COVID-19 subject UPHS-1368

2021-06-23

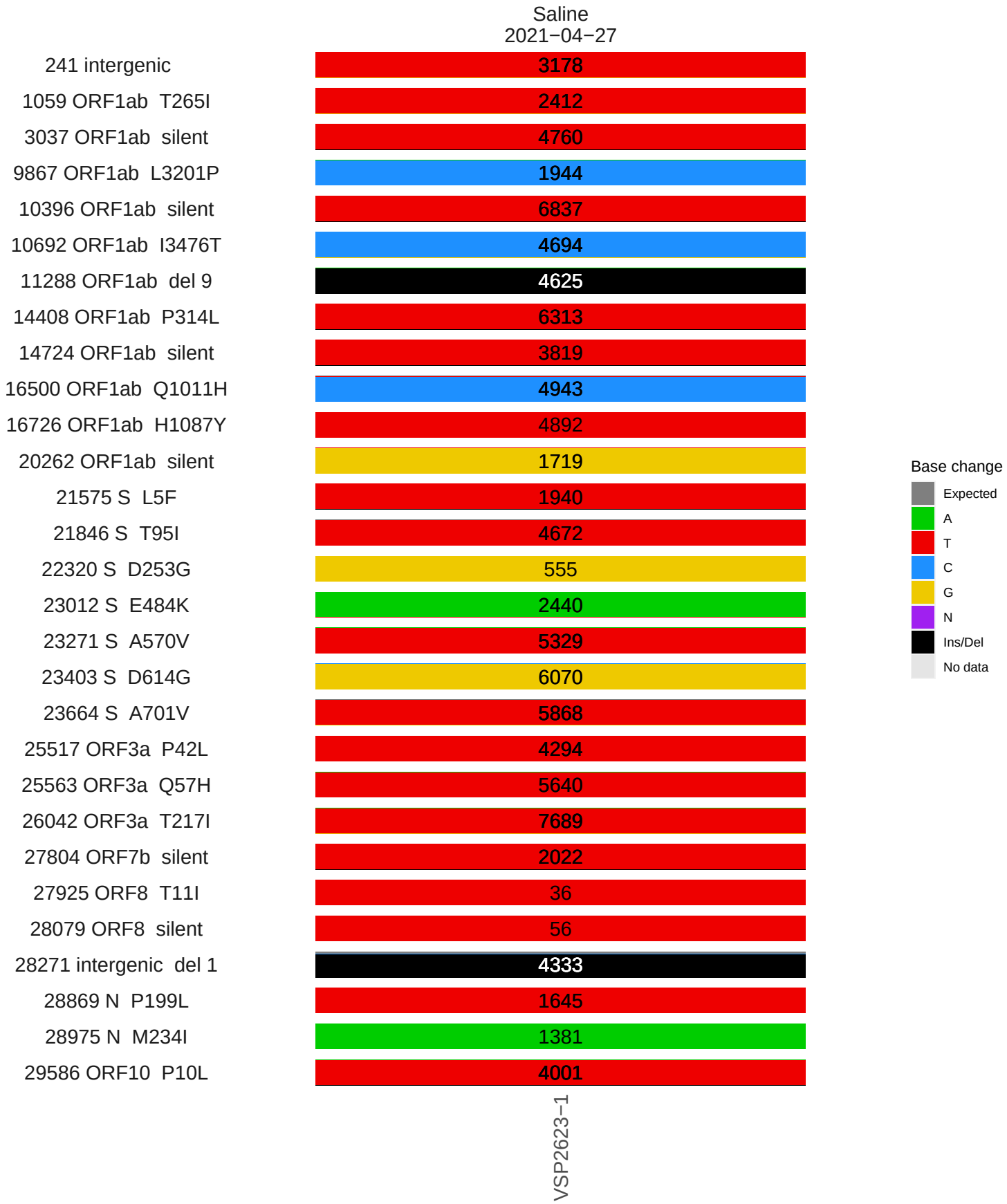
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2623-1	single experiment	NA	Saline	2021-04-27	29.82	B.1.526	99.8%	99.7%

