COVID-19 subject UPHS-1079

2021-05-10

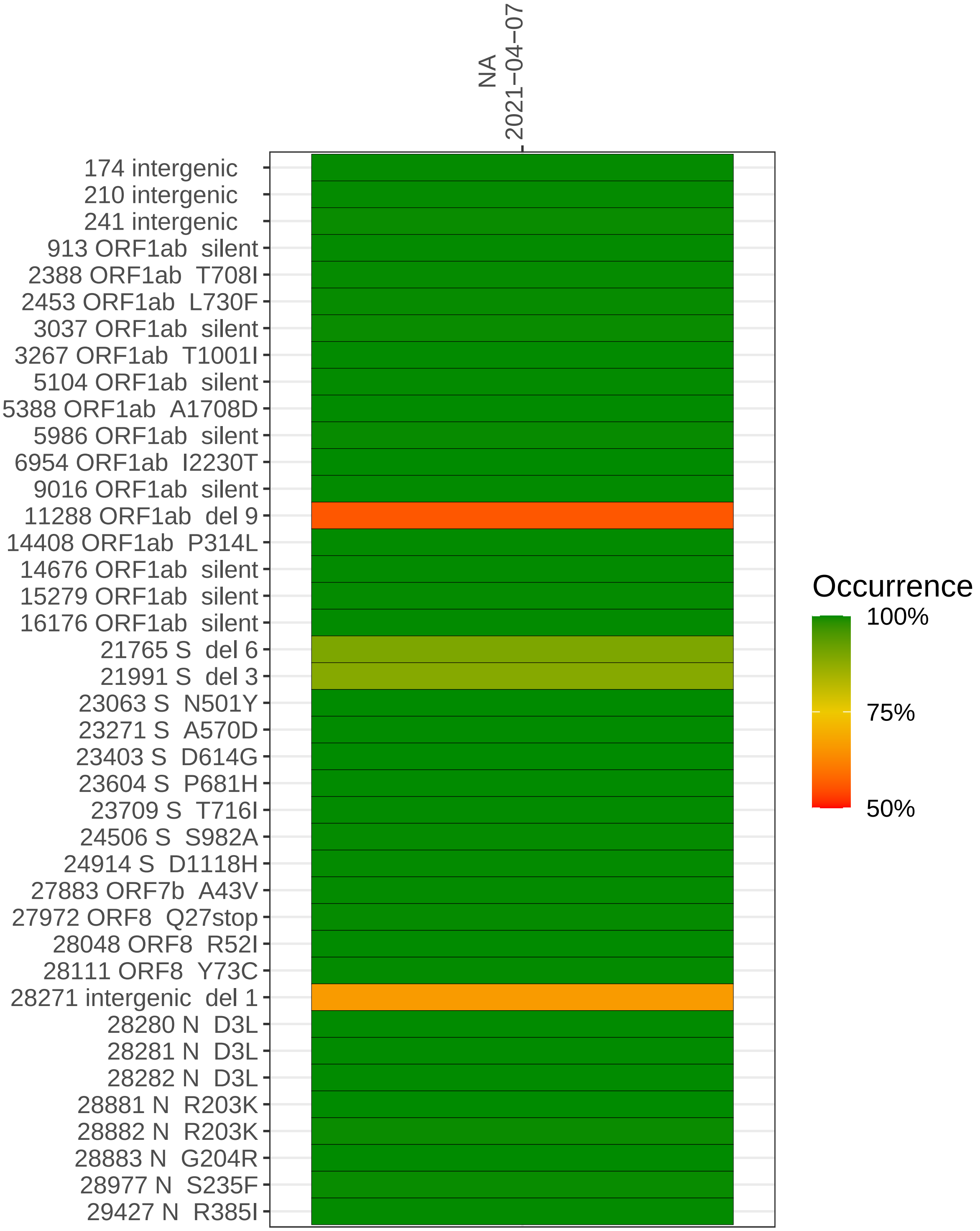
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

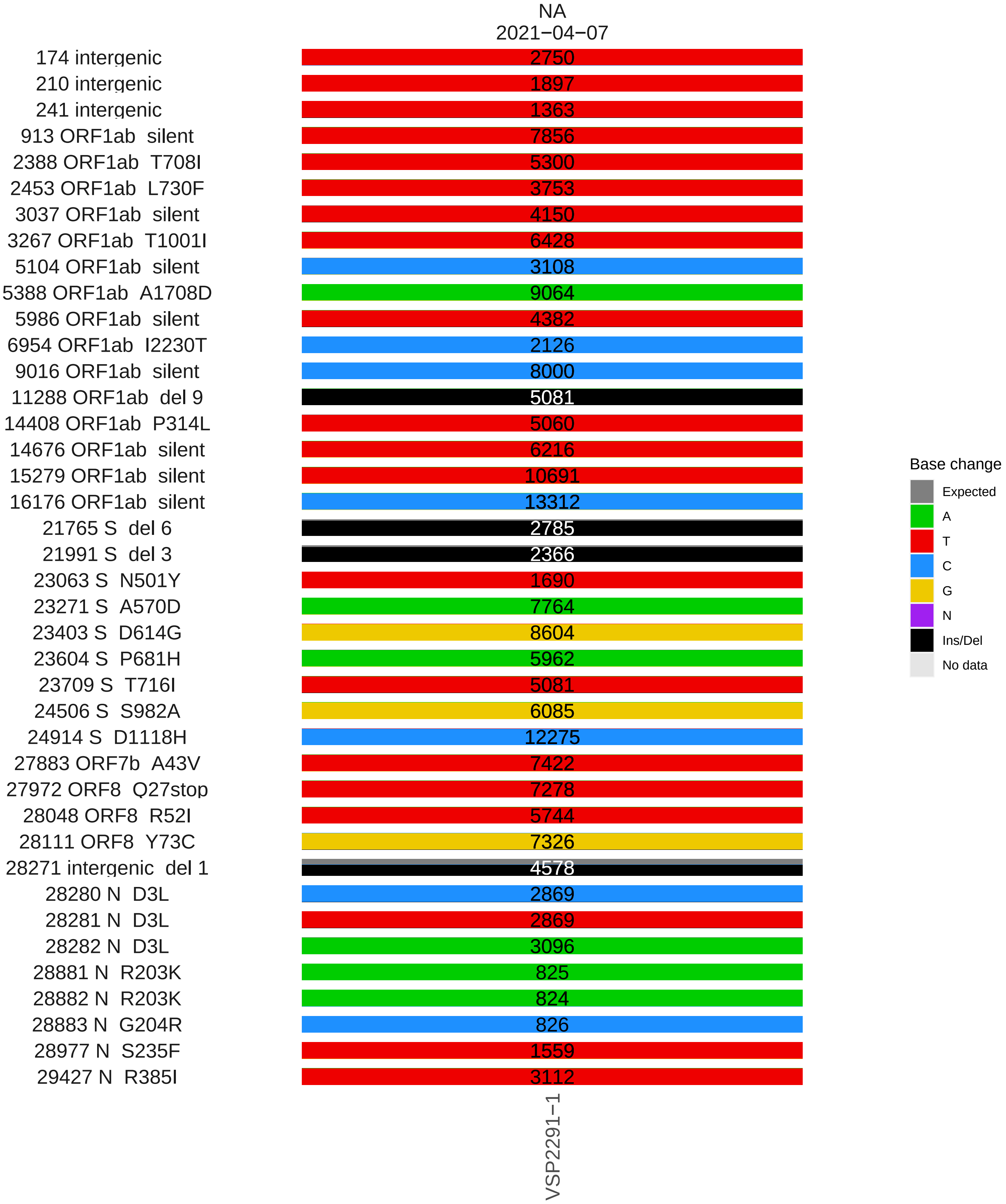
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2291-1	single experiment	NA	NA	2021-04-07	29.82	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

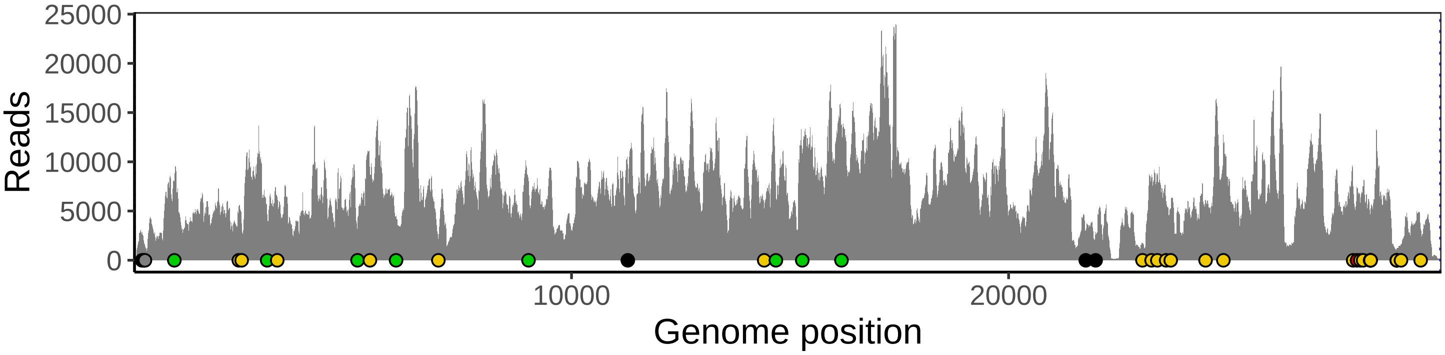



NA
2021−04−07
174 intergenic
2750
210 intergenic
1897
241 intergenic
1363
913 ORF1ab silent
7856
2388 ORF1ab T708I
5300
2453 ORF1ab L730F
3753
3037 ORF1ab silent
4150
3267 ORF1ab T1001I
6428
5104 ORF1ab silent
3108
5388 ORF1ab A1708D
9064
5986 ORF1ab silent
4382
6954 ORF1ab I2230T
2126
9016 ORF1ab silent
8000
11288 ORF1ab del 9
5081
14408 ORF1ab P314L
5060
14676 ORF1ab silent
6216
15279 ORF1ab silent
10691
16176 ORF1ab silent
13312
21765 S del 6
2785
21991 S del 3
2366
23063 S N501Y
1690
23271 S A570D
7764
23403 S D614G
8604
23604 S P681H
5962
23709 S T716I
5081
24506 S S982A
6085
24914 S D1118H
12275
27883 ORF7b A43V
7422
27972 ORF8 Q27stop
7278
28048 ORF8 R52I
5744
28111 ORF8 Y73C
7326
28271 intergenic del 1
4578
28280 N D3L
2869
28281 N D3L
2869
28282 N D3L
3096
28881 N R203K
825
28882 N R203K
824
28883 N G204R
826
28977 N S235F
1559
29427 N R385I
3112
VSP2291−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

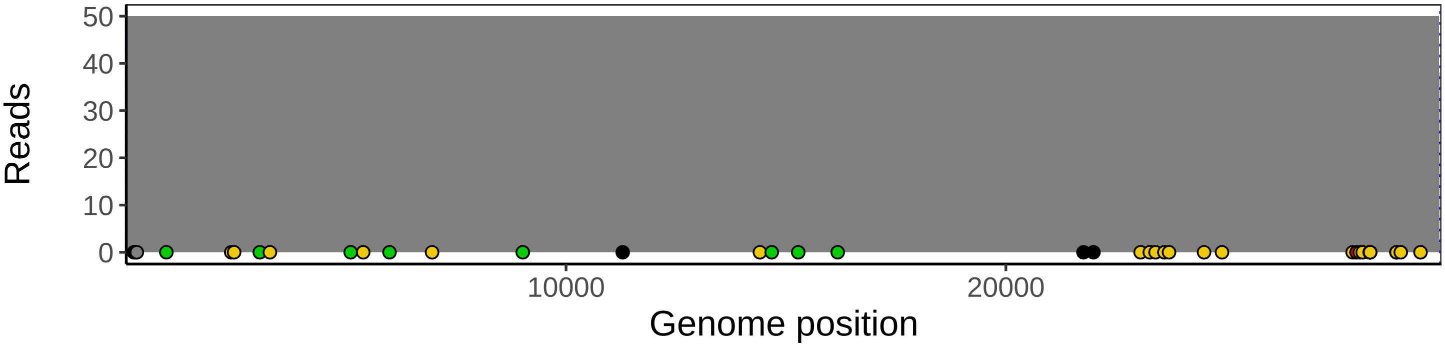
Analyses of individual experiments and composite results

VSP2291-1 | 2021-04-07 | NA | UPHS-1079 | genomes | single experiment

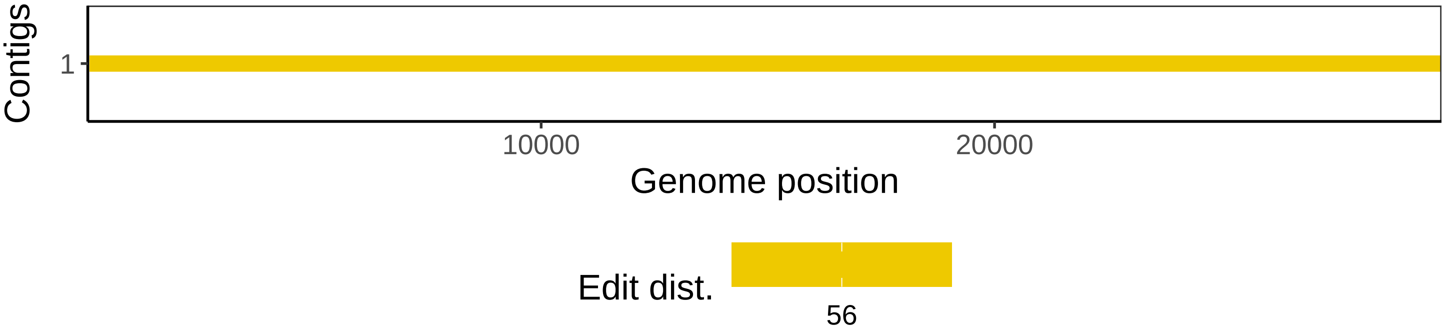
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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