COVID-19 subject UPHS-0312

2021-05-05

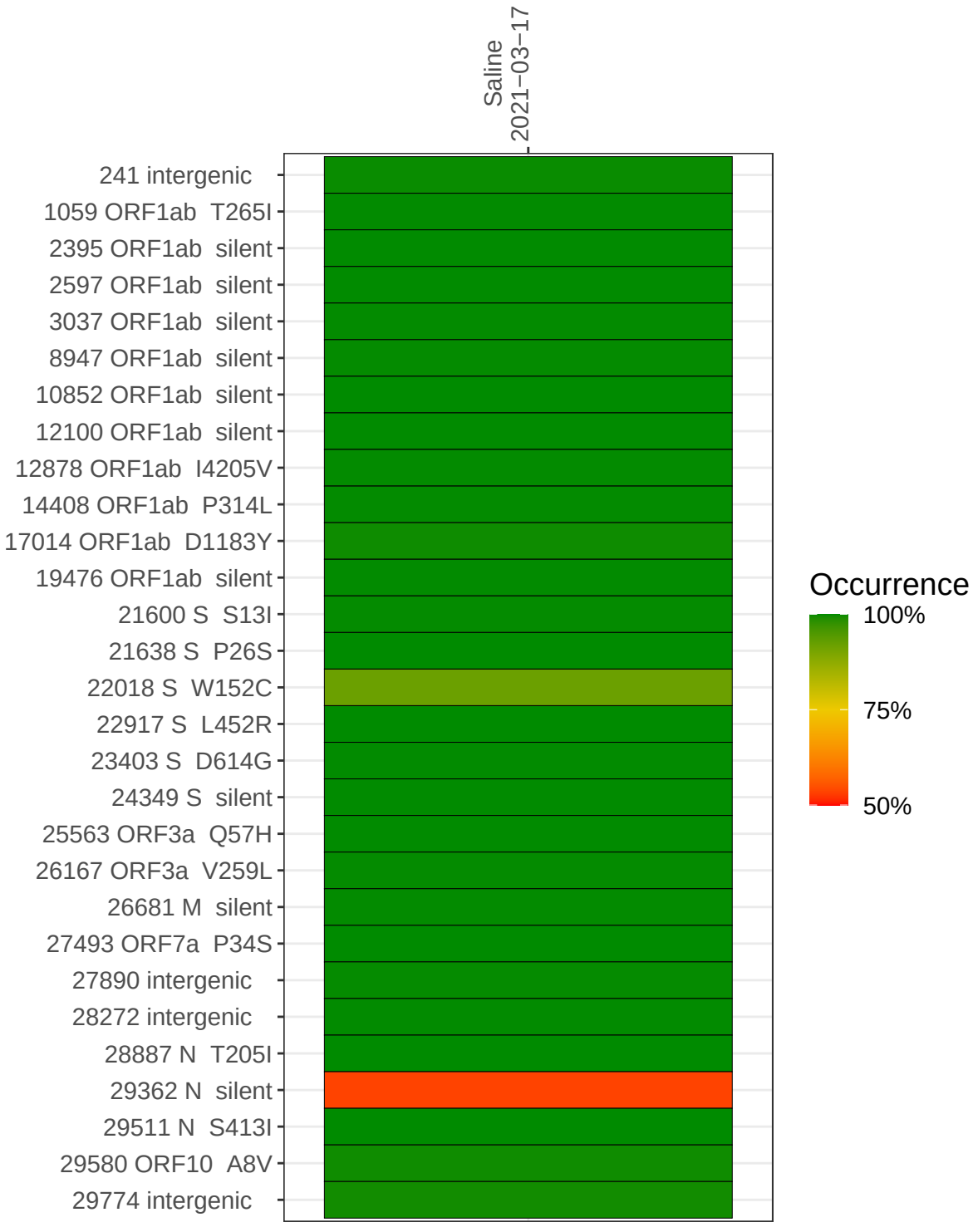
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

