COVID-19 subject UPHS-0265

2021-04-17

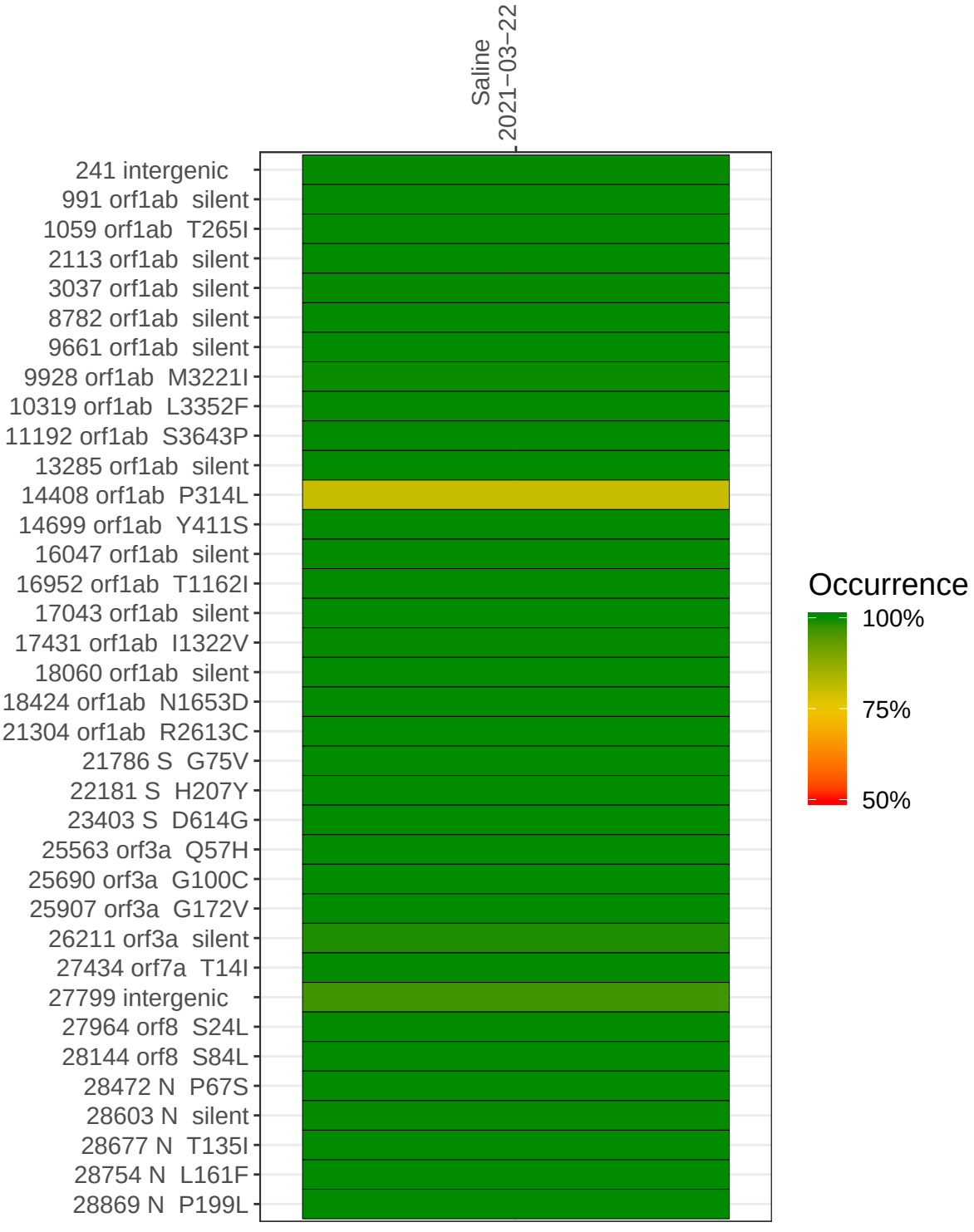
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

