COVID-19 subject UPHS-1592

2021-06-03

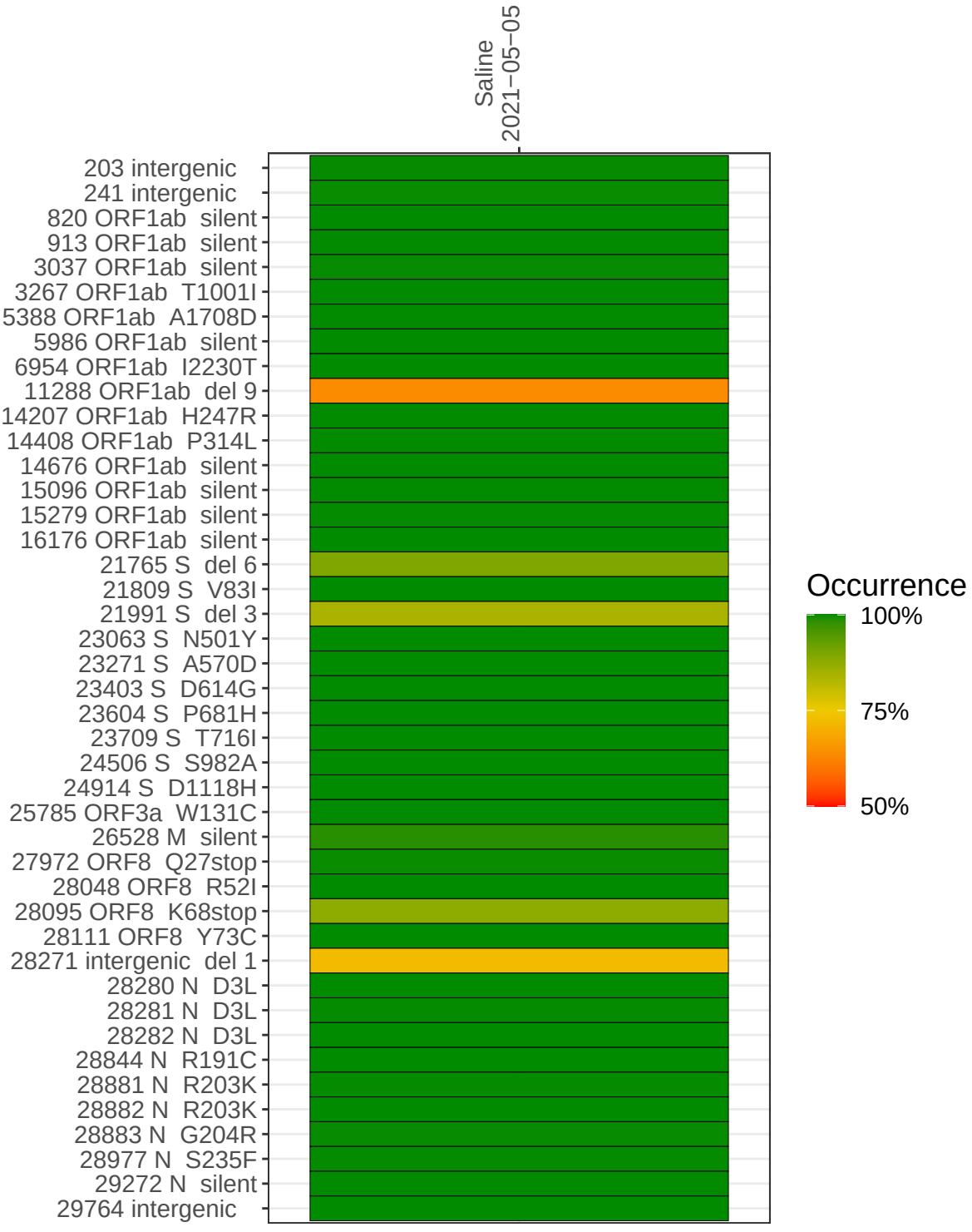
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

