COVID-19 subject UPHS-0124

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)
VSP1109-1	single experiment	NA	VTM	2021-03-15	29.89	B.1.2	99.8%	99.8%

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.

VTM
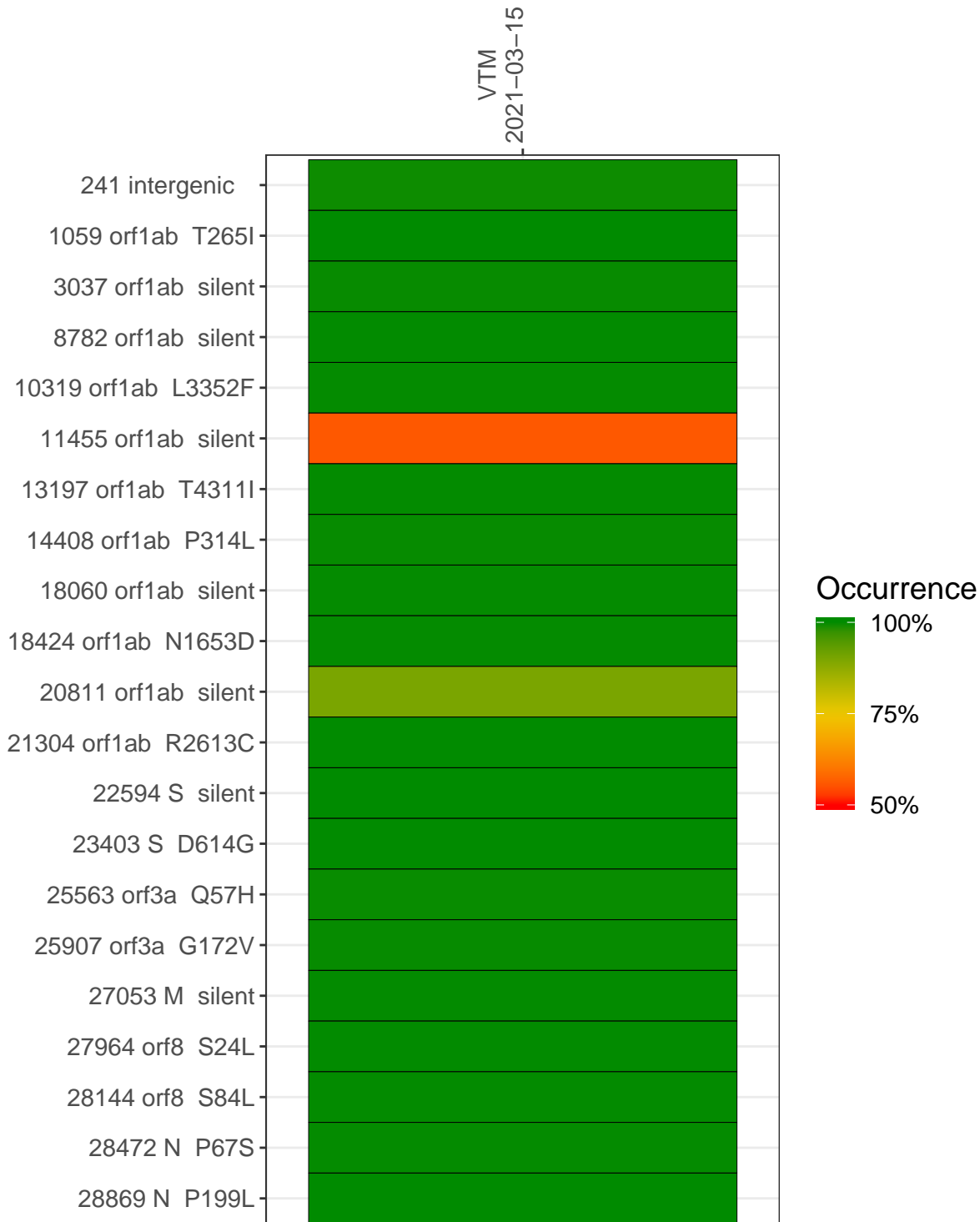
Position	VSP1109-1
241 intergenic	1585
1059 orf1ab T265I	3477
3037 orf1ab silent	5841
8782 orf1ab silent	5898
10319 orf1ab L3352F	8954
11455 orf1ab silent	12767
13197 orf1ab T4311I	15031
14408 orf1ab P314L	8677
18060 orf1ab silent	6699
18424 orf1ab N1653D	6792
20811 orf1ab silent	9158
21304 orf1ab R2613C	5941
22594 S silent	1930
23403 S D614G	6775
25563 orf3a Q57H	3546
25907 orf3a G172V	3487
27053 M silent	7248
27964 orf8 S24L	9100
28144 orf8 S84L	4418
28472 N P67S	4485
28869 N P199L	926

Base change

- Expected (grey)
- A (green)
- T (red)
- C (blue)
- G (yellow)
- N (purple)
- Ins/Del (black)
- No data (light grey)

Analyses of individual experiments and composite results

## VSP1109-1 | 2021-03-15 | VTM | UPHS-0124 | 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.
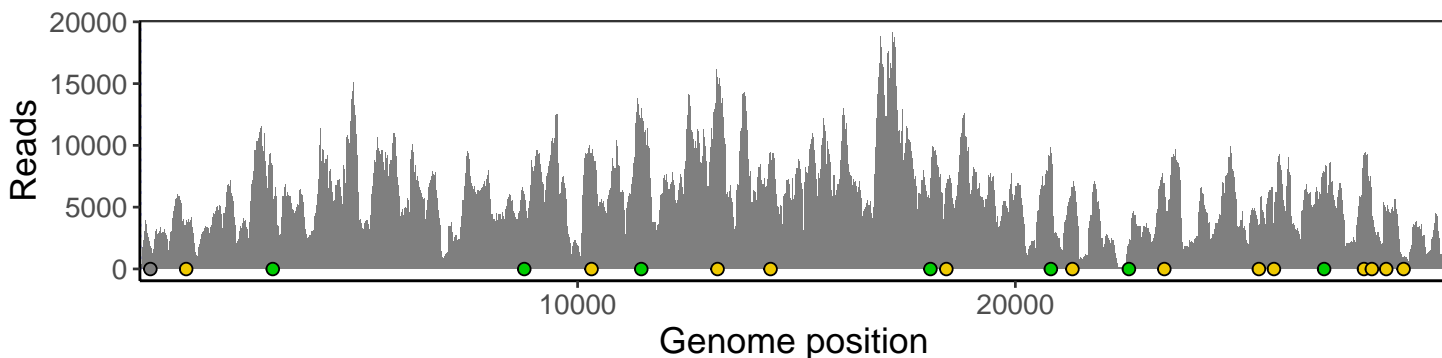
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
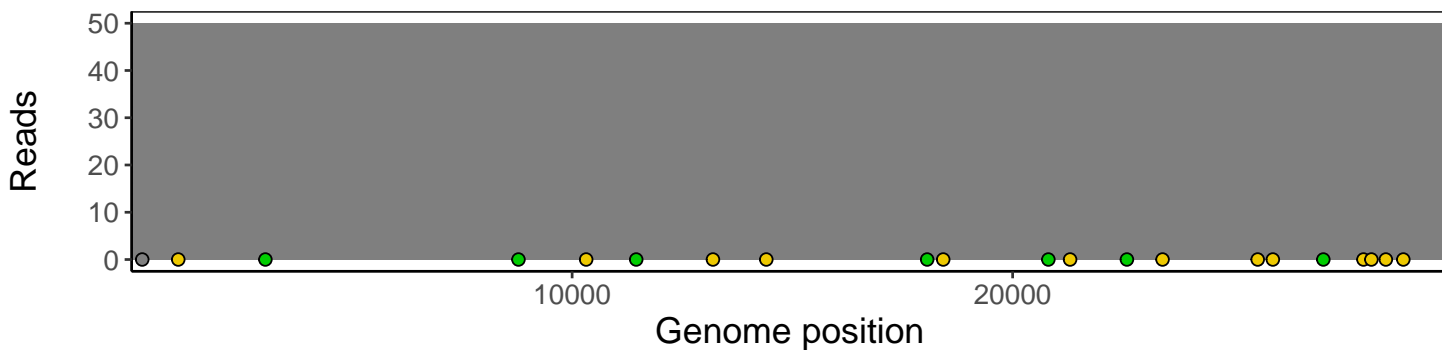
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
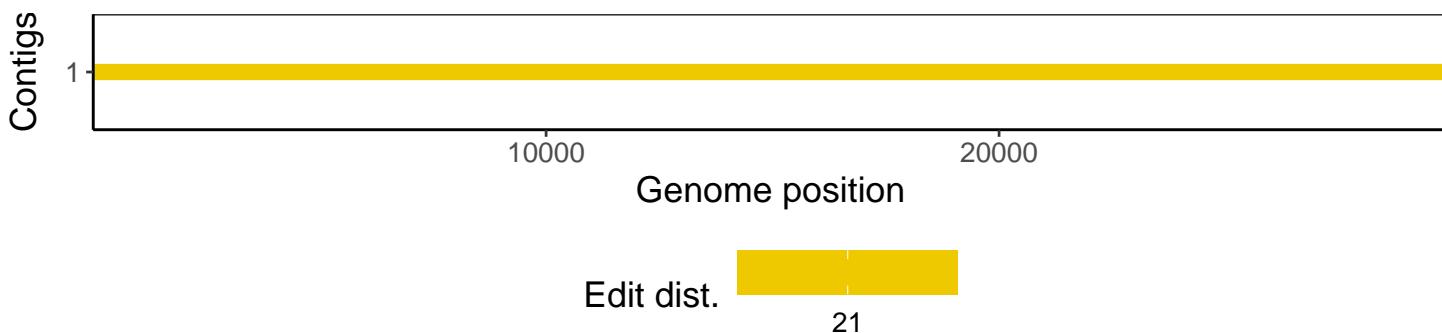
Software environment

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