COVID-19 subject UPHS-0418

2021-06-01

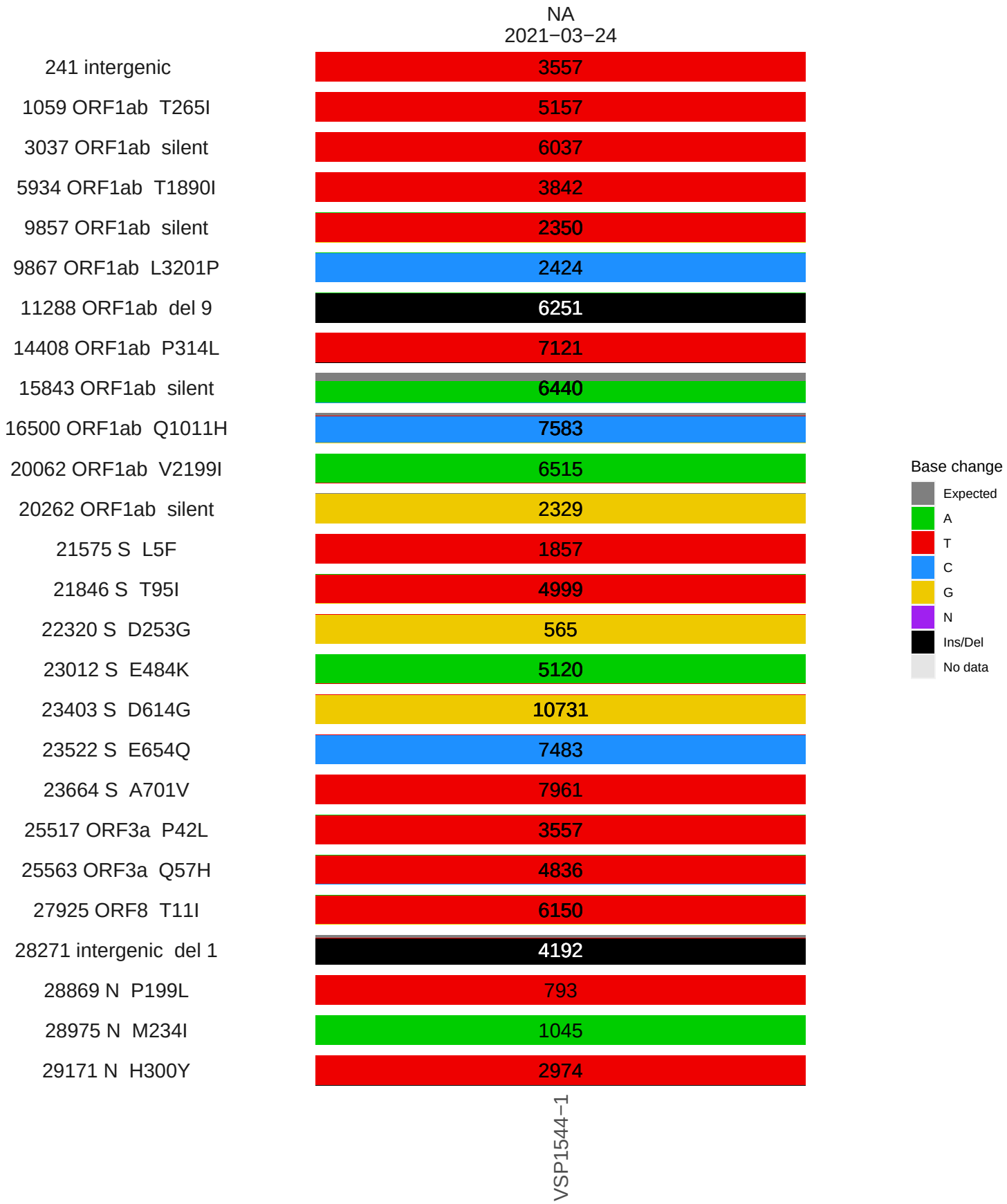
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1544-1	single experiment	NA	NA	2021-03-24	29.83	B.1.526	99.9%	99.7%

Variants shared across samples

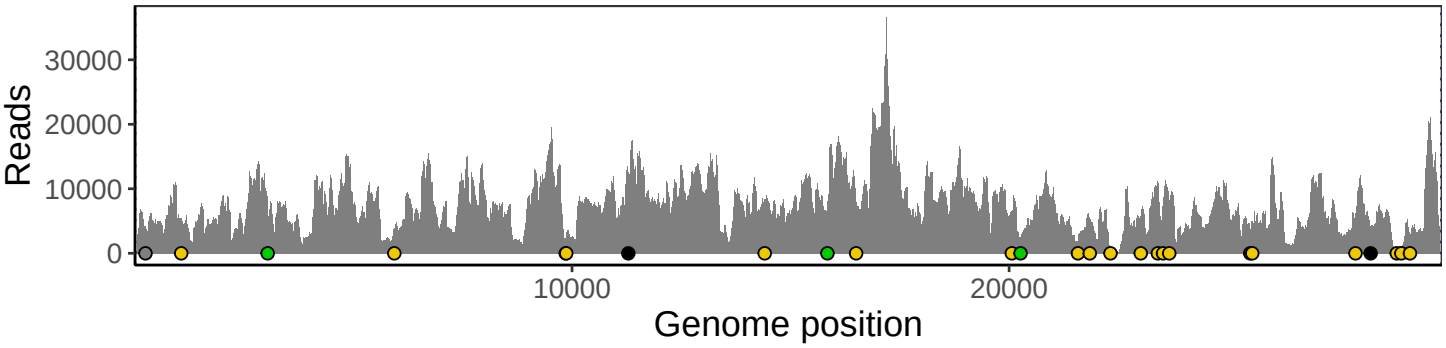
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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.