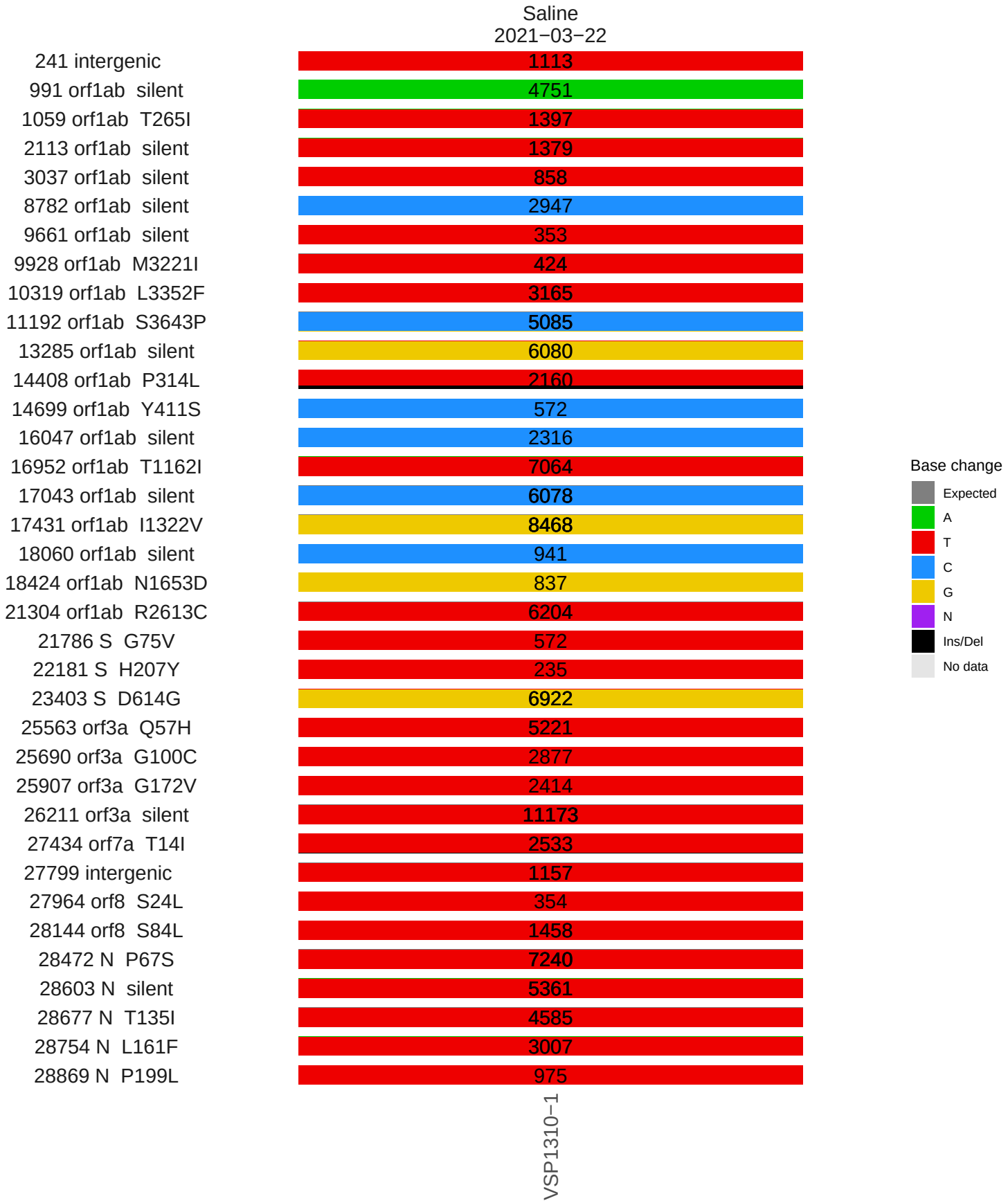
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1310-1	single experiment	NA	Saline	2021-03-22	21.46	B.1.2	98.5%	98.5%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

