COVID-19 subject UPHS-0455

2021-06-01

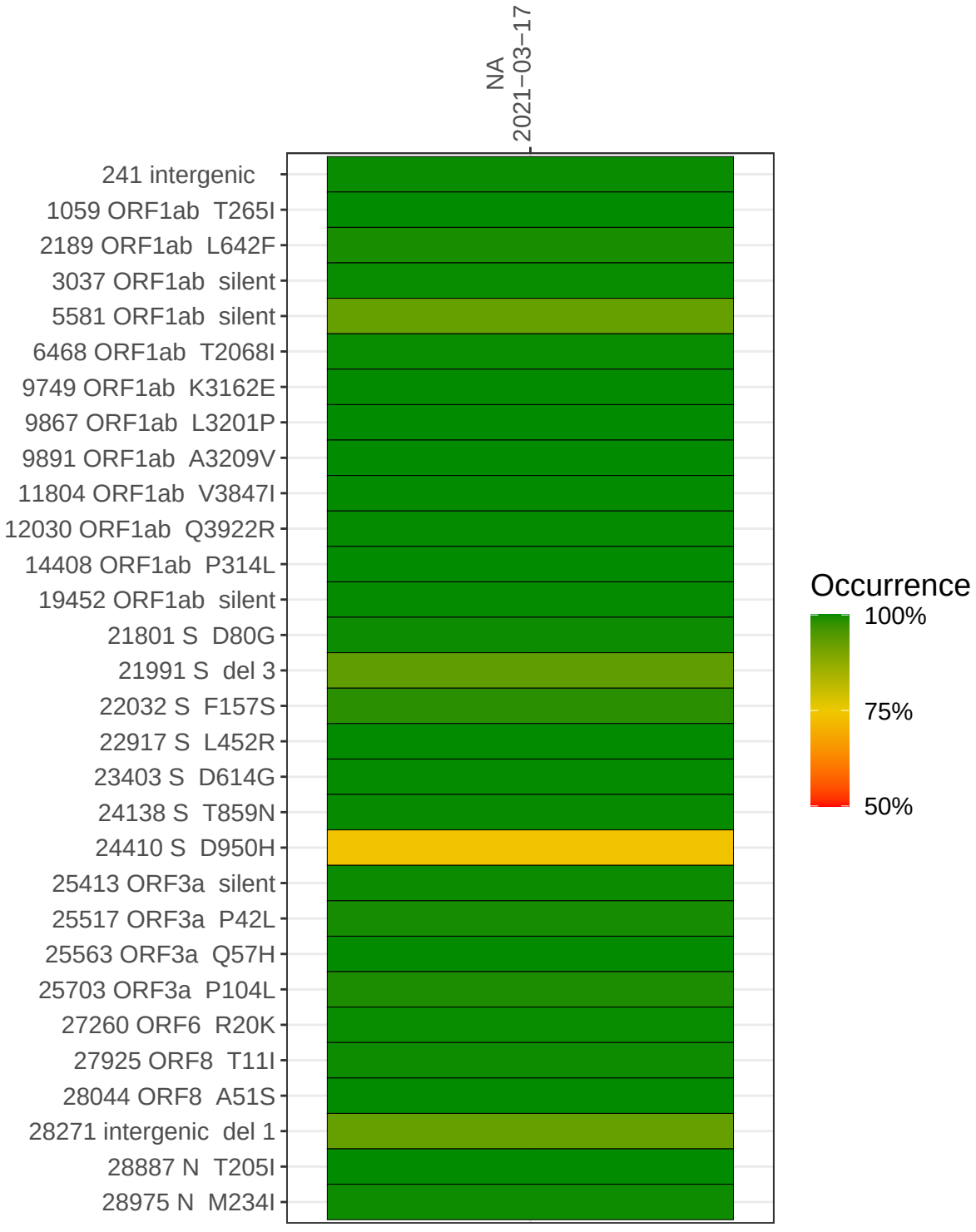
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

