COVID-19 subject UPHS-1182

2021-06-23

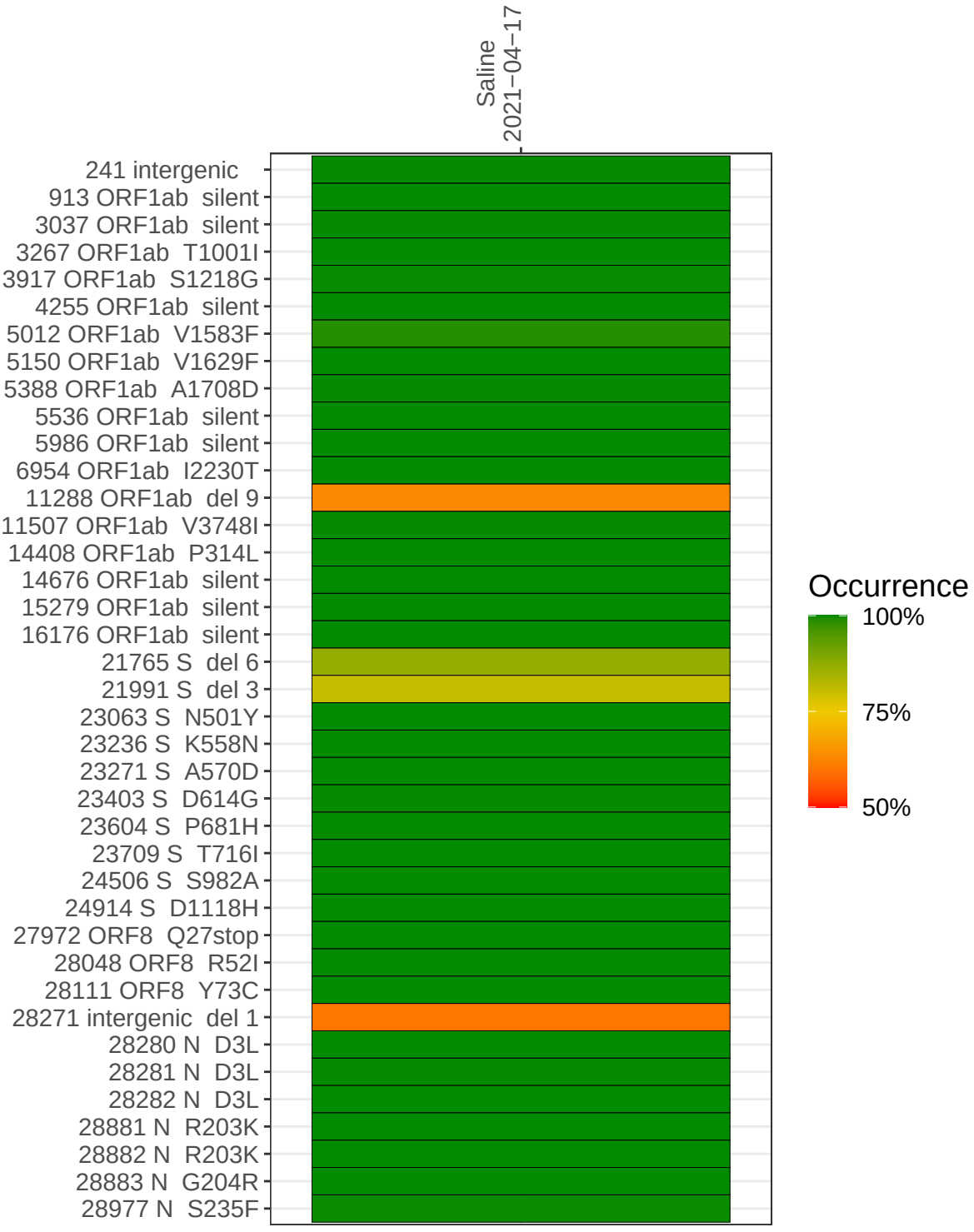
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

