COVID-19 subject UPHS-1497

2021-06-23

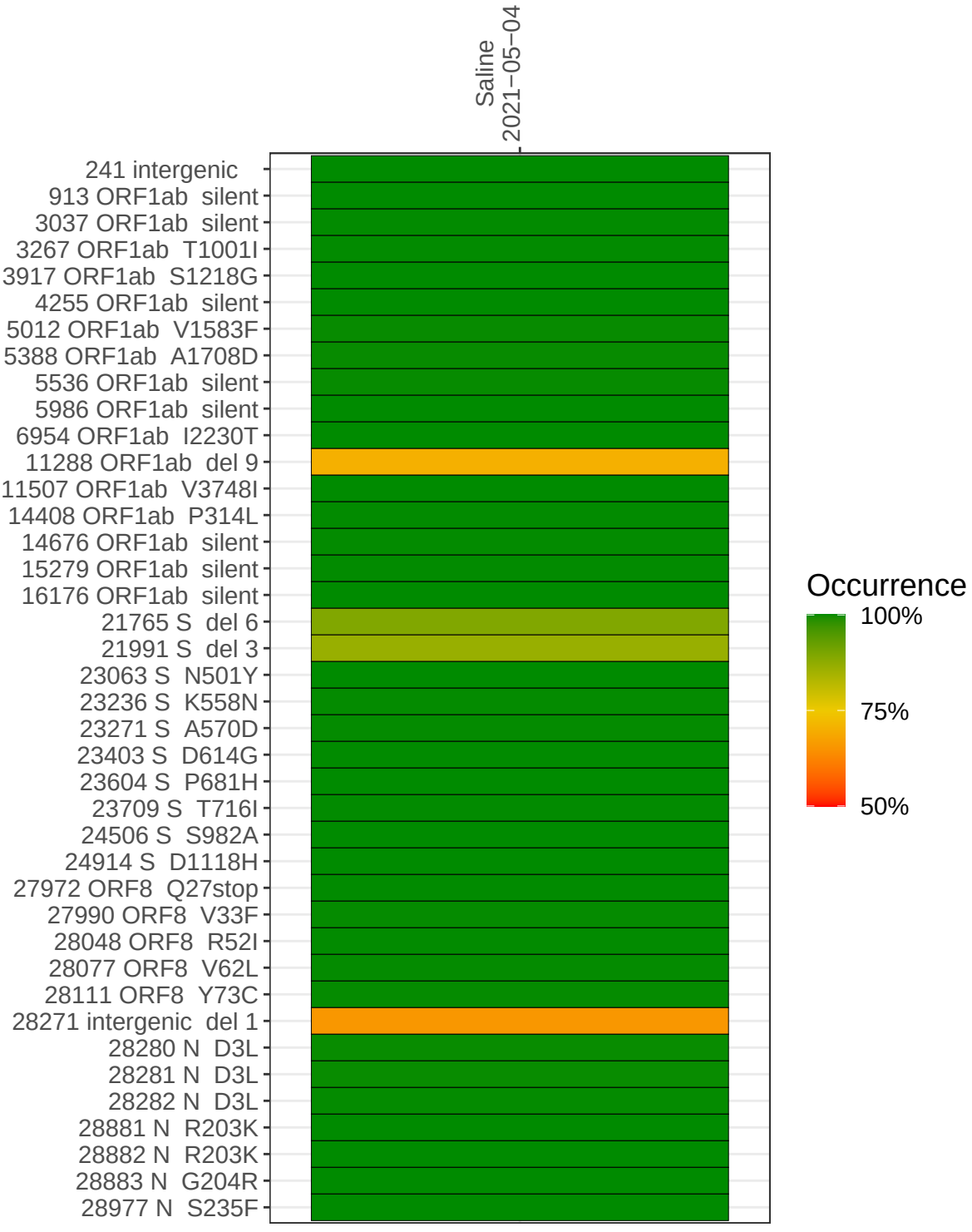
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

