COVID-19 subject UPHS-0506

2021-06-01

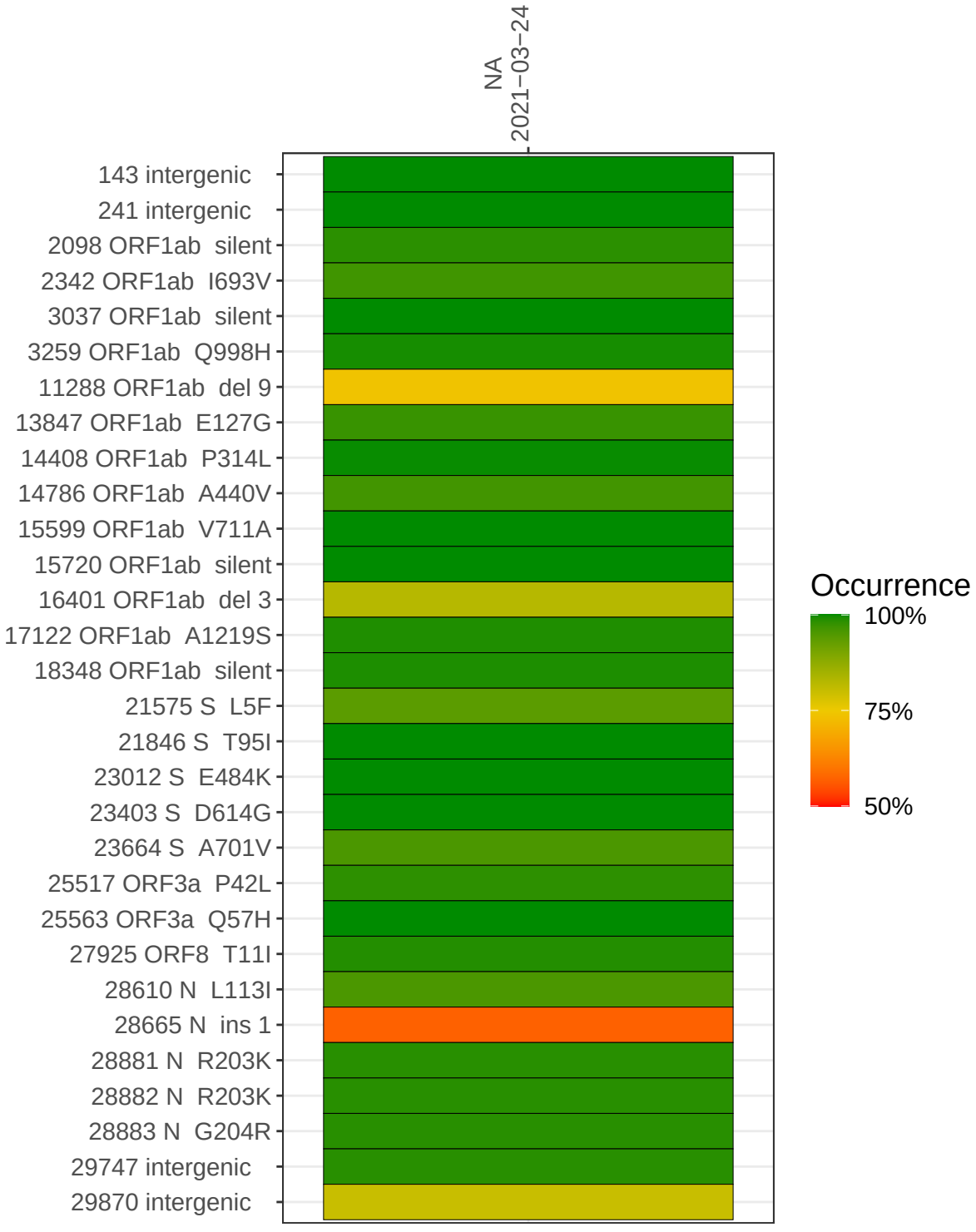
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