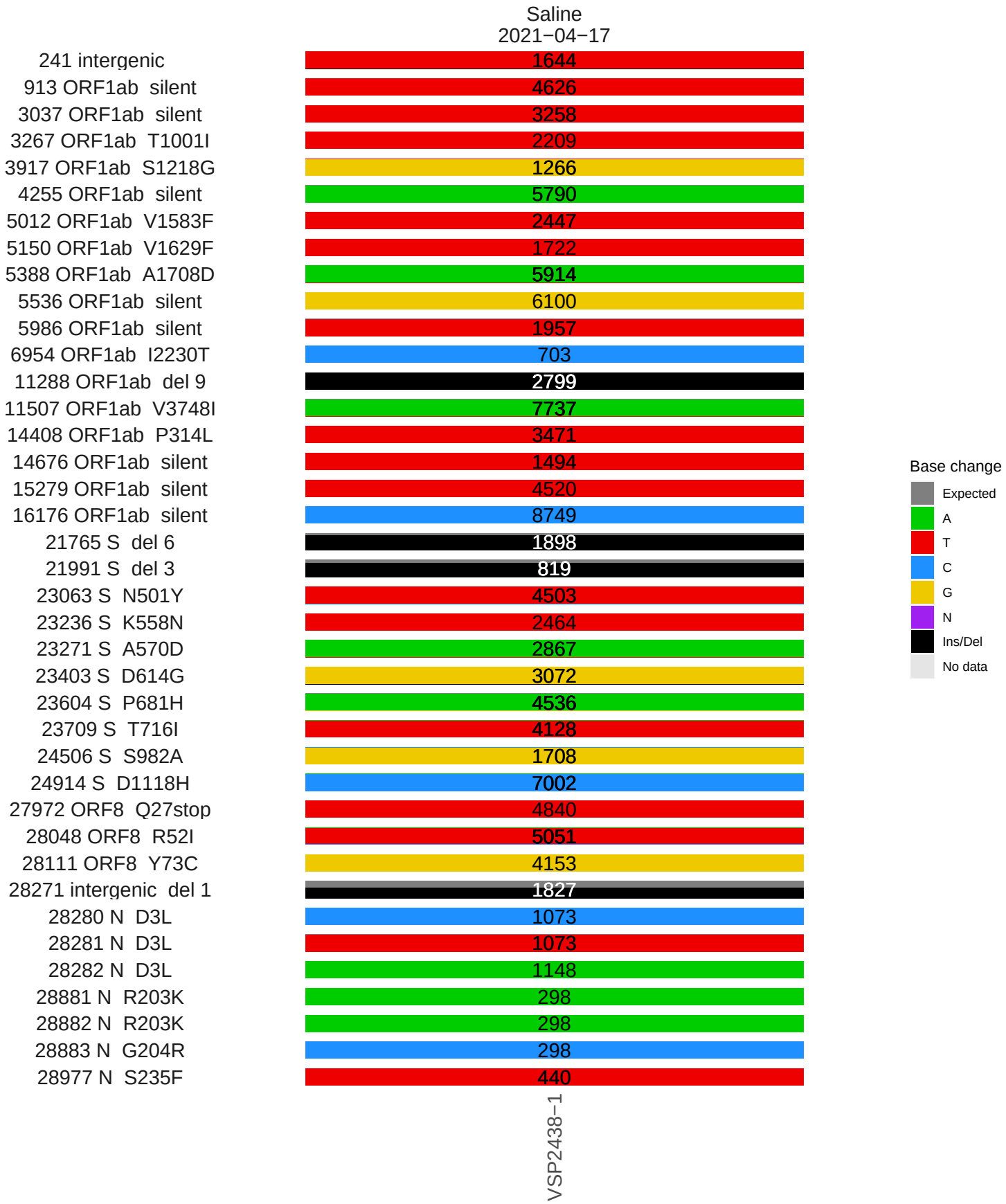
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2438-1	single experiment	NA	Saline	2021-04-17	29.83	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.

