COVID-19 subject UPHS-1161

2021-06-23

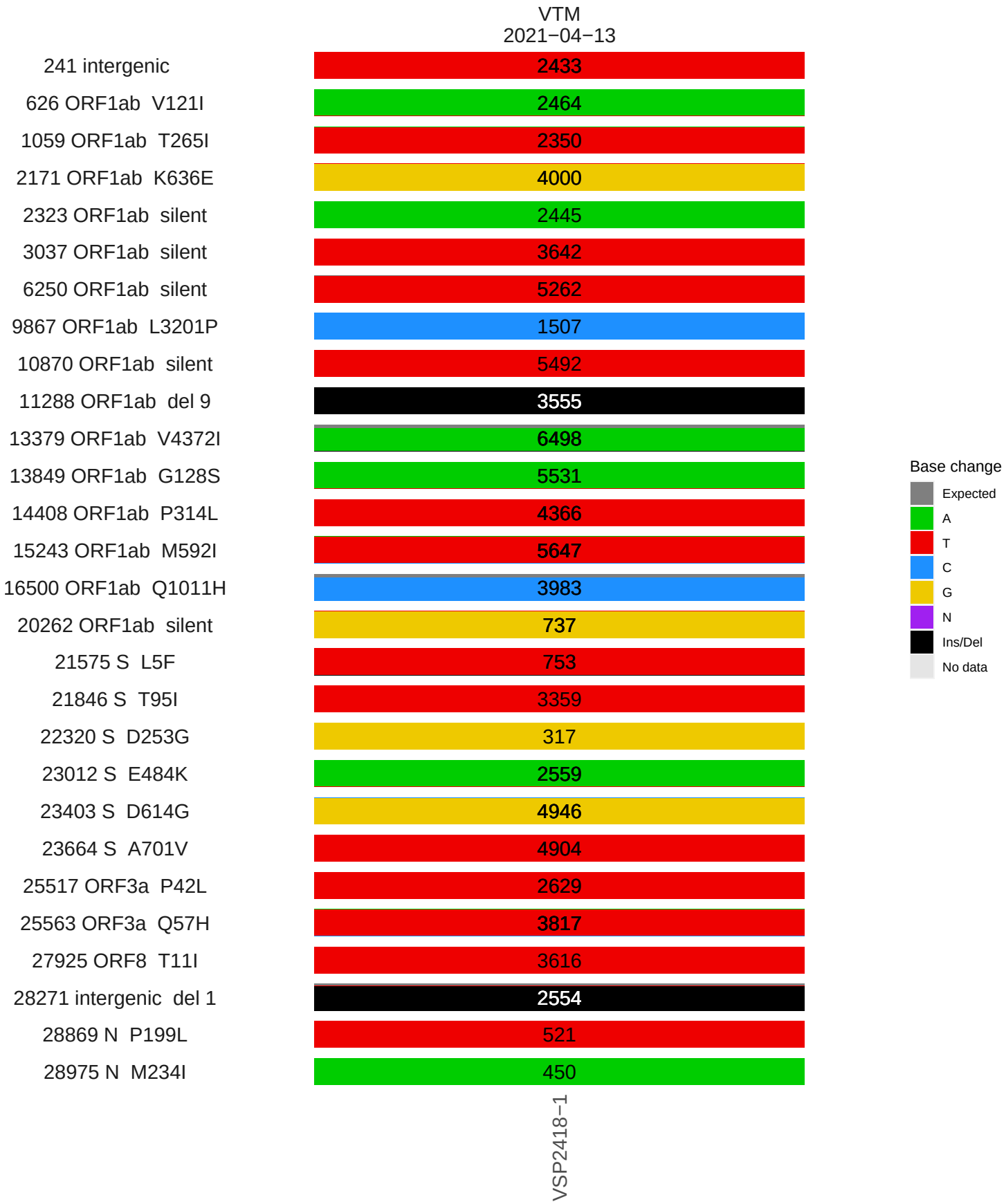
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2418-1	single experiment	NA	VTM	2021-04-13	29.83	B.1.526	99.8%	99.7%

Variants shared across samples

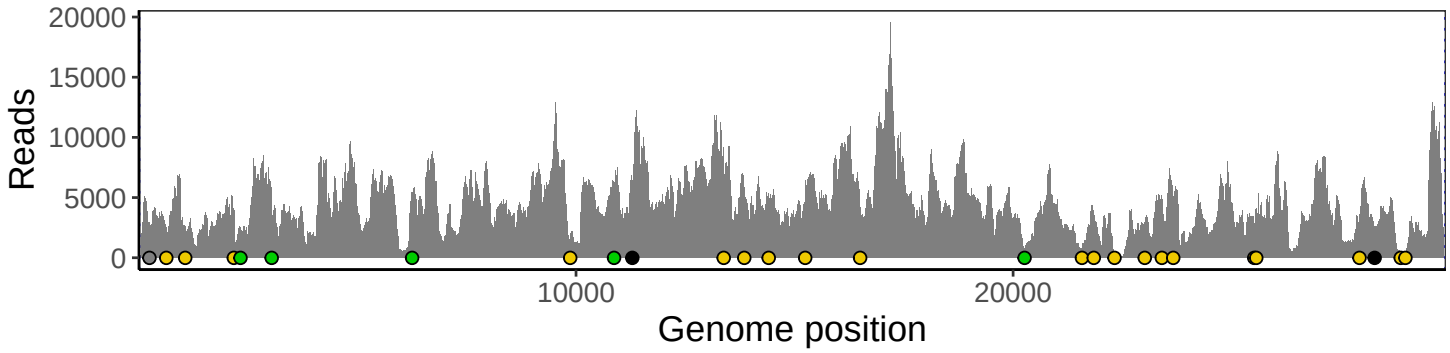
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of read pairs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