Variants shared across samples

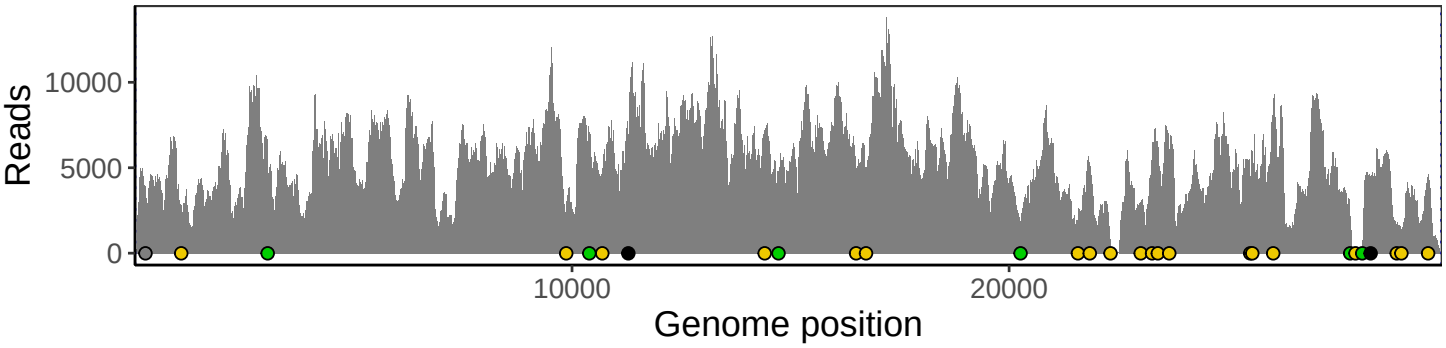
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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
2021−04−27
241 intergenic
3178
1059 ORF1ab T265I
2412
3037 ORF1ab silent
4760
9867 ORF1ab L3201P
1944
10396 ORF1ab silent
6837
10692 ORF1ab I3476T
4694
11288 ORF1ab del 9
4625
14408 ORF1ab P314L
6313
14724 ORF1ab silent
3819
16500 ORF1ab Q1011H
4943
16726 ORF1ab H1087Y
4892
20262 ORF1ab silent
1719
21575 S L5F
1940
21846 S T95I
4672
22320 S D253G
555
23012 S E484K
2440
23271 S A570V
5329
23403 S D614G
6070
23664 S A701V
5868
25517 ORF3a P42L
4294
25563 ORF3a Q57H
5640
26042 ORF3a T217I
7689
27804 ORF7b silent
2022
27925 ORF8 T11I
36
28079 ORF8 silent
56
28271 intergenic del 1
4333
28869 N P199L
1645
28975 N M234I
1381
29586 ORF10 P10L
4001
VSP2623−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

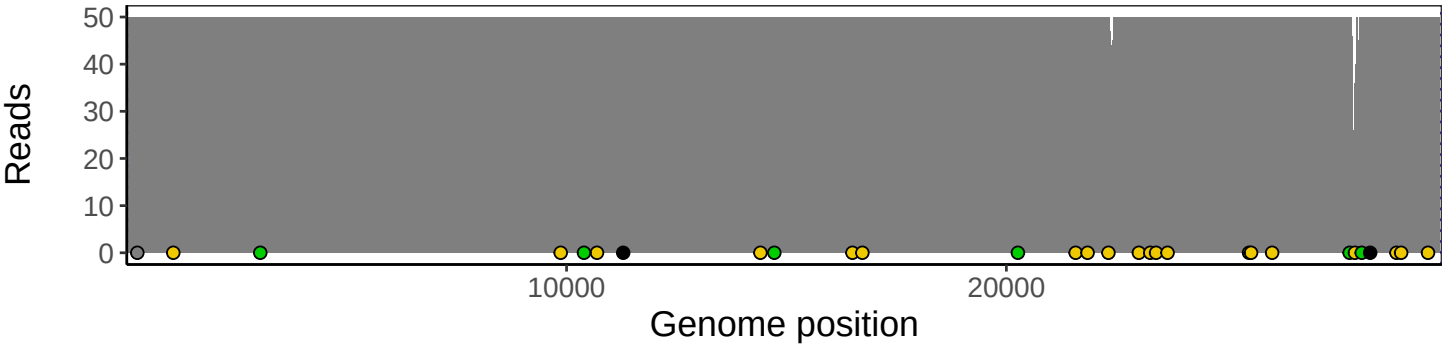
Analyses of individual experiments and composite results

VSP2623-1 | 2021-04-27 | Saline | UPHS-1368 | genomes | single experiment

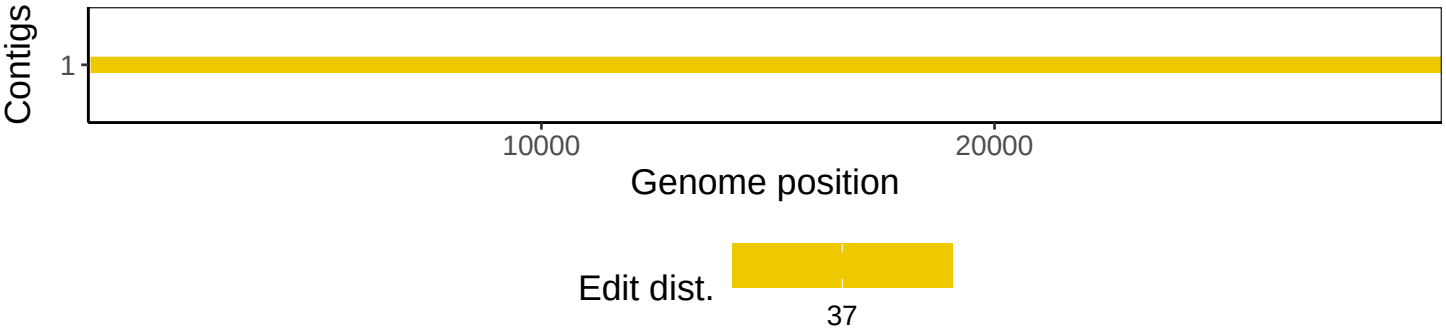
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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