COVID-19 subject AHVYTNAFX2-1

2021-06-23

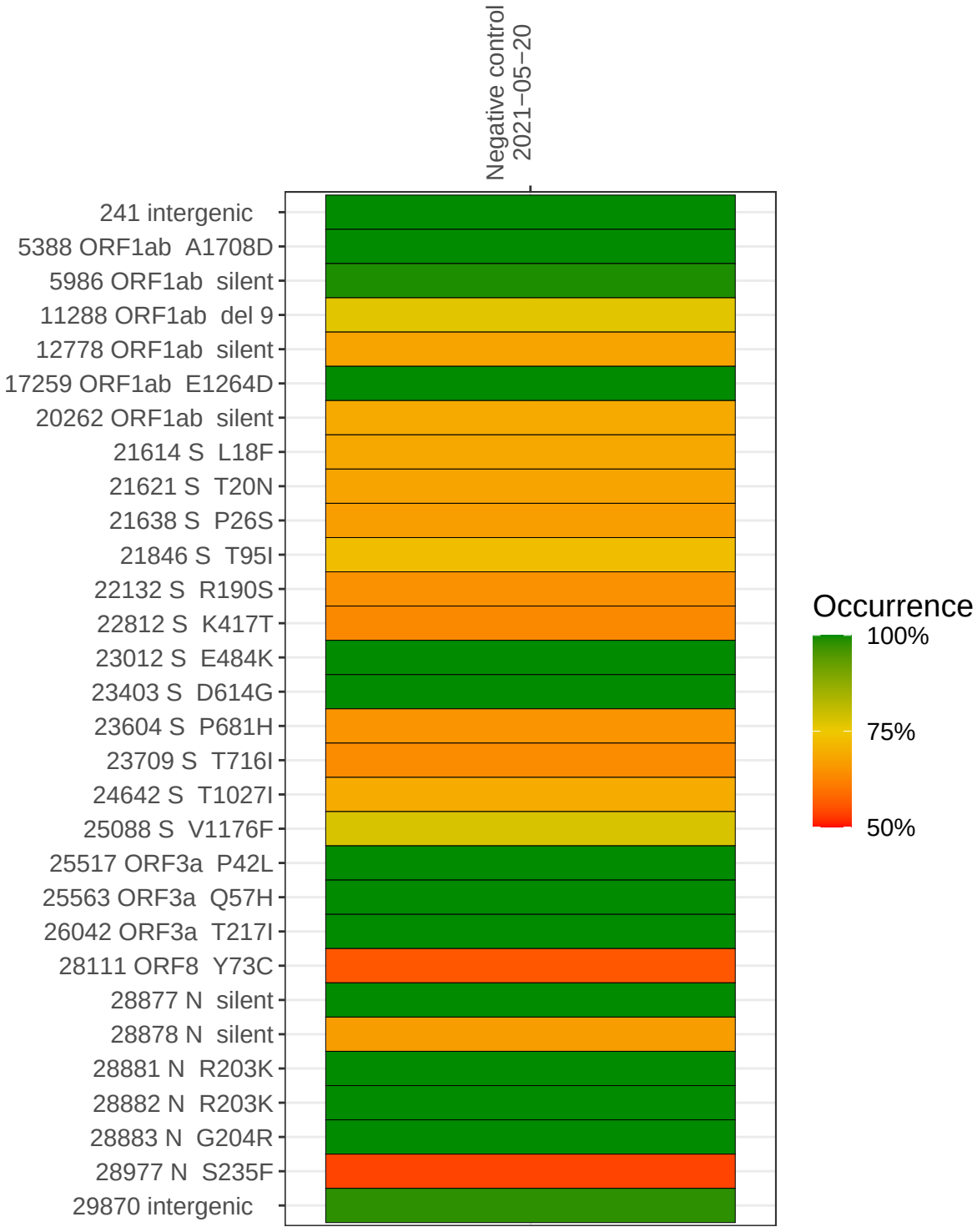
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

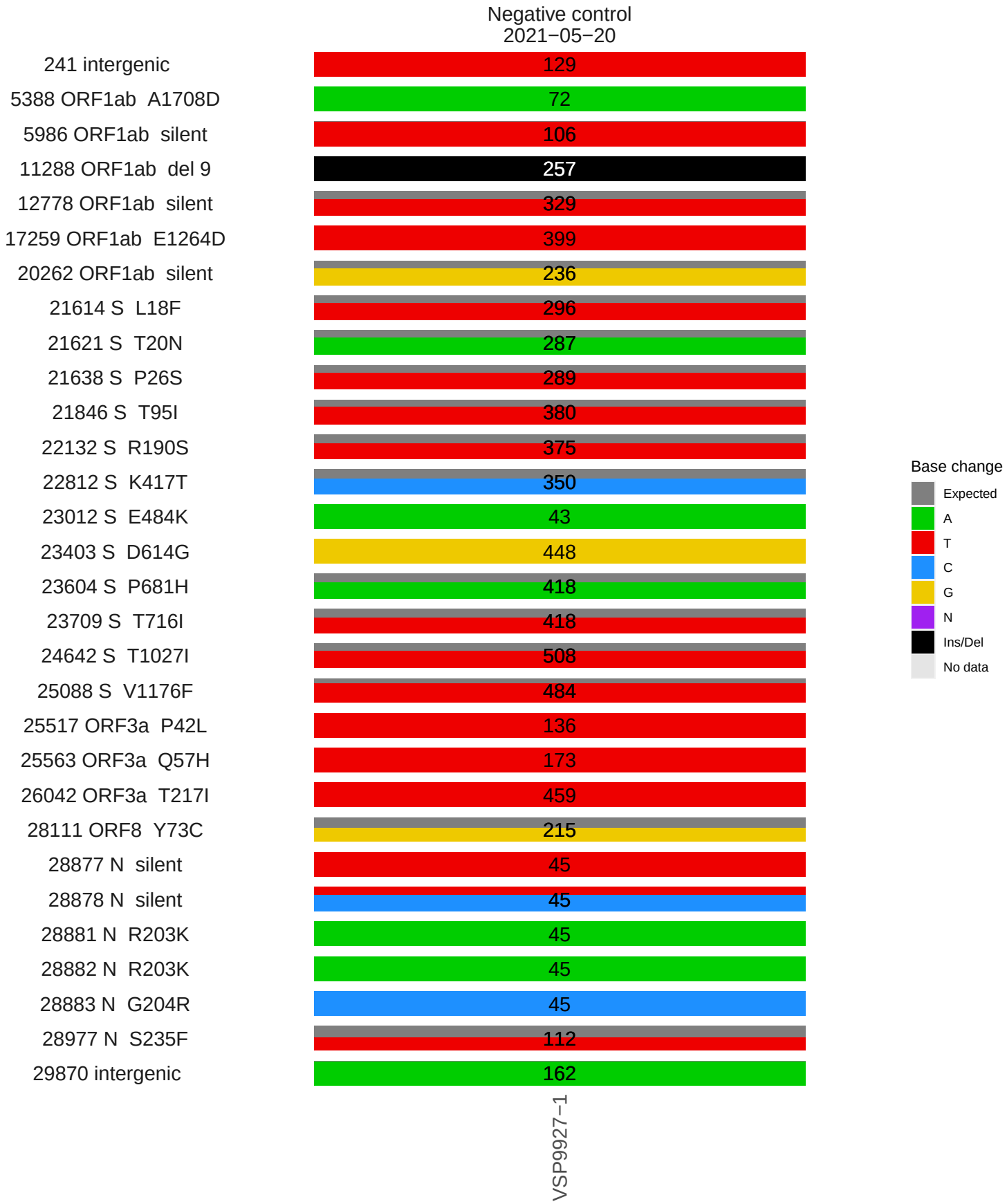
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP9927-1	single experiment	NA	Negative control	2021-05-20	4.11	NA	74.7%	73.2%

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.

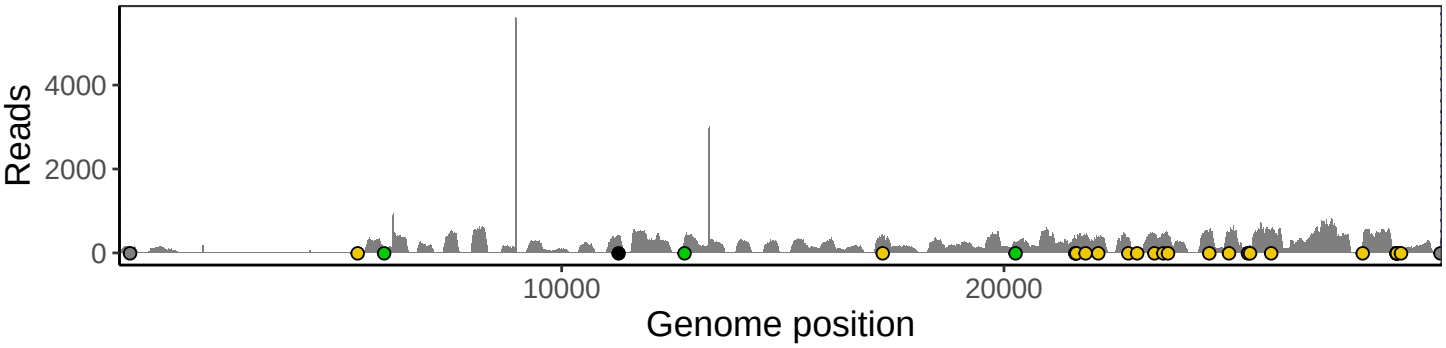



Negative control
2021−05−20
241 intergenic
5388 ORF1ab A1708D
5986 ORF1ab silent
11288 ORF1ab del 9
12778 ORF1ab silent
17259 ORF1ab E1264D
20262 ORF1ab silent
21614 S L18F
21621 S T20N
21638 S P26S
21846 S T95I
22132 S R190S
22812 S K417T
23012 S E484K
23403 S D614G
23604 S P681H
23709 S T716I
24642 S T1027I
25088 S V1176F
25517 ORF3a P42L
25563 ORF3a Q57H
26042 ORF3a T217I
28111 ORF8 Y73C
28877 N silent
28878 N silent
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29870 intergenic
129
72
106
257
329
399
236
296
287
289
380
375
350
43
448
418
418
508
484
136
173
459
215
45
45
45
45
45
112
162
VSP9927−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

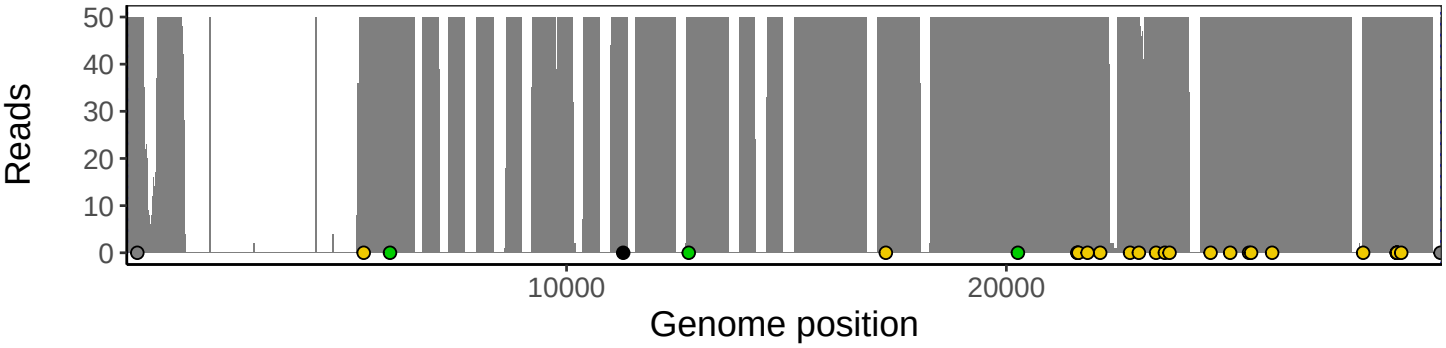
Analyses of individual experiments and composite results

VSP9927-1 | 2021-05-20 | Negative control | AHVYTNAFX2-1 | genomes | single experiment

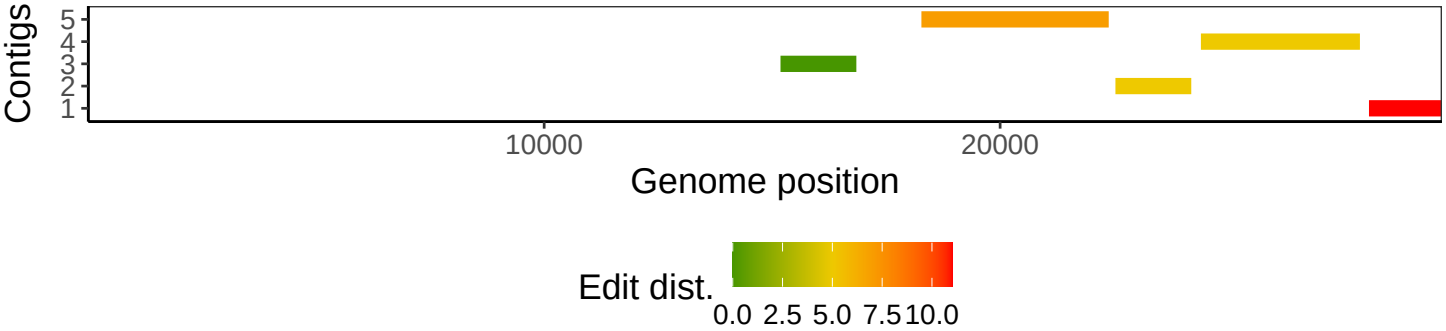
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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