COVID-19 subject UPHS-0054

2021-04-17

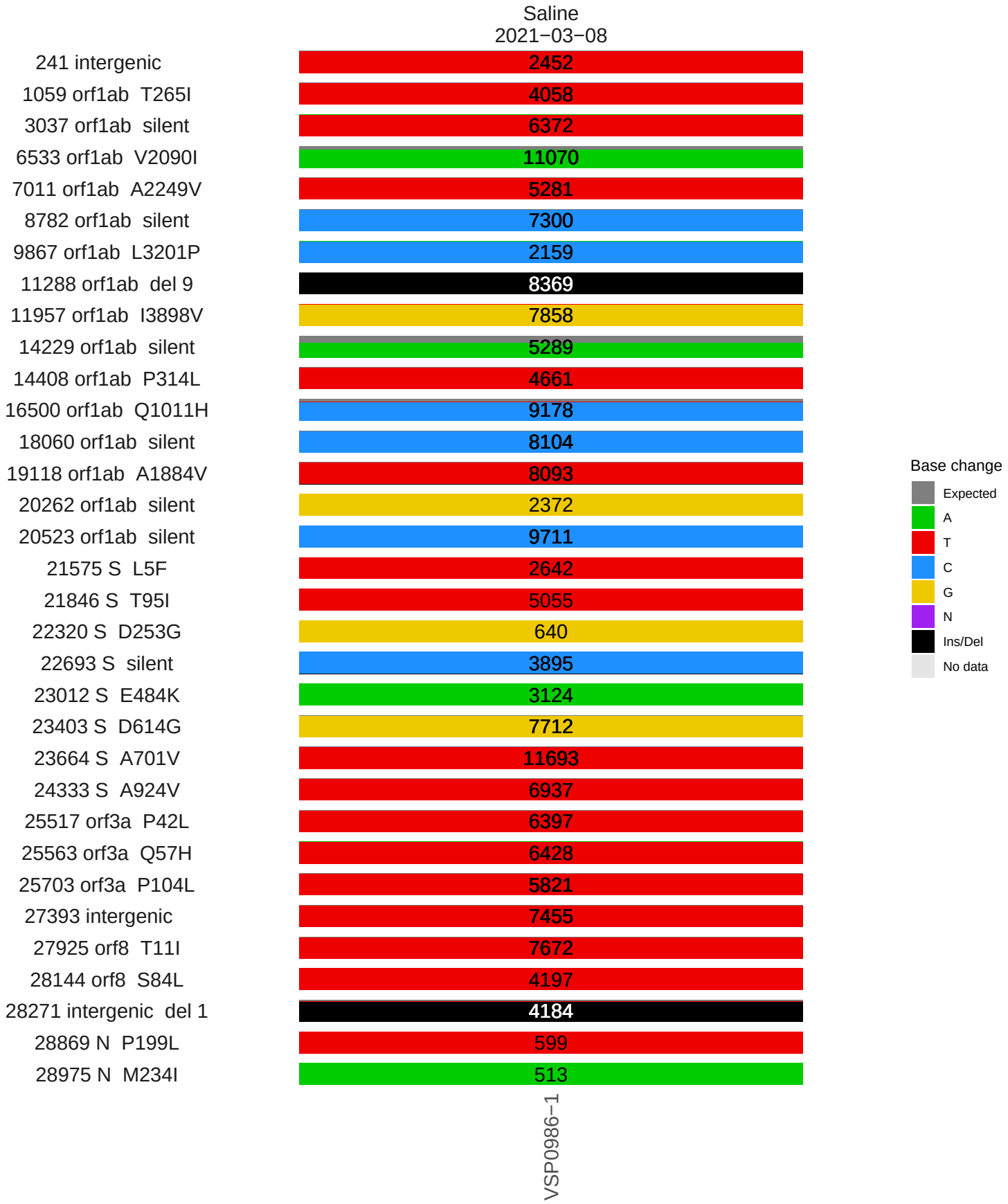
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0986-1	single experiment	NA	Saline	2021-03-08	29.87	B.1.526	99.8%	99.8%

