COVID-19 subject UPHS-0326

2021-05-05

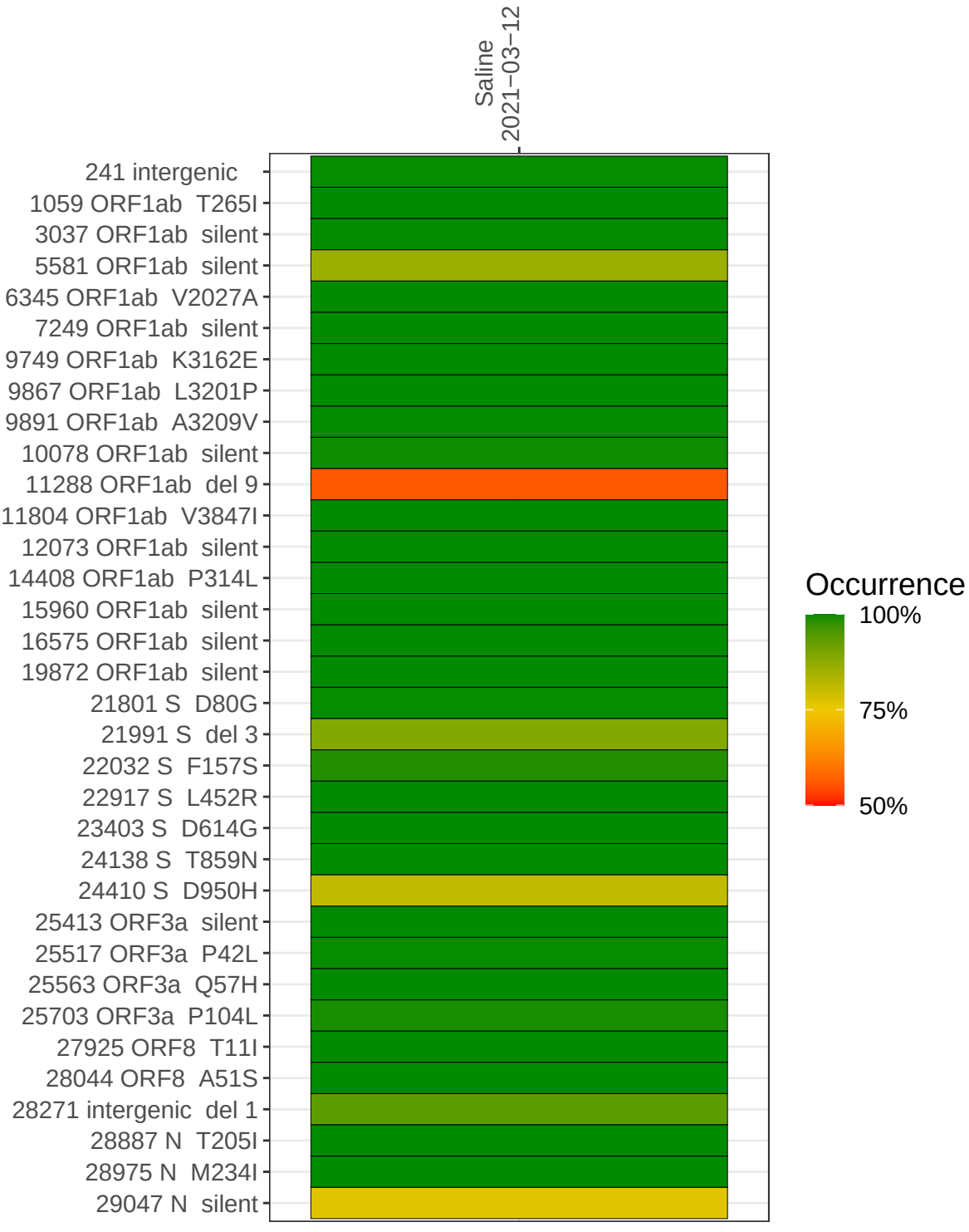
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