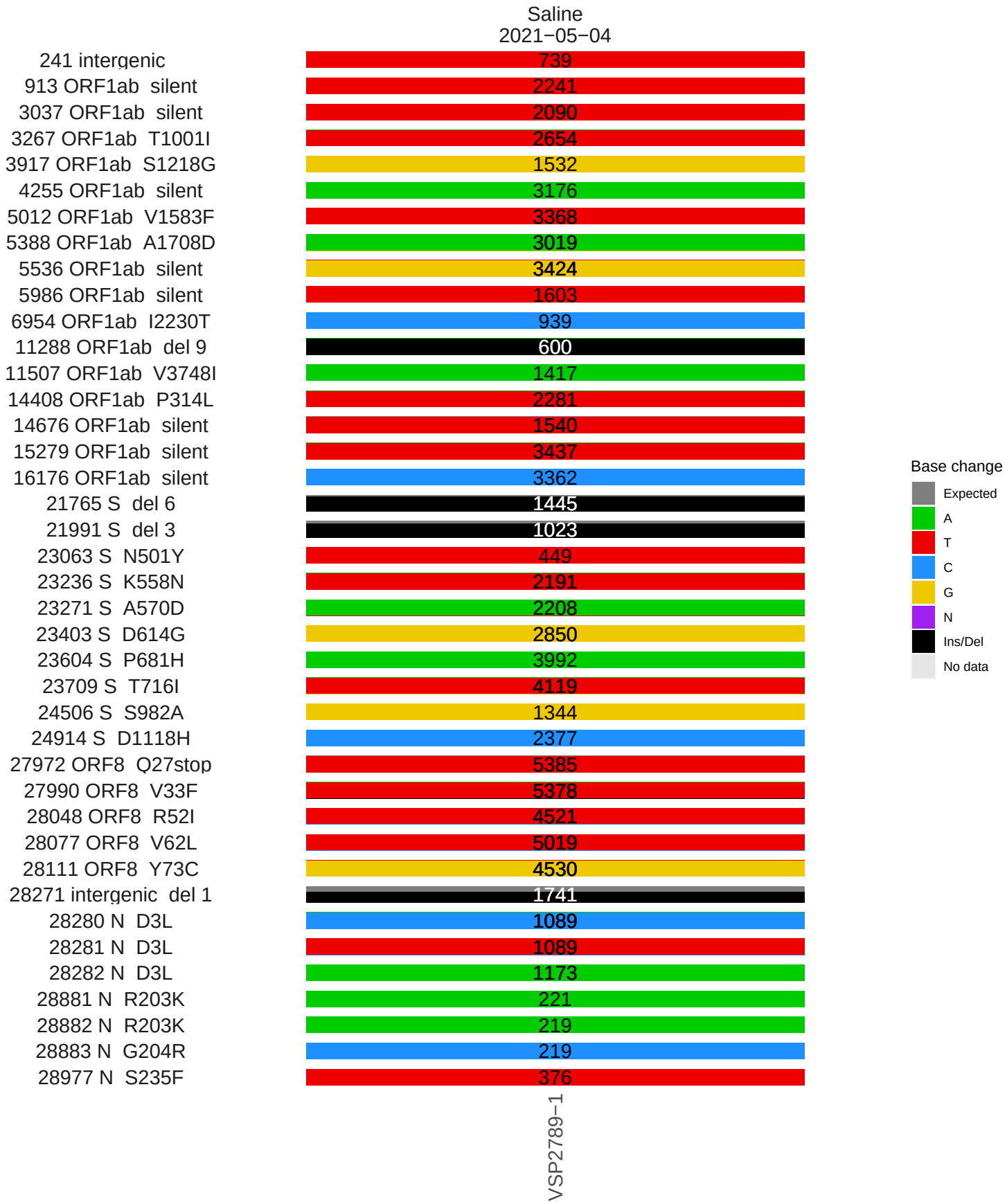
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2789-1	single experiment	NA	Saline	2021-05-04	29.82	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.

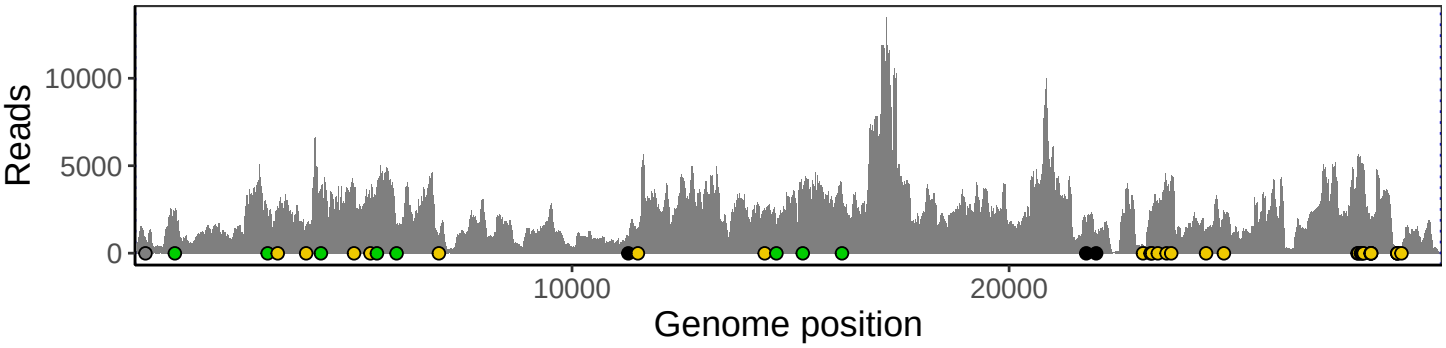



Saline
2021−05−04
241 intergenic 739
913 ORF1ab silent 2241
3037 ORF1ab silent 2090
3267 ORF1ab T1001I 2654
3917 ORF1ab S1218G 1532
4255 ORF1ab silent 3176
5012 ORF1ab V1583F 3368
5388 ORF1ab A1708D 3019
5536 ORF1ab silent 3424
5986 ORF1ab silent 1603
6954 ORF1ab I2230T 939
11288 ORF1ab del 9 600
11507 ORF1ab V3748I 1417
14408 ORF1ab P314L 2281
14676 ORF1ab silent 1540
15279 ORF1ab silent 3437
16176 ORF1ab silent 3362
21765 S del 6 1445
21991 S del 3 1023
23063 S N501Y 449
23236 S K558N 2191
23271 S A570D 2208
23403 S D614G 2850
23604 S P681H 3992
23709 S T716I 4119
24506 S S982A 1344
24914 S D1118H 2377
27972 ORF8 Q27stop 5385
27990 ORF8 V33F 5378
28048 ORF8 R52I 4521
28077 ORF8 V62L 5019
28111 ORF8 Y73C 4530
28271 intergenic del 1 1741
28280 N D3L 1089
28281 N D3L 1089
28282 N D3L 1173
28881 N R203K 221
28882 N R203K 219
28883 N G204R 219
28977 N S235F 376
VSP2789−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

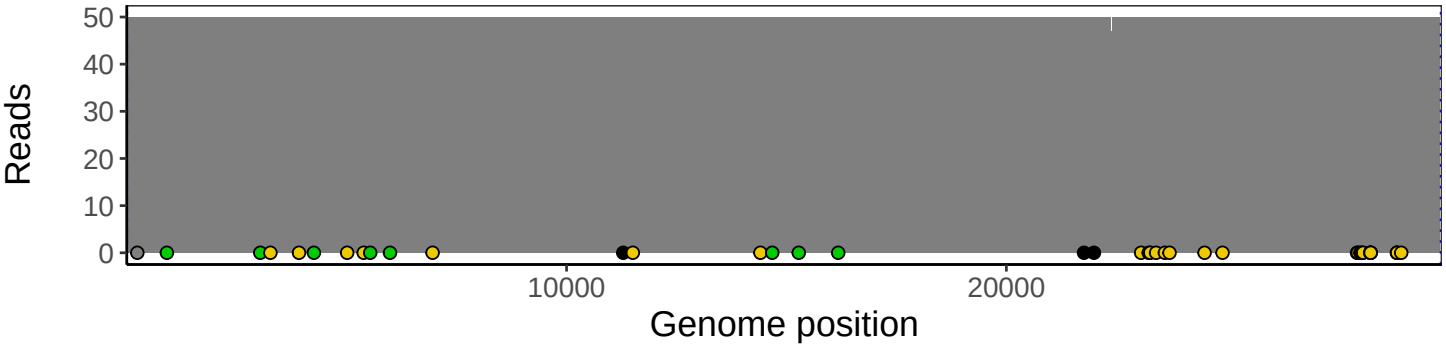
Analyses of individual experiments and composite results

VSP2789-1 | 2021-05-04 | Saline | UPHS-1497 | genomes | single experiment

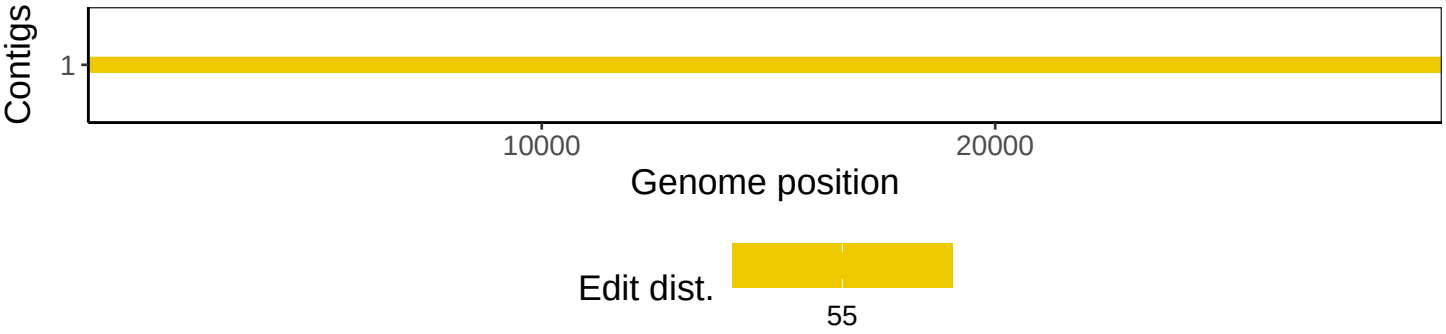
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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