COVID-19 subject UPHS-0866

2021-05-21

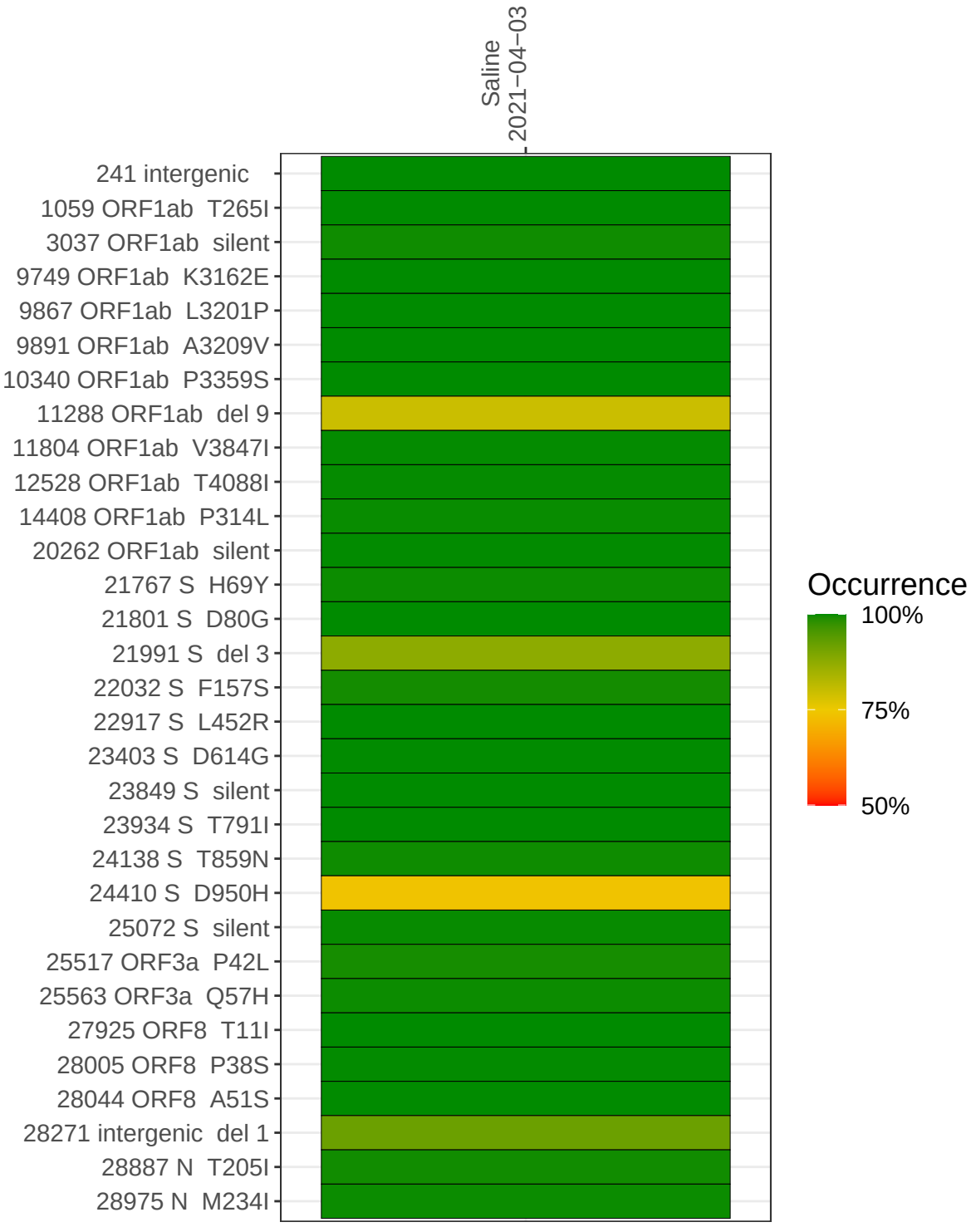
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

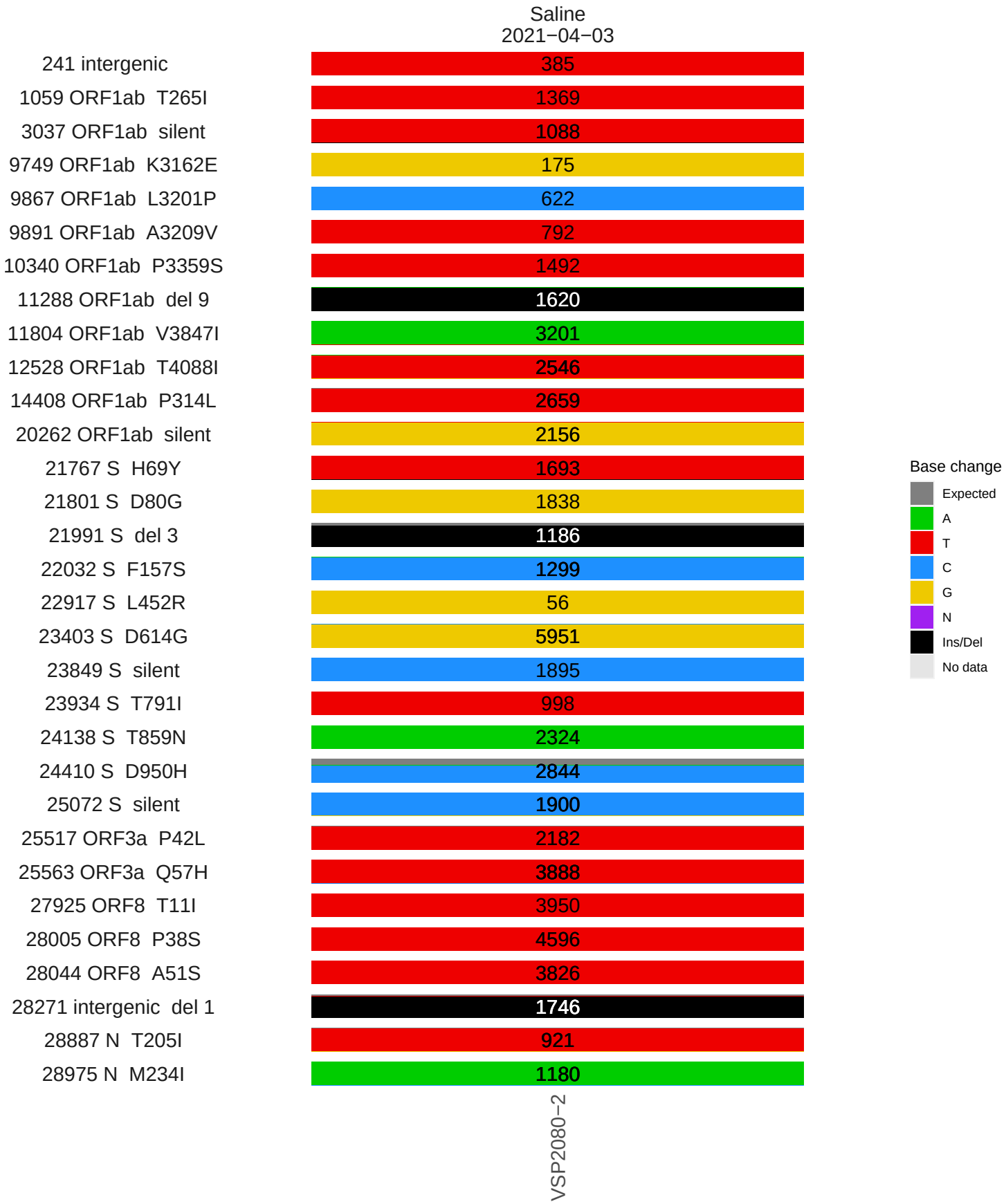
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2080-2	single experiment	NA	Saline	2021-04-03	29.84	B.1.526.1	99.9%	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.

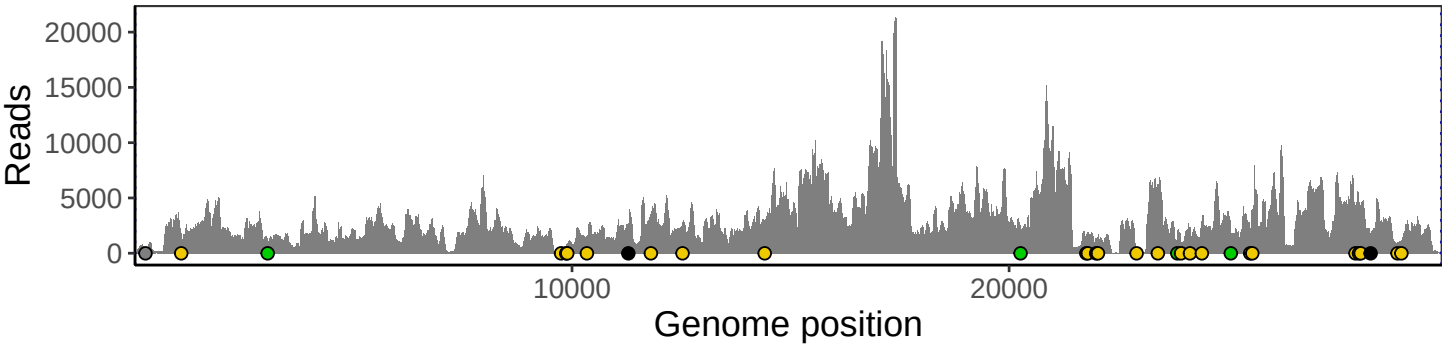



Saline
2021−04−03
241 intergenic
385
1059 ORF1ab T265I
1369
3037 ORF1ab silent
1088
9749 ORF1ab K3162E
175
9867 ORF1ab L3201P
622
9891 ORF1ab A3209V
792
10340 ORF1ab P3359S
1492
11288 ORF1ab del 9
1620
11804 ORF1ab V3847I
3201
12528 ORF1ab T4088I
2546
14408 ORF1ab P314L
2659
20262 ORF1ab silent
2156
21767 S H69Y
1693
21801 S D80G
1838
21991 S del 3
1186
22032 S F157S
1299
22917 S L452R
56
23403 S D614G
5951
23849 S silent
1895
23934 S T791I
998
24138 S T859N
2324
24410 S D950H
2844
25072 S silent
1900
25517 ORF3a P42L
2182
25563 ORF3a Q57H
3888
27925 ORF8 T11I
3950
28005 ORF8 P38S
4596
28044 ORF8 A51S
3826
28271 intergenic del 1
1746
28887 N T205I
921
28975 N M234I
1180
VSP2080−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

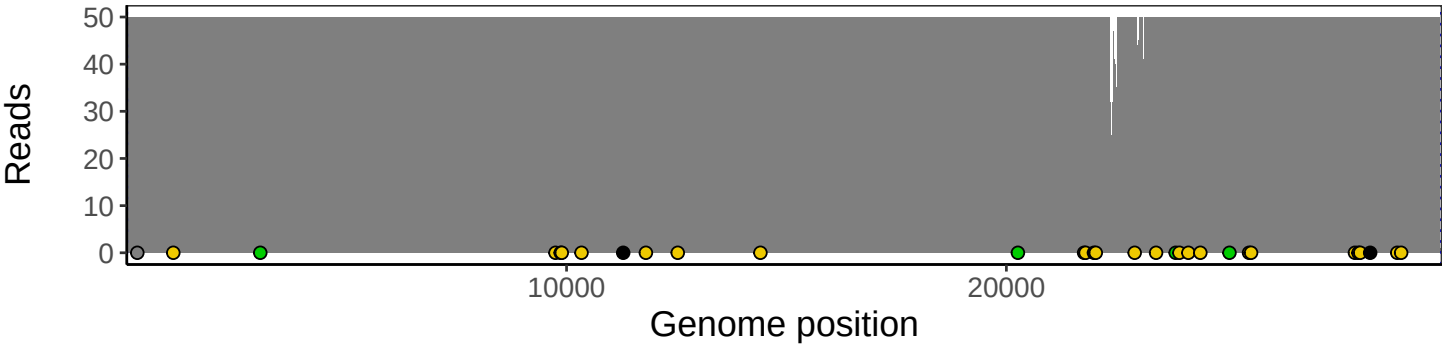
Analyses of individual experiments and composite results

VSP2080-2 | 2021-04-03 | Saline | UPHS-0866 | genomes | single experiment

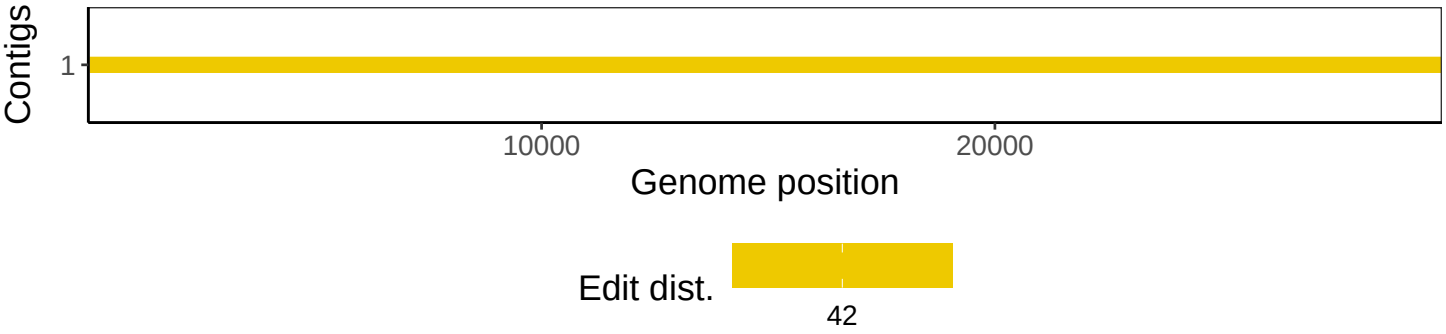
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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