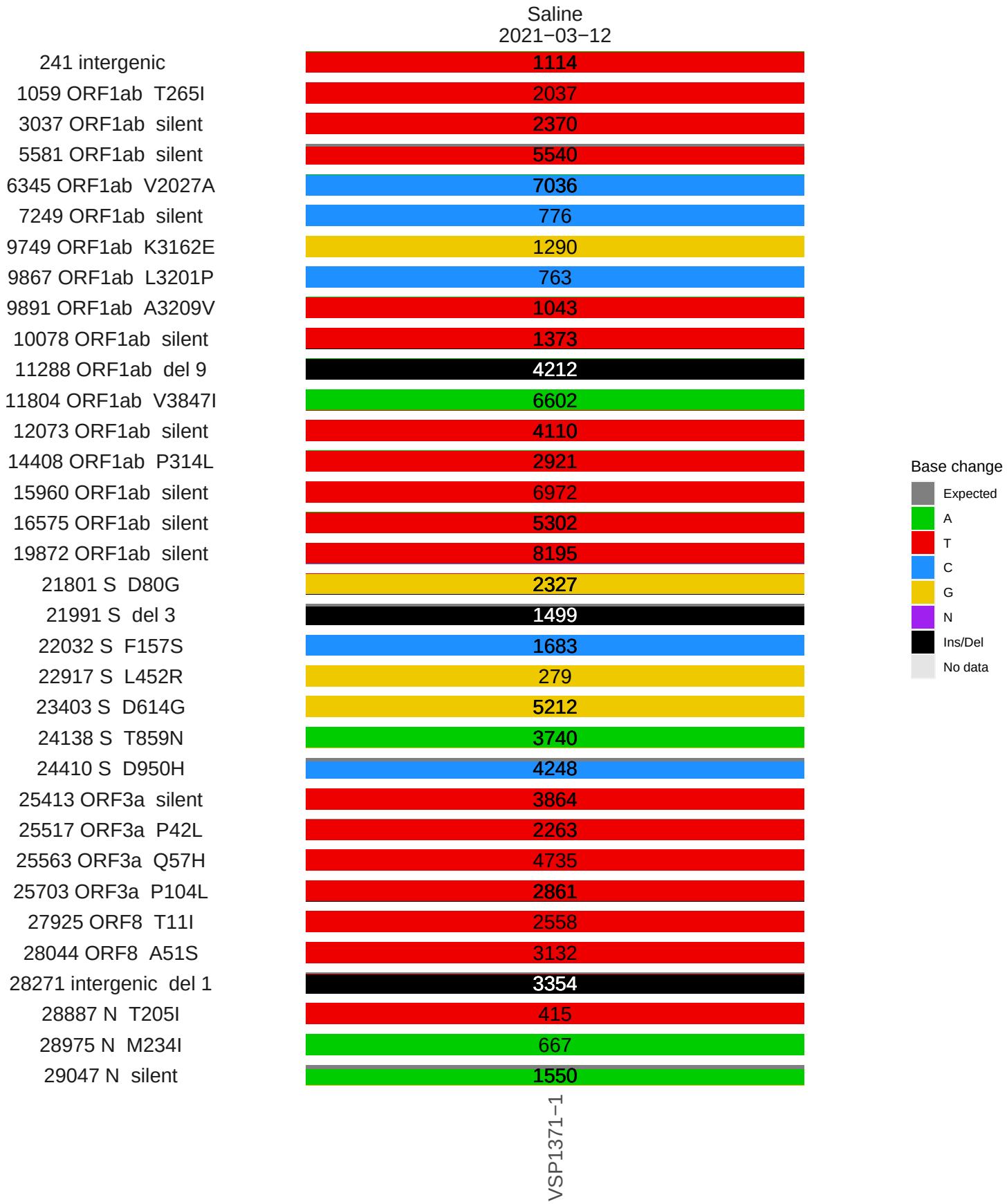
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1371-1	single experiment	NA	Saline	2021-03-12	29.80	B.1.526.1	99.7%	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.

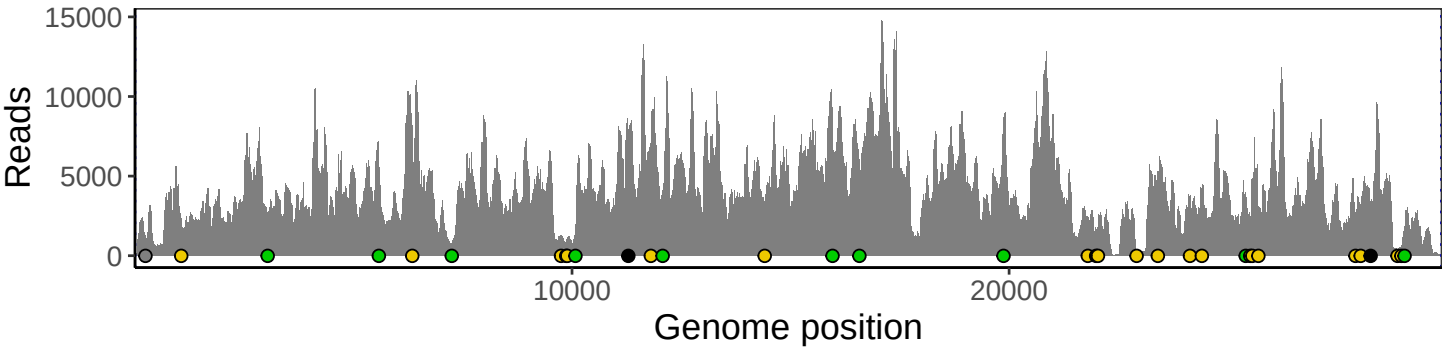



Saline
2021−03−12
241 intergenic 1114
1059 ORF1ab T265I 2037
3037 ORF1ab silent 2370
5581 ORF1ab silent 5540
6345 ORF1ab V2027A 7036
7249 ORF1ab silent 776
9749 ORF1ab K3162E 1290
9867 ORF1ab L3201P 763
9891 ORF1ab A3209V 1043
10078 ORF1ab silent 1373
11288 ORF1ab del 9 4212
11804 ORF1ab V3847I 6602
12073 ORF1ab silent 4110
14408 ORF1ab P314L 2921
15960 ORF1ab silent 6972
16575 ORF1ab silent 5302
19872 ORF1ab silent 8195
21801 S D80G 2327
21991 S del 3 1499
22032 S F157S 1683
22917 S L452R 279
23403 S D614G 5212
24138 S T859N 3740
24410 S D950H 4248
25413 ORF3a silent 3864
25517 ORF3a P42L 2263
25563 ORF3a Q57H 4735
25703 ORF3a P104L 2861
27925 ORF8 T11I 2558
28044 ORF8 A51S 3132
28271 intergenic del 1 3354
28887 N T205I 415
28975 N M234I 667
29047 N silent 1550
VSP1371−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

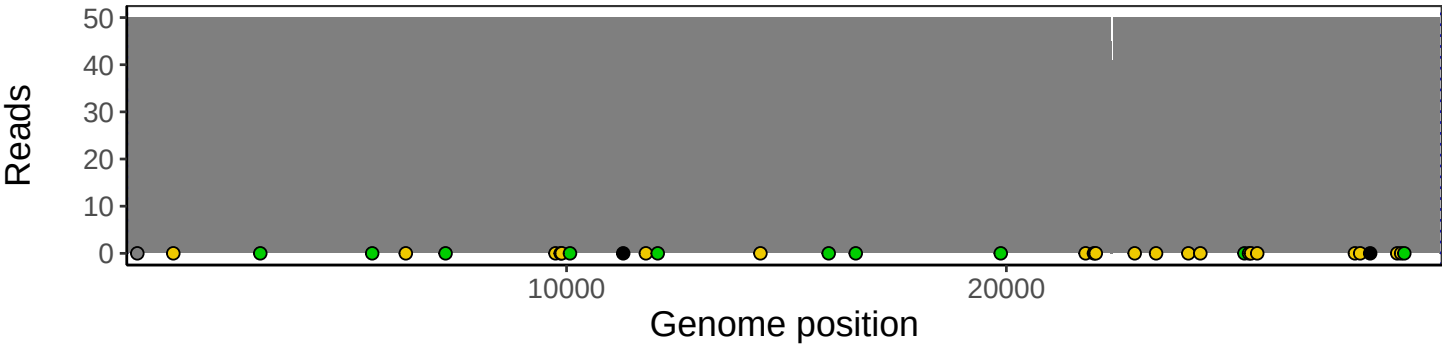
Analyses of individual experiments and composite results

VSP1371-1 | 2021-03-12 | Saline | UPHS-0326 | genomes | single experiment

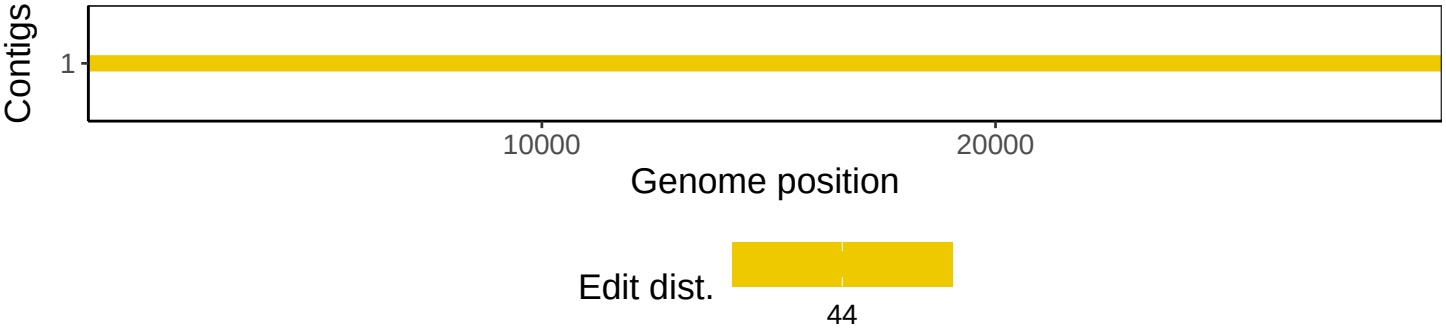
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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