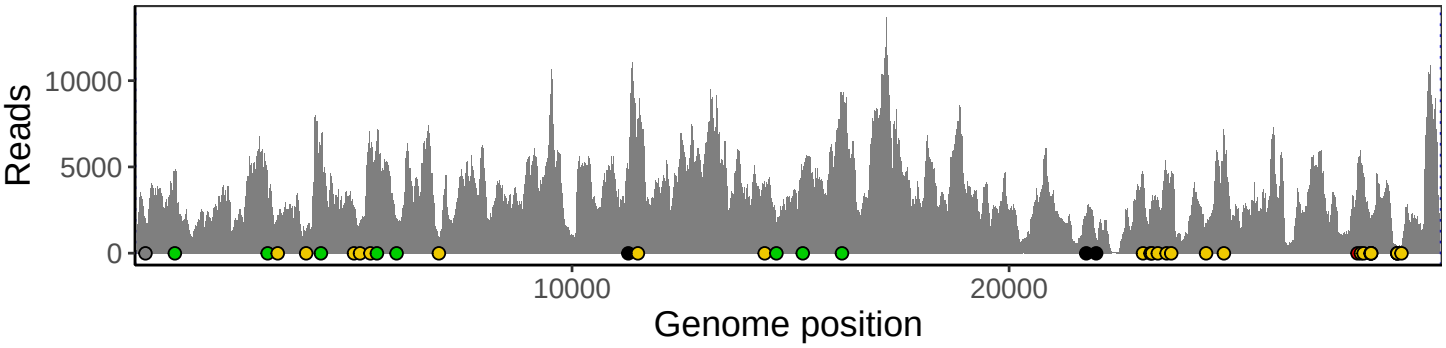



Saline
2021−04−17
241 intergenic 1644
913 ORF1ab silent 4626
3037 ORF1ab silent 3258
3267 ORF1ab T1001I 2209
3917 ORF1ab S1218G 1266
4255 ORF1ab silent 5790
5012 ORF1ab V1583F 2447
5150 ORF1ab V1629F 1722
5388 ORF1ab A1708D 5914
5536 ORF1ab silent 6100
5986 ORF1ab silent 1957
6954 ORF1ab I2230T 703
11288 ORF1ab del 9 2799
11507 ORF1ab V3748I 7737
14408 ORF1ab P314L 3471
14676 ORF1ab silent 1494
15279 ORF1ab silent 4520
16176 ORF1ab silent 8749
21765 S del 6 1898
21991 S del 3 819
23063 S N501Y 4503
23236 S K558N 2464
23271 S A570D 2867
23403 S D614G 3072
23604 S P681H 4536
23709 S T716I 4128
24506 S S982A 1708
24914 S D1118H 7002
27972 ORF8 Q27stop 4840
28048 ORF8 R52I 5051
28111 ORF8 Y73C 4153
28271 intergenic del 1 1827
28280 N D3L 1073
28281 N D3L 1073
28282 N D3L 1148
28881 N R203K 298
28882 N R203K 298
28883 N G204R 298
28977 N S235F 440
VSP2438−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

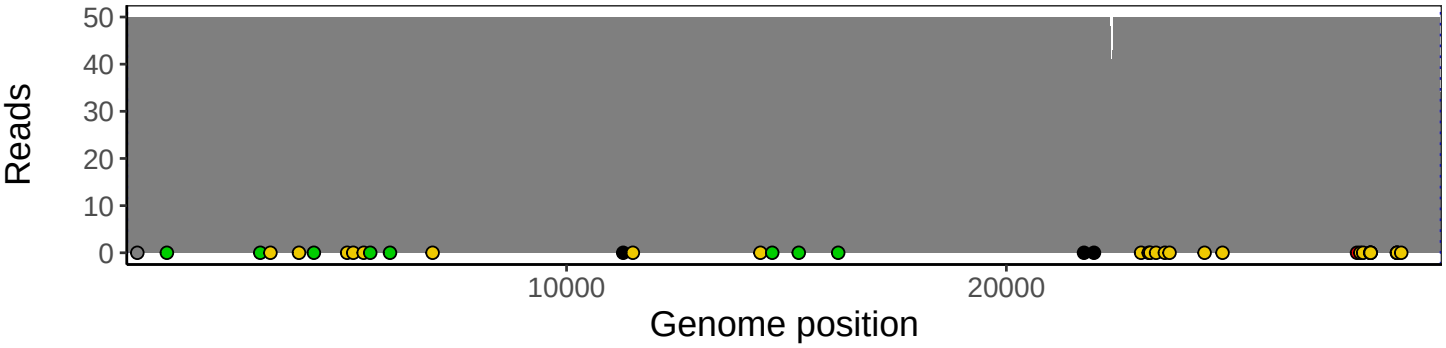
Analyses of individual experiments and composite results

VSP2438-1 | 2021-04-17 | Saline | UPHS-1182 | genomes | single experiment

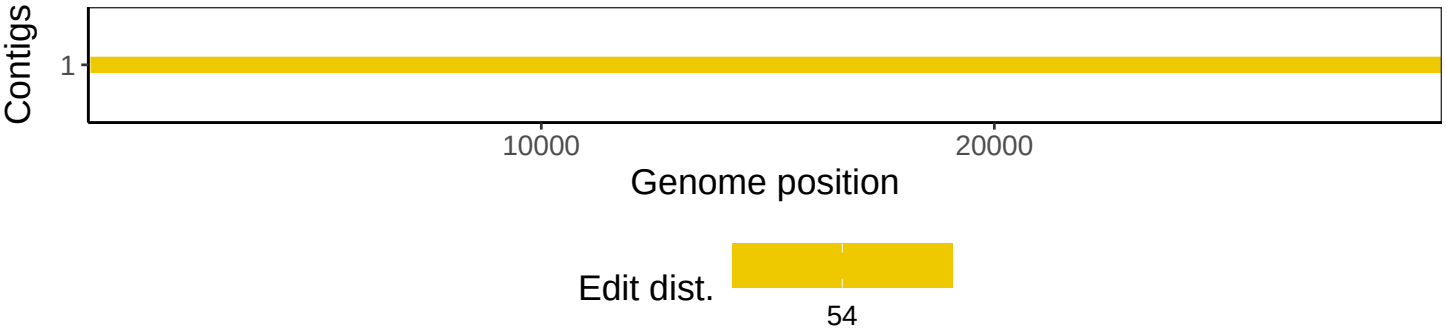
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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