COVID-19 subject UPHS-0488

2021-06-01

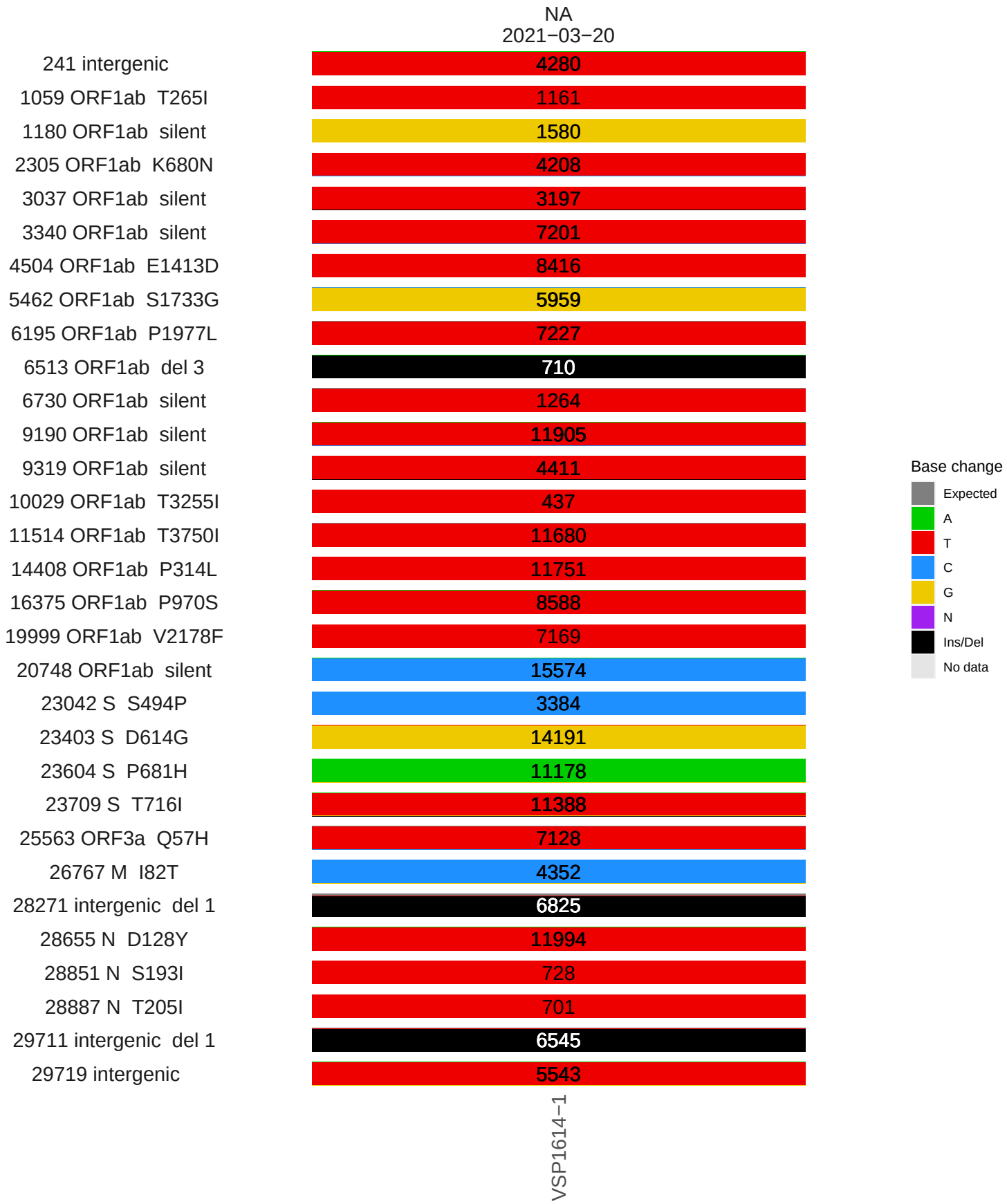
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1614-1	single experiment	NA	NA	2021-03-20	22.98	B.1.575	99.9%	99.6%

