COVID-19 subject UPHS-0041

2021-04-17

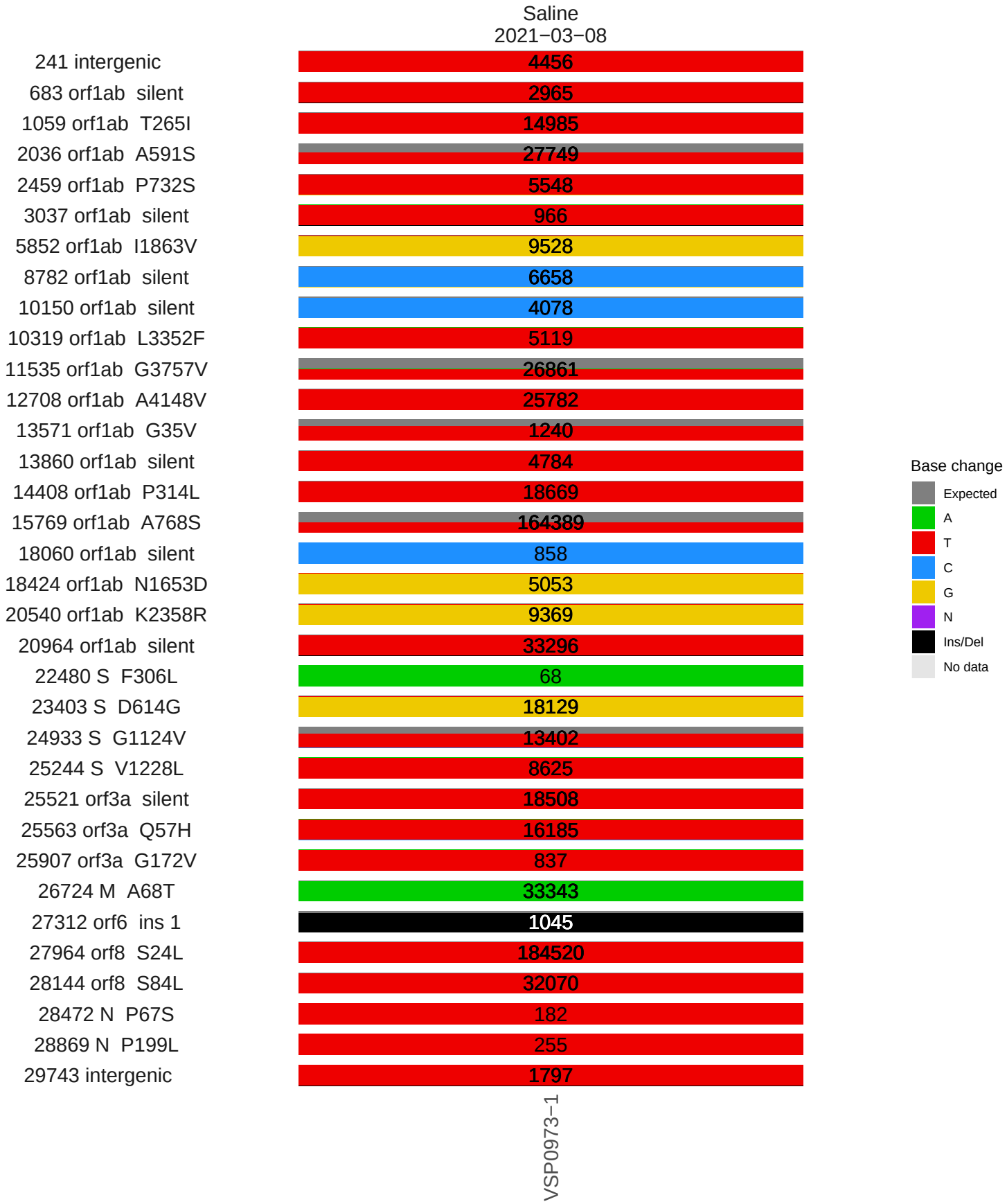
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0973-1	single experiment	NA	Saline	2021-03-08	29.84	B.1.596	99.9%	99.9%

