COVID-19 subject UPHS-1363

2021-05-21

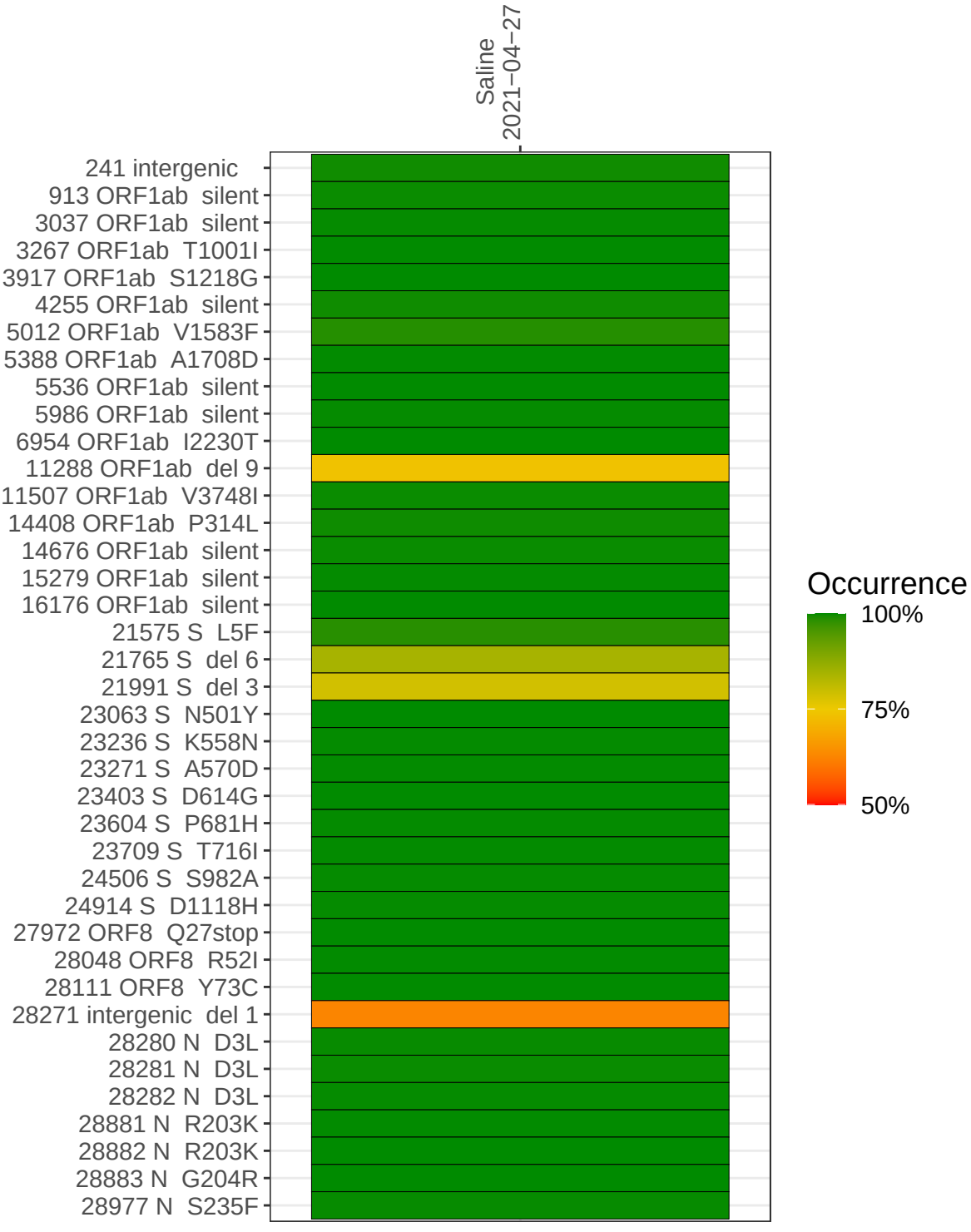
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