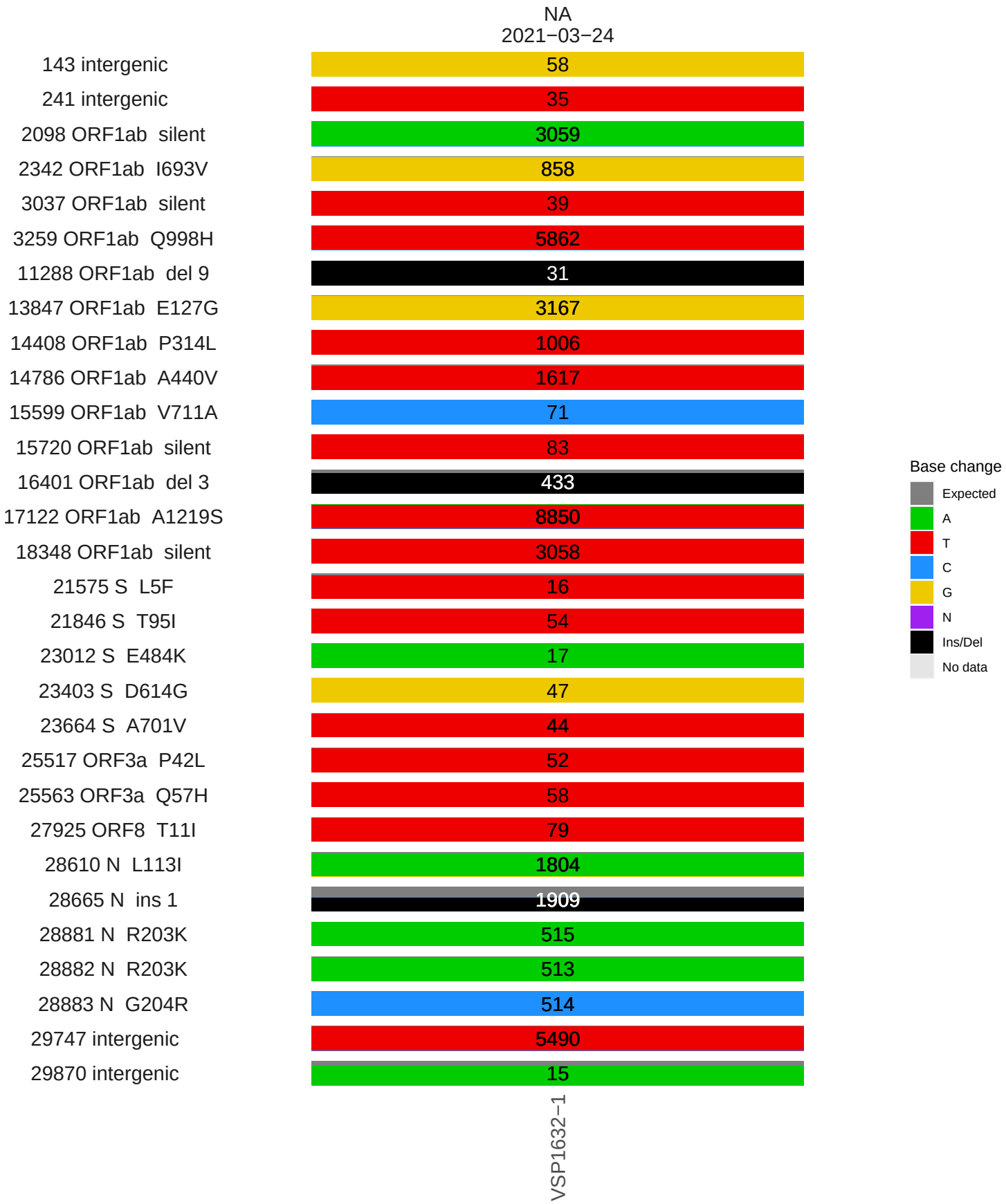
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1632-1	single experiment	NA	NA	2021-03-24	16.20	B.1.1.434	99.2%	98.8%

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.

