COVID-19 subject UPHS-1176

2021-06-23

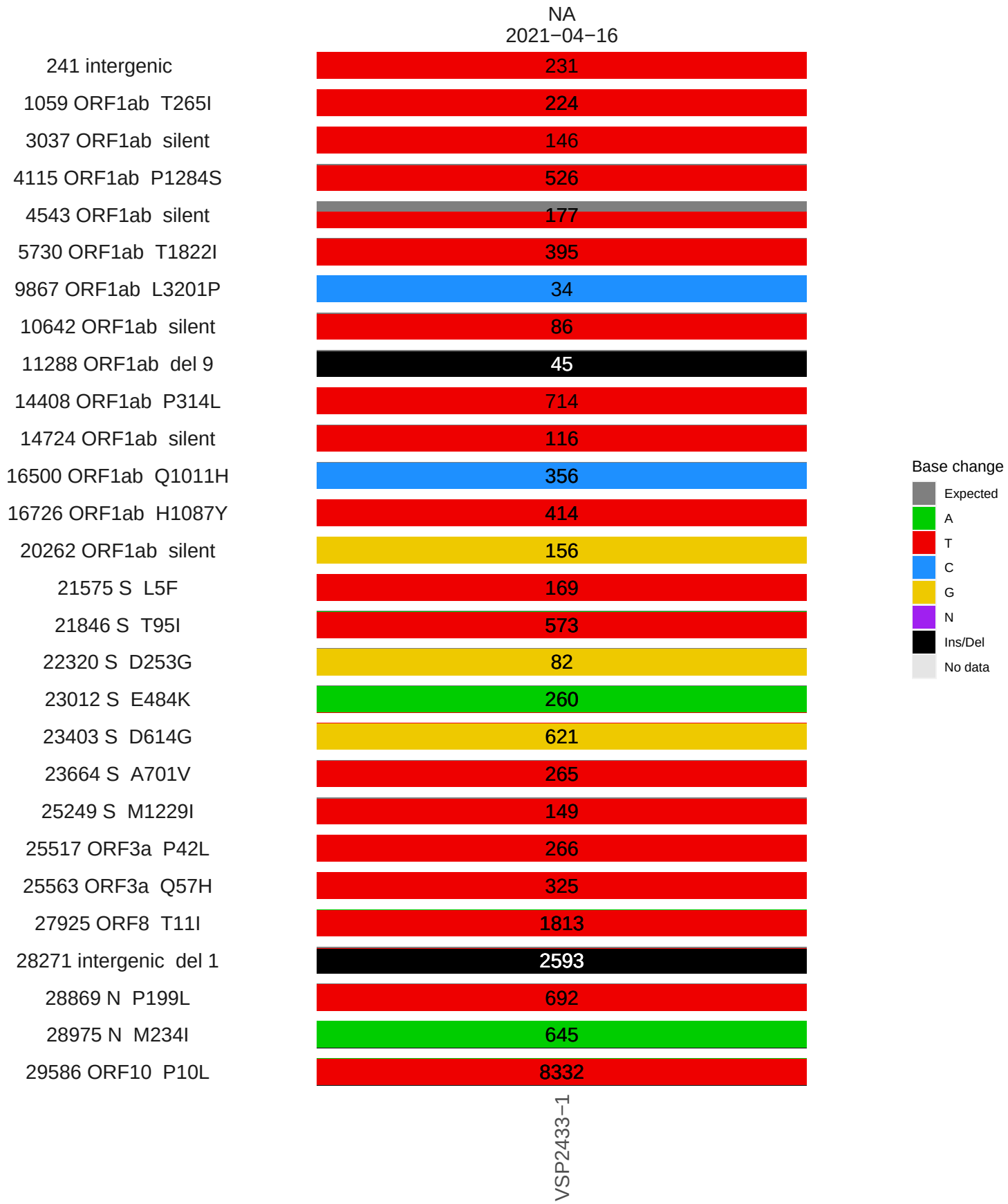
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2433-1	single experiment	NA	NA	2021-04-16	29.89	B.1.526	99.9%	99.8%

Variants shared across samples

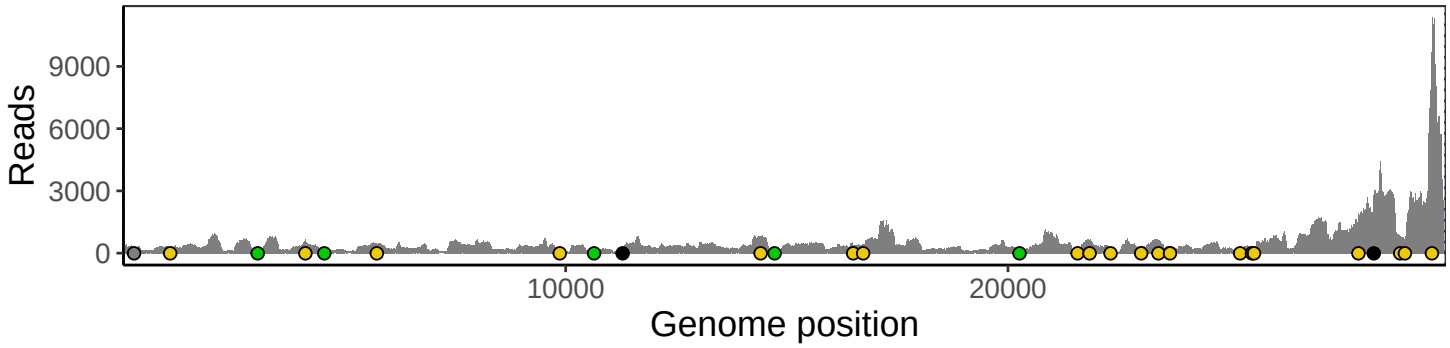
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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
2021−04−16
241 intergenic
231
1059 ORF1ab T265I
224
3037 ORF1ab silent
146
4115 ORF1ab P1284S
526
4543 ORF1ab silent
177
5730 ORF1ab T1822I
395
9867 ORF1ab L3201P
34
10642 ORF1ab silent
86
11288 ORF1ab del 9
45
14408 ORF1ab P314L
714
14724 ORF1ab silent
116
16500 ORF1ab Q1011H
356
16726 ORF1ab H1087Y
414
20262 ORF1ab silent
156
21575 S L5F
169
21846 S T95I
573
22320 S D253G
82
23012 S E484K
260
23403 S D614G
621
23664 S A701V
265
25249 S M1229I
149
25517 ORF3a P42L
266
25563 ORF3a Q57H
325
27925 ORF8 T11I
1813
28271 intergenic del 1
2593
28869 N P199L
692
28975 N M234I
645
29586 ORF10 P10L
8332
VSP2433−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

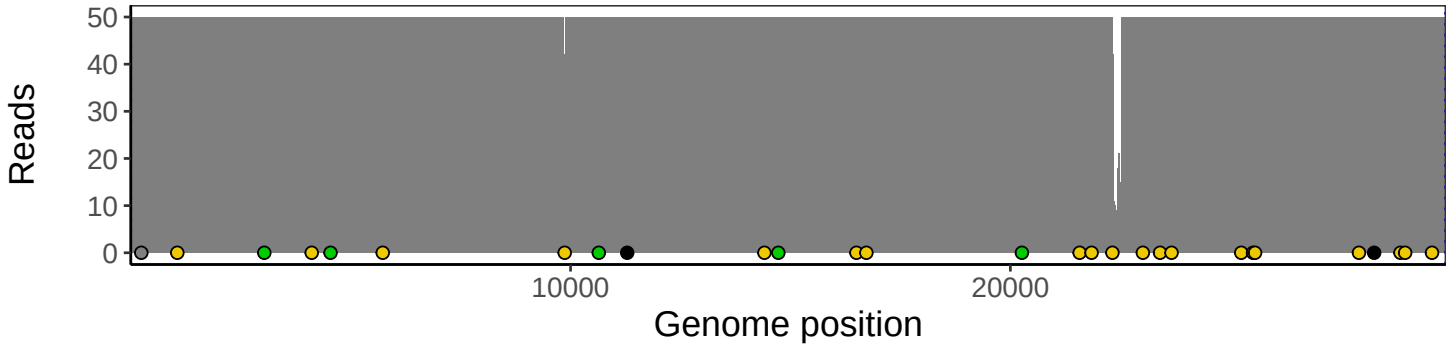
Analyses of individual experiments and composite results

VSP2433-1 | 2021-04-16 | NA | UPHS-1176 | genomes | single experiment

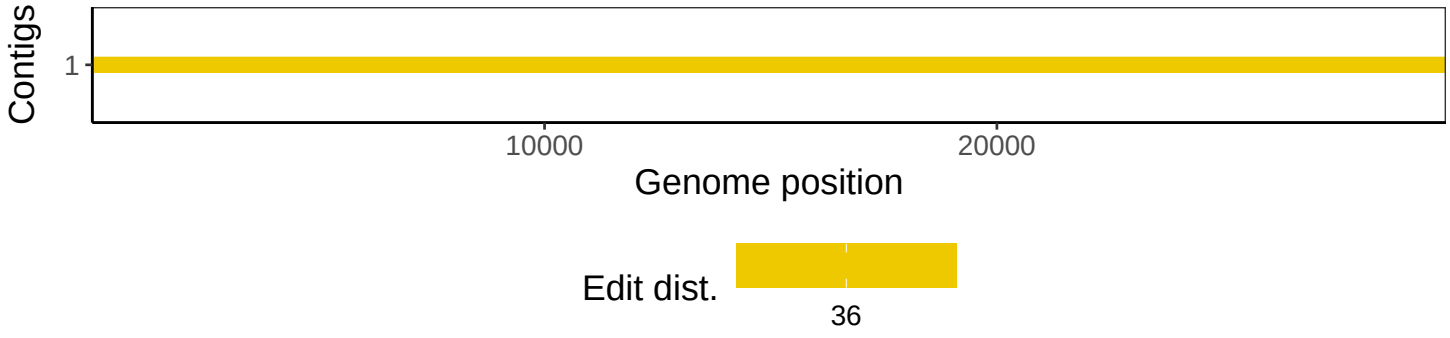
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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