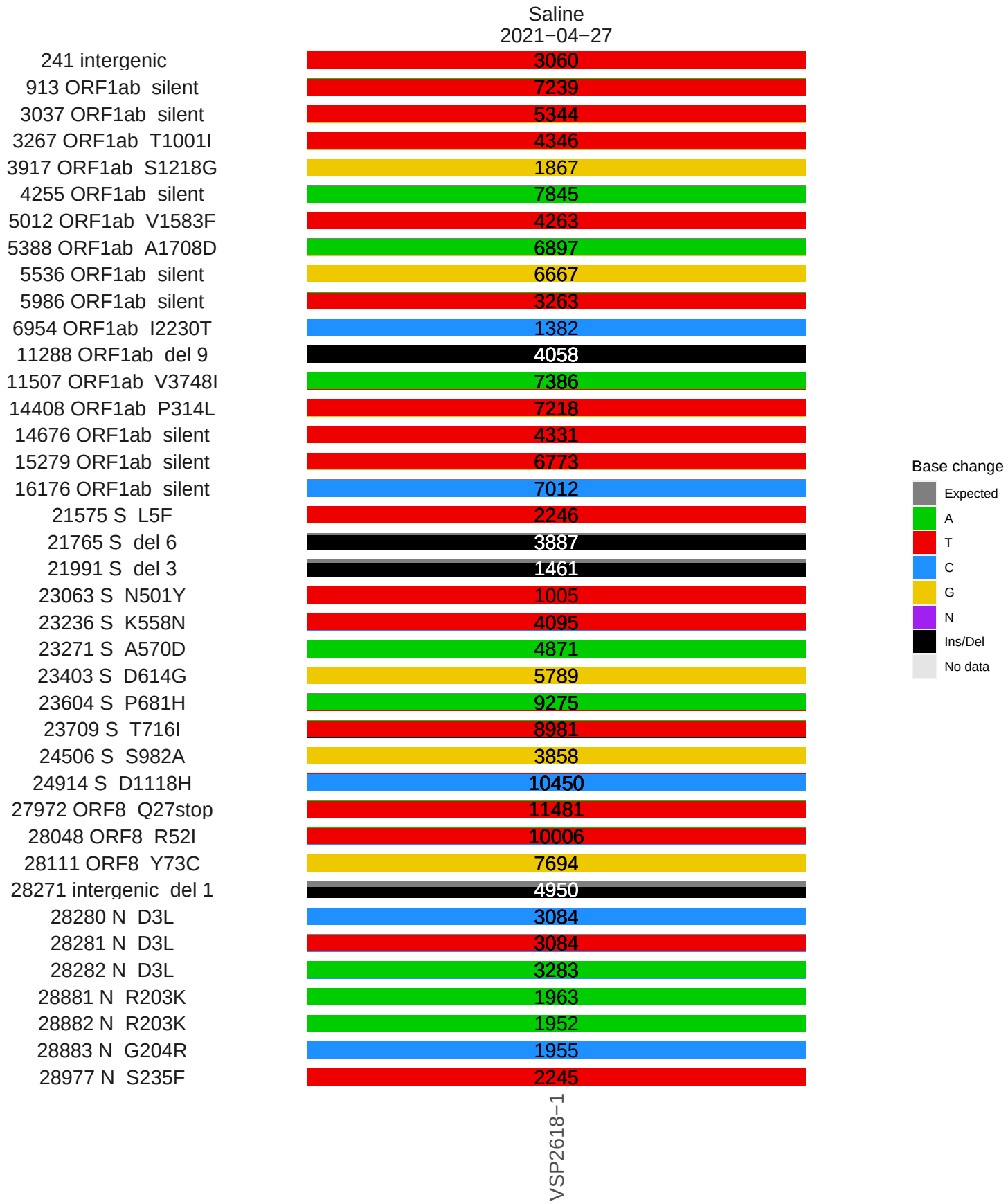
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2618-1	single experiment	NA	Saline	2021-04-27	29.82	B.1.1.7	99.8%	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.

