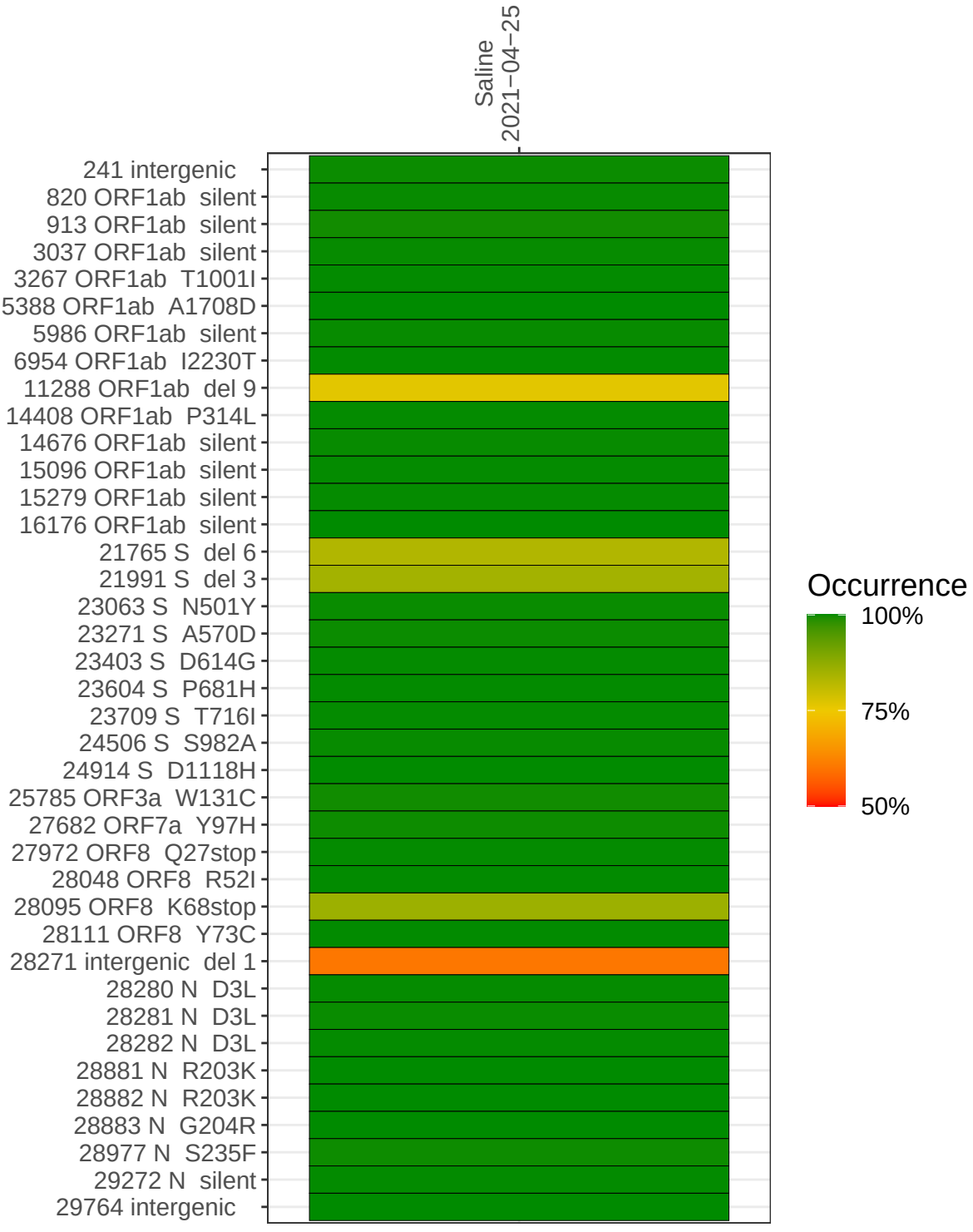
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