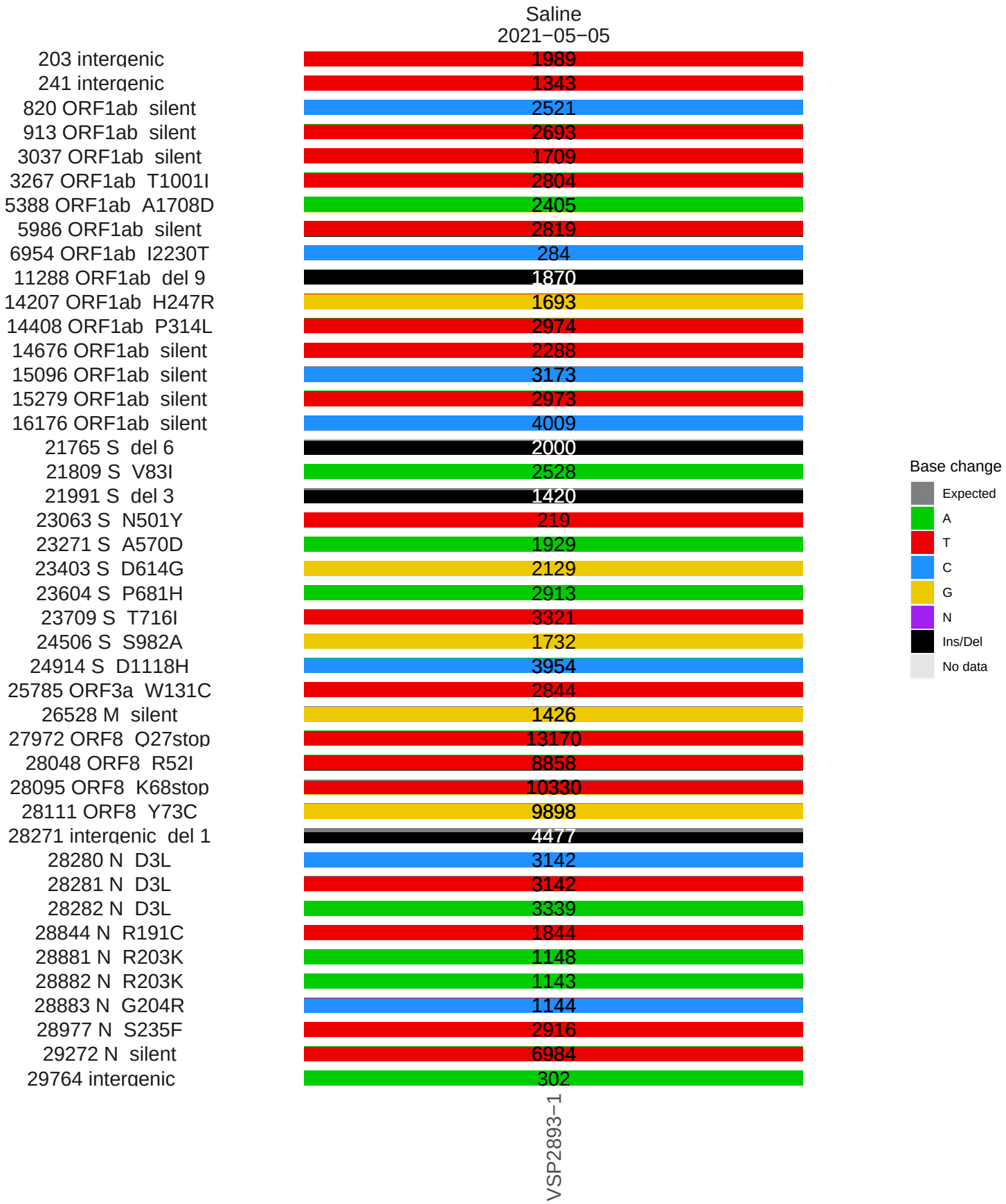
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2893-1	single experiment	NA	Saline	2021-05-05	29.80	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.