Variants shared across samples

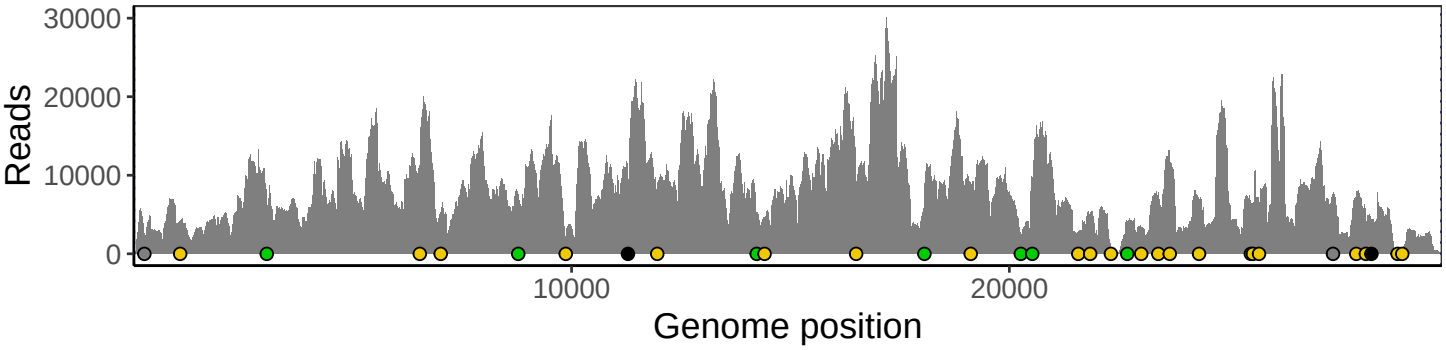
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% 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
2021−03−08
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
6533 orf1ab V2090I
7011 orf1ab A2249V
8782 orf1ab silent
9867 orf1ab L3201P
11288 orf1ab del 9
11957 orf1ab I3898V
14229 orf1ab silent
14408 orf1ab P314L
16500 orf1ab Q1011H
18060 orf1ab silent
19118 orf1ab A1884V
20262 orf1ab silent
20523 orf1ab silent
21575 S L5F
21846 S T95I
22320 S D253G
22693 S silent
23012 S E484K
23403 S D614G
23664 S A701V
24333 S A924V
25517 orf3a P42L
25563 orf3a Q57H
25703 orf3a P104L
27393 intergenic
27925 orf8 T11I
28144 orf8 S84L
28271 intergenic del 1
28869 N P199L
28975 N M234I
2452
4058
6372
11070
5281
7300
2159
8369
7858
5289
4661
9178
8104
8093
2372
9711
2642
5055
640
3895
3124
7712
11693
6937
6397
6428
5821
7455
7672
4197
4184
599
513
VSP0986−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

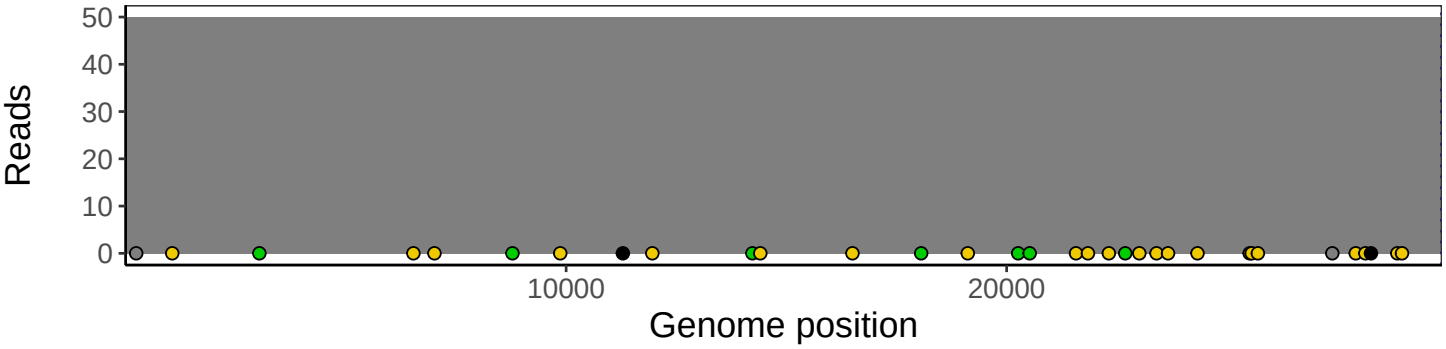
Analyses of individual experiments and composite results

VSP0986-1 | 2021-03-08 | Saline | UPHS-0054 | genomes | single experiment

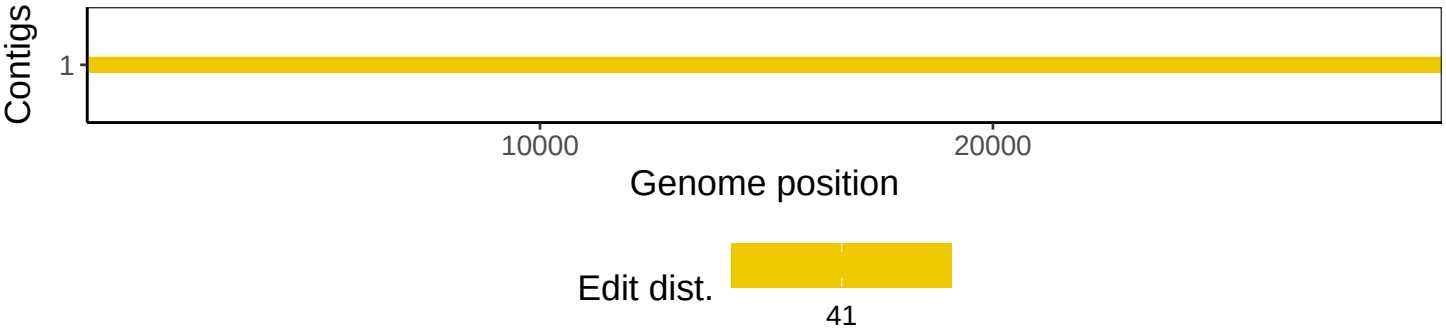
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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