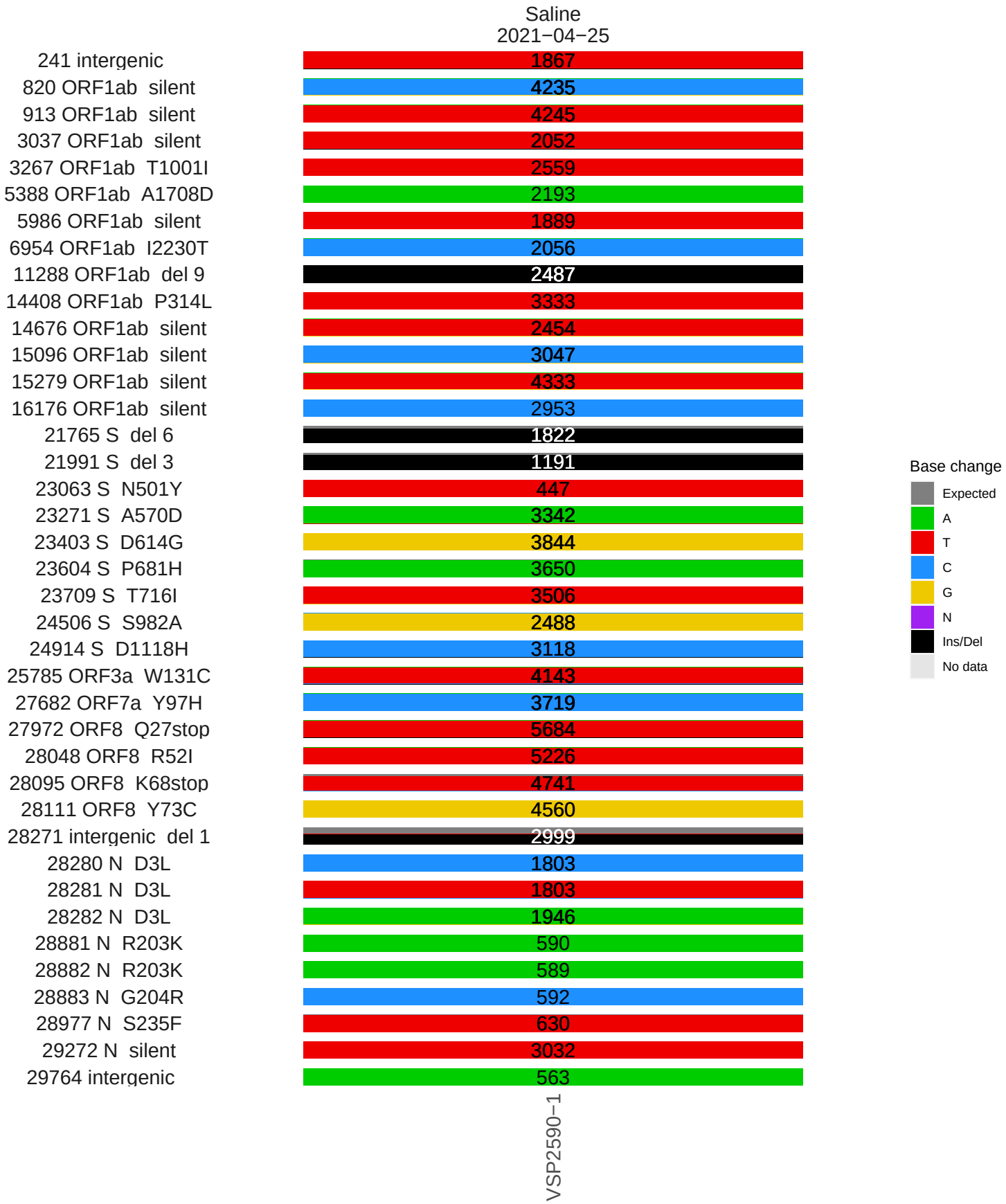
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2590-1	single experiment	NA	Saline	2021-04-25	29.80	B.1.1.7	99.8%	99.8%

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.