NA
2021−03−24
241 intergenic
3557
1059 ORF1ab T265I
5157
3037 ORF1ab silent
6037
5934 ORF1ab T1890I
3842
9857 ORF1ab silent
2350
9867 ORF1ab L3201P
2424
11288 ORF1ab del 9
6251
14408 ORF1ab P314L
7121
15843 ORF1ab silent
6440
16500 ORF1ab Q1011H
7583
20062 ORF1ab V2199I
6515
20262 ORF1ab silent
2329
21575 S L5F
1857
21846 S T95I
4999
22320 S D253G
565
23012 S E484K
5120
23403 S D614G
10731
23522 S E654Q
7483
23664 S A701V
7961
25517 ORF3a P42L
3557
25563 ORF3a Q57H
4836
27925 ORF8 T11I
6150
28271 intergenic del 1
4192
28869 N P199L
793
28975 N M234I
1045
29171 N H300Y
2974
VSP1544−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

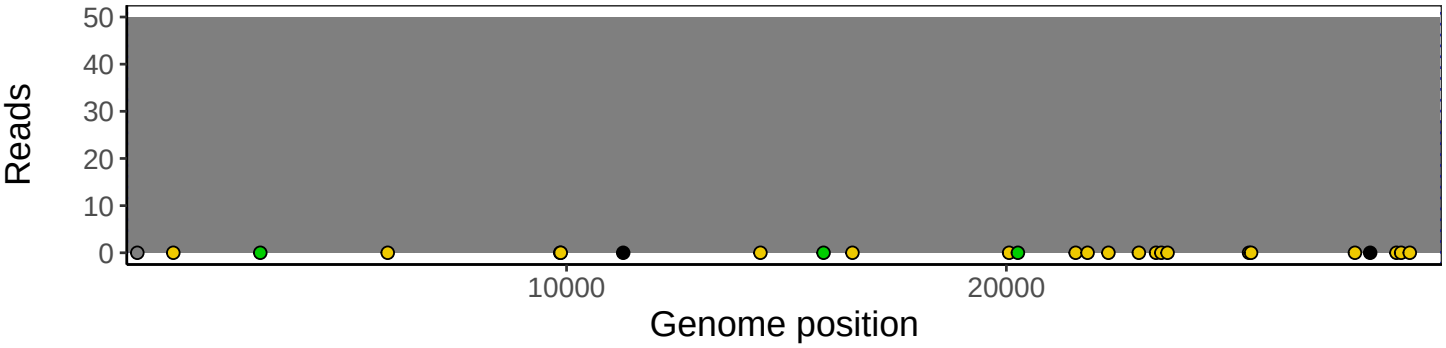
Analyses of individual experiments and composite results

VSP1544-1 | 2021-03-24 | NA | UPHS-0418 | genomes | single experiment

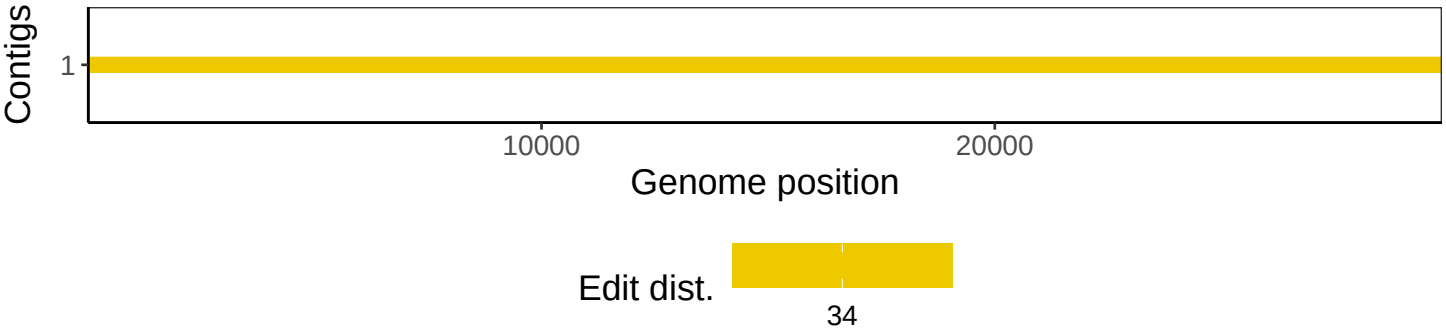
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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