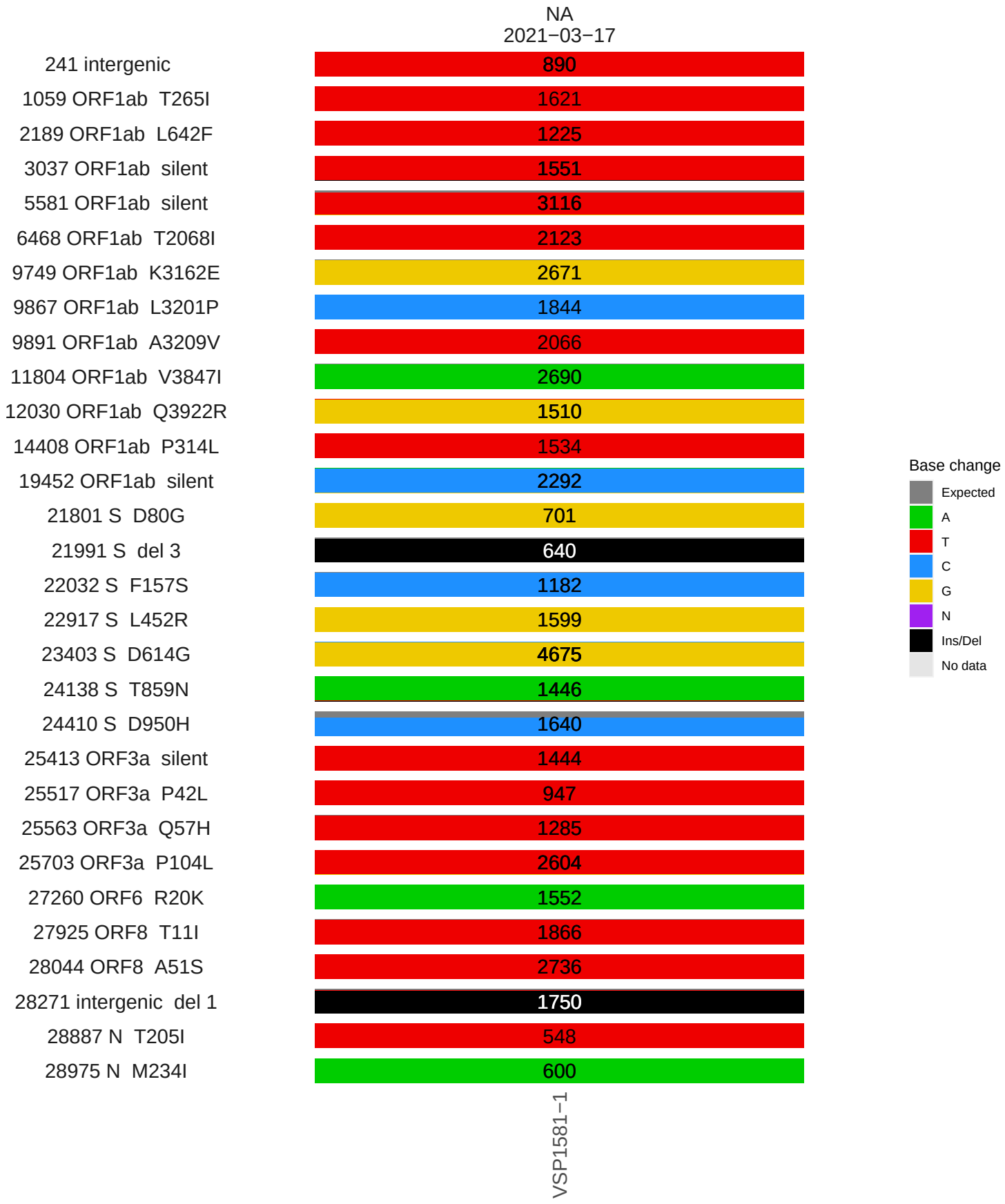
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1581-1	single experiment	NA	NA	2021-03-17	27.41	B.1	99.9%	99.5%

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.

