COVID-19 subject UPHS-1052

2021-06-23

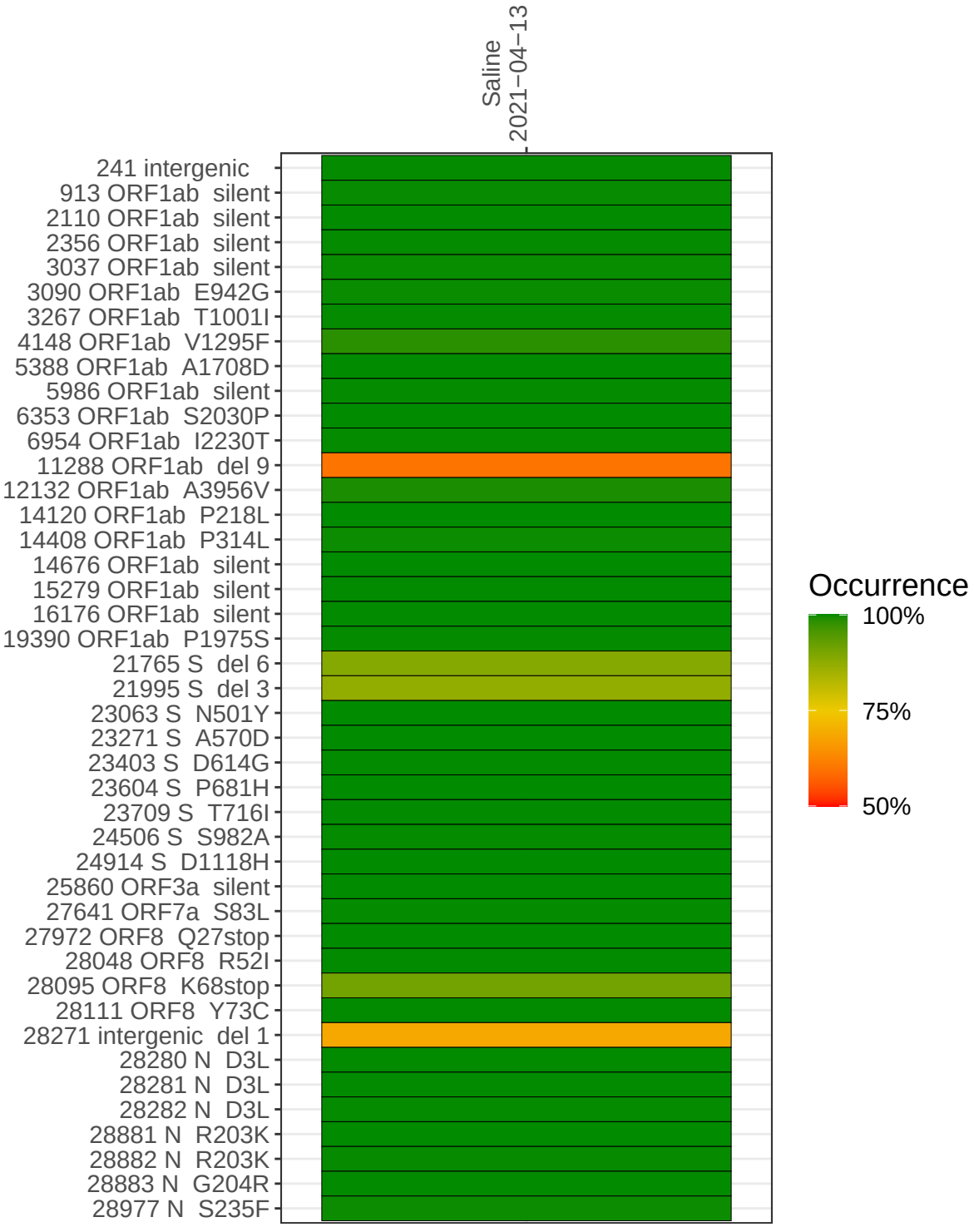
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