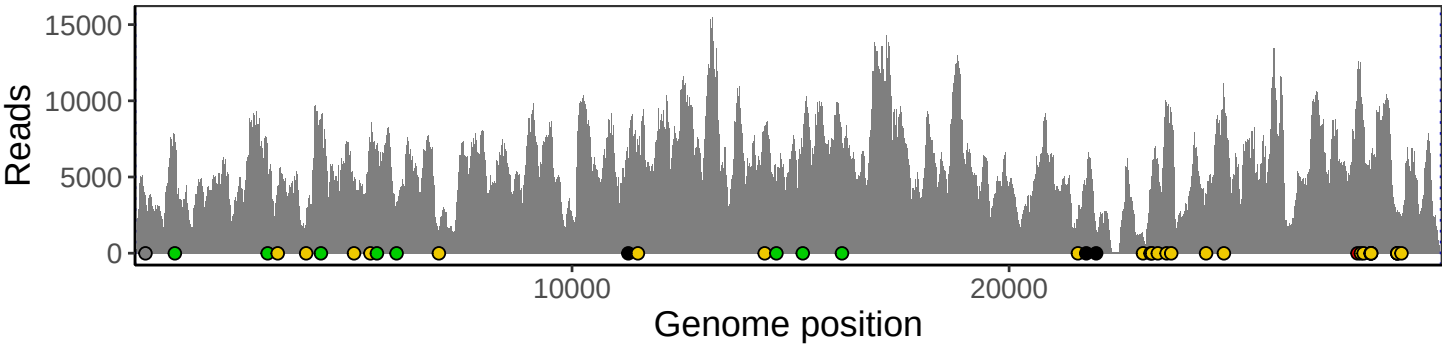



Saline
2021−04−27
241 intergenic 3060
913 ORF1ab silent 7239
3037 ORF1ab silent 5344
3267 ORF1ab T1001I 4346
3917 ORF1ab S1218G 1867
4255 ORF1ab silent 7845
5012 ORF1ab V1583F 4263
5388 ORF1ab A1708D 6897
5536 ORF1ab silent 6667
5986 ORF1ab silent 3263
6954 ORF1ab I2230T 1382
11288 ORF1ab del 9 4058
11507 ORF1ab V3748I 7386
14408 ORF1ab P314L 7218
14676 ORF1ab silent 4331
15279 ORF1ab silent 6773
16176 ORF1ab silent 7012
21575 S L5F 2246
21765 S del 6 3887
21991 S del 3 1461
23063 S N501Y 1005
23236 S K558N 4095
23271 S A570D 4871
23403 S D614G 5789
23604 S P681H 9275
23709 S T716I 8981
24506 S S982A 3858
24914 S D1118H 10450
27972 ORF8 Q27stop 11481
28048 ORF8 R52I 10006
28111 ORF8 Y73C 7694
28271 intergenic del 1 4950
28280 N D3L 3084
28281 N D3L 3084
28282 N D3L 3283
28881 N R203K 1963
28882 N R203K 1952
28883 N G204R 1955
28977 N S235F 2245
VSP2618−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

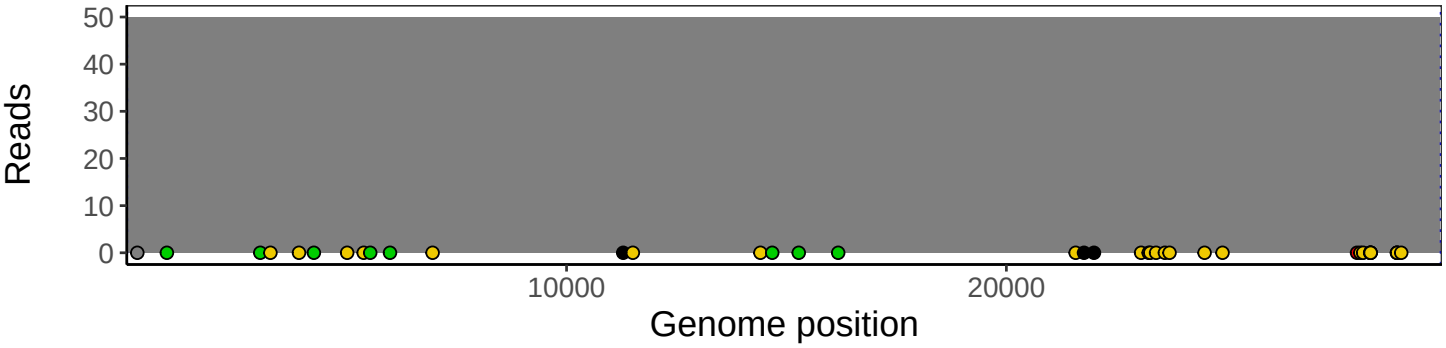
Analyses of individual experiments and composite results

VSP2618-1 | 2021-04-27 | Saline | UPHS-1363 | genomes | single experiment

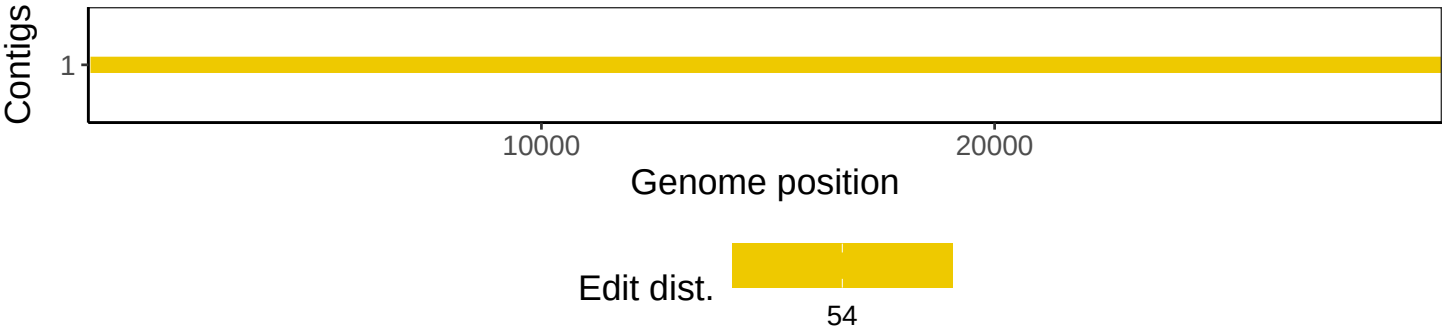
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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