COVID-19 subject UPHS-0155

2021-04-17

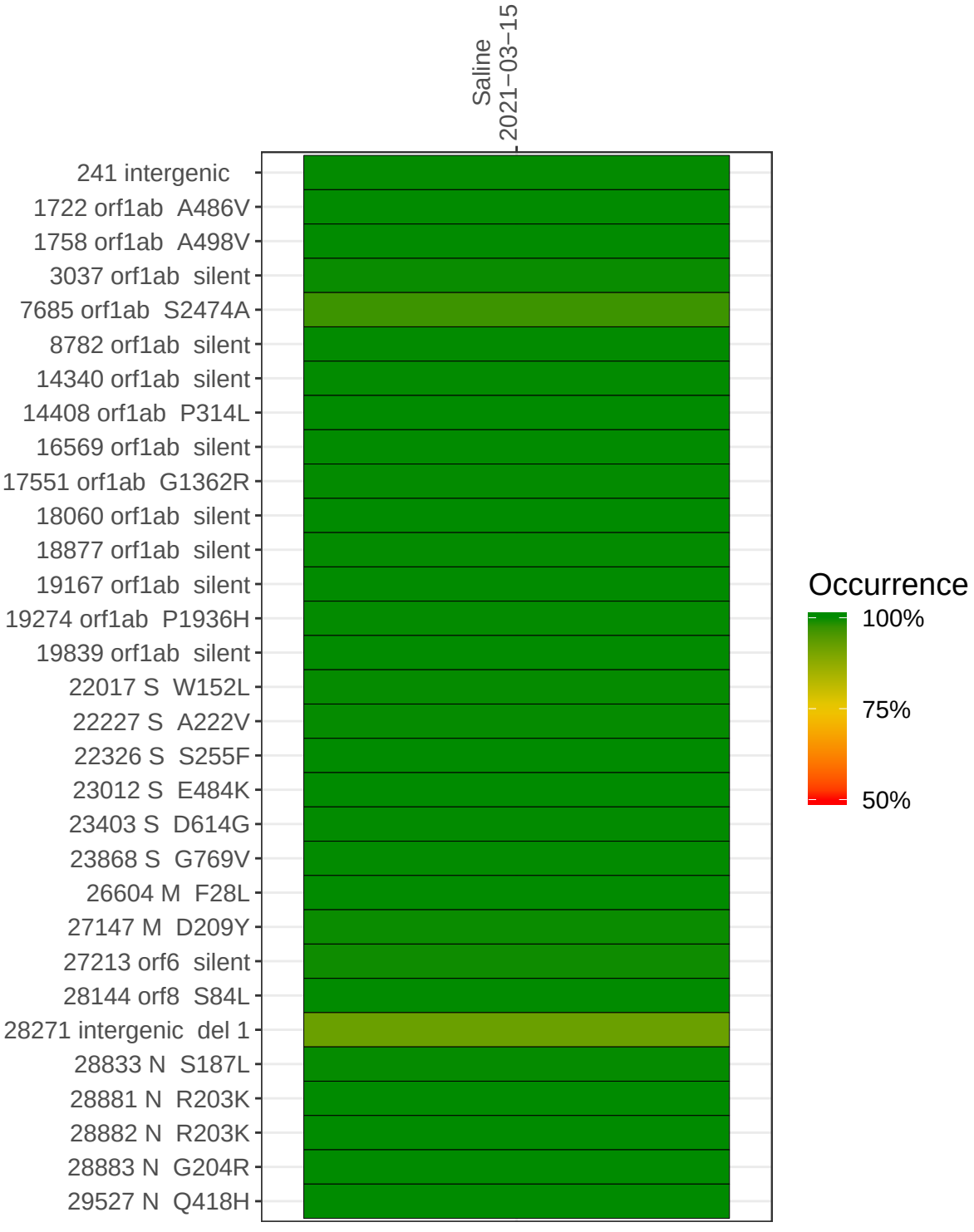
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

