COVID-19 subject UPHS-1165

2021-06-23

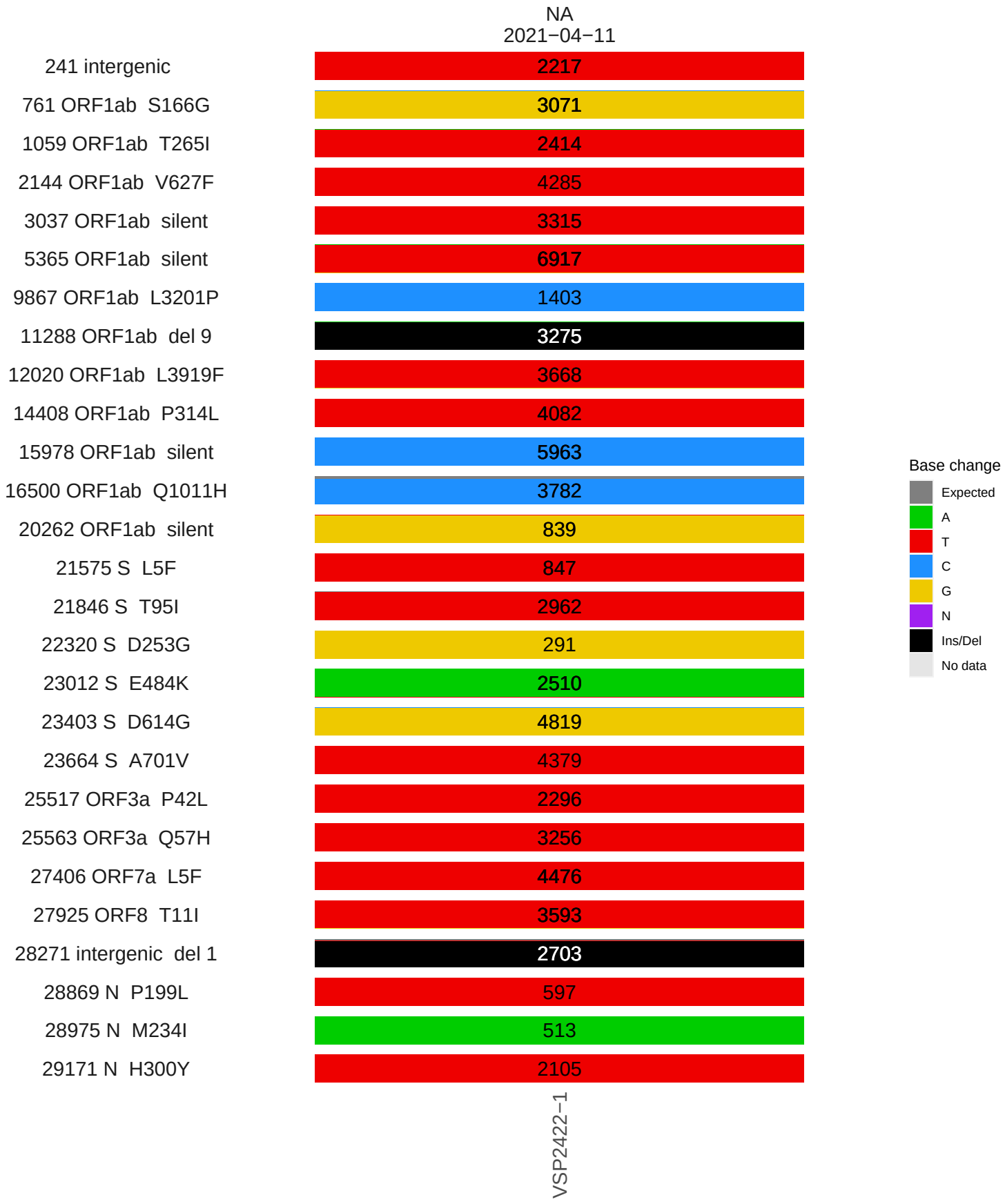
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2422-1	single experiment	NA	NA	2021-04-11	29.92	B.1.526	99.8%	99.7%

Variants shared across samples

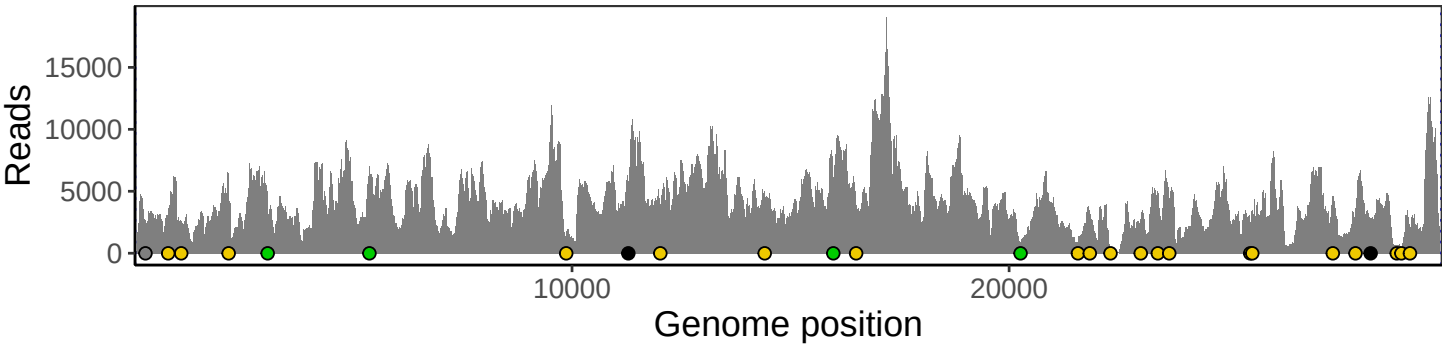
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of read pairs 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
2021−04−11
241 intergenic
2217
761 ORF1ab S166G
3071
1059 ORF1ab T265I
2414
2144 ORF1ab V627F
4285
3037 ORF1ab silent
3315
5365 ORF1ab silent
6917
9867 ORF1ab L3201P
1403
11288 ORF1ab del 9
3275
12020 ORF1ab L3919F
3668
14408 ORF1ab P314L
4082
15978 ORF1ab silent
5963
16500 ORF1ab Q1011H
3782
20262 ORF1ab silent
839
21575 S L5F
847
21846 S T95I
2962
22320 S D253G
291
23012 S E484K
2510
23403 S D614G
4819
23664 S A701V
4379
25517 ORF3a P42L
2296
25563 ORF3a Q57H
3256
27406 ORF7a L5F
4476
27925 ORF8 T11I
3593
28271 intergenic del 1
2703
28869 N P199L
597
28975 N M234I
513
29171 N H300Y
2105
VSP2422−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

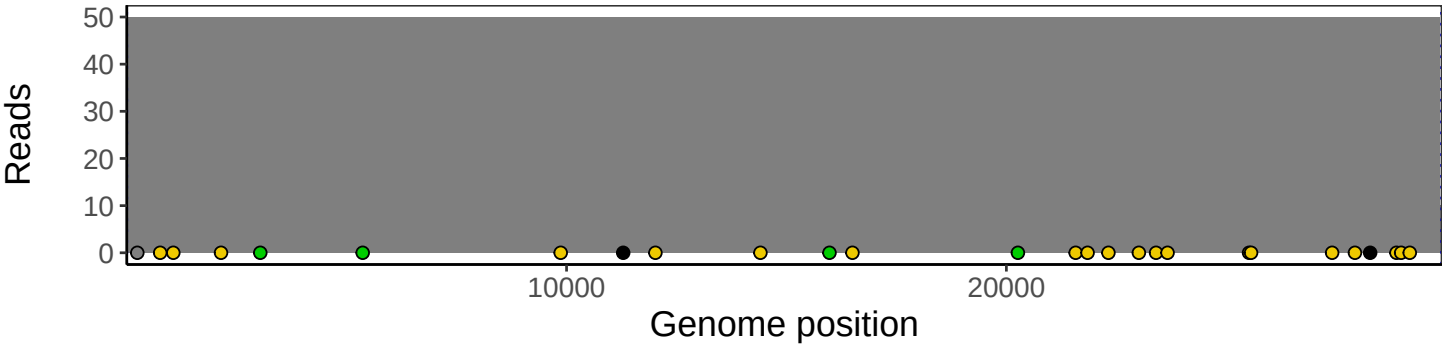
Analyses of individual experiments and composite results

VSP2422-1 | 2021-04-11 | NA | UPHS-1165 | genomes | single experiment

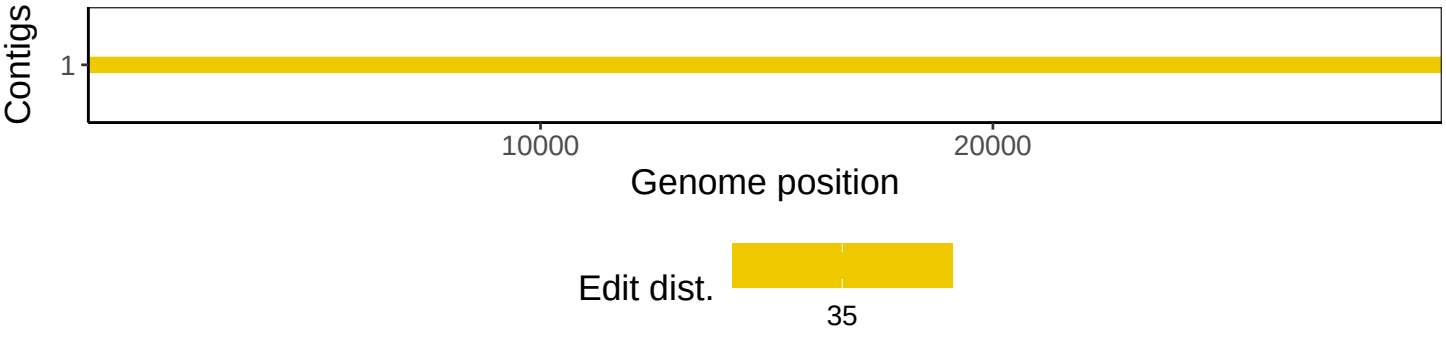
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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