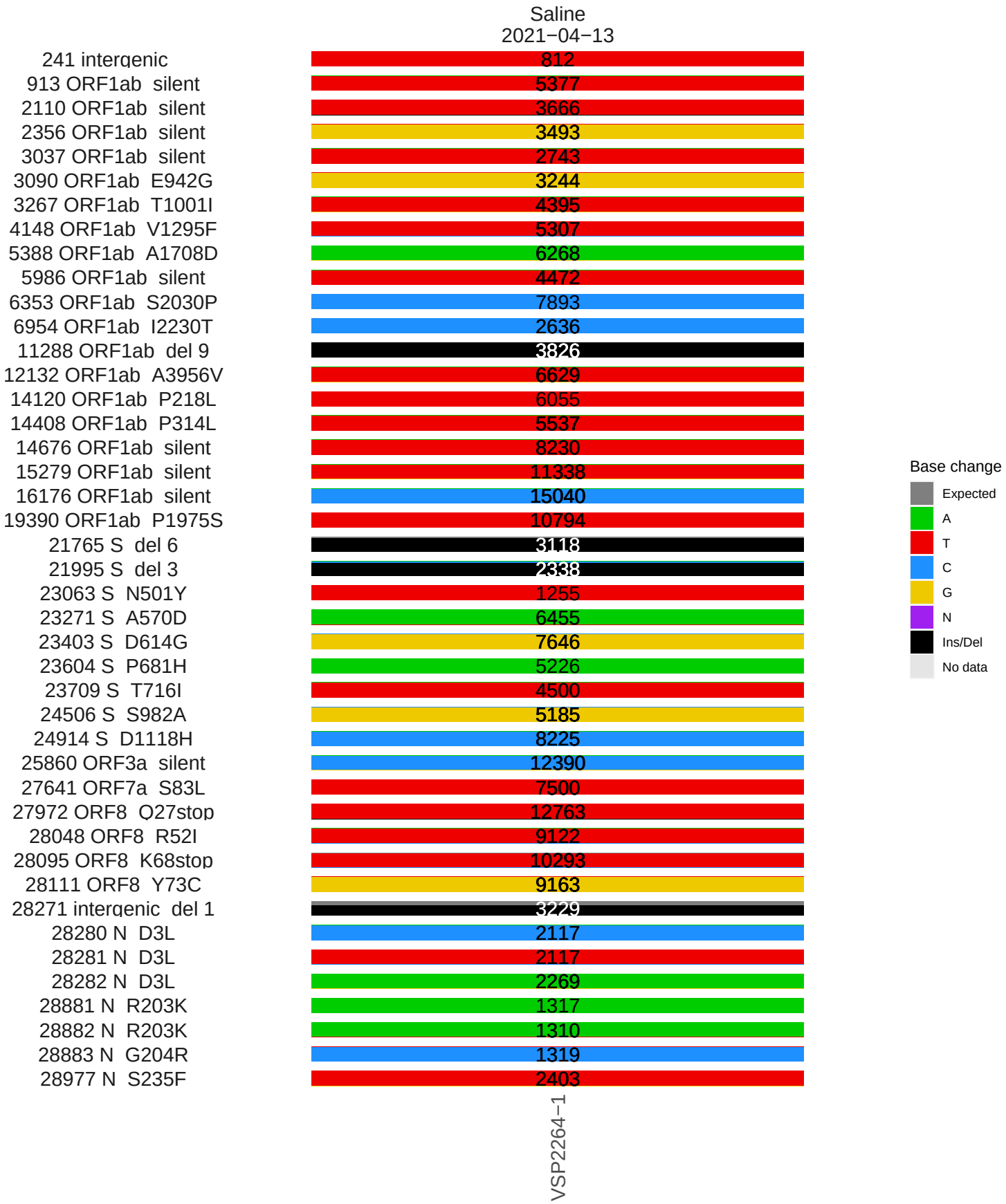
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2264-1	single experiment	NA	Saline	2021-04-13	29.85	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.