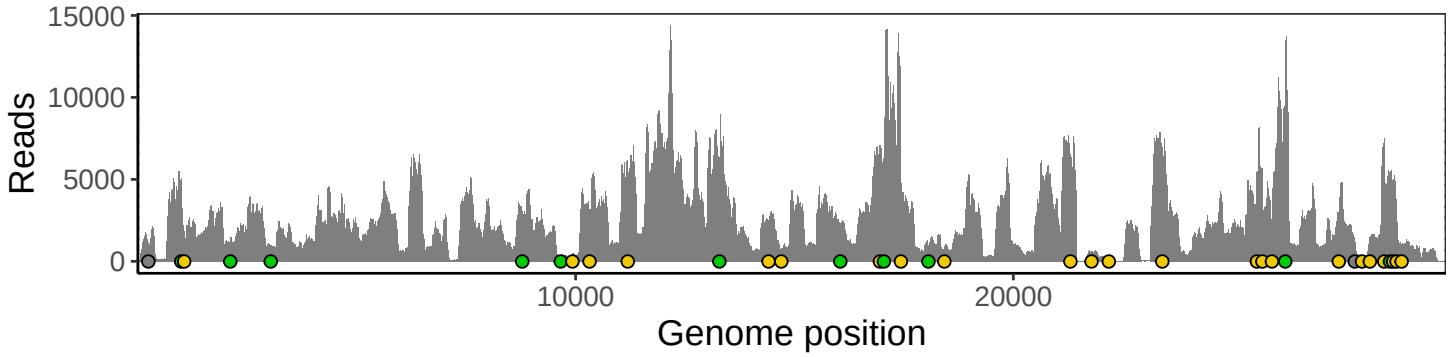



Saline
2021−03−22
241 intergenic
991 orf1ab silent
1059 orf1ab T265I
2113 orf1ab silent
3037 orf1ab silent
8782 orf1ab silent
9661 orf1ab silent
9928 orf1ab M3221I
10319 orf1ab L3352F
11192 orf1ab S3643P
13285 orf1ab silent
14408 orf1ab P314L
14699 orf1ab Y411S
16047 orf1ab silent
16952 orf1ab T1162I
17043 orf1ab silent
17431 orf1ab I1322V
18060 orf1ab silent
18424 orf1ab N1653D
21304 orf1ab R2613C
21786 S G75V
22181 S H207Y
23403 S D614G
25563 orf3a Q57H
25690 orf3a G100C
25907 orf3a G172V
26211 orf3a silent
27434 orf7a T14I
27799 intergenic
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28603 N silent
28677 N T135I
28754 N L161F
28869 N P199L
1113
4751
1397
1379
858
2947
353
424
3165
5085
6080
2160
572
2316
7064
6078
8468
941
837
6204
572
235
6922
5221
2877
2414
11173
2533
1157
354
1458
7240
5361
4585
3007
975
VSP1310−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

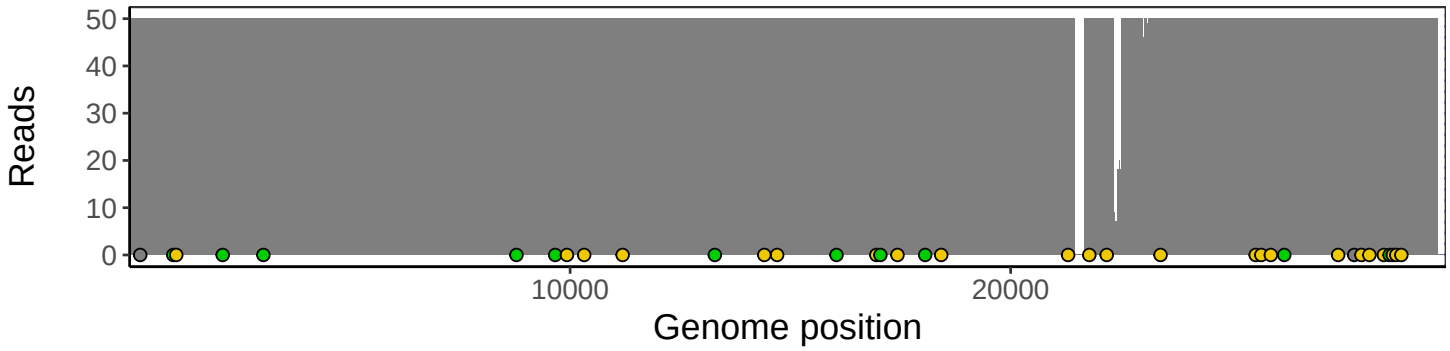
Analyses of individual experiments and composite results

VSP1310-1 | 2021-03-22 | Saline | UPHS-0265 | genomes | single experiment

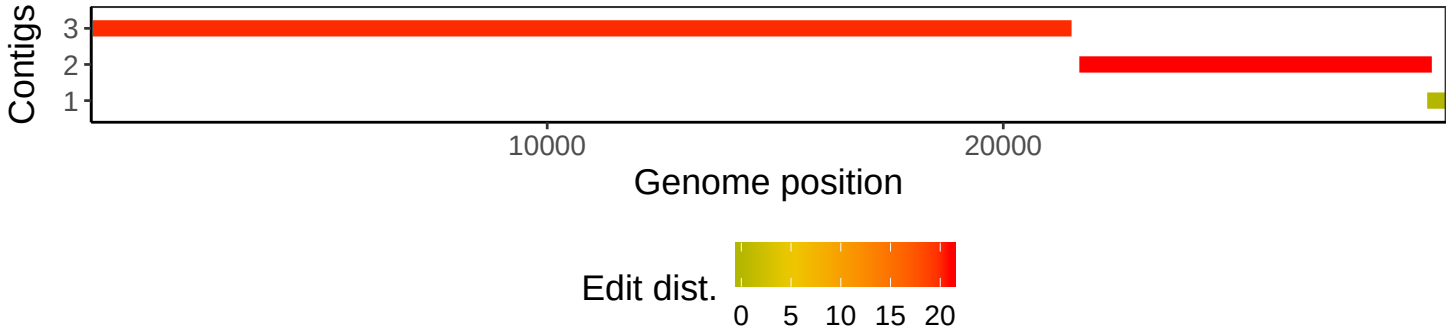
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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