Variants shared across samples

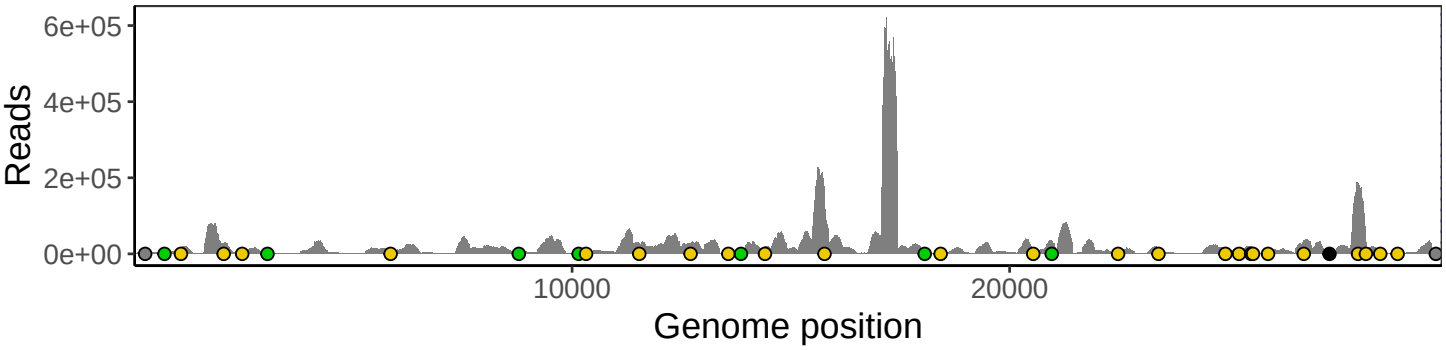
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% 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
683 orf1ab silent
1059 orf1ab T265I
2036 orf1ab A591S
2459 orf1ab P732S
3037 orf1ab silent
5852 orf1ab I1863V
8782 orf1ab silent
10150 orf1ab silent
10319 orf1ab L3352F
11535 orf1ab G3757V
12708 orf1ab A4148V
13571 orf1ab G35V
13860 orf1ab silent
14408 orf1ab P314L
15769 orf1ab A768S
18060 orf1ab silent
18424 orf1ab N1653D
20540 orf1ab K2358R
20964 orf1ab silent
22480 S F306L
23403 S D614G
24933 S G1124V
25244 S V1228L
25521 orf3a silent
25563 orf3a Q57H
25907 orf3a G172V
26724 M A68T
27312 orf6 ins 1
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28869 N P199L
29743 intergenic
4456
2965
14985
27749
5548
966
9528
6658
4078
5119
26861
25782
1240
4784
18669
164389
858
5053
9369
33296
68
18129
13402
8625
18508
16185
837
33343
1045
184520
32070
182
255
1797
VSP0973−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

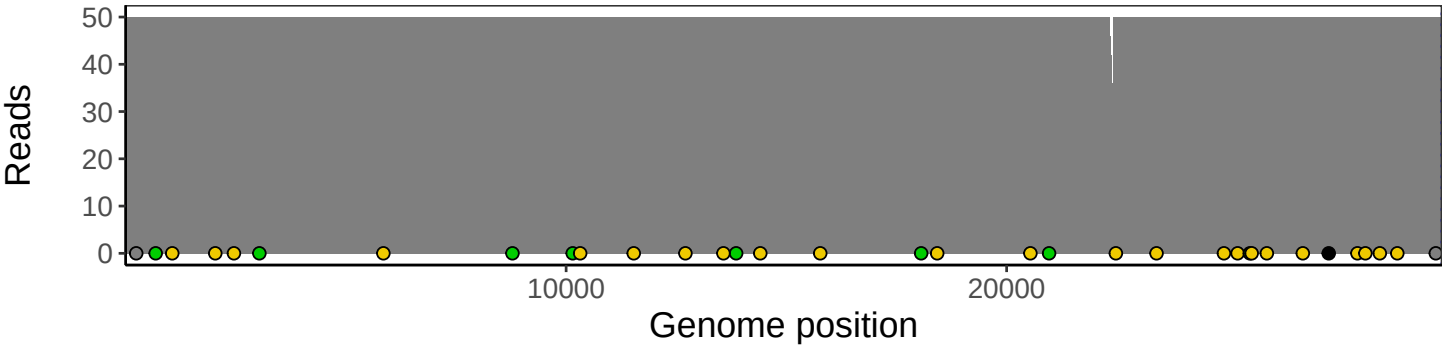
Analyses of individual experiments and composite results

VSP0973-1 | 2021-03-08 | Saline | UPHS-0041 | genomes | single experiment

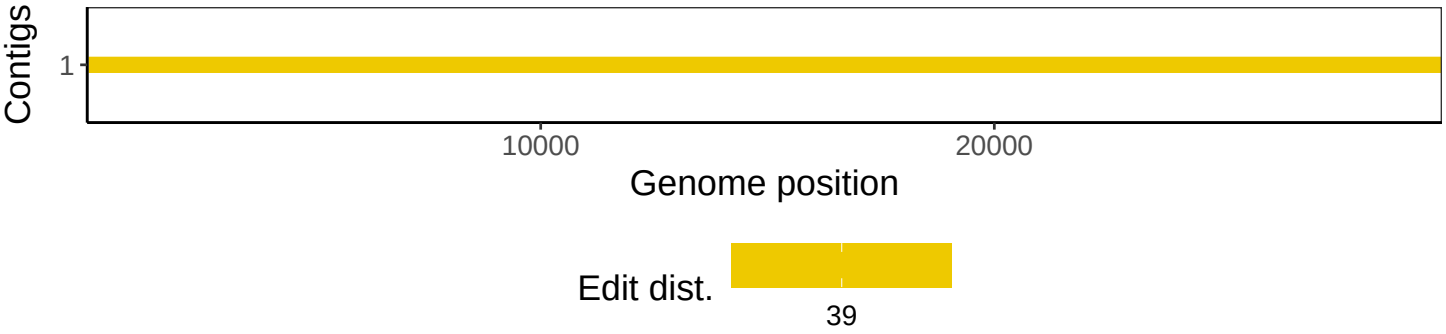
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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