

# COVID-19 subject UPHS-0580

*2021-06-03*

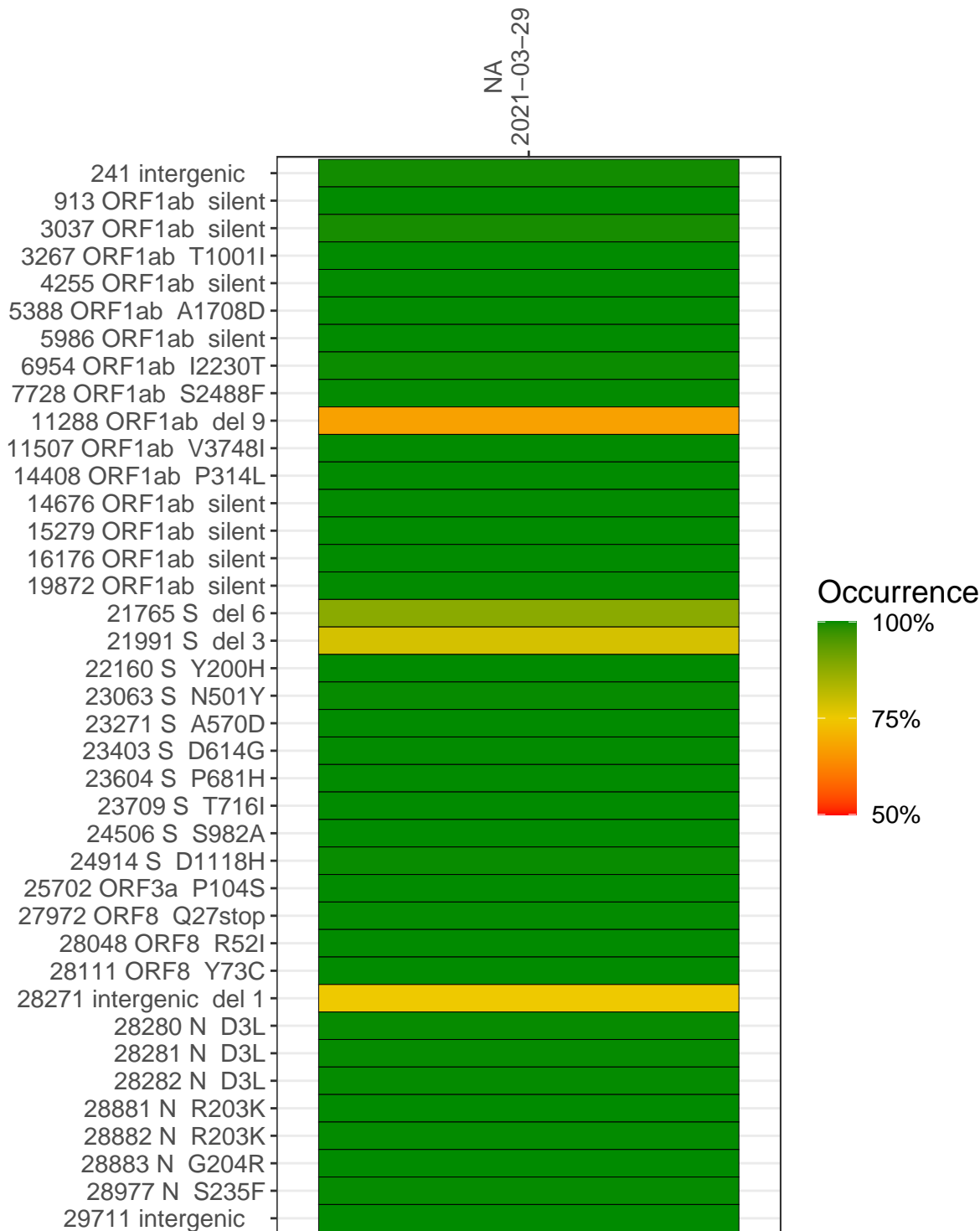
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1705-1	single experiment	NA	NA	2021-03-29	29.87	B.1.1.7	99.9%	99.9%

## 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 2021-03-29	
241 intergenic	1446	
913 ORF1ab silent	9823	
3037 ORF1ab silent	8132	
3267 ORF1ab T1001I	6744	
4255 ORF1ab silent	10068	
5388 ORF1ab A1708D	9931	
5986 ORF1ab silent	3905	
6954 ORF1ab I2230T	1529	
7728 ORF1ab S2488F	6523	
11288 ORF1ab del 9	5663	
11507 ORF1ab V3748I	9955	
14408 ORF1ab P314L	9292	
14676 ORF1ab silent	3990	
15279 ORF1ab silent	6510	
16176 ORF1ab silent	16852	
19872 ORF1ab silent	6317	
21765 S del 6	4091	
21991 S del 3	1678	
22160 S Y200H	2429	
23063 S N501Y	2211	
23271 S A570D	6342	
23403 S D614G	6657	
23604 S P681H	14099	
23709 S T716I	11761	
24506 S S982A	1789	
24914 S D1118H	7598	
25702 ORF3a P104S	7317	
27972 ORF8 Q27stop	20672	
28048 ORF8 R52I	21235	
28111 ORF8 Y73C	13871	
28271 intergenic del 1	5981	
28280 N D3L	4403	
28281 N D3L	4403	
28282 N D3L	4617	
28881 N R203K	1590	
28882 N R203K	1587	
28883 N G204R	1591	
28977 N S235F	2556	
29711 intergenic	1350	
	VSP1705-1	

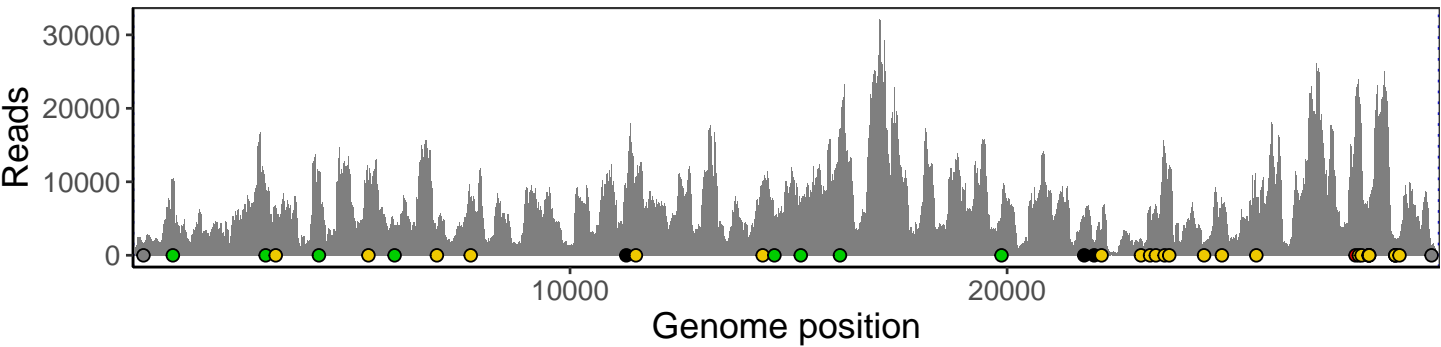
Base change

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

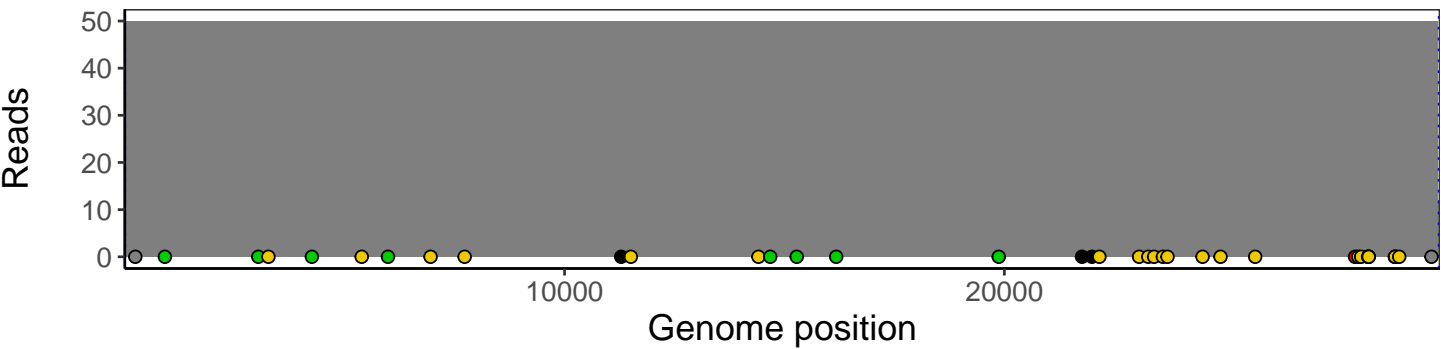
# Analyses of individual experiments and composite results

VSP1705-1 | 2021-03-29 | NA | UPHS-0580 | genomes | single experiment

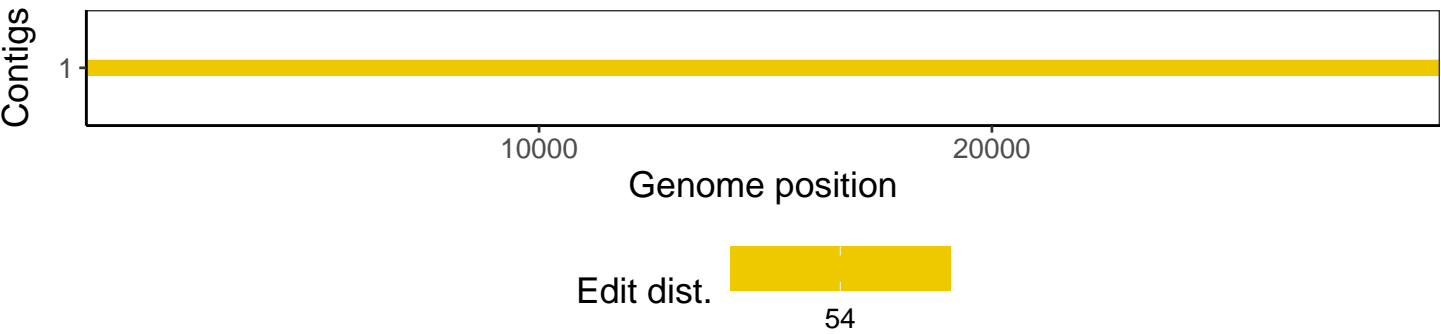
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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