

COVID-19 subject 369

2021-04-17

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.

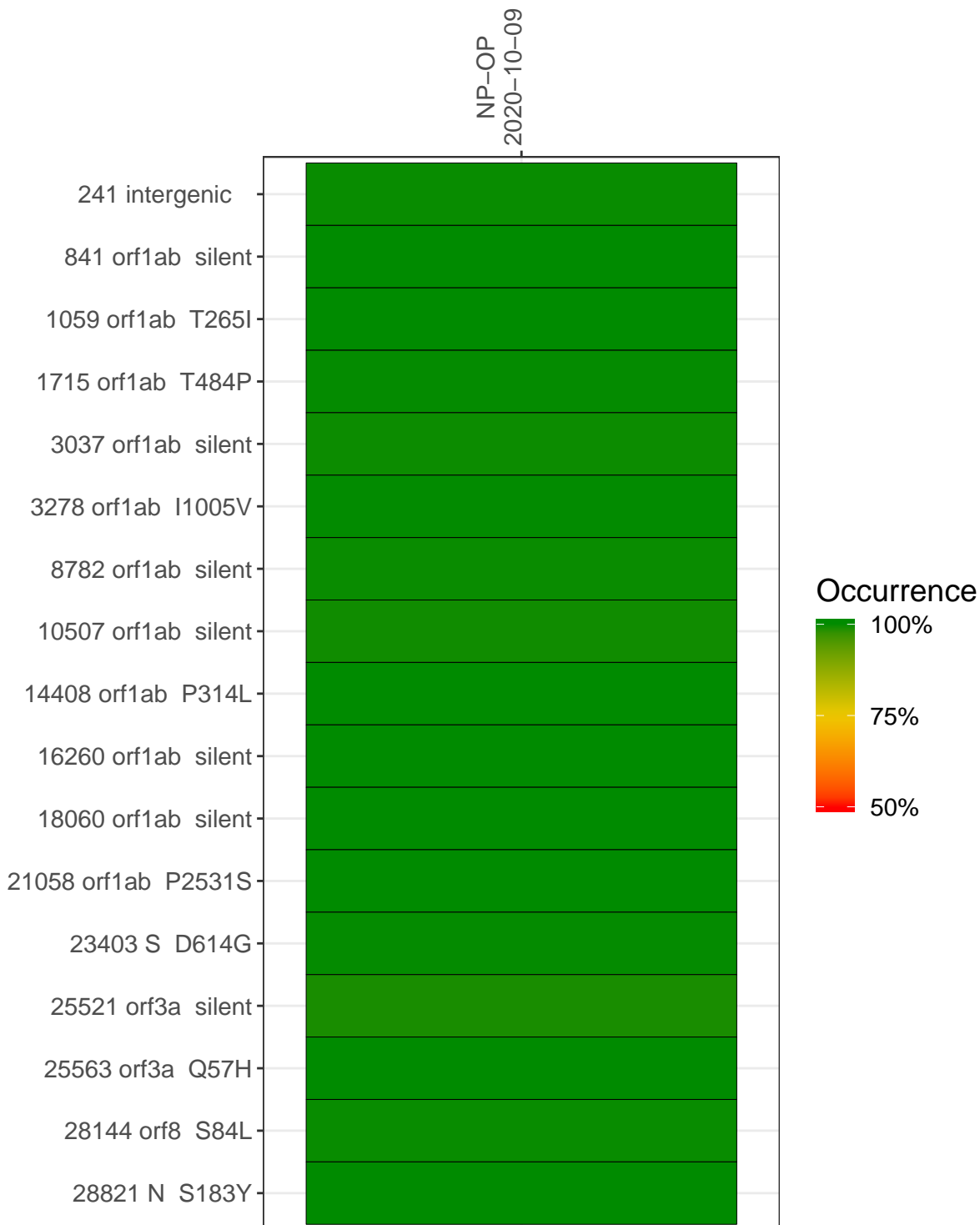
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0393-1	single experiment	NA	NP-OP	2020-10-09	29.60	B.1	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome `/home/everett/projects/SARS-CoV-2-Philadelphia/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.



NP-OP
2020-10-09

241 intergenic	3793
841 orf1ab silent	6244
1059 orf1ab T265I	2283
1715 orf1ab T484P	6181
3037 orf1ab silent	711
3278 orf1ab I1005V	4307
8782 orf1ab silent	896
10507 orf1ab silent	1698
14408 orf1ab P314L	2167
16260 orf1ab silent	680
18060 orf1ab silent	584
21058 orf1ab P2531S	3411
23403 S D614G	11409
25521 orf3a silent	3912
25563 orf3a Q57H	3236
28144 orf8 S84L	7866
28821 N S183Y	1760

Base change

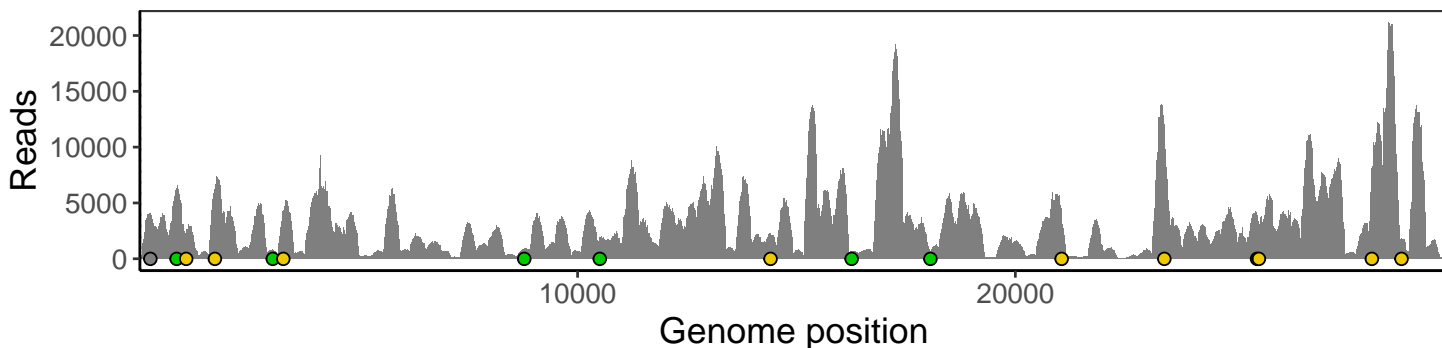


VSP0393-1

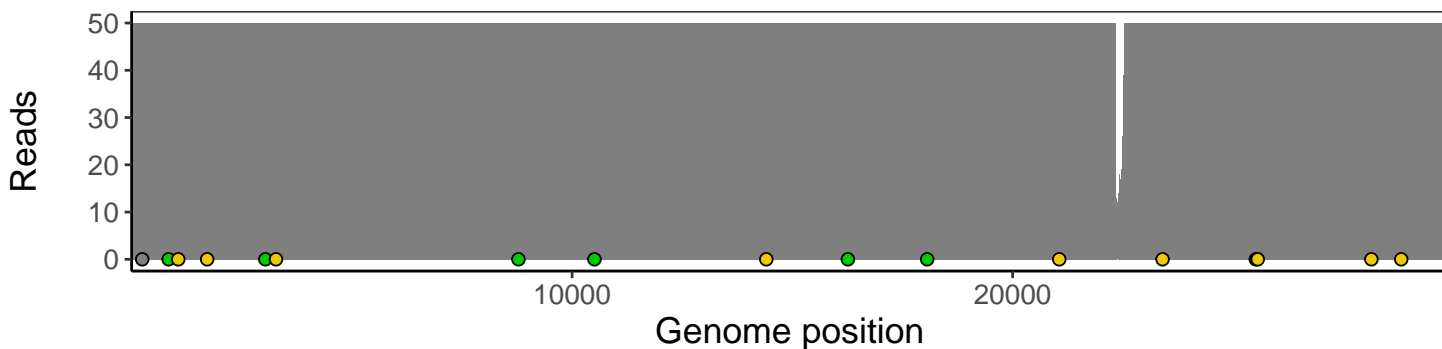
Analyses of individual experiments and composite results

VSP0393-1 | 2020-10-09 | NP-OP | 369no-q | genomes | single experiment

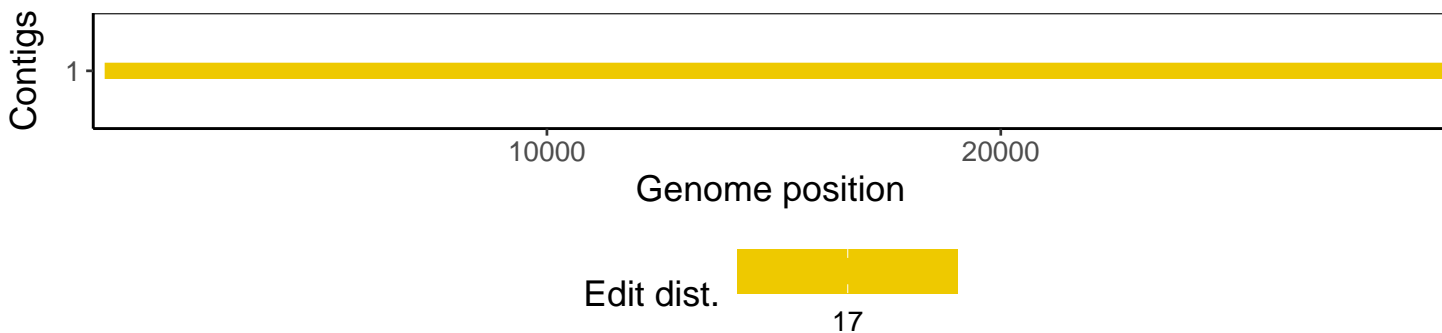
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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