VTM
2021−04−13
241 intergenic
2433
626 ORF1ab V121I
2464
1059 ORF1ab T265I
2350
2171 ORF1ab K636E
4000
2323 ORF1ab silent
2445
3037 ORF1ab silent
3642
6250 ORF1ab silent
5262
9867 ORF1ab L3201P
1507
10870 ORF1ab silent
5492
11288 ORF1ab del 9
3555
13379 ORF1ab V4372I
6498
13849 ORF1ab G128S
5531
14408 ORF1ab P314L
4366
15243 ORF1ab M592I
5647
16500 ORF1ab Q1011H
3983
20262 ORF1ab silent
737
21575 S L5F
753
21846 S T95I
3359
22320 S D253G
317
23012 S E484K
2559
23403 S D614G
4946
23664 S A701V
4904
25517 ORF3a P42L
2629
25563 ORF3a Q57H
3817
27925 ORF8 T11I
3616
28271 intergenic del 1
2554
28869 N P199L
521
28975 N M234I
450
VSP2418−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

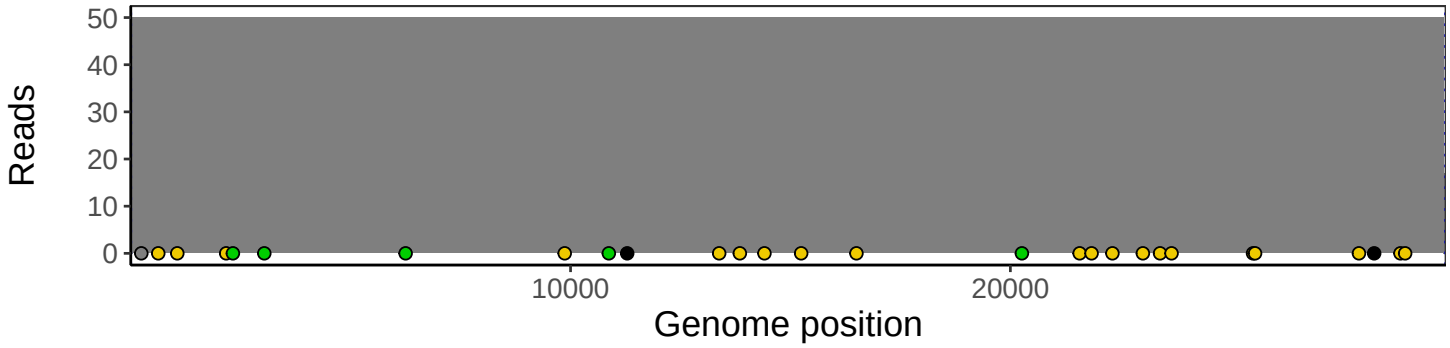
Analyses of individual experiments and composite results

VSP2418-1 | 2021-04-13 | VTM | UPHS-1161 | genomes | single experiment

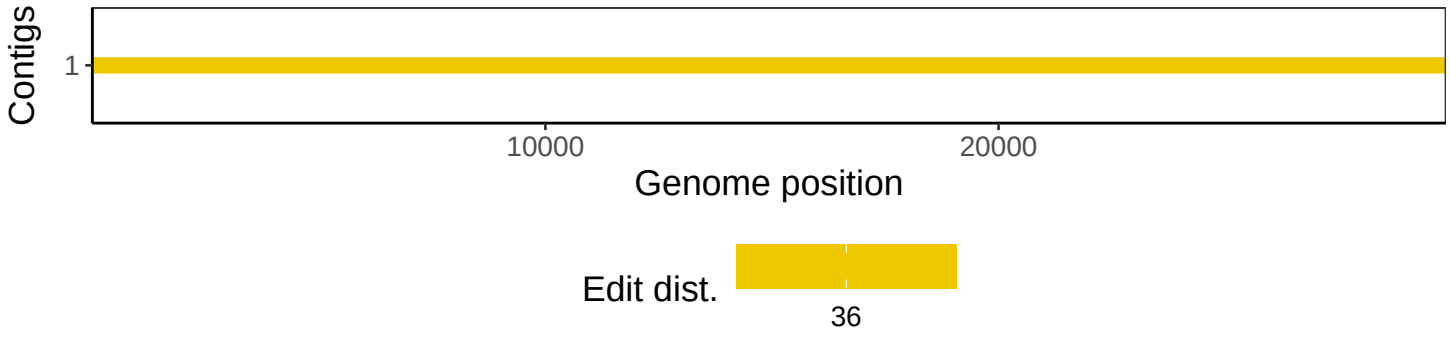
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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