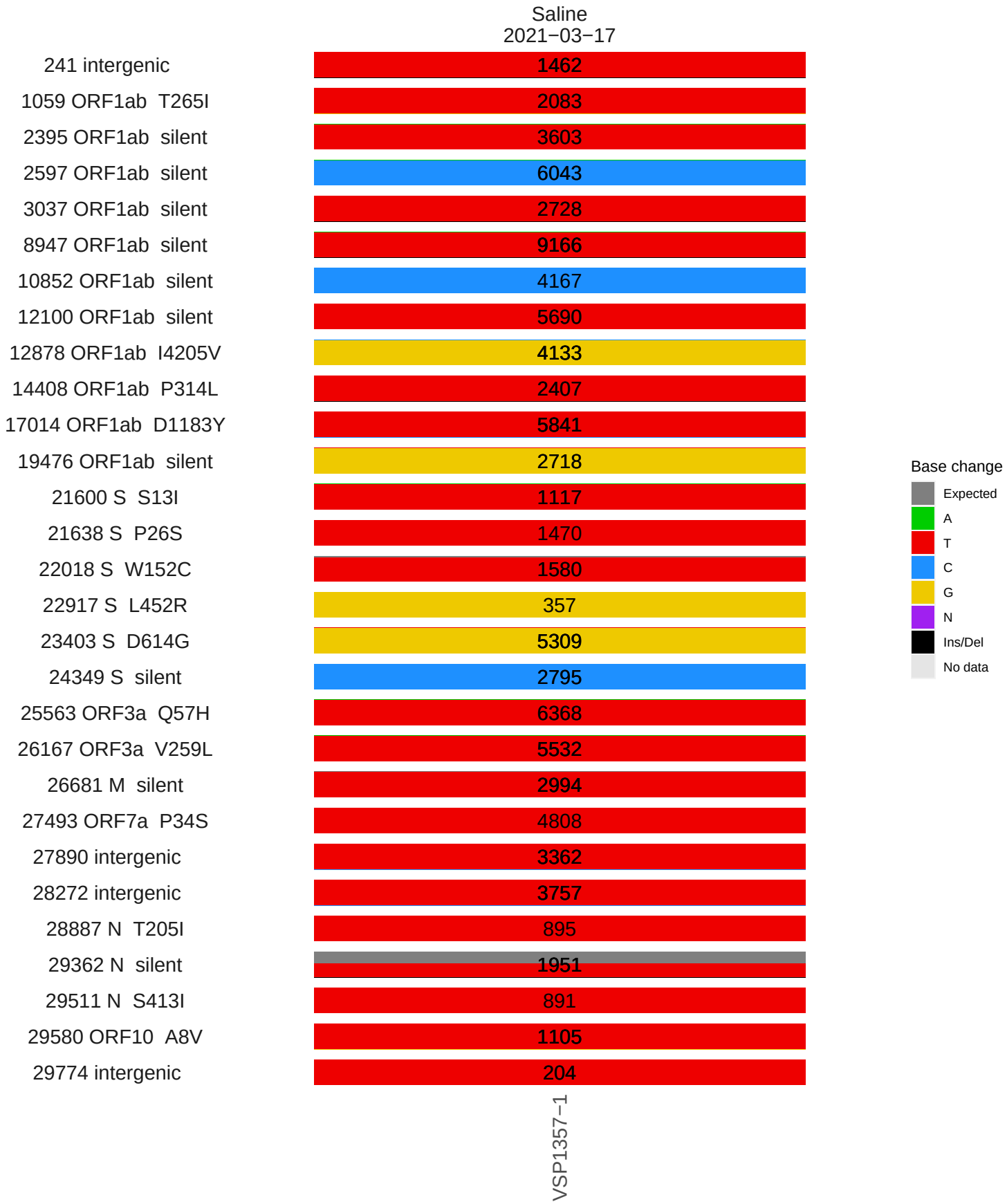
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1357-1	single experiment	NA	Saline	2021-03-17	29.91	B.1.429	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.

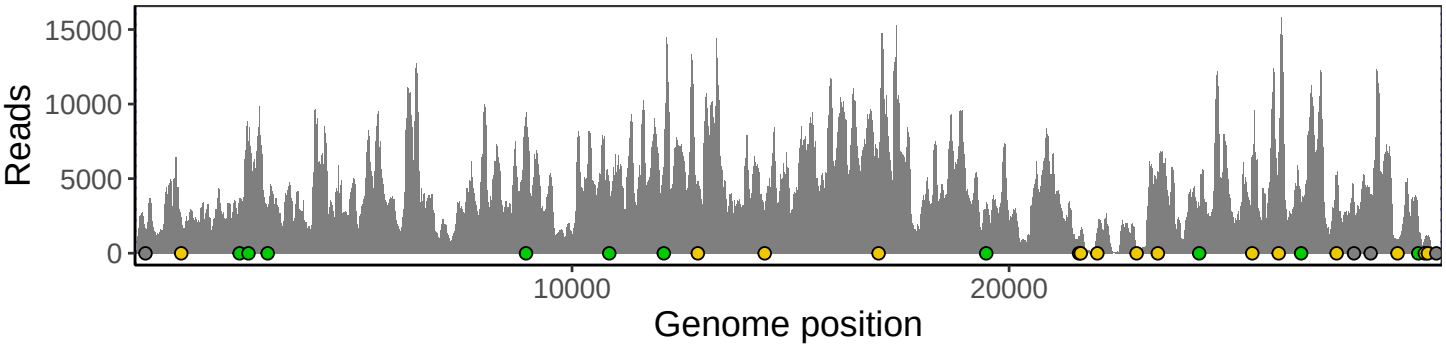



Saline
2021−03−17
241 intergenic
1059 ORF1ab T265I
2395 ORF1ab silent
2597 ORF1ab silent
3037 ORF1ab silent
8947 ORF1ab silent
10852 ORF1ab silent
12100 ORF1ab silent
12878 ORF1ab I4205V
14408 ORF1ab P314L
17014 ORF1ab D1183Y
19476 ORF1ab silent
21600 S S13I
21638 S P26S
22018 S W152C
22917 S L452R
23403 S D614G
24349 S silent
25563 ORF3a Q57H
26167 ORF3a V259L
26681 M silent
27493 ORF7a P34S
27890 intergenic
28272 intergenic
28887 N T205I
29362 N silent
29511 N S413I
29580 ORF10 A8V
29774 intergenic
1462
2083
3603
6043
2728
9166
4167
5690
4133
2407
5841
2718
1117
1470
1580
357
5309
2795
6368
5532
2994
4808
3362
3757
895
1951
891
1105
204
VSP1357−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

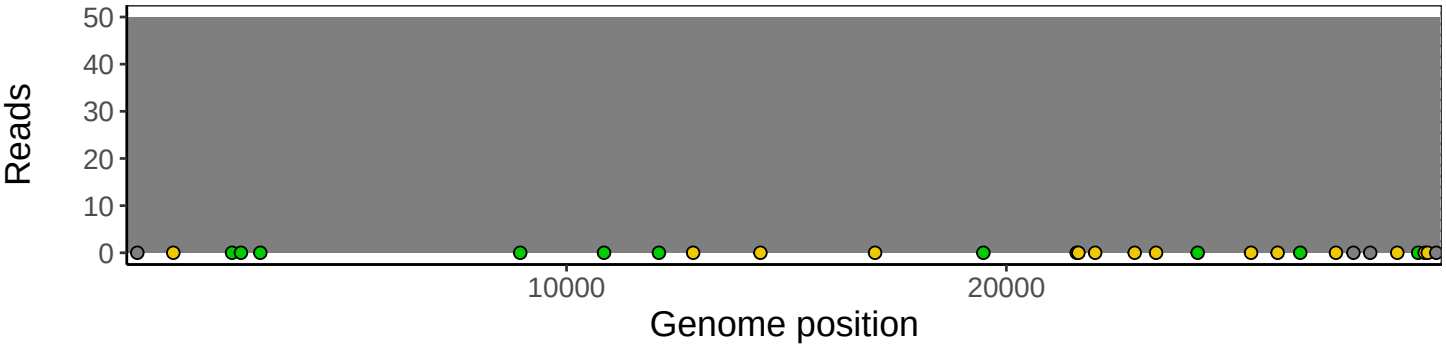
Analyses of individual experiments and composite results

VSP1357-1 | 2021-03-17 | Saline | UPHS-0312 | genomes | single experiment

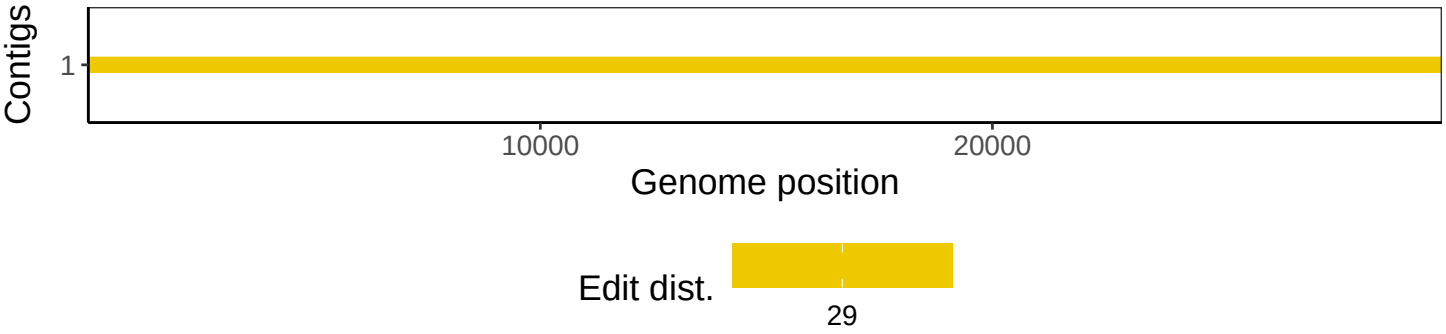
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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