COVID-19 subject UPHS-0093

2021-05-05

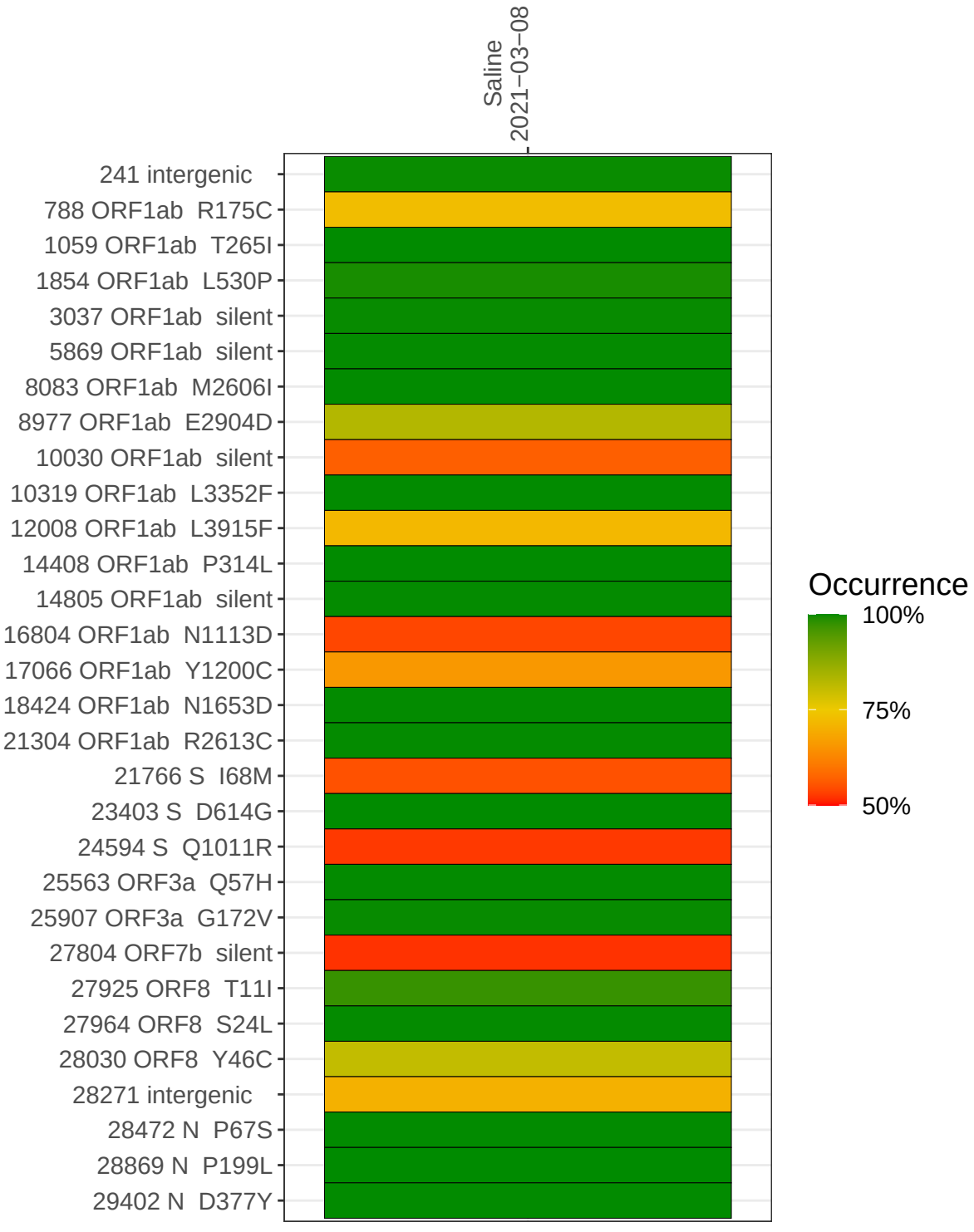
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

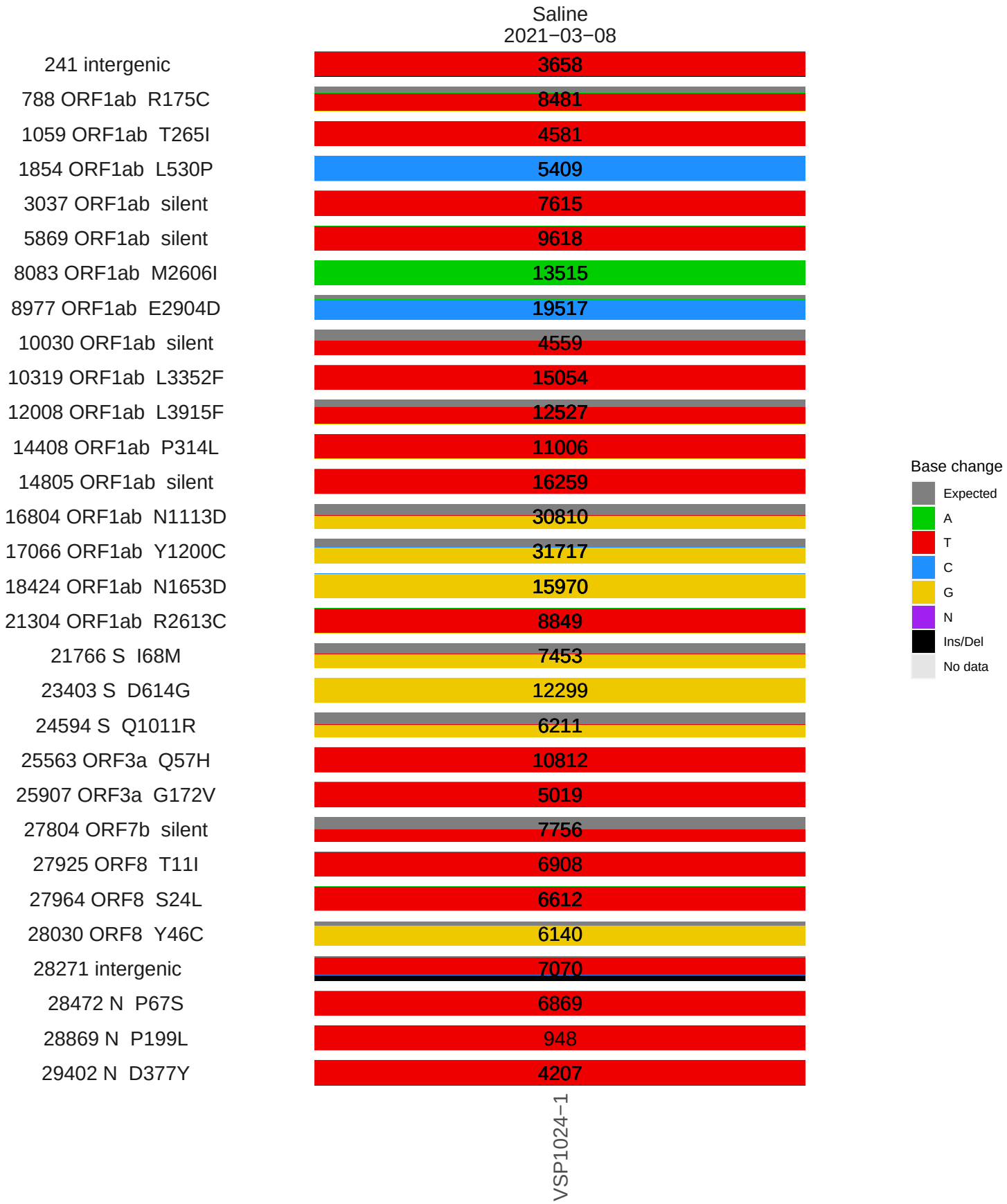
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1024-1	single experiment	NA	Saline	2021-03-08	29.86	B.1.2	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.

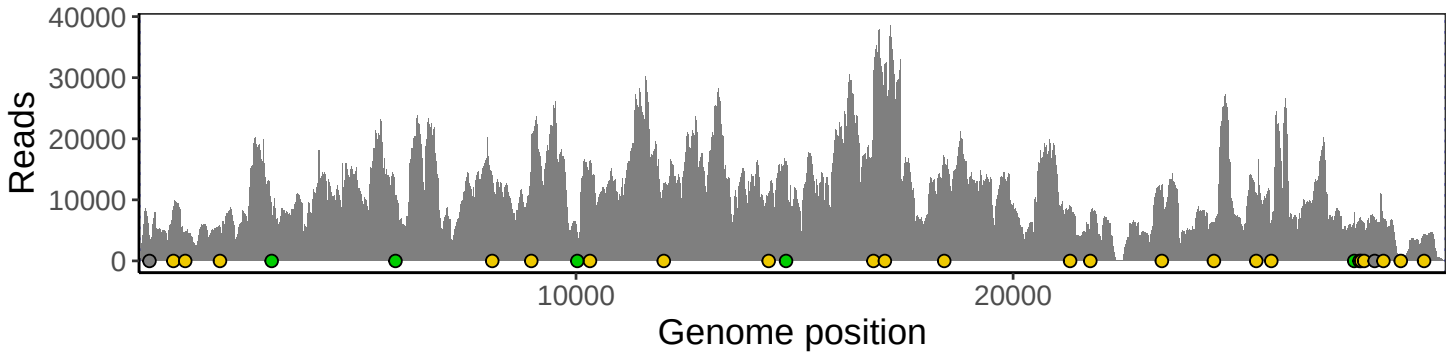



Saline
2021−03−08
241 intergenic
788 ORF1ab R175C
1059 ORF1ab T265I
1854 ORF1ab L530P
3037 ORF1ab silent
5869 ORF1ab silent
8083 ORF1ab M2606I
8977 ORF1ab E2904D
10030 ORF1ab silent
10319 ORF1ab L3352F
12008 ORF1ab L3915F
14408 ORF1ab P314L
14805 ORF1ab silent
16804 ORF1ab N1113D
17066 ORF1ab Y1200C
18424 ORF1ab N1653D
21304 ORF1ab R2613C
21766 S I68M
23403 S D614G
24594 S Q1011R
25563 ORF3a Q57H
25907 ORF3a G172V
27804 ORF7b silent
27925 ORF8 T11I
27964 ORF8 S24L
28030 ORF8 Y46C
28271 intergenic
28472 N P67S
28869 N P199L
29402 N D377Y
3658
8481
4581
5409
7615
9618
13515
19517
4559
15054
12527
11006
16259
30810
31717
15970
8849
7453
12299
6211
10812
5019
7756
6908
6612
6140
7070
6869
948
4207
VSP1024−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

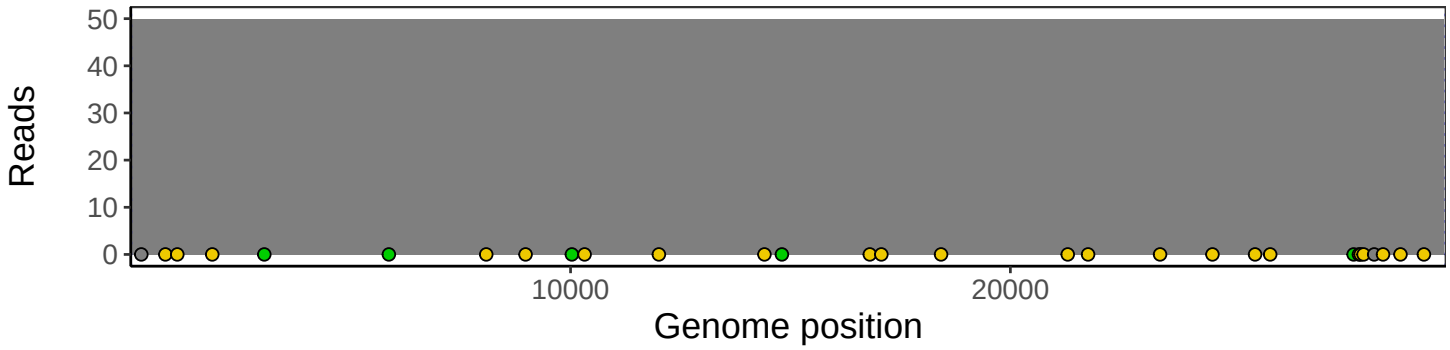
Analyses of individual experiments and composite results

VSP1024-1 | 2021-03-08 | Saline | UPHS-0093 | genomes | single experiment

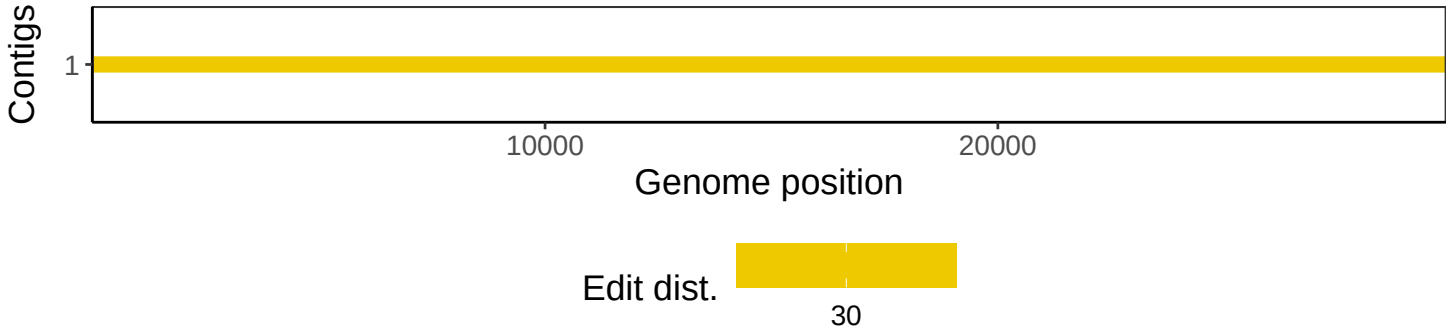
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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