

# COVID-19 subject UPHS-0459

*2021-06-01*

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.

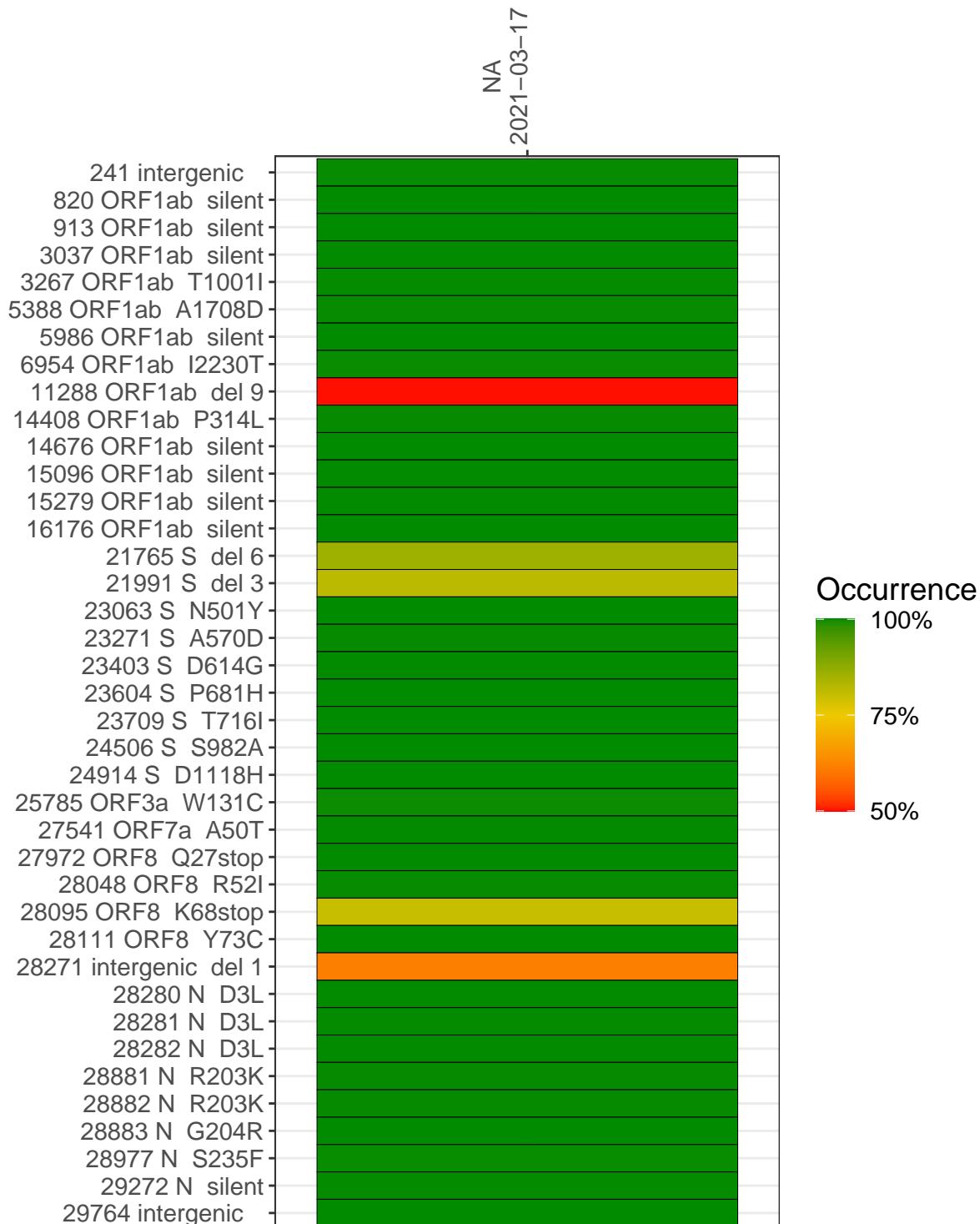
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP1585-1	single experiment	NA	NA	2021-03-17	29.84	B.1.1.7	100.0%	100.0%

## 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.



	NA 2021-03-17	
241 intergenic	2449	
820 ORF1ab silent	6838	
913 ORF1ab silent	8347	
3037 ORF1ab silent	3779	
3267 ORF1ab T1001I	5716	
5388 ORF1ab A1708D	4170	
5986 ORF1ab silent	2917	
6954 ORF1ab I2230T	1355	
11288 ORF1ab del 9	5358	
14408 ORF1ab P314L	5230	
14676 ORF1ab silent	3001	
15096 ORF1ab silent	5464	
15279 ORF1ab silent	6529	
16176 ORF1ab silent	11542	
21765 S del 6	2505	
21991 S del 3	1162	
23063 S N501Y	4087	
23271 S A570D	5817	
23403 S D614G	8862	
23604 S P681H	8044	
23709 S T716I	6835	
24506 S S982A	3536	
24914 S D1118H	6673	
25785 ORF3a W131C	4691	
27541 ORF7a A50T	4069	
27972 ORF8 Q27stop	11152	
28048 ORF8 R52I	13525	
28095 ORF8 K68stop	11673	
28111 ORF8 Y73C	9372	
28271 intergenic del 1	5136	
28280 N D3L	3126	
28281 N D3L	3126	
28282 N D3L	3368	
28881 N R203K	707	
28882 N R203K	706	
28883 N G204R	708	
28977 N S235F	1065	
29272 N silent	9294	
29764 intergenic	19276	
	VSP1585-1	

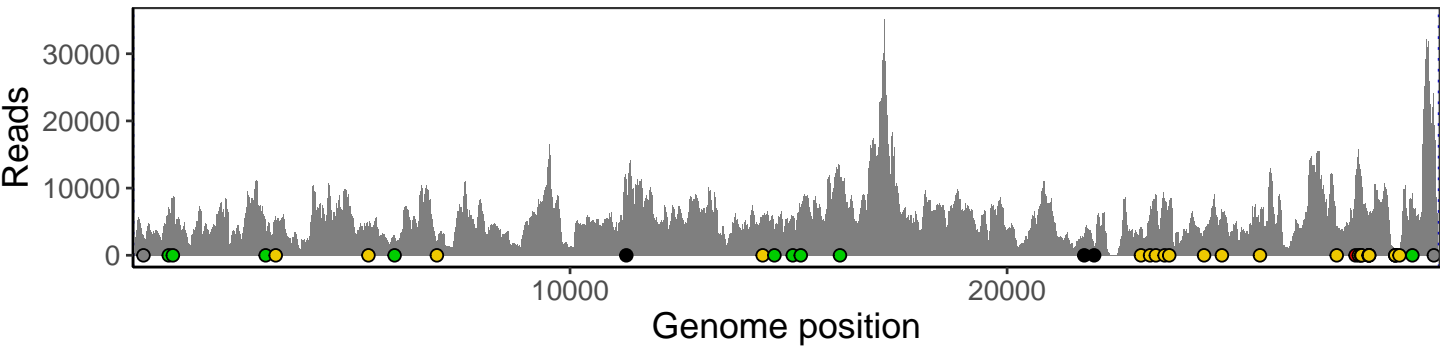
Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

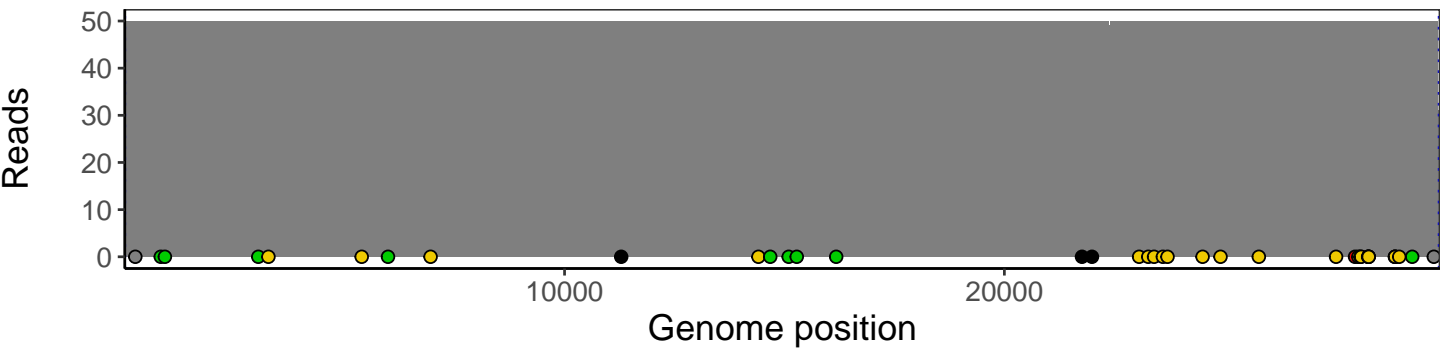
# Analyses of individual experiments and composite results

VSP1585-1 | 2021-03-17 | NA | UPHS-0459 | genomes | single experiment

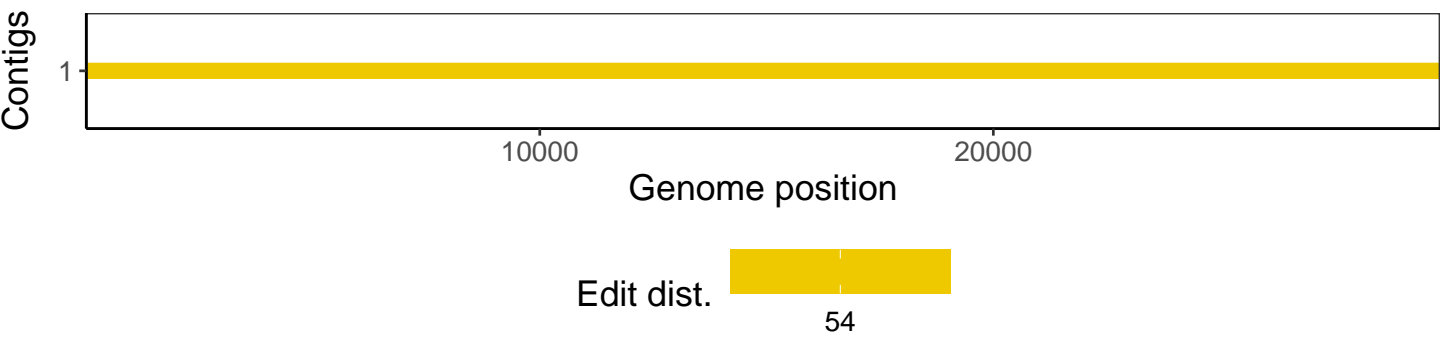
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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	3.3.3
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