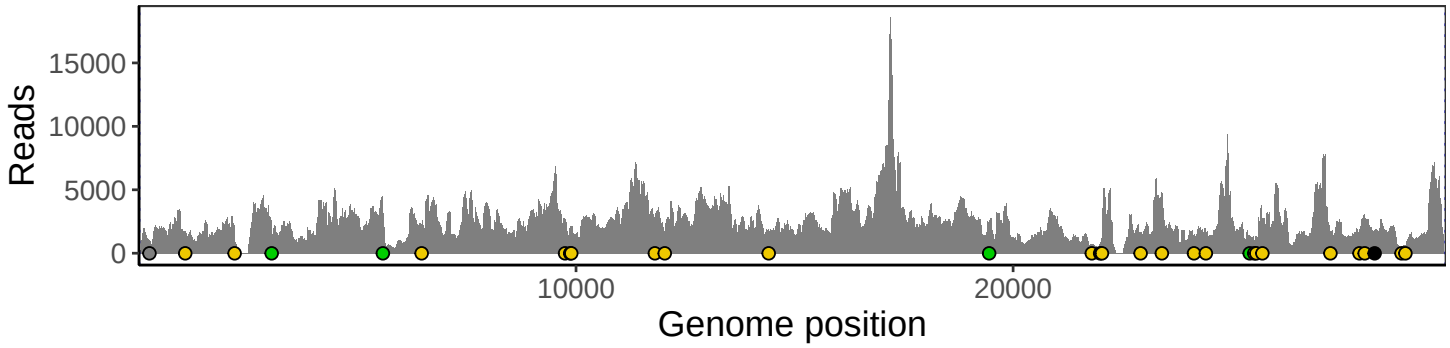



NA
2021−03−17
241 intergenic
890
1059 ORF1ab T265I
1621
2189 ORF1ab L642F
1225
3037 ORF1ab silent
1551
5581 ORF1ab silent
3116
6468 ORF1ab T2068I
2123
9749 ORF1ab K3162E
2671
9867 ORF1ab L3201P
1844
9891 ORF1ab A3209V
2066
11804 ORF1ab V3847I
2690
12030 ORF1ab Q3922R
1510
14408 ORF1ab P314L
1534
19452 ORF1ab silent
2292
21801 S D80G
701
21991 S del 3
640
22032 S F157S
1182
22917 S L452R
1599
23403 S D614G
4675
24138 S T859N
1446
24410 S D950H
1640
25413 ORF3a silent
1444
25517 ORF3a P42L
947
25563 ORF3a Q57H
1285
25703 ORF3a P104L
2604
27260 ORF6 R20K
1552
27925 ORF8 T11I
1866
28044 ORF8 A51S
2736
28271 intergenic del 1
1750
28887 N T205I
548
28975 N M234I
600
VSP1581−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

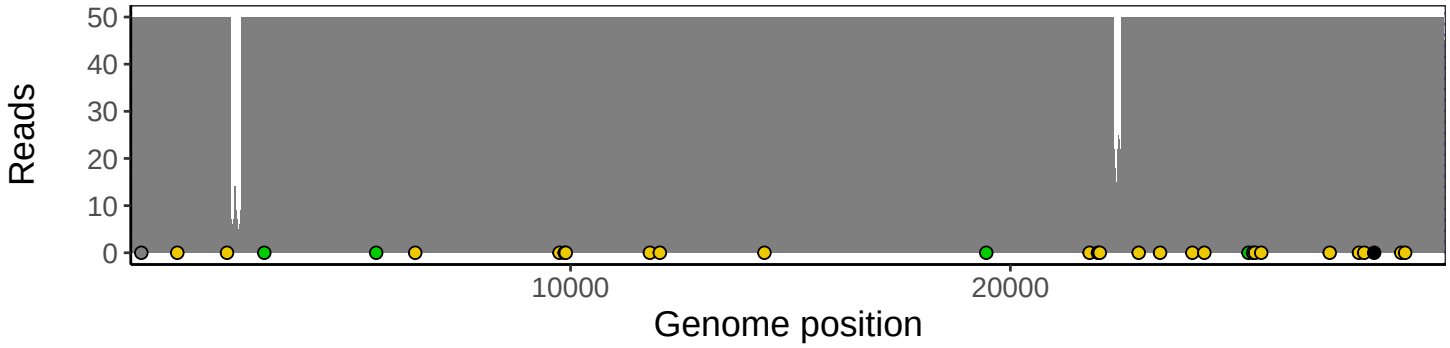
Analyses of individual experiments and composite results

VSP1581-1 | 2021-03-17 | NA | UPHS-0455 | genomes | single experiment

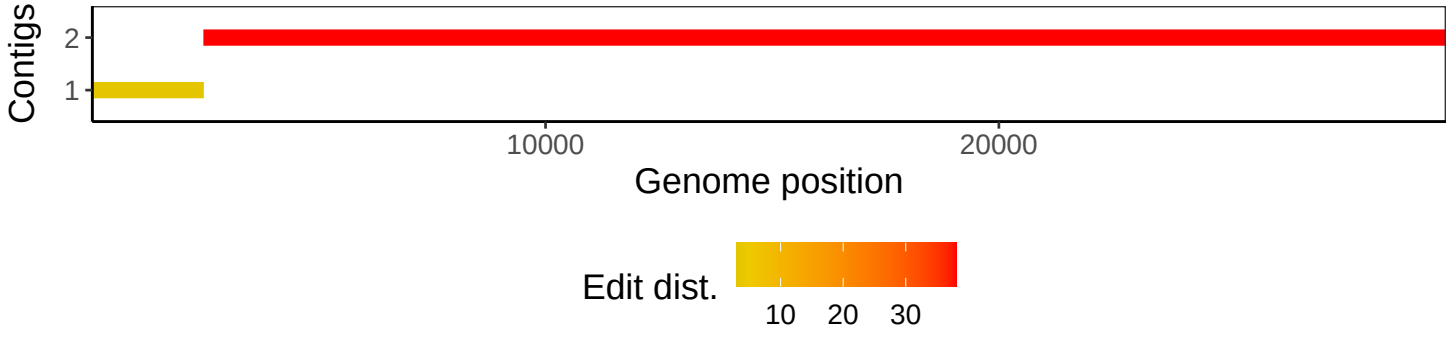
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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