COVID-19 subject AHTMV3AFX4

2021-03-29

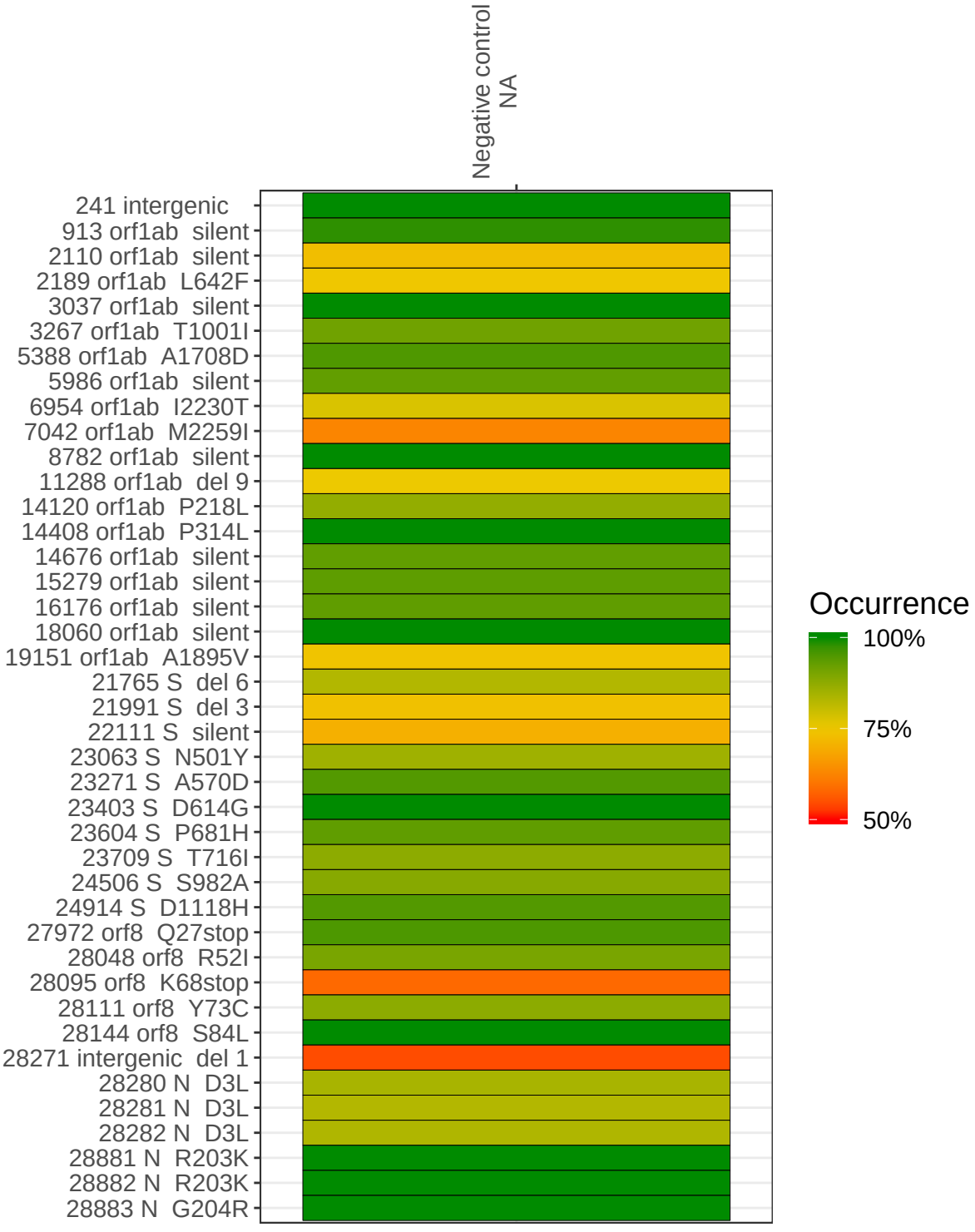
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

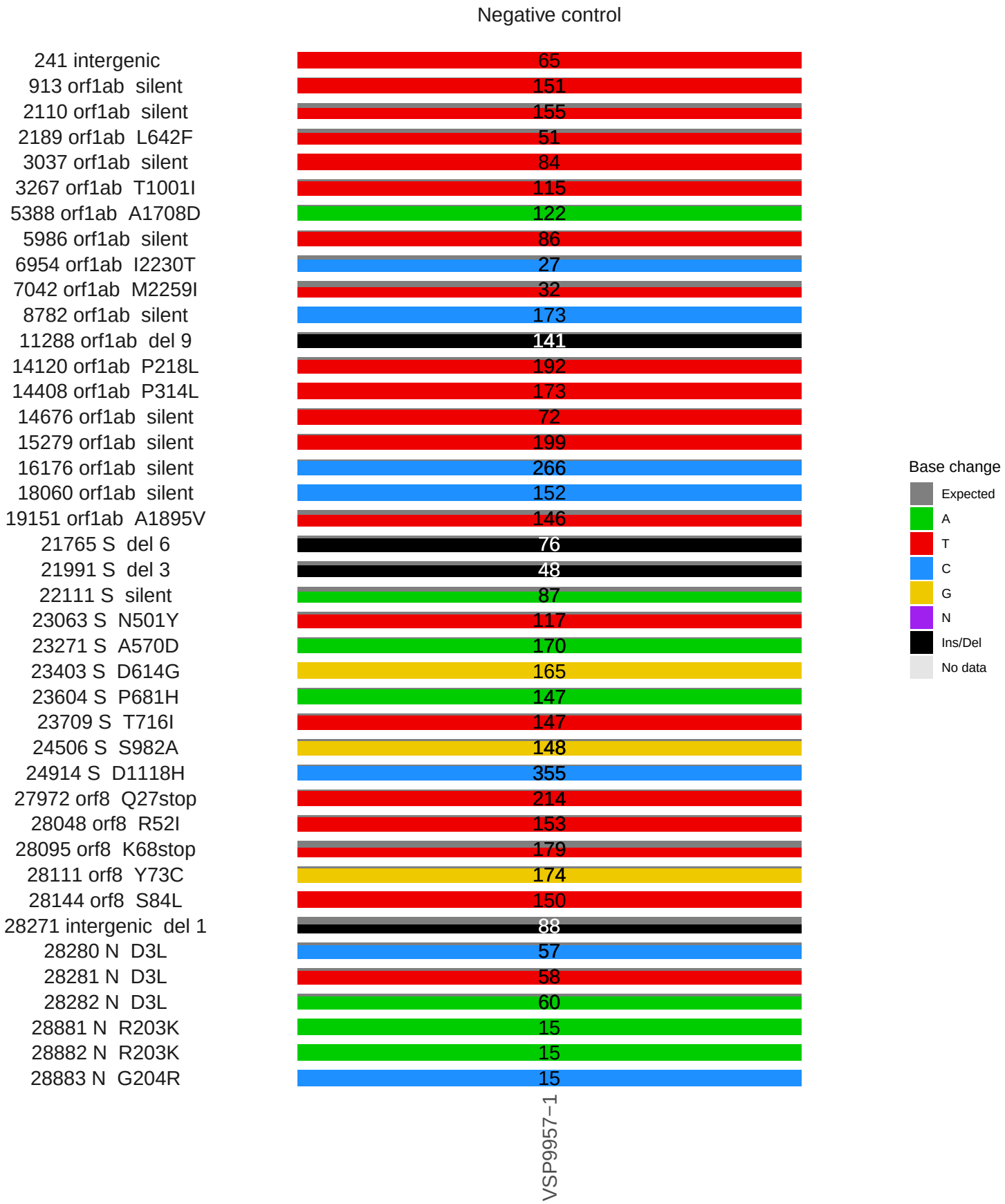
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP9957-1	single experiment	NA	Negative control	NA	22.28	B.1.1.7	99.2%	99.1%

Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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.

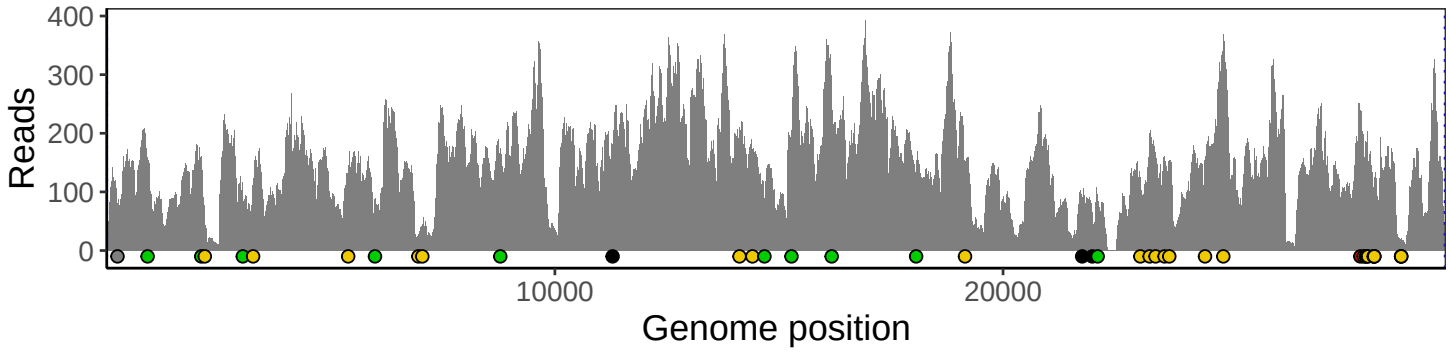



Negative control
241 intergenic 65
913 orf1ab silent 151
2110 orf1ab silent 155
2189 orf1ab L642F 51
3037 orf1ab silent 84
3267 orf1ab T1001I 115
5388 orf1ab A1708D 122
5986 orf1ab silent 86
6954 orf1ab I2230T 27
7042 orf1ab M2259I 32
8782 orf1ab silent 173
11288 orf1ab del 9 141
14120 orf1ab P218L 192
14408 orf1ab P314L 173
14676 orf1ab silent 72
15279 orf1ab silent 199
16176 orf1ab silent 266
18060 orf1ab silent 152
19151 orf1ab A1895V 146
21765 S del 6 76
21991 S del 3 48
22111 S silent 87
23063 S N501Y 117
23271 S A570D 170
23403 S D614G 165
23604 S P681H 147
23709 S T716I 147
24506 S S982A 148
24914 S D1118H 355
27972 orf8 Q27stop 214
28048 orf8 R52I 153
28095 orf8 K68stop 179
28111 orf8 Y73C 174
28144 orf8 S84L 150
28271 intergenic del 1 88
28280 N D3L 57
28281 N D3L 58
28282 N D3L 60
28881 N R203K 15
28882 N R203K 15
28883 N G204R 15
VSP9957−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

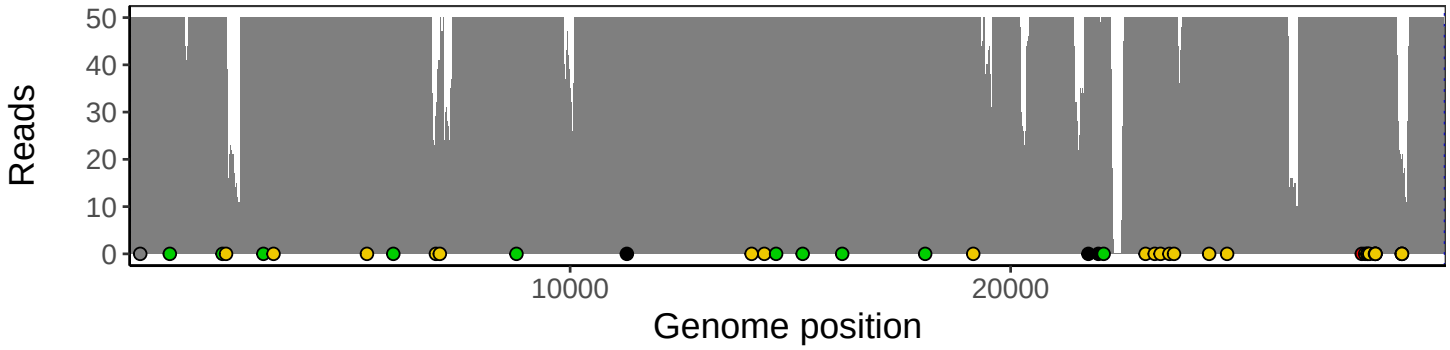
Analyses of individual experiments and composite results

VSP9957-1 | NA | Negative control | AHTMV3AFX4 | genomes | single experiment

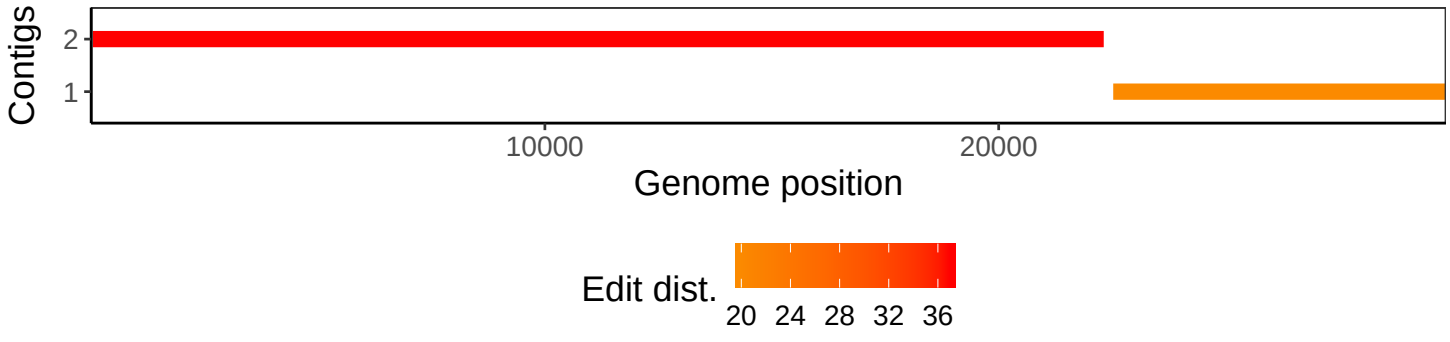
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
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