COVID-19 subject UPHS-0475

2021-06-01

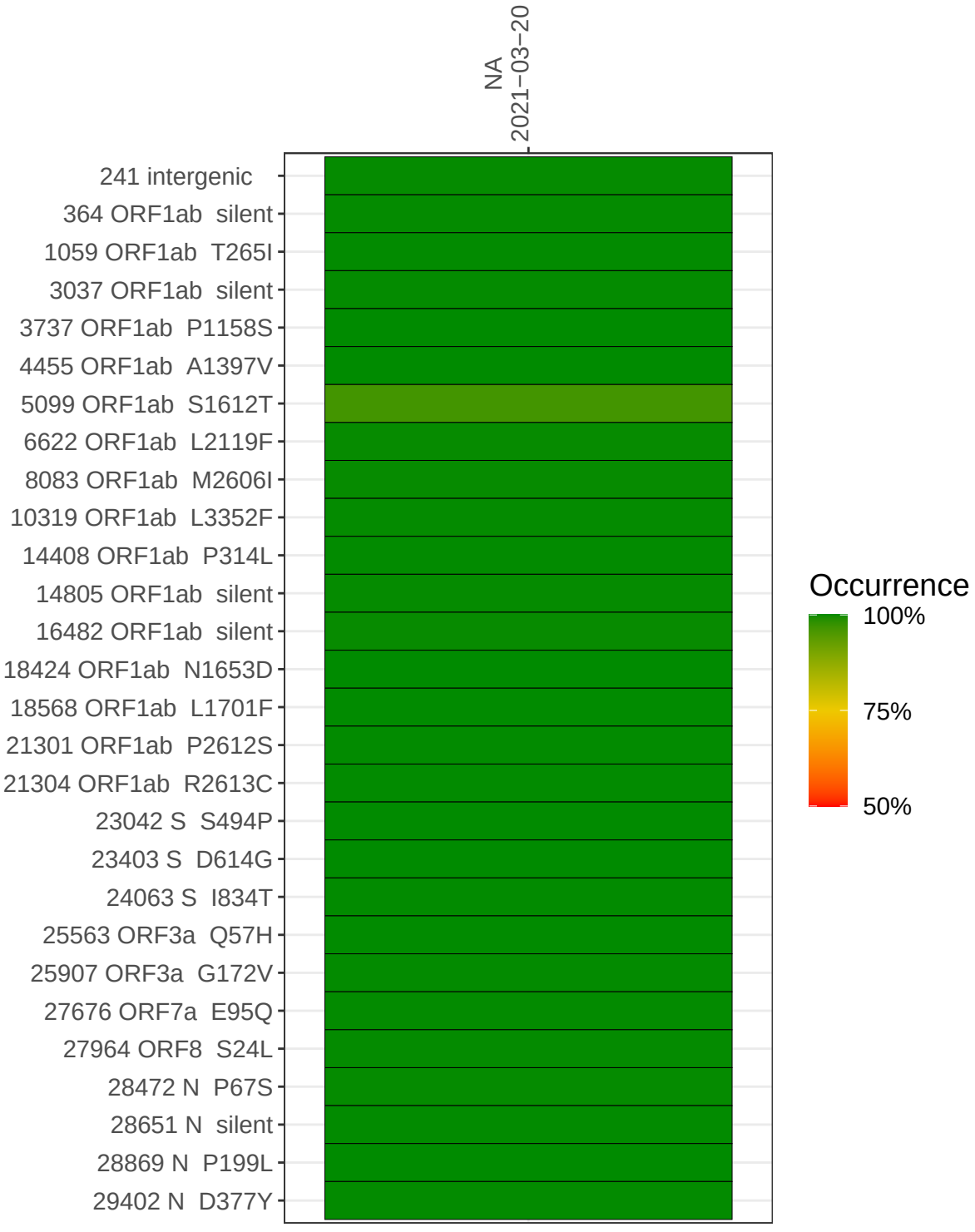
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

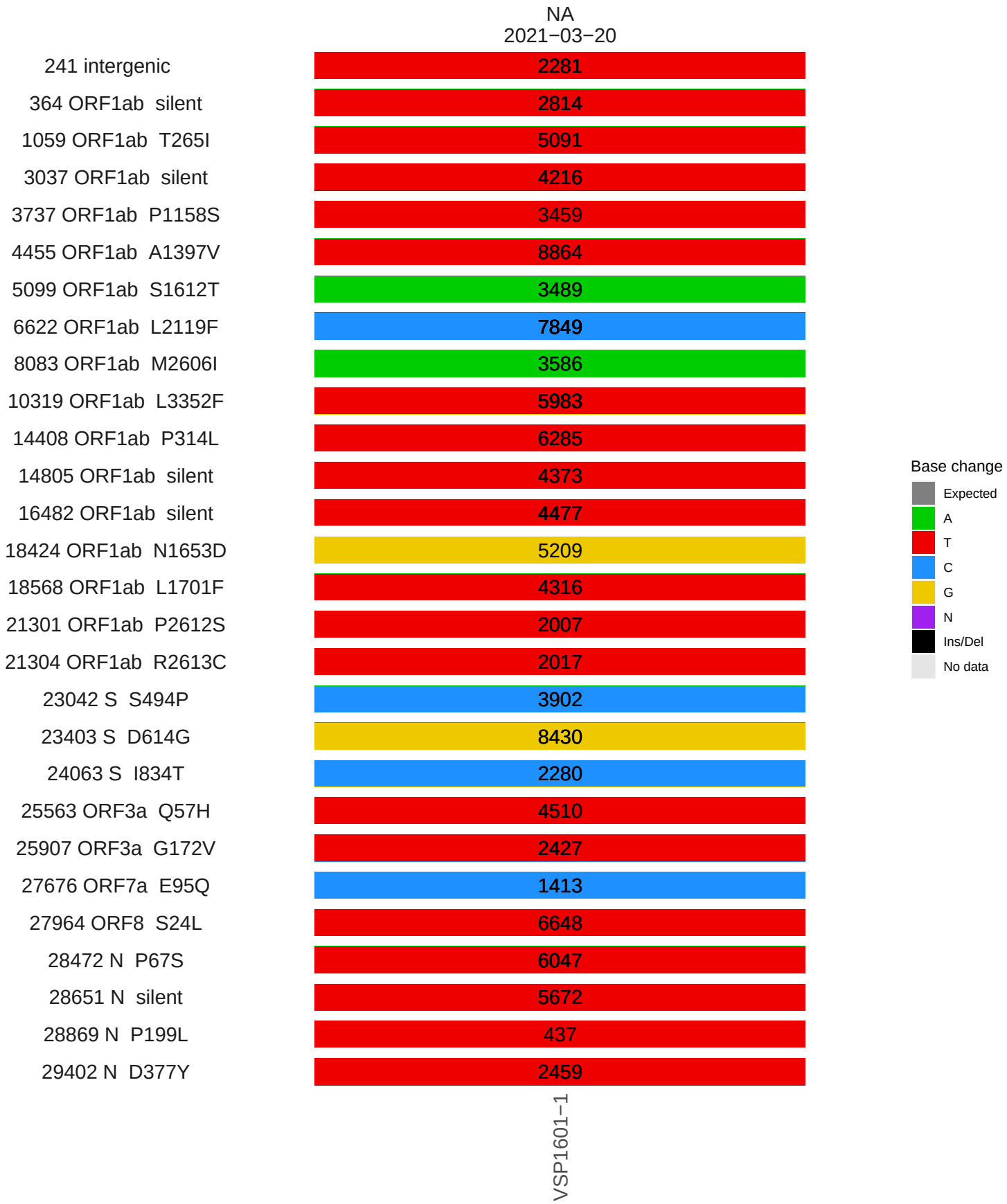
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1601-1	single experiment	NA	NA	2021-03-20	29.90	B.1.2	100.0%	99.8%

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.

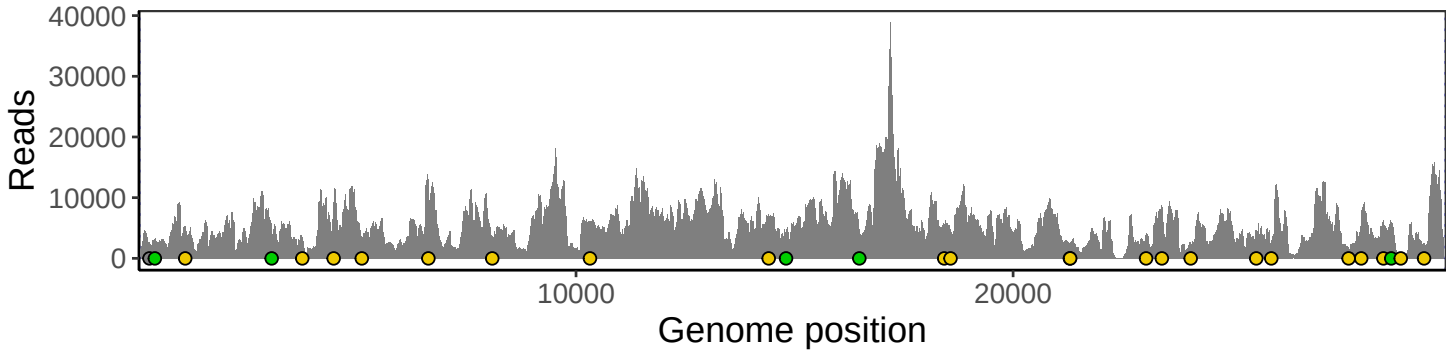



NA
2021−03−20
241 intergenic
2281
364 ORF1ab silent
2814
1059 ORF1ab T265I
5091
3037 ORF1ab silent
4216
3737 ORF1ab P1158S
3459
4455 ORF1ab A1397V
8864
5099 ORF1ab S1612T
3489
6622 ORF1ab L2119F
7849
8083 ORF1ab M2606I
3586
10319 ORF1ab L3352F
5983
14408 ORF1ab P314L
6285
14805 ORF1ab silent
4373
16482 ORF1ab silent
4477
18424 ORF1ab N1653D
5209
18568 ORF1ab L1701F
4316
21301 ORF1ab P2612S
2007
21304 ORF1ab R2613C
2017
23042 S S494P
3902
23403 S D614G
8430
24063 S I834T
2280
25563 ORF3a Q57H
4510
25907 ORF3a G172V
2427
27676 ORF7a E95Q
1413
27964 ORF8 S24L
6648
28472 N P67S
6047
28651 N silent
5672
28869 N P199L
437
29402 N D377Y
2459
VSP1601−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

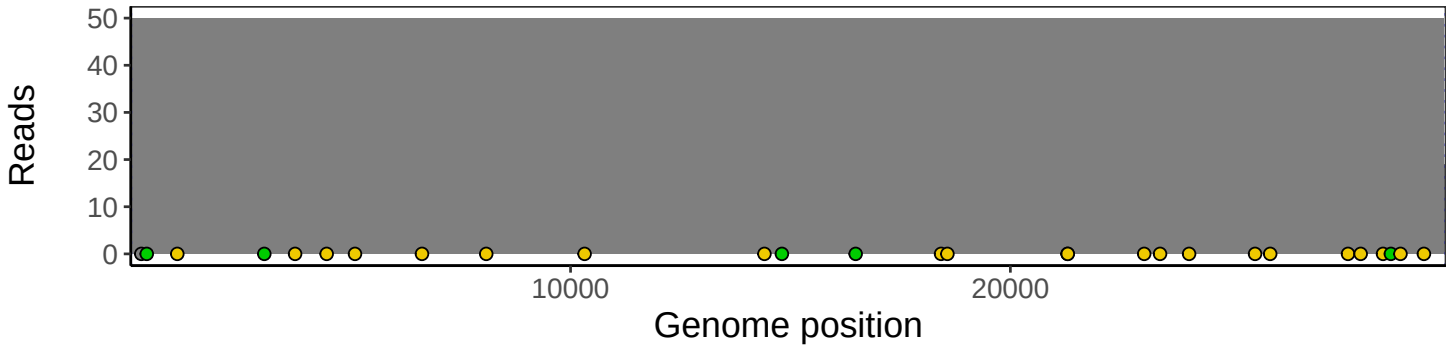
Analyses of individual experiments and composite results

VSP1601-1 | 2021-03-20 | NA | UPHS-0475 | genomes | single experiment

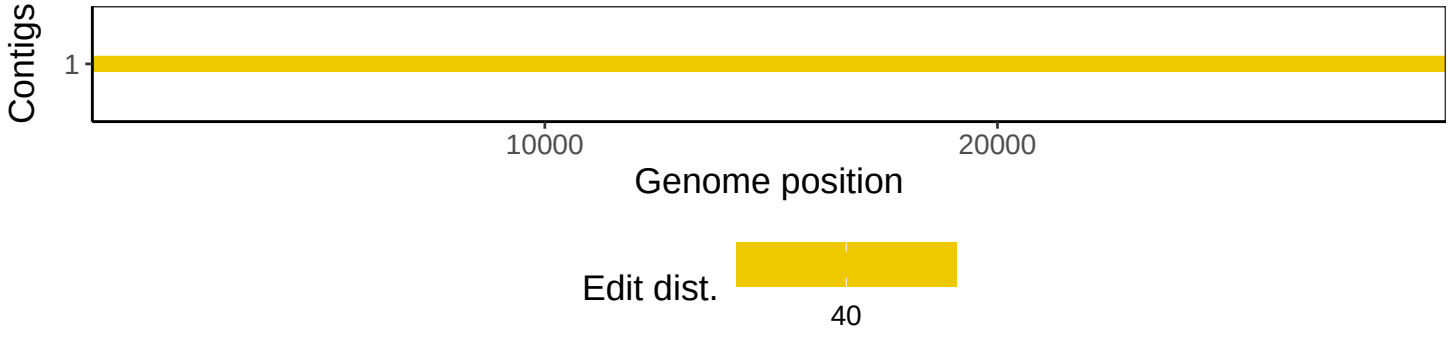
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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