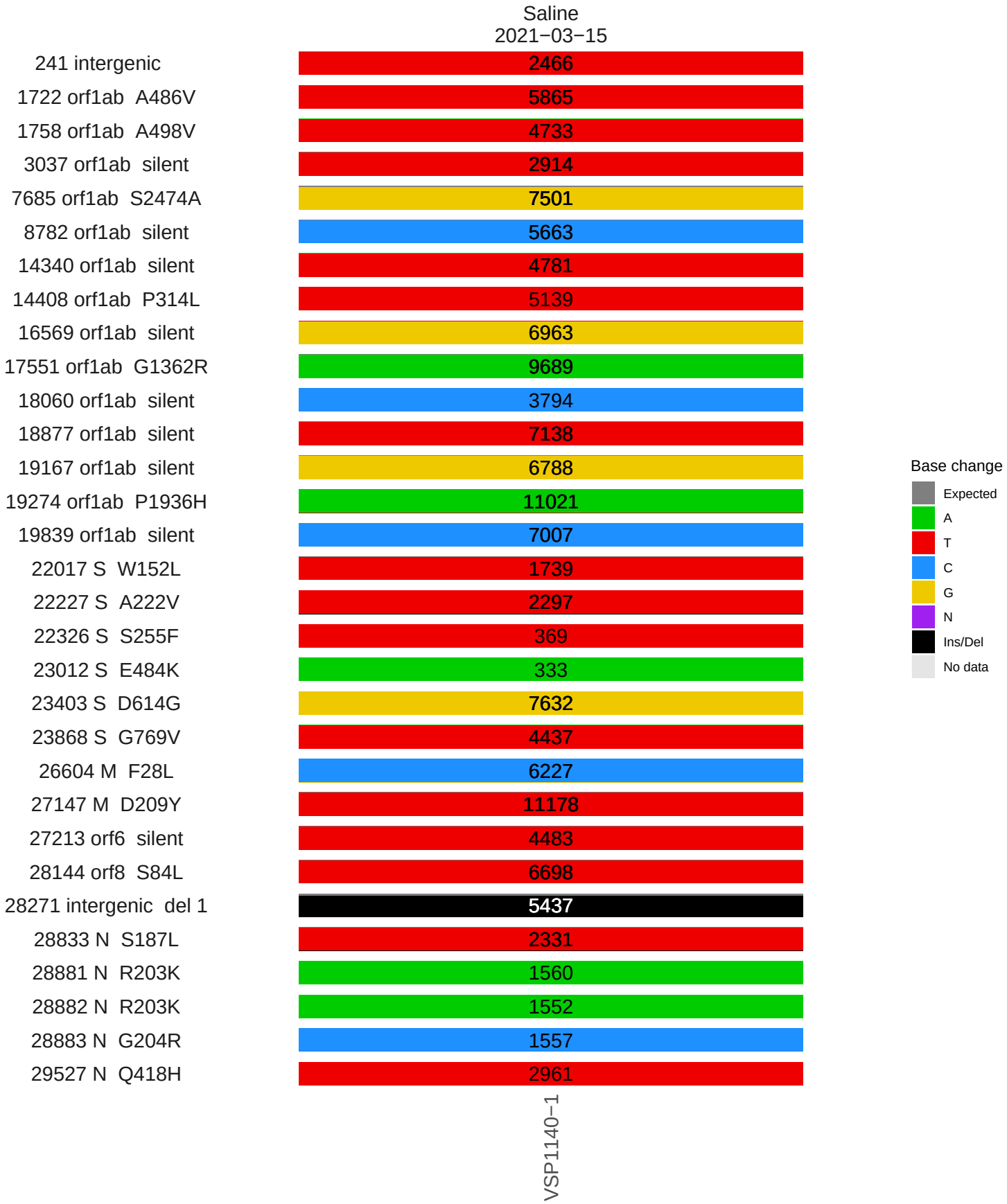
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1140-1	single experiment	NA	Saline	2021-03-15	29.70	R.1	99.2%	99.2%

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.

