COVID-19 subject UPHS-0997

2021-05-10

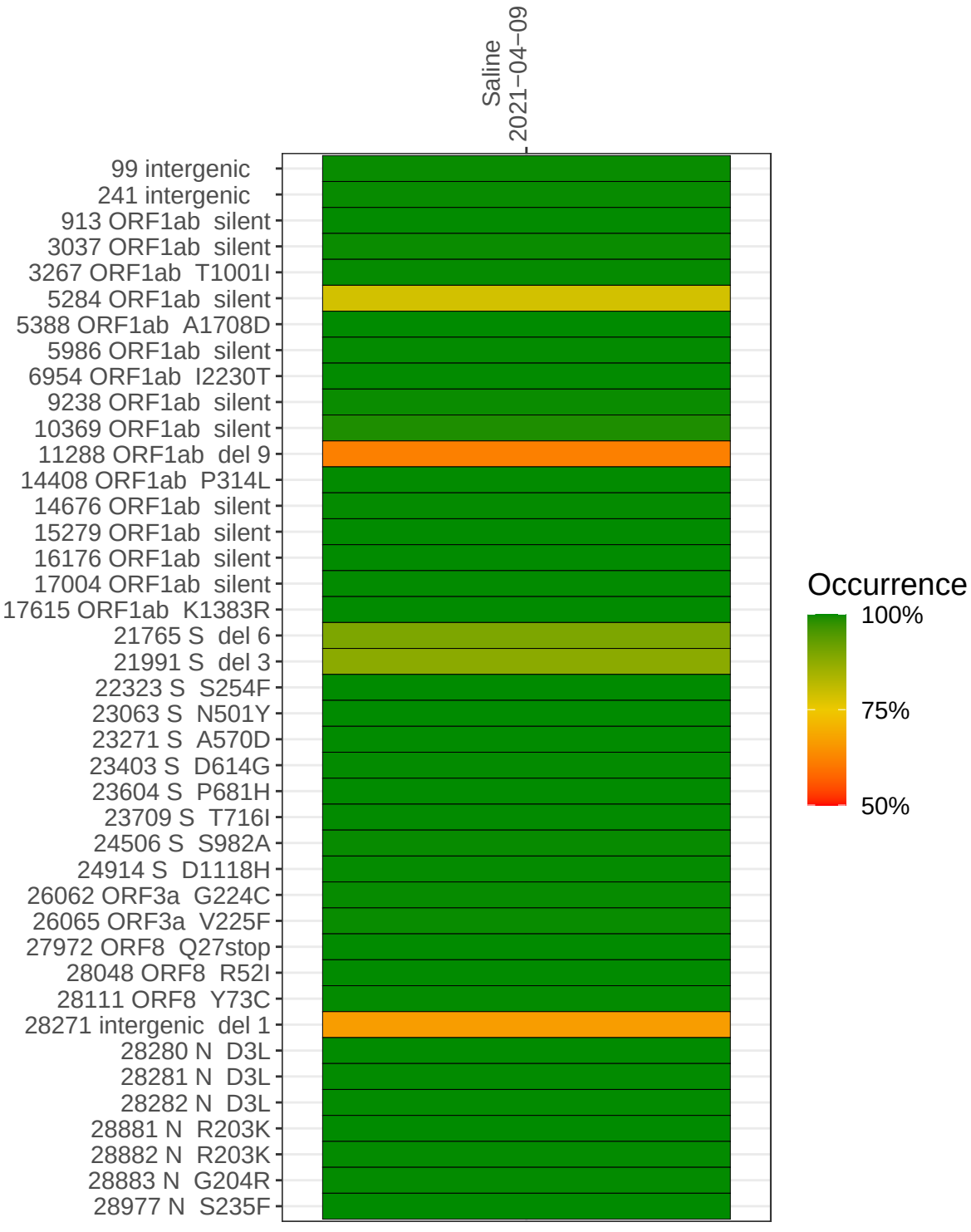
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

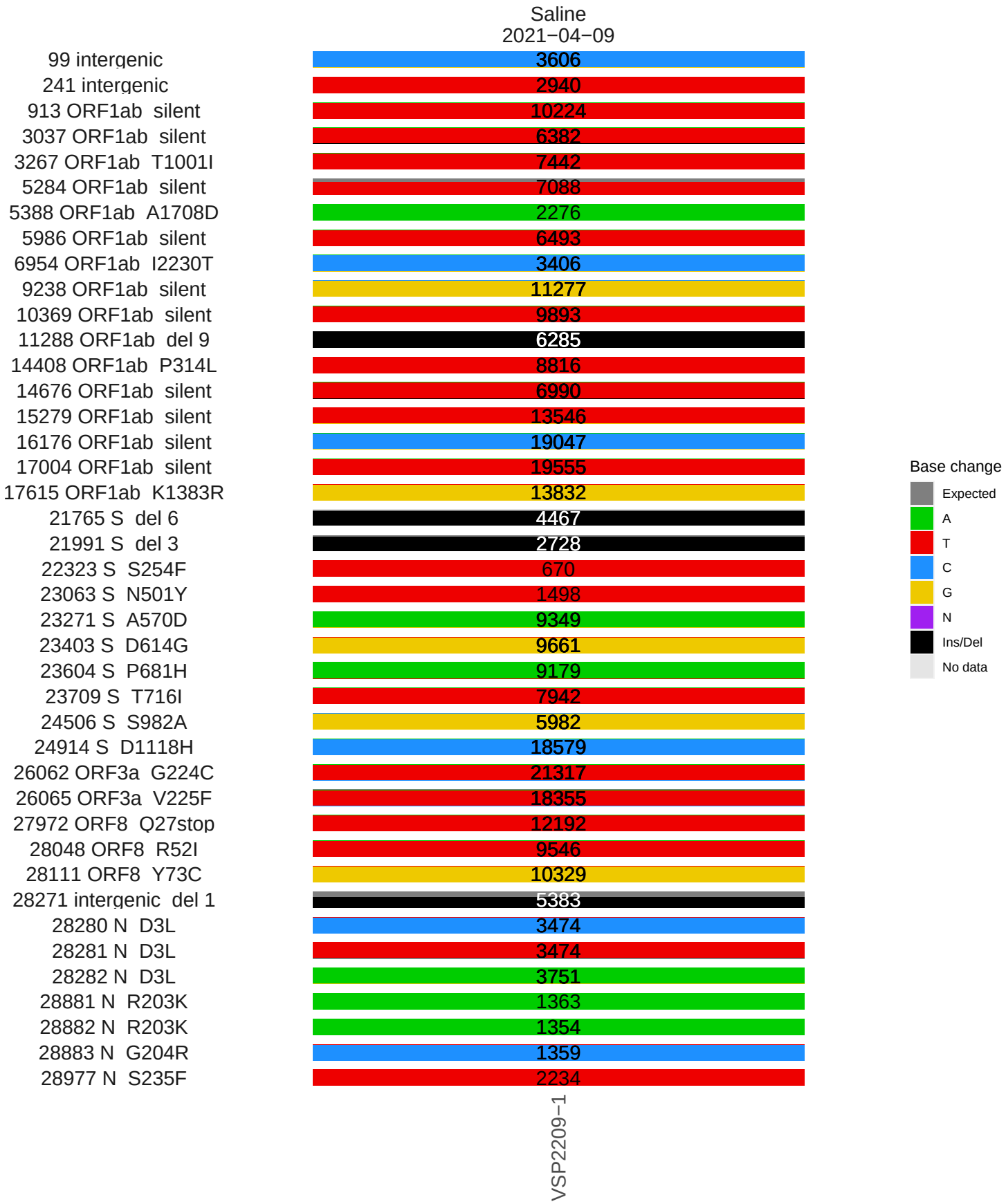
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2209-1	single experiment	NA	Saline	2021-04-09	29.87	B.1.1.7	99.9%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

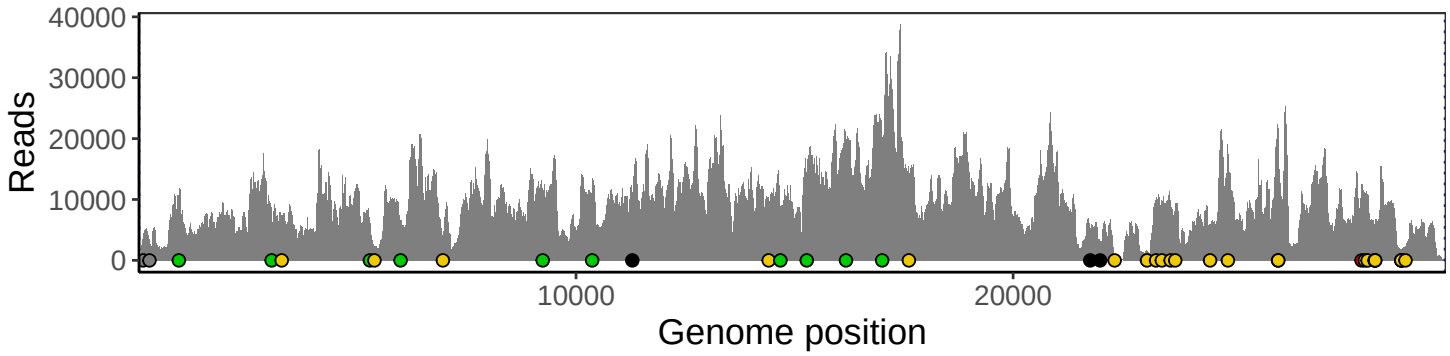



Saline
2021−04−09
99 intergenic 3606
241 intergenic 2940
913 ORF1ab silent 10224
3037 ORF1ab silent 6382
3267 ORF1ab T1001I 7442
5284 ORF1ab silent 7088
5388 ORF1ab A1708D 2276
5986 ORF1ab silent 6493
6954 ORF1ab I2230T 3406
9238 ORF1ab silent 11277
10369 ORF1ab silent 9893
11288 ORF1ab del 9 6285
14408 ORF1ab P314L 8816
14676 ORF1ab silent 6990
15279 ORF1ab silent 13546
16176 ORF1ab silent 19047
17004 ORF1ab silent 19555
17615 ORF1ab K1383R 13832
21765 S del 6 4467
21991 S del 3 2728
22323 S S254F 670
23063 S N501Y 1498
23271 S A570D 9349
23403 S D614G 9661
23604 S P681H 9179
23709 S T716I 7942
24506 S S982A 5982
24914 S D1118H 18579
26062 ORF3a G224C 21317
26065 ORF3a V225F 18355
27972 ORF8 Q27stop 12192
28048 ORF8 R52I 9546
28111 ORF8 Y73C 10329
28271 intergenic del 1 5383
28280 N D3L 3474
28281 N D3L 3474
28282 N D3L 3751
28881 N R203K 1363
28882 N R203K 1354
28883 N G204R 1359
28977 N S235F 2234
VSP2209−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

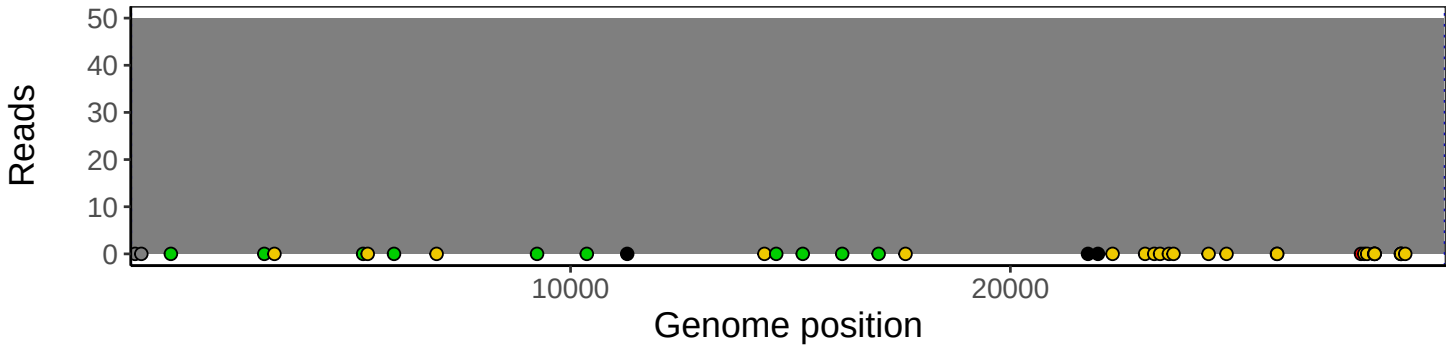
Analyses of individual experiments and composite results

VSP2209-1 | 2021-04-09 | Saline | UPHS-0997 | genomes | single experiment

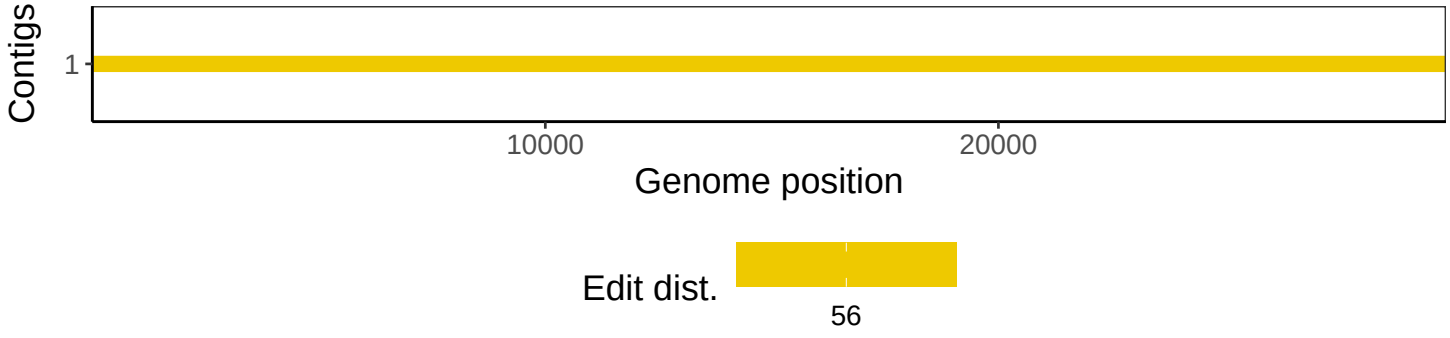
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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