COVID-19 subject UPHS-1074

2021-06-23

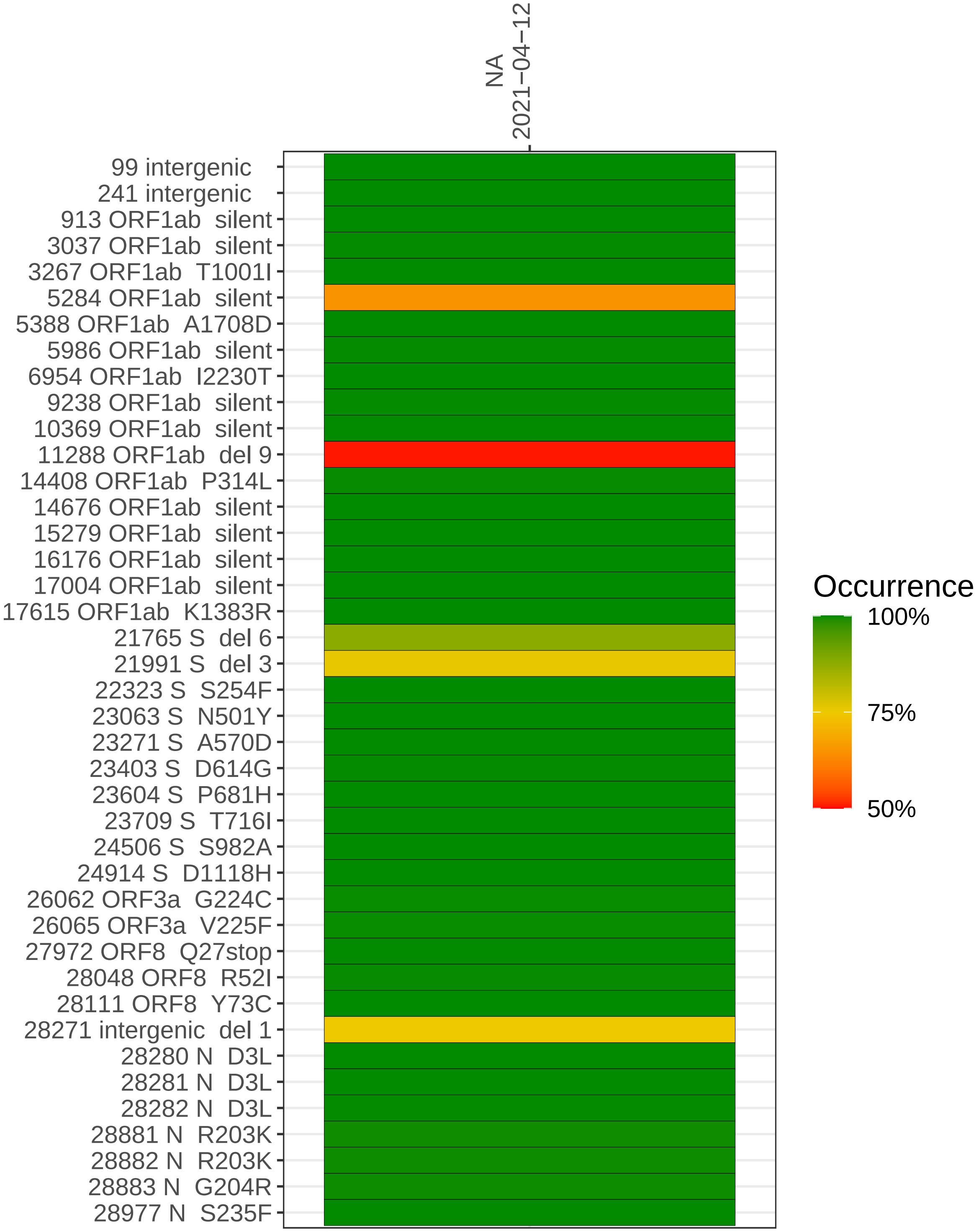
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

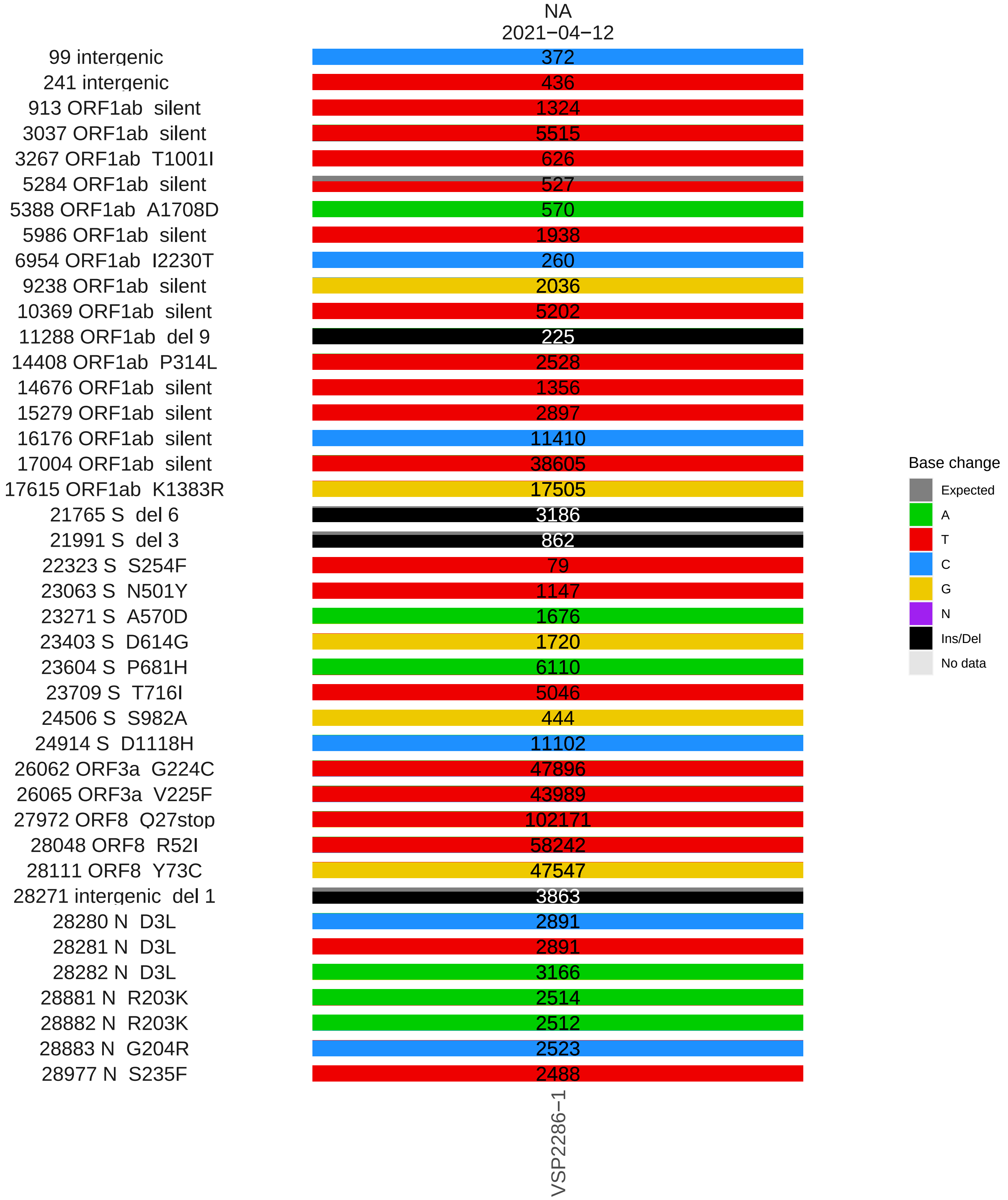
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2286-1	single experiment	NA	NA	2021-04-12	29.81	B.1.1.7	99.7%	99.7%

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.

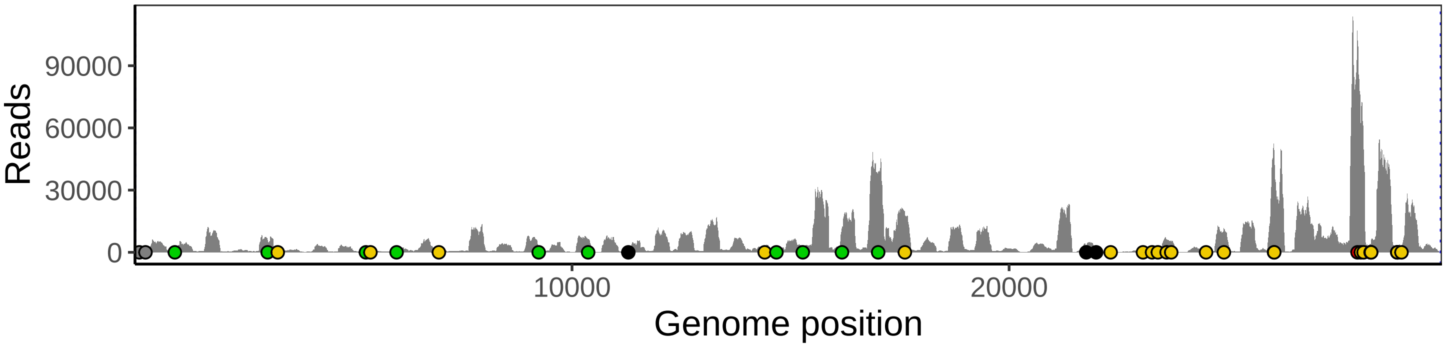



NA
2021−04−12
99 intergenic
372
241 intergenic
436
913 ORF1ab silent
1324
3037 ORF1ab silent
5515
3267 ORF1ab T1001I
626
5284 ORF1ab silent
527
5388 ORF1ab A1708D
570
5986 ORF1ab silent
1938
6954 ORF1ab I2230T
260
9238 ORF1ab silent
2036
10369 ORF1ab silent
5202
11288 ORF1ab del 9
225
14408 ORF1ab P314L
2528
14676 ORF1ab silent
1356
15279 ORF1ab silent
2897
16176 ORF1ab silent
11410
17004 ORF1ab silent
38605
17615 ORF1ab K1383R
17505
21765 S del 6
3186
21991 S del 3
862
22323 S S254F
79
23063 S N501Y
1147
23271 S A570D
1676
23403 S D614G
1720
23604 S P681H
6110
23709 S T716I
5046
24506 S S982A
444
24914 S D1118H
11102
26062 ORF3a G224C
47896
26065 ORF3a V225F
43989
27972 ORF8 Q27stop
102171
28048 ORF8 R52I
58242
28111 ORF8 Y73C
47547
28271 intergenic del 1
3863
28280 N D3L
2891
28281 N D3L
2891
28282 N D3L
3166
28881 N R203K
2514
28882 N R203K
2512
28883 N G204R
2523
28977 N S235F
2488
VSP2286−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

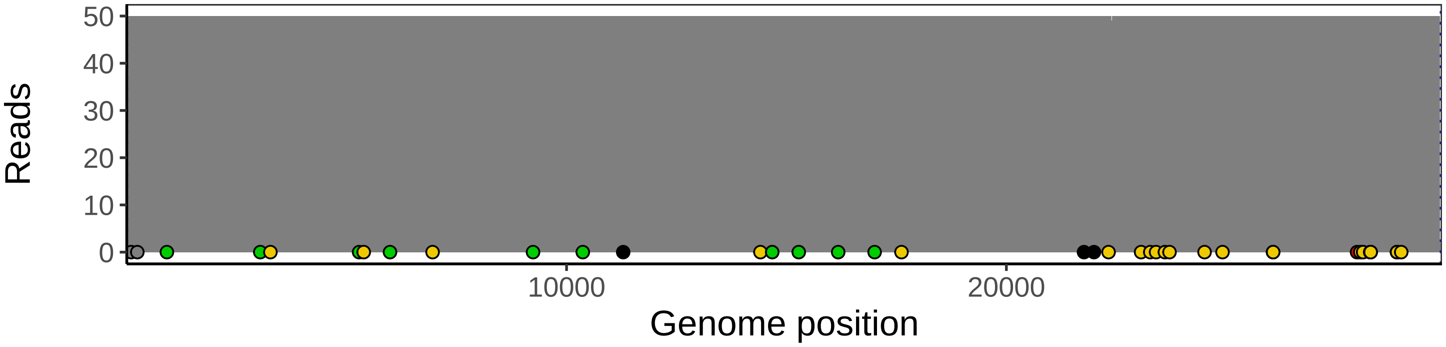
Analyses of individual experiments and composite results

VSP2286-1 | 2021-04-12 | NA | UPHS-1074 | genomes | single experiment

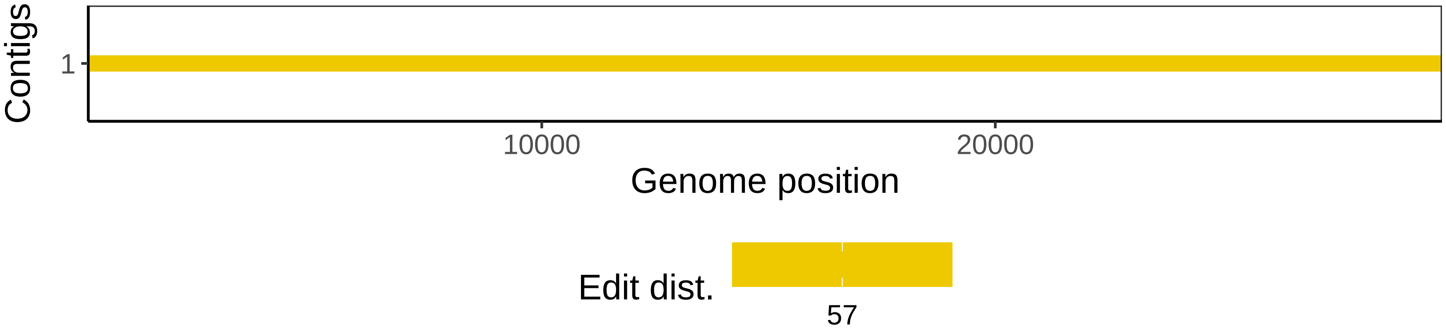
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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