COVID-19 subject UPHS-0584

2021-06-03

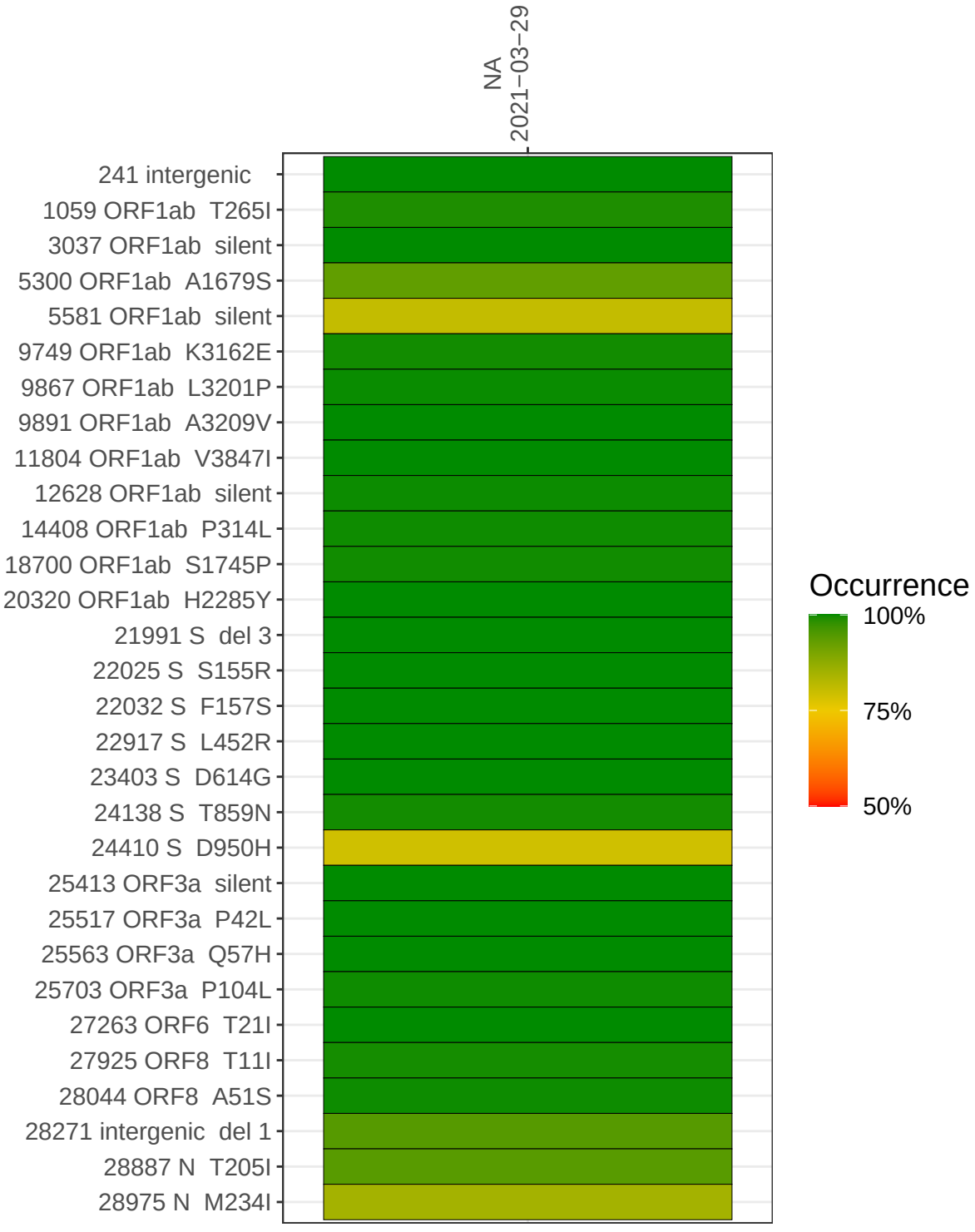
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

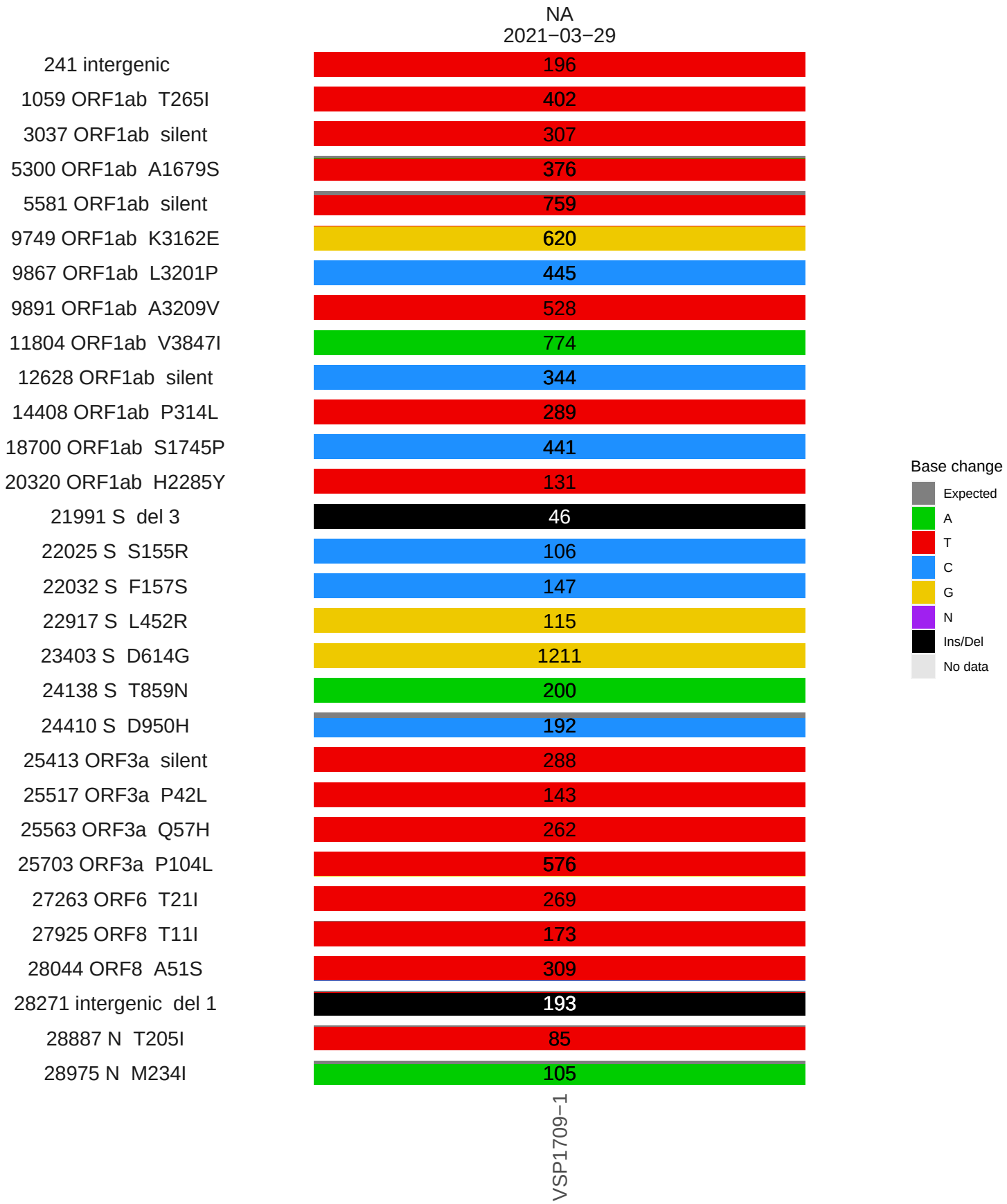
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1709-1	single experiment	NA	NA	2021-03-29	21.69	B.1	98.9%	98.9%

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.

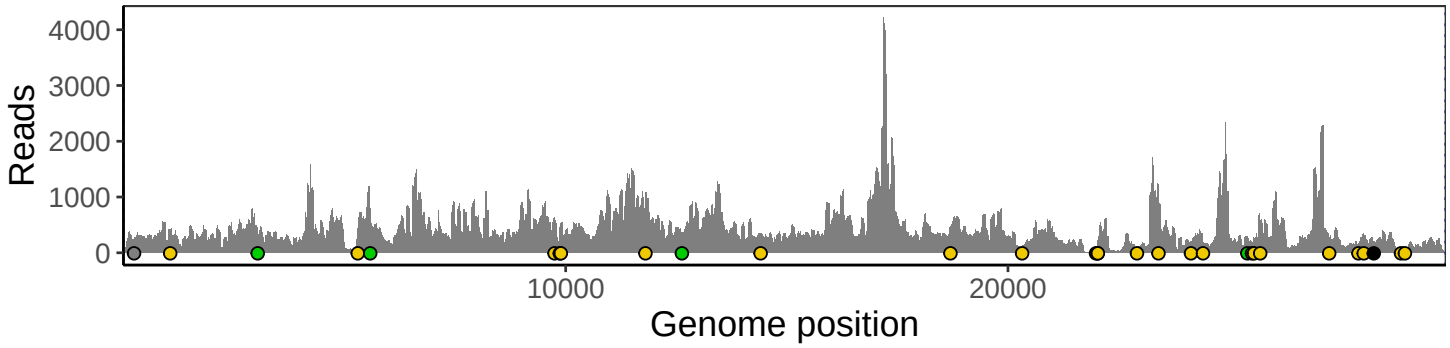



NA
2021−03−29
241 intergenic
196
1059 ORF1ab T265I
402
3037 ORF1ab silent
307
5300 ORF1ab A1679S
376
5581 ORF1ab silent
759
9749 ORF1ab K3162E
620
9867 ORF1ab L3201P
445
9891 ORF1ab A3209V
528
11804 ORF1ab V3847I
774
12628 ORF1ab silent
344
14408 ORF1ab P314L
289
18700 ORF1ab S1745P
441
20320 ORF1ab H2285Y
131
21991 S del 3
46
22025 S S155R
106
22032 S F157S
147
22917 S L452R
115
23403 S D614G
1211
24138 S T859N
200
24410 S D950H
192
25413 ORF3a silent
288
25517 ORF3a P42L
143
25563 ORF3a Q57H
262
25703 ORF3a P104L
576
27263 ORF6 T21I
269
27925 ORF8 T11I
173
28044 ORF8 A51S
309
28271 intergenic del 1
193
28887 N T205I
85
28975 N M234I
105
VSP1709−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

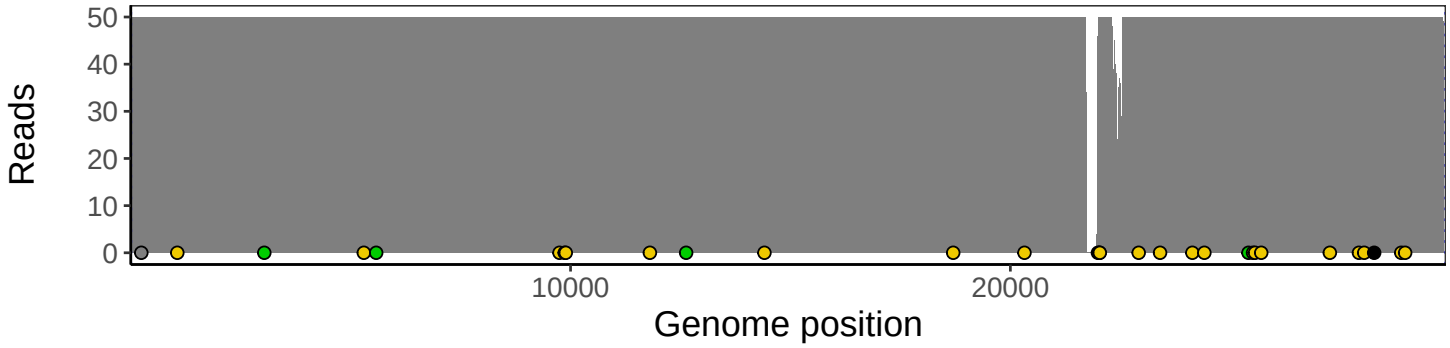
Analyses of individual experiments and composite results

VSP1709-1 | 2021-03-29 | NA | UPHS-0584 | genomes | single experiment

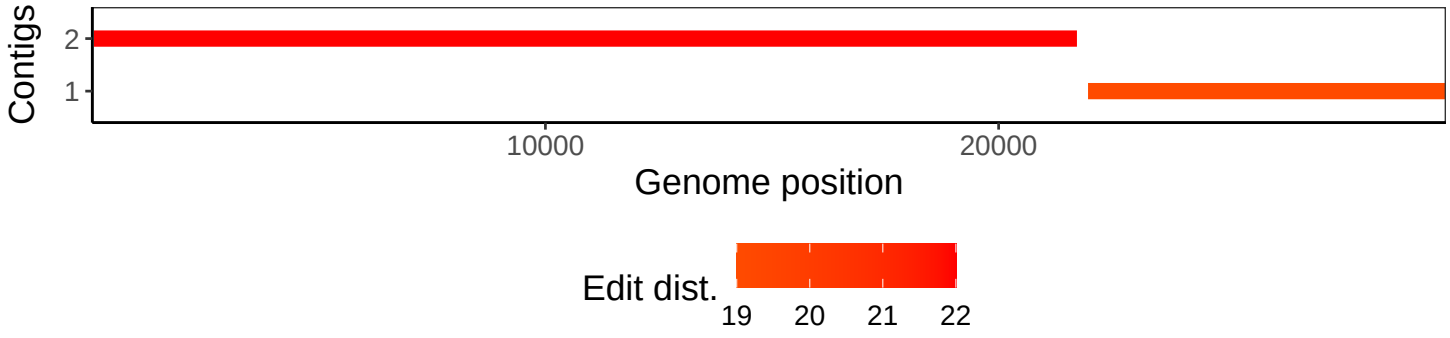
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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