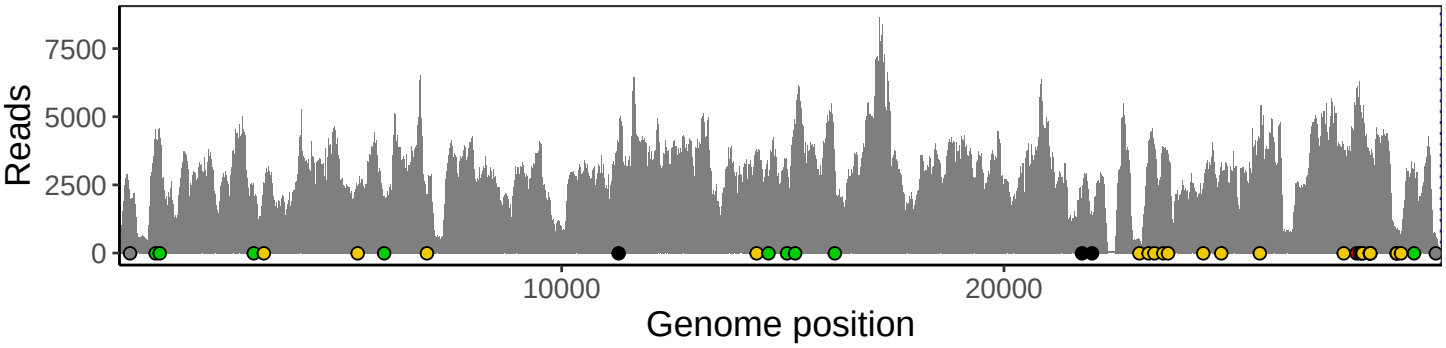



Saline
2021−04−25
241 intergenic 1867
820 ORF1ab silent 4235
913 ORF1ab silent 4245
3037 ORF1ab silent 2052
3267 ORF1ab T1001I 2559
5388 ORF1ab A1708D 2193
5986 ORF1ab silent 1889
6954 ORF1ab I2230T 2056
11288 ORF1ab del 9 2487
14408 ORF1ab P314L 3333
14676 ORF1ab silent 2454
15096 ORF1ab silent 3047
15279 ORF1ab silent 4333
16176 ORF1ab silent 2953
21765 S del 6 1822
21991 S del 3 1191
23063 S N501Y 447
23271 S A570D 3342
23403 S D614G 3844
23604 S P681H 3650
23709 S T716I 3506
24506 S S982A 2488
24914 S D1118H 3118
25785 ORF3a W131C 4143
27682 ORF7a Y97H 3719
27972 ORF8 Q27stop 5684
28048 ORF8 R52I 5226
28095 ORF8 K68stop 4741
28111 ORF8 Y73C 4560
28271 intergenic del 1 2999
28280 N D3L 1803
28281 N D3L 1803
28282 N D3L 1946
28881 N R203K 590
28882 N R203K 589
28883 N G204R 592
28977 N S235F 630
29272 N silent 3032
29764 intergenic 563
VSP2590−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

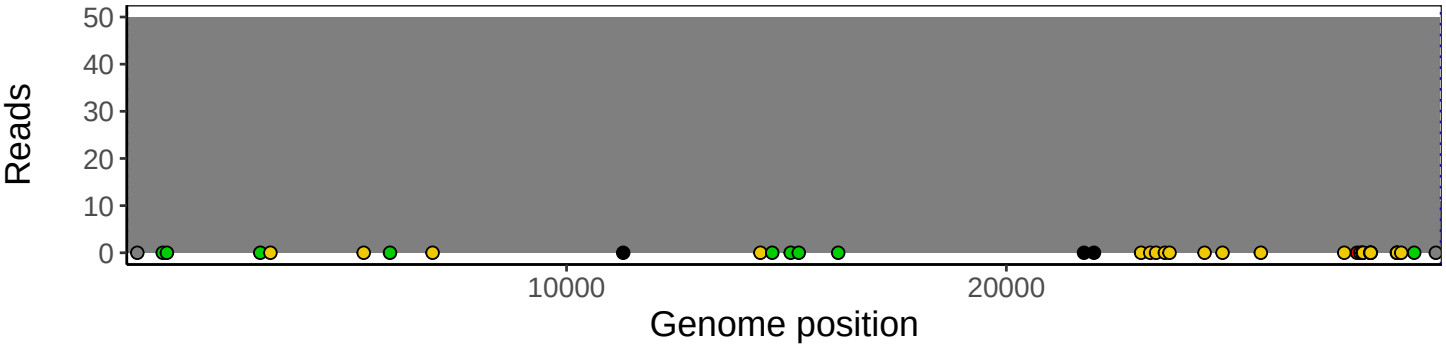
Analyses of individual experiments and composite results

VSP2590-1 | 2021-04-25 | Saline | UPHS-1334 | genomes | single experiment

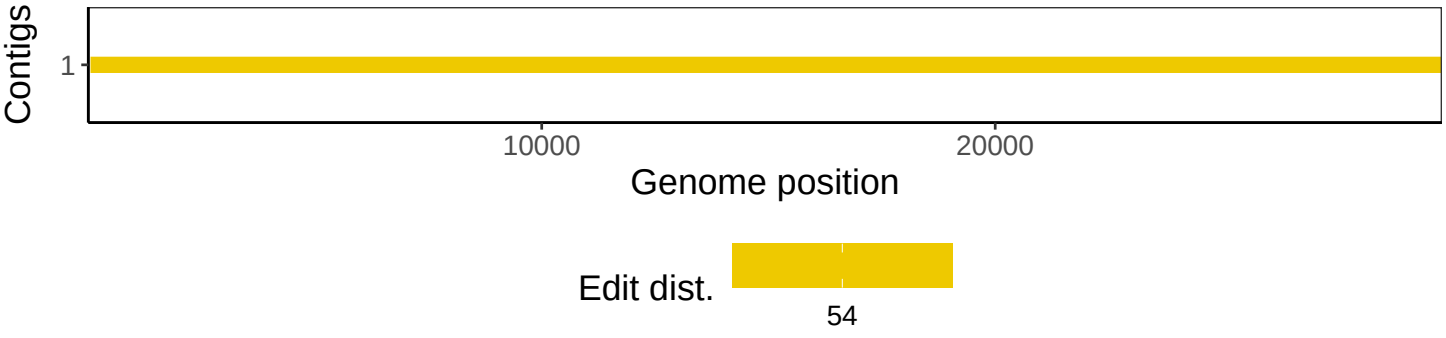
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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