COVID-19 subject UPHS-0005

2021-03-25

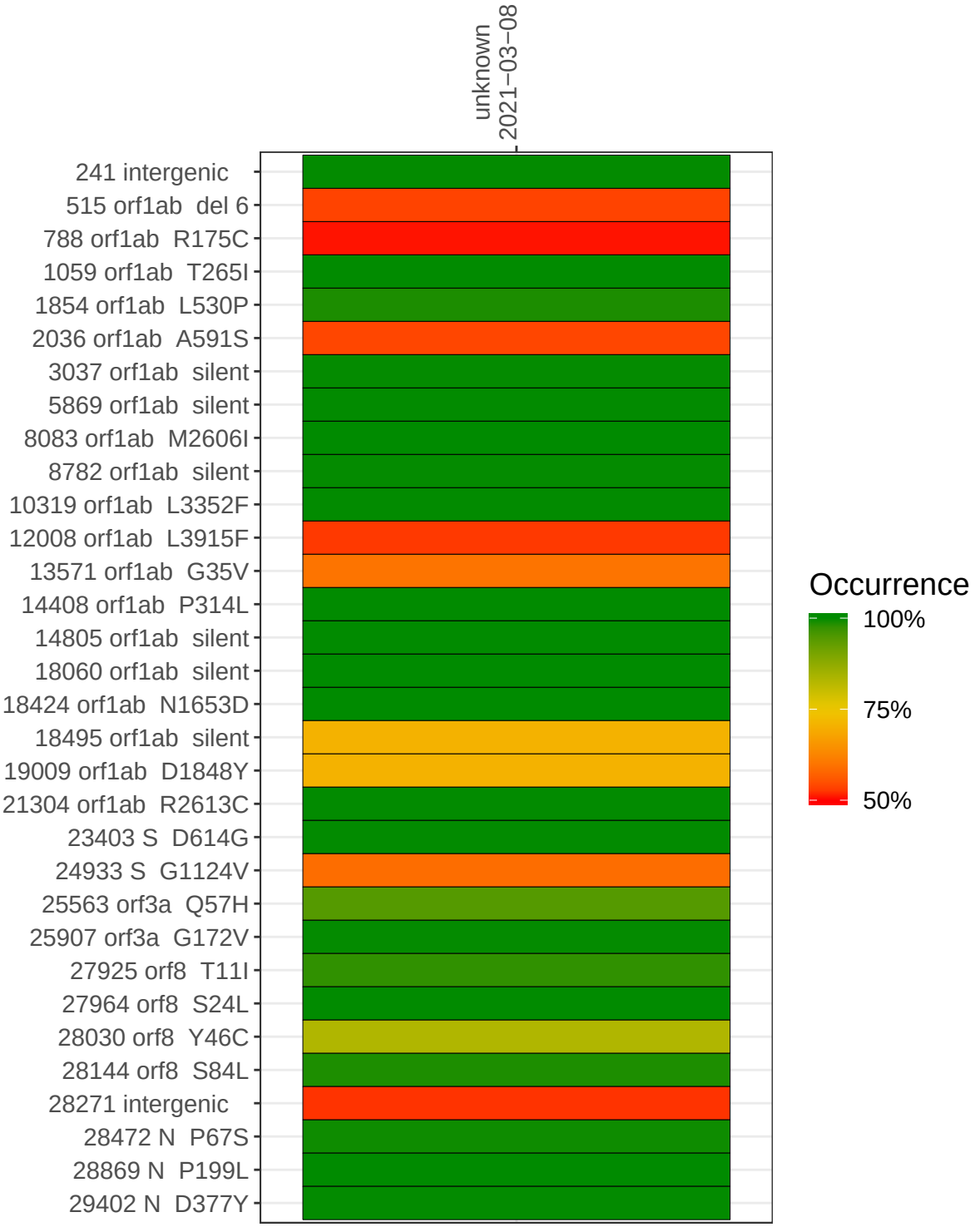
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

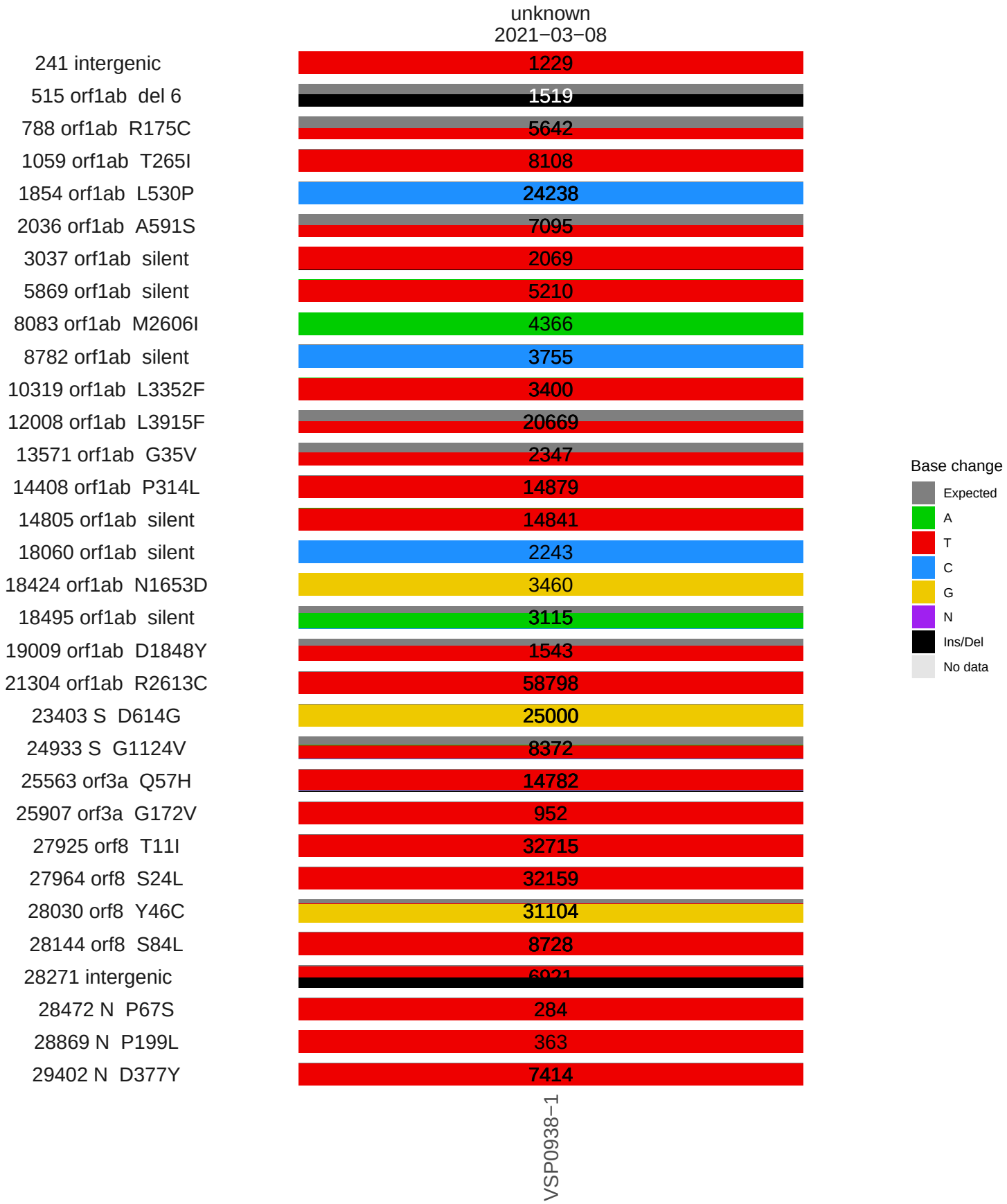
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0938-1	single experiment	NA	unknown	2021-03-08	29.68	B.1.2	99.2%	99.2%

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.

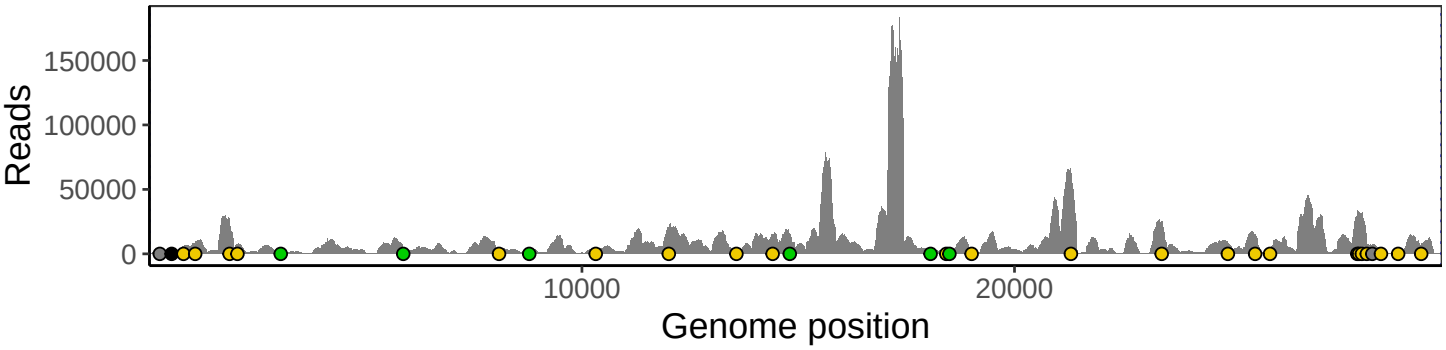



unknown
2021−03−08
241 intergenic
515 orf1ab del 6
788 orf1ab R175C
1059 orf1ab T265I
1854 orf1ab L530P
2036 orf1ab A591S
3037 orf1ab silent
5869 orf1ab silent
8083 orf1ab M2606I
8782 orf1ab silent
10319 orf1ab L3352F
12008 orf1ab L3915F
13571 orf1ab G35V
14408 orf1ab P314L
14805 orf1ab silent
18060 orf1ab silent
18424 orf1ab N1653D
18495 orf1ab silent
19009 orf1ab D1848Y
21304 orf1ab R2613C
23403 S D614G
24933 S G1124V
25563 orf3a Q57H
25907 orf3a G172V
27925 orf8 T11I
27964 orf8 S24L
28030 orf8 Y46C
28144 orf8 S84L
28271 intergenic
28472 N P67S
28869 N P199L
29402 N D377Y
1229
1519
5642
8108
24238
7095
2069
5210
4366
3755
3400
20669
2347
14879
14841
2243
3460
3115
1543
58798
25000
8372
14782
952
32715
32159
31104
8728
6921
284
363
7414
VSP0938−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

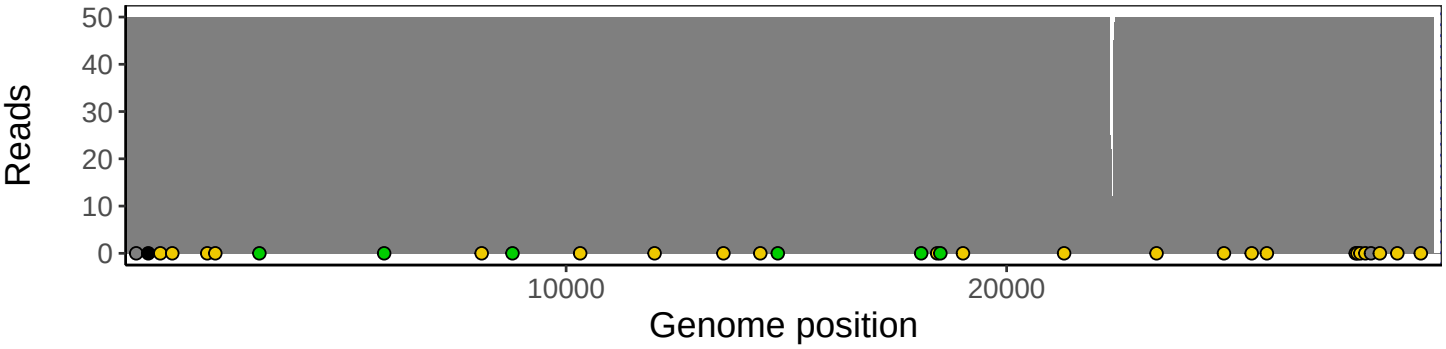
Analyses of individual experiments and composite results

VSP0938-1 | 2021-03-08 | unknown | UPHS-0005 | genomes | single experiment

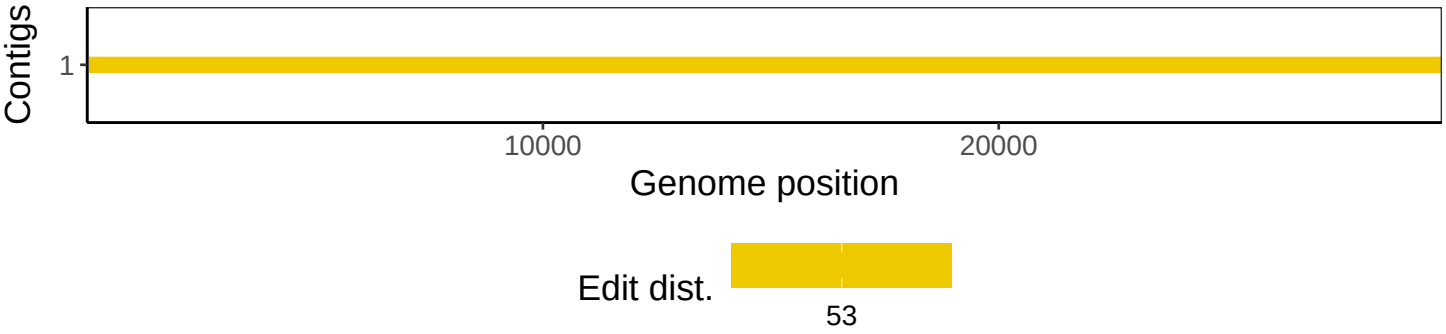
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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