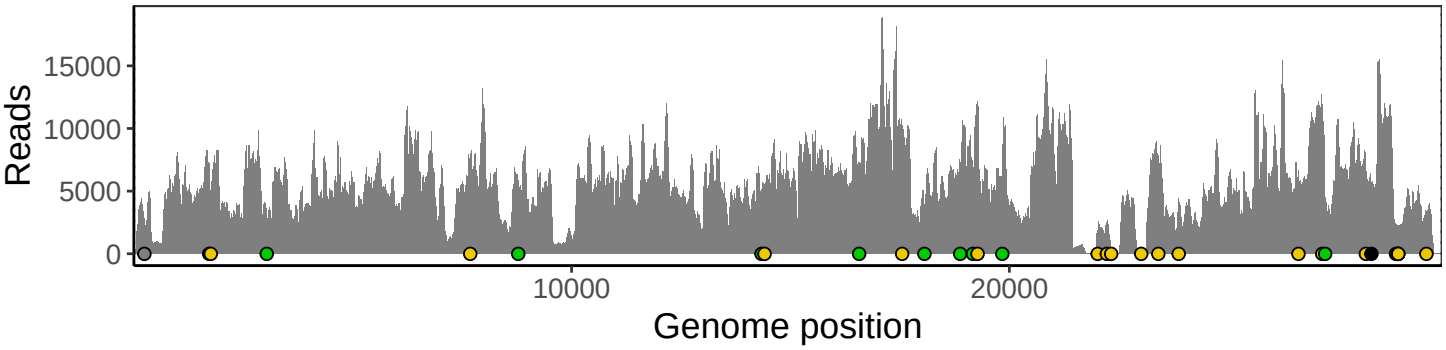



Saline
2021−03−15
241 intergenic
2466
1722 orf1ab A486V
5865
1758 orf1ab A498V
4733
3037 orf1ab silent
2914
7685 orf1ab S2474A
7501
8782 orf1ab silent
5663
14340 orf1ab silent
4781
14408 orf1ab P314L
5139
16569 orf1ab silent
6963
17551 orf1ab G1362R
9689
18060 orf1ab silent
3794
18877 orf1ab silent
7138
19167 orf1ab silent
6788
19274 orf1ab P1936H
11021
19839 orf1ab silent
7007
22017 S W152L
1739
22227 S A222V
2297
22326 S S255F
369
23012 S E484K
333
23403 S D614G
7632
23868 S G769V
4437
26604 M F28L
6227
27147 M D209Y
11178
27213 orf6 silent
4483
28144 orf8 S84L
6698
28271 intergenic del 1
5437
28833 N S187L
2331
28881 N R203K
1560
28882 N R203K
1552
28883 N G204R
1557
29527 N Q418H
2961
VSP1140−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

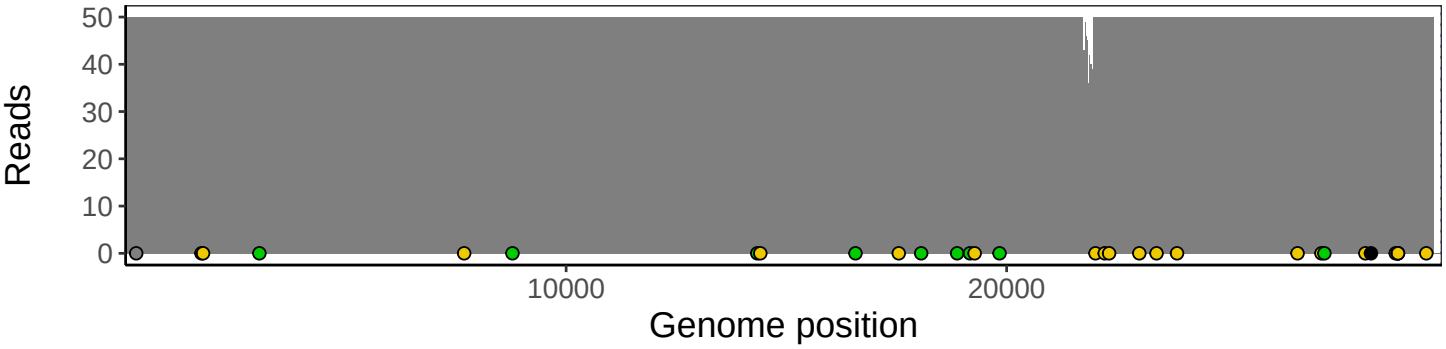
Analyses of individual experiments and composite results

VSP1140-1 | 2021-03-15 | Saline | UPHS-0155 | genomes | single experiment

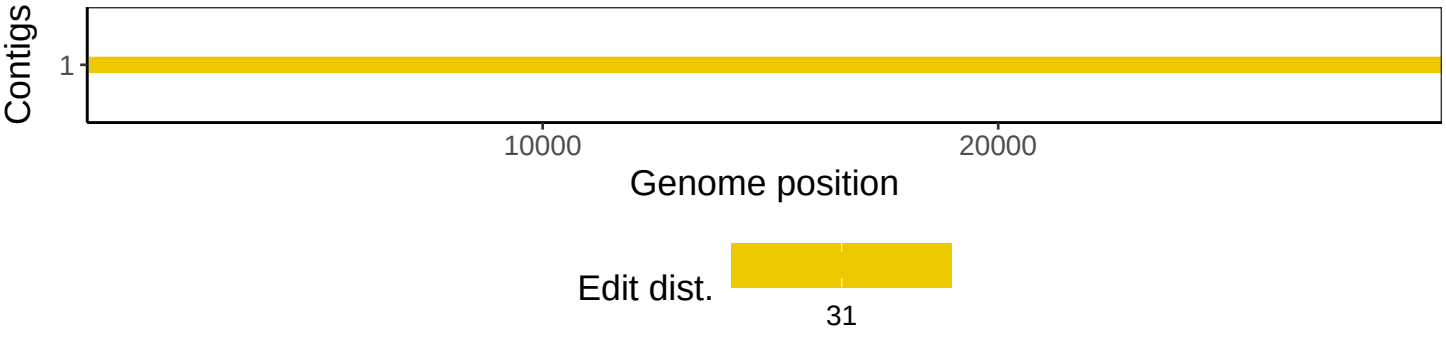
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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