COVID-19 subject UPHS-1633

2021-06-03

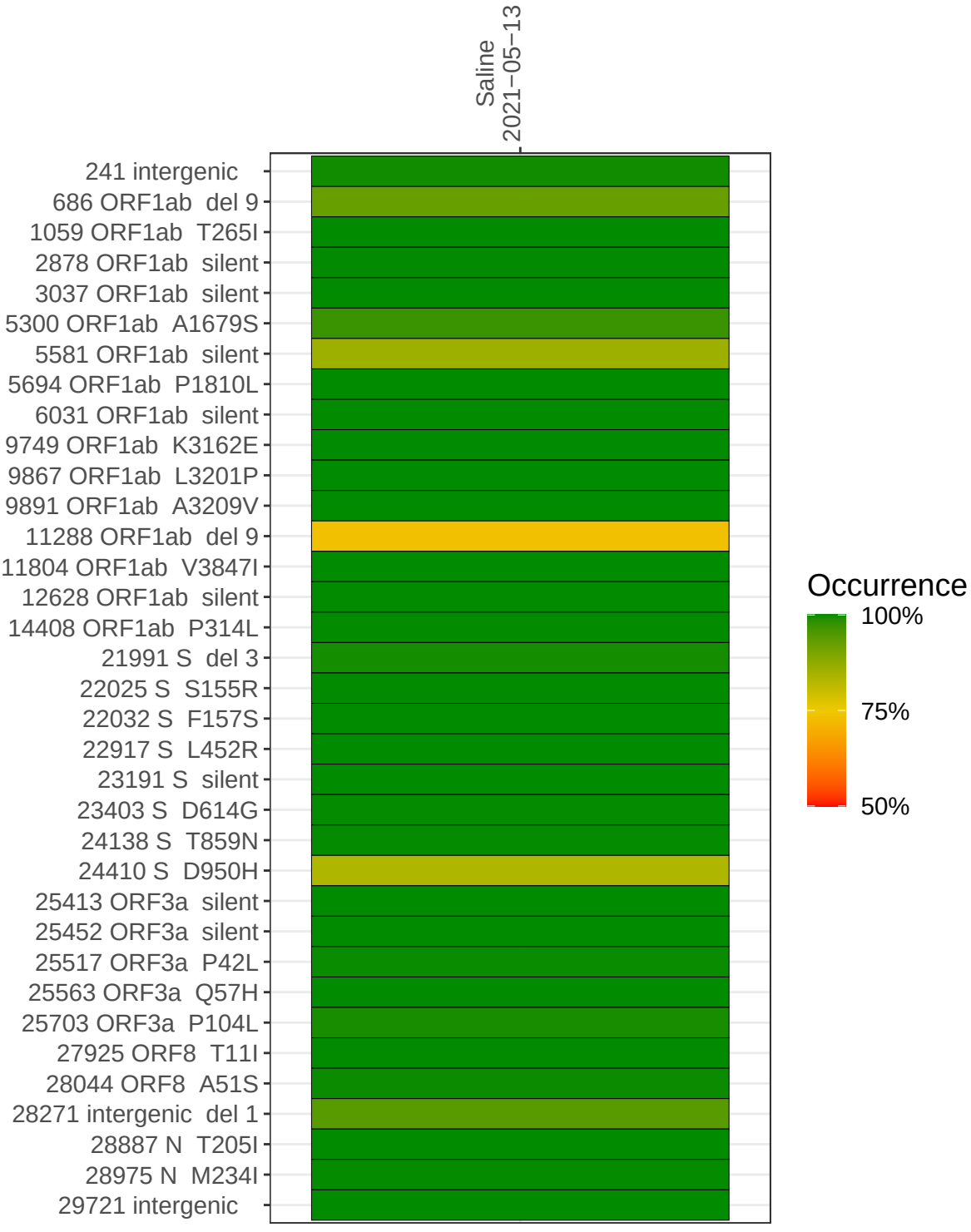
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

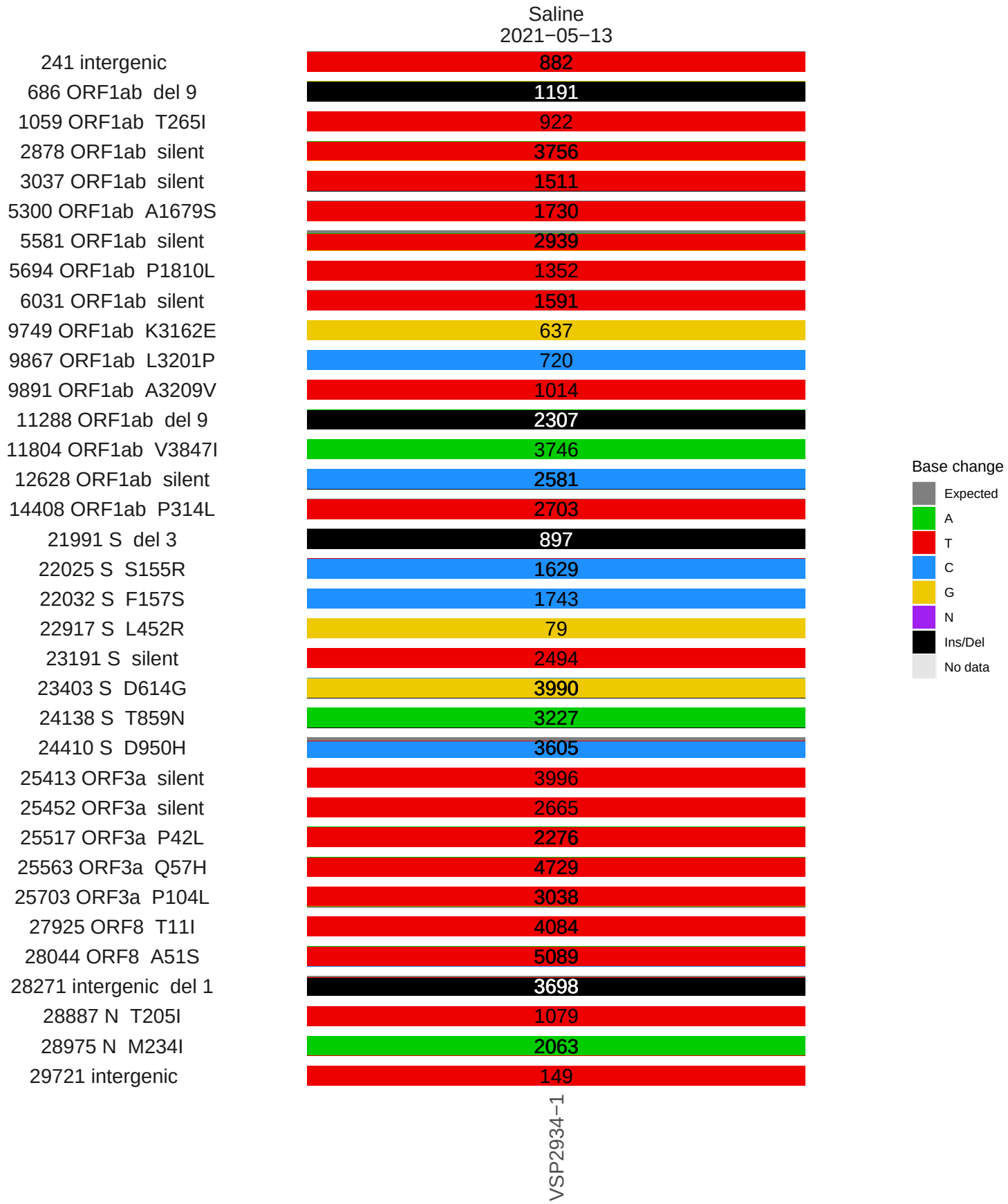
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2934-1	single experiment	NA	Saline	2021-05-13	29.75	B.1.526.1	99.7%	99.0%

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.

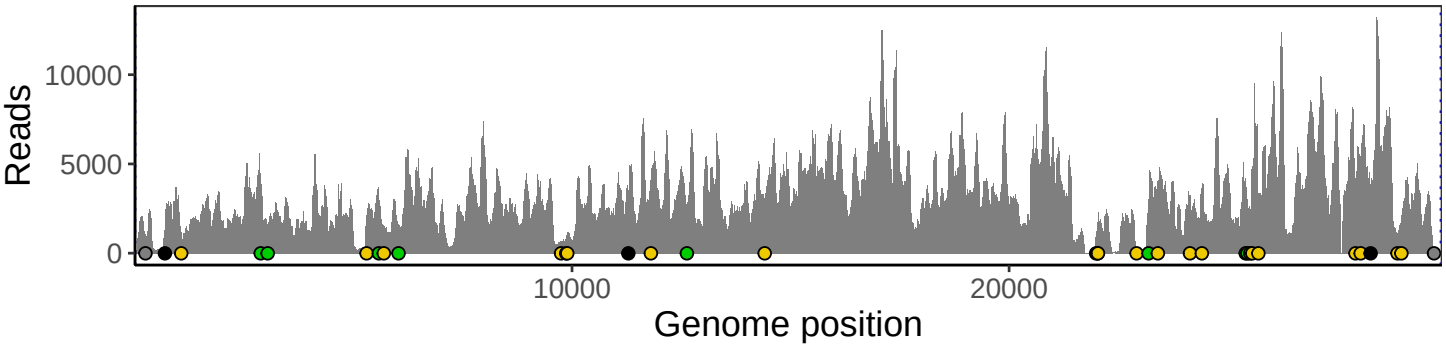



Saline
2021−05−13
241 intergenic
882
686 ORF1ab del 9
1191
1059 ORF1ab T265I
922
2878 ORF1ab silent
3756
3037 ORF1ab silent
1511
5300 ORF1ab A1679S
1730
5581 ORF1ab silent
2939
5694 ORF1ab P1810L
1352
6031 ORF1ab silent
1591
9749 ORF1ab K3162E
637
9867 ORF1ab L3201P
720
9891 ORF1ab A3209V
1014
11288 ORF1ab del 9
2307
11804 ORF1ab V3847I
3746
12628 ORF1ab silent
2581
14408 ORF1ab P314L
2703
21991 S del 3
897
22025 S S155R
1629
22032 S F157S
1743
22917 S L452R
79
23191 S silent
2494
23403 S D614G
3990
24138 S T859N
3227
24410 S D950H
3605
25413 ORF3a silent
3996
25452 ORF3a silent
2665
25517 ORF3a P42L
2276
25563 ORF3a Q57H
4729
25703 ORF3a P104L
3038
27925 ORF8 T11I
4084
28044 ORF8 A51S
5089
28271 intergenic del 1
3698
28887 N T205I
1079
28975 N M234I
2063
29721 intergenic
149
VSP2934−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

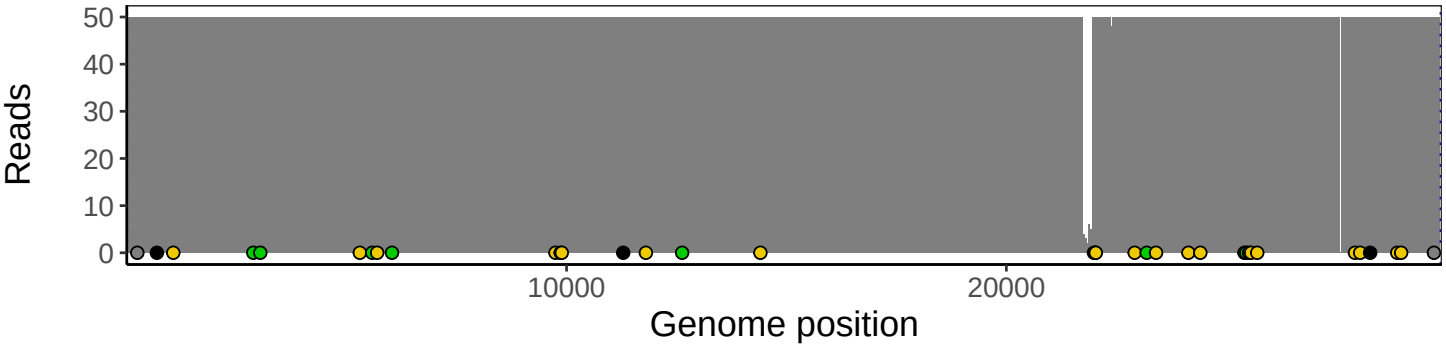
Analyses of individual experiments and composite results

VSP2934-1 | 2021-05-13 | Saline | UPHS-1633 | genomes | single experiment

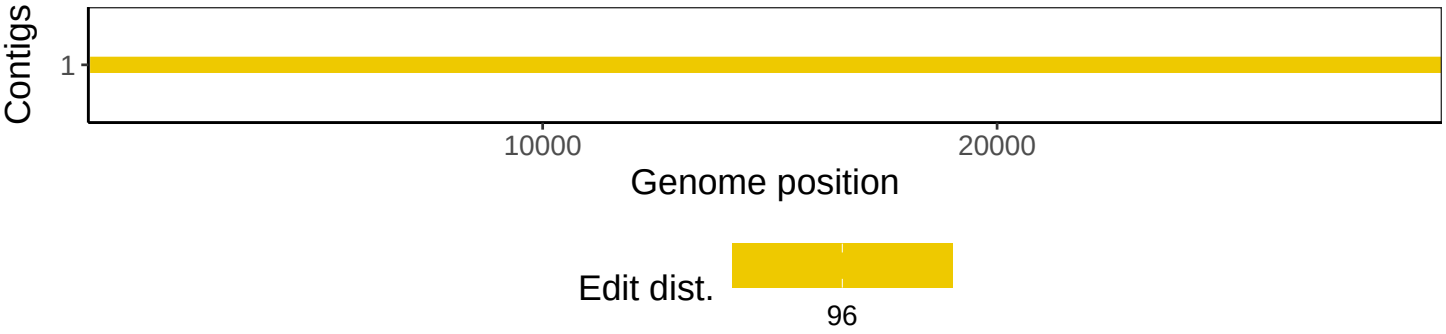
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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