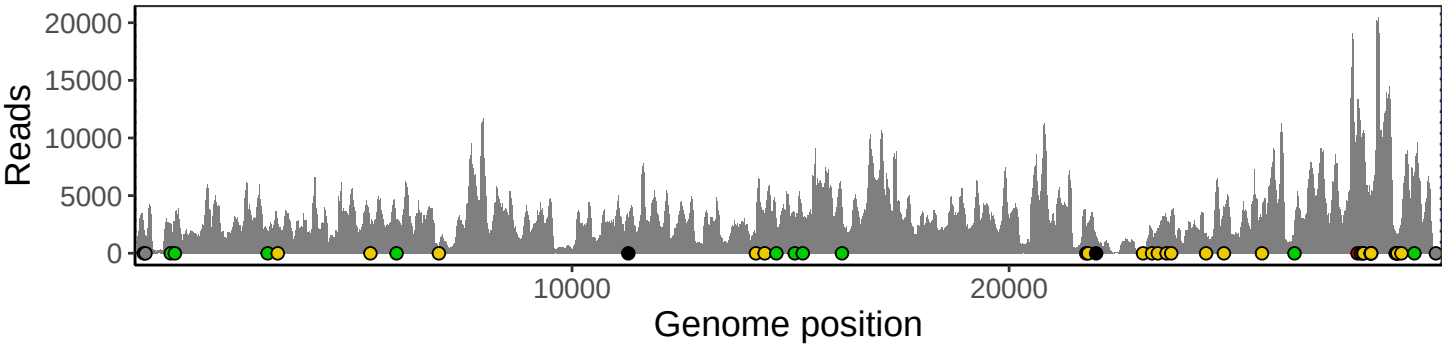



Saline
2021−05−05
203 intergenic 1989
241 intergenic 1343
820 ORF1ab silent 2521
913 ORF1ab silent 2693
3037 ORF1ab silent 1709
3267 ORF1ab T1001I 2804
5388 ORF1ab A1708D 2405
5986 ORF1ab silent 2819
6954 ORF1ab I2230T 284
11288 ORF1ab del 9 1870
14207 ORF1ab H247R 1693
14408 ORF1ab P314L 2974
14676 ORF1ab silent 2288
15096 ORF1ab silent 3173
15279 ORF1ab silent 2973
16176 ORF1ab silent 4009
21765 S del 6 2000
21809 S V83I 2528
21991 S del 3 1420
23063 S N501Y 219
23271 S A570D 1929
23403 S D614G 2129
23604 S P681H 2913
23709 S T716I 3321
24506 S S982A 1732
24914 S D1118H 3954
25785 ORF3a W131C 2844
26528 M silent 1426
27972 ORF8 Q27stop 13170
28048 ORF8 R52I 8858
28095 ORF8 K68stop 10330
28111 ORF8 Y73C 9898
28271 intergenic del 1 4477
28280 N D3L 3142
28281 N D3L 3142
28282 N D3L 3339
28844 N R191C 1844
28881 N R203K 1148
28882 N R203K 1143
28883 N G204R 1144
28977 N S235F 2916
29272 N silent 6984
29764 intergenic 302
VSP2893−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

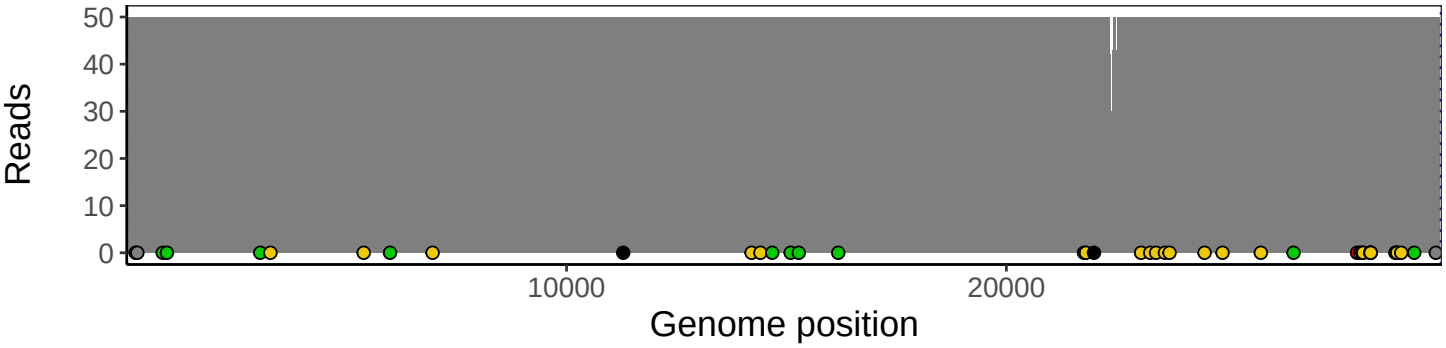
Analyses of individual experiments and composite results

VSP2893-1 | 2021-05-05 | Saline | UPHS-1592 | genomes | single experiment

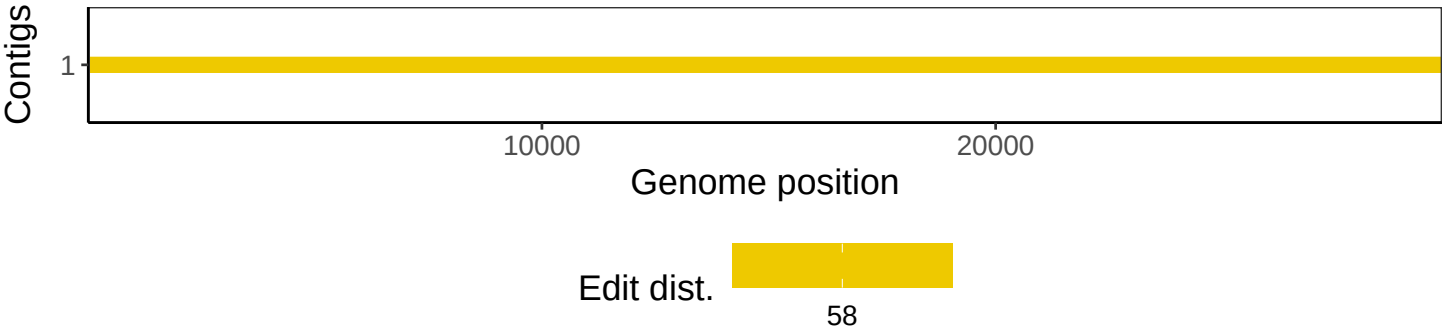
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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