Variants shared across samples

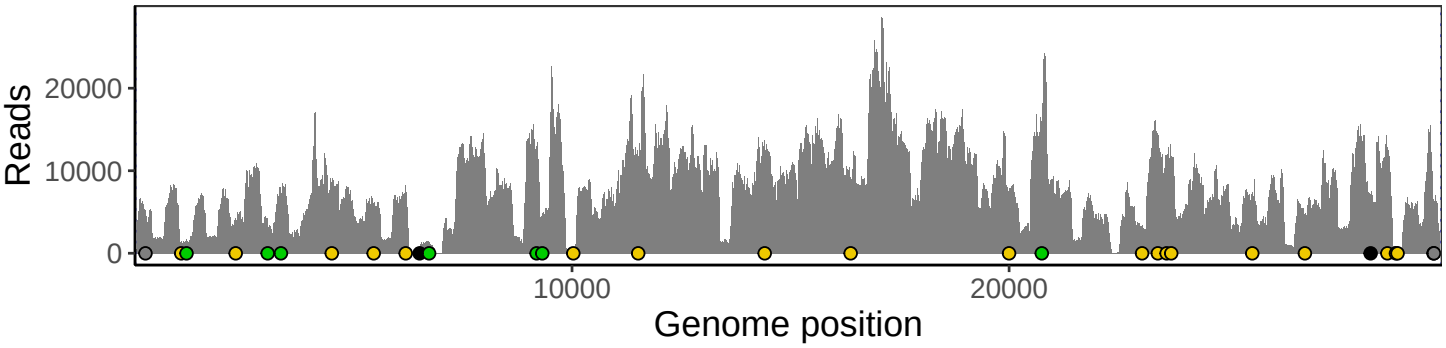
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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
2021−03−20
241 intergenic
1059 ORF1ab T265I
1180 ORF1ab silent
2305 ORF1ab K680N
3037 ORF1ab silent
3340 ORF1ab silent
4504 ORF1ab E1413D
5462 ORF1ab S1733G
6195 ORF1ab P1977L
6513 ORF1ab del 3
6730 ORF1ab silent
9190 ORF1ab silent
9319 ORF1ab silent
10029 ORF1ab T3255I
11514 ORF1ab T3750I
14408 ORF1ab P314L
16375 ORF1ab P970S
19999 ORF1ab V2178F
20748 ORF1ab silent
23042 S S494P
23403 S D614G
23604 S P681H
23709 S T716I
25563 ORF3a Q57H
26767 M I82T
28271 intergenic del 1
28655 N D128Y
28851 N S193I
28887 N T205I
29711 intergenic del 1
29719 intergenic
4280
1161
1580
4208
3197
7201
8416
5959
7227
710
1264
11905
4411
437
11680
11751
8588
7169
15574
3384
14191
11178
11388
7128
4352
6825
11994
728
701
6545
5543
VSP1614−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

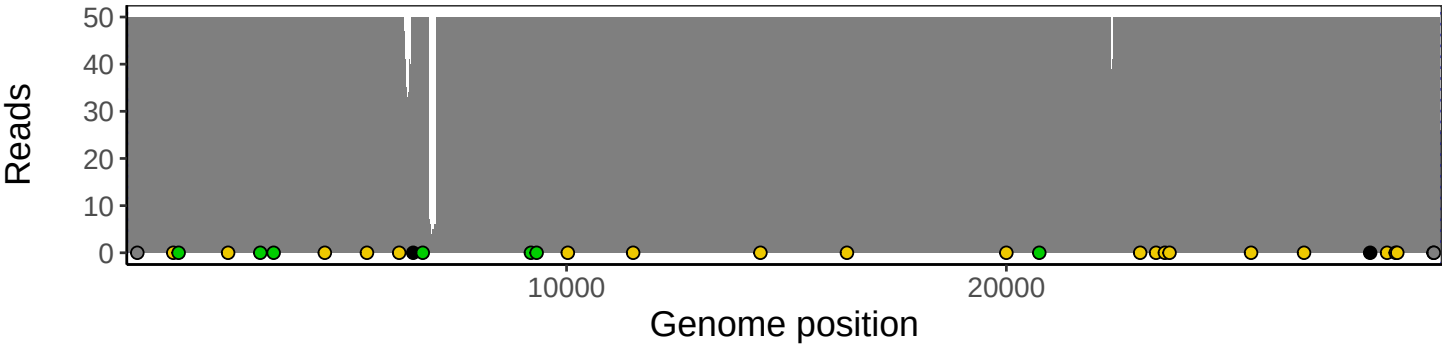
Analyses of individual experiments and composite results

VSP1614-1 | 2021-03-20 | NA | UPHS-0488 | genomes | single experiment

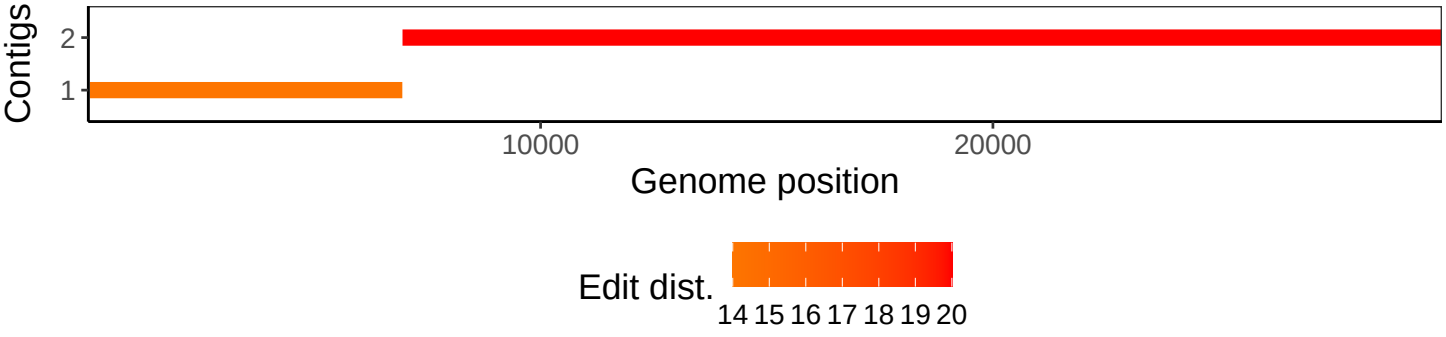
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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