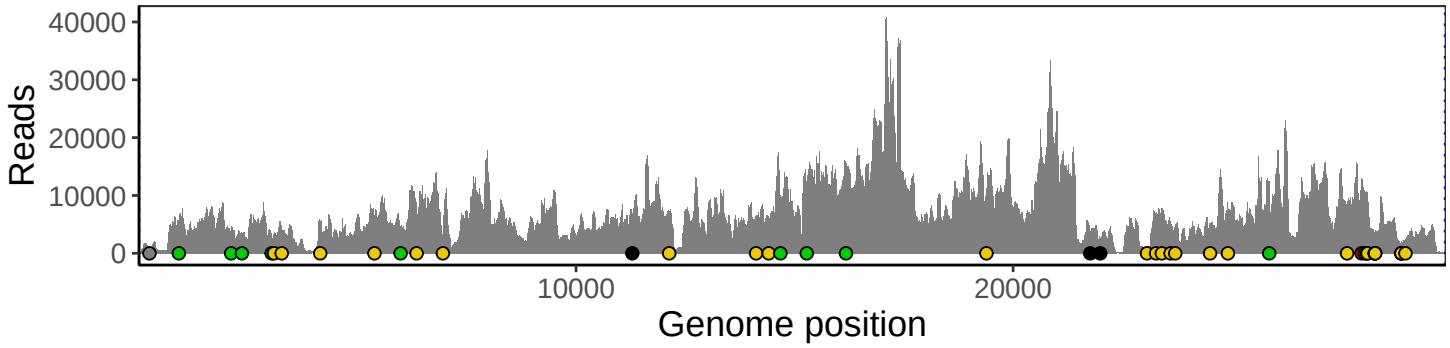



Saline
2021−04−13
241 intergenic 812
913 ORF1ab silent 5377
2110 ORF1ab silent 3666
2356 ORF1ab silent 3493
3037 ORF1ab silent 2743
3090 ORF1ab E942G 3244
3267 ORF1ab T1001I 4395
4148 ORF1ab V1295F 5307
5388 ORF1ab A1708D 6268
5986 ORF1ab silent 4472
6353 ORF1ab S2030P 7893
6954 ORF1ab I2230T 2636
11288 ORF1ab del 9 3826
12132 ORF1ab A3956V 6629
14120 ORF1ab P218L 6055
14408 ORF1ab P314L 5537
14676 ORF1ab silent 8230
15279 ORF1ab silent 11338
16176 ORF1ab silent 15040
19390 ORF1ab P1975S 10794
21765 S del 6 3118
21995 S del 3 2338
23063 S N501Y 1255
23271 S A570D 6455
23403 S D614G 7646
23604 S P681H 5226
23709 S T716I 4500
24506 S S982A 5185
24914 S D1118H 8225
25860 ORF3a silent 12390
27641 ORF7a S83L 7500
27972 ORF8 Q27stop 12763
28048 ORF8 R52I 9122
28095 ORF8 K68stop 10293
28111 ORF8 Y73C 9163
28271 intergenic del 1 3229
28280 N D3L 2117
28281 N D3L 2117
28282 N D3L 2269
28881 N R203K 1317
28882 N R203K 1310
28883 N G204R 1319
28977 N S235F 2403
VSP2264−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

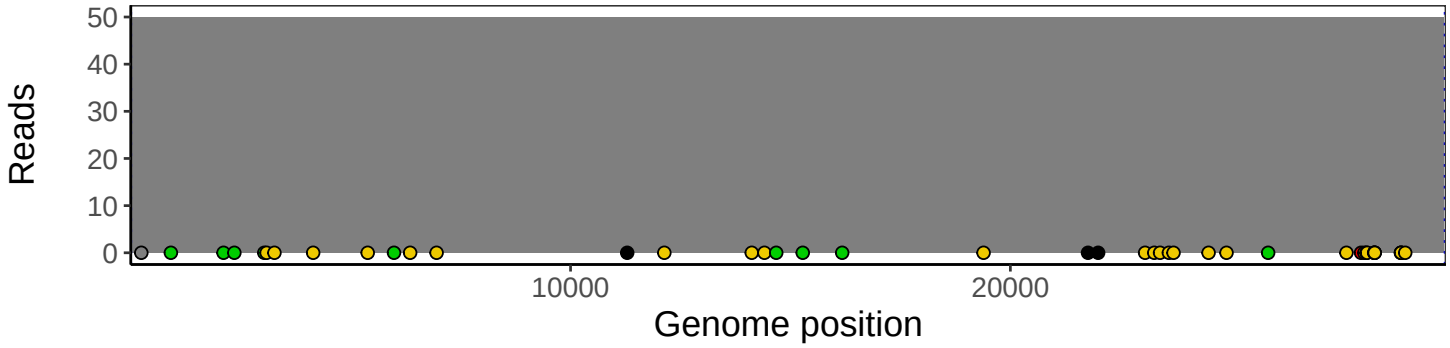
Analyses of individual experiments and composite results

VSP2264-1 | 2021-04-13 | Saline | UPHS-1052 | genomes | single experiment

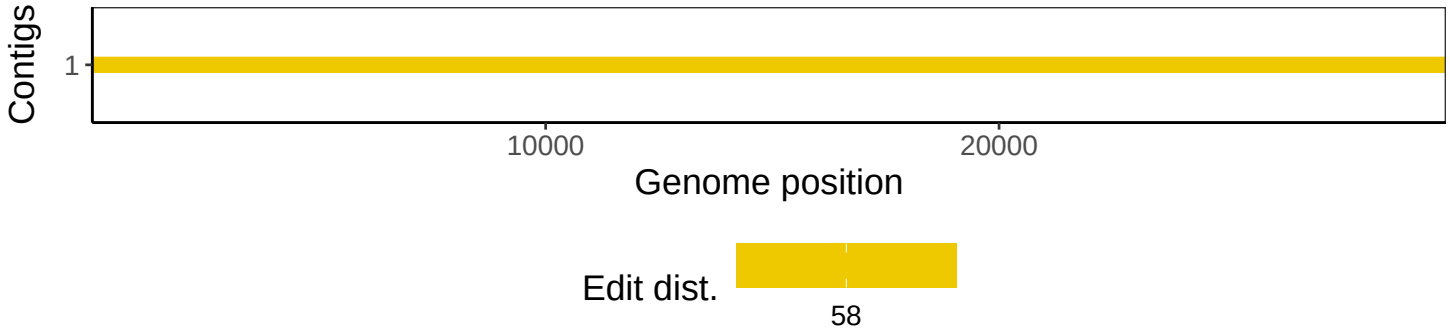
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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