

COVID-19 subject HUP-Q-0013

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)
VSP0881-1	single experiment	NA	unknown	2021-02-22	29.83	B.1.1.519	99.9%	99.8%

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.



unknown
2021-02-22

203 intergenic	2419
222 intergenic	2256
241 intergenic	1924
3037 ORF1ab silent	4011
3140 ORF1ab P959S	2399
5974 ORF1ab silent	5614
10029 ORF1ab T3255I	1955
10954 ORF1ab silent	8387
11117 ORF1ab I3618V	7478
12789 ORF1ab T4175I	11018
14408 ORF1ab P314L	11309
19839 ORF1ab silent	13730
21306 ORF1ab silent	5860
22995 S T478K	7526
23403 S D614G	15614
23604 S P681H	11370
23756 S T732A	9866
27904 ORF8 L4P	12447
28087 ORF8 A65V	11464
28881 N R203K	1075
28882 N R203K	1071
28883 N G204R	1076
29197 N silent	9569

Base change

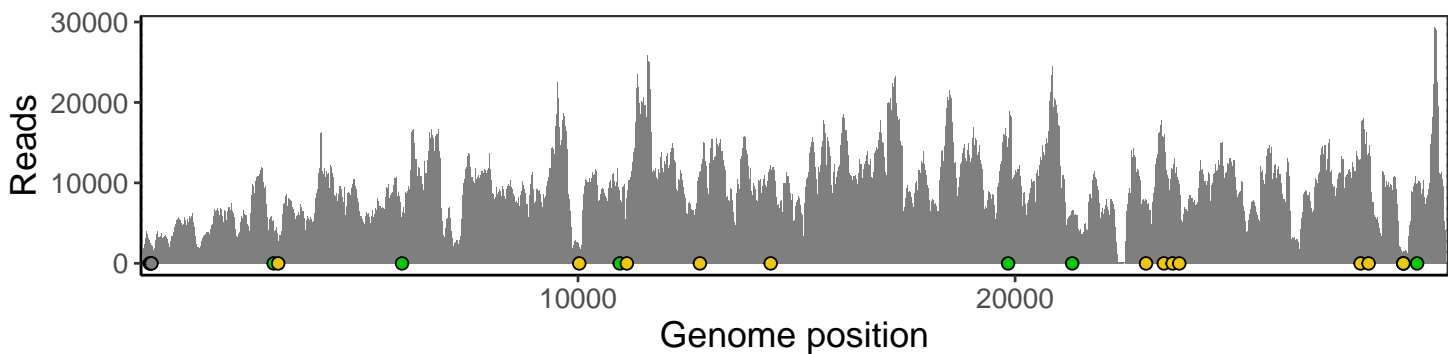


VSP0881-1

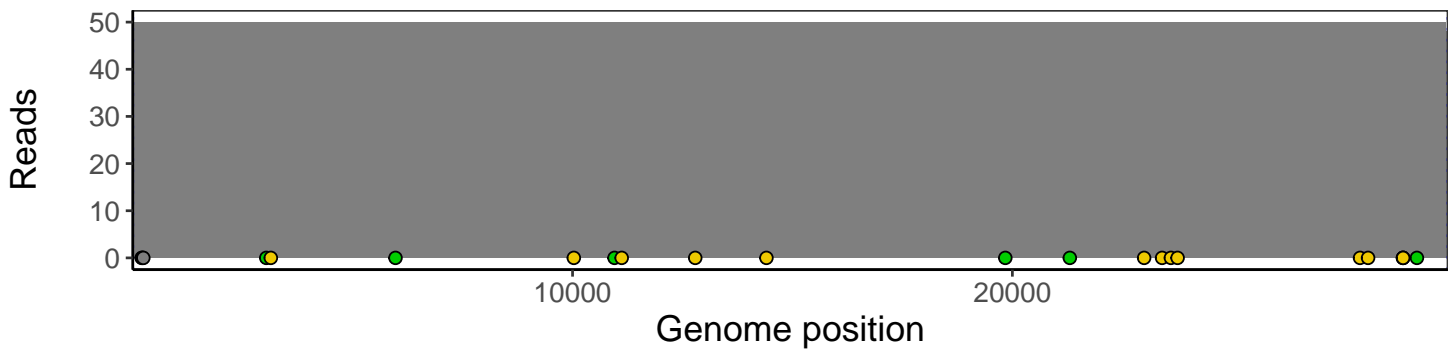
Analyses of individual experiments and composite results

VSP0881-1 | 2021-02-22 | unknown | HUP-Q-0013 | genomes | single experiment

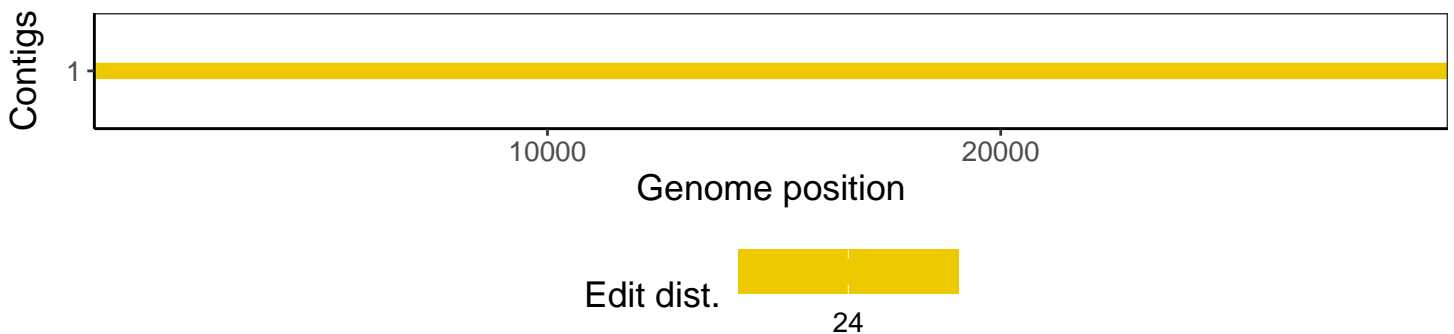
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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