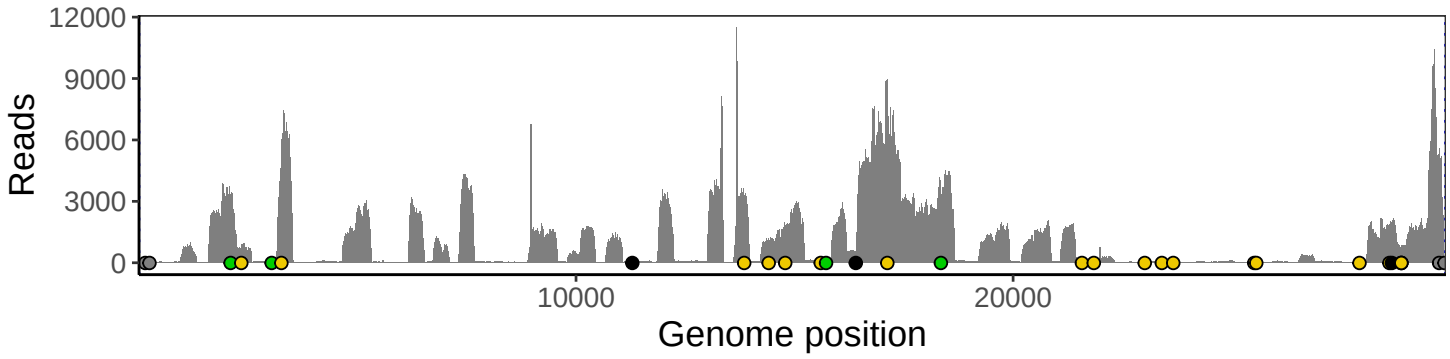



NA
2021−03−24
143 intergenic
241 intergenic
2098 ORF1ab silent
2342 ORF1ab I693V
3037 ORF1ab silent
3259 ORF1ab Q998H
11288 ORF1ab del 9
13847 ORF1ab E127G
14408 ORF1ab P314L
14786 ORF1ab A440V
15599 ORF1ab V711A
15720 ORF1ab silent
16401 ORF1ab del 3
17122 ORF1ab A1219S
18348 ORF1ab silent
21575 S L5F
21846 S T95I
23012 S E484K
23403 S D614G
23664 S A701V
25517 ORF3a P42L
25563 ORF3a Q57H
27925 ORF8 T11I
28610 N L113I
28665 N ins 1
28881 N R203K
28882 N R203K
28883 N G204R
29747 intergenic
29870 intergenic
58
35
3059
858
39
5862
31
3167
1006
1617
71
83
433
8850
3058
16
54
17
47
44
52
58
79
1804
1909
515
513
514
5490
15
VSP1632−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

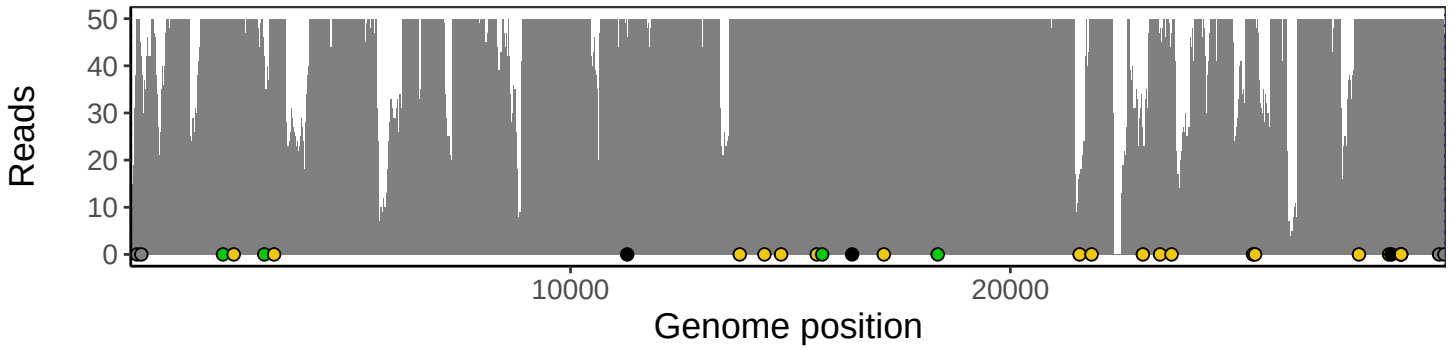
Analyses of individual experiments and composite results

VSP1632-1 | 2021-03-24 | NA | UPHS-0506 | genomes | single experiment

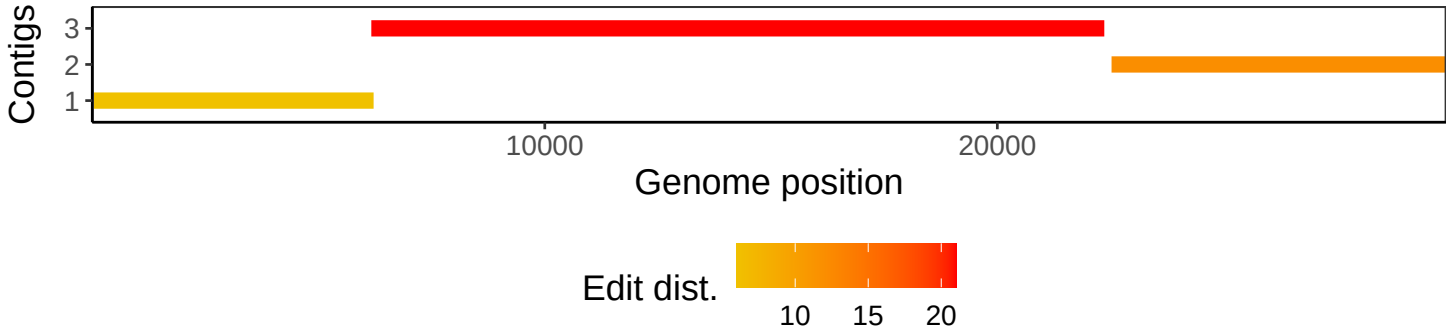
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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