# COVID-19 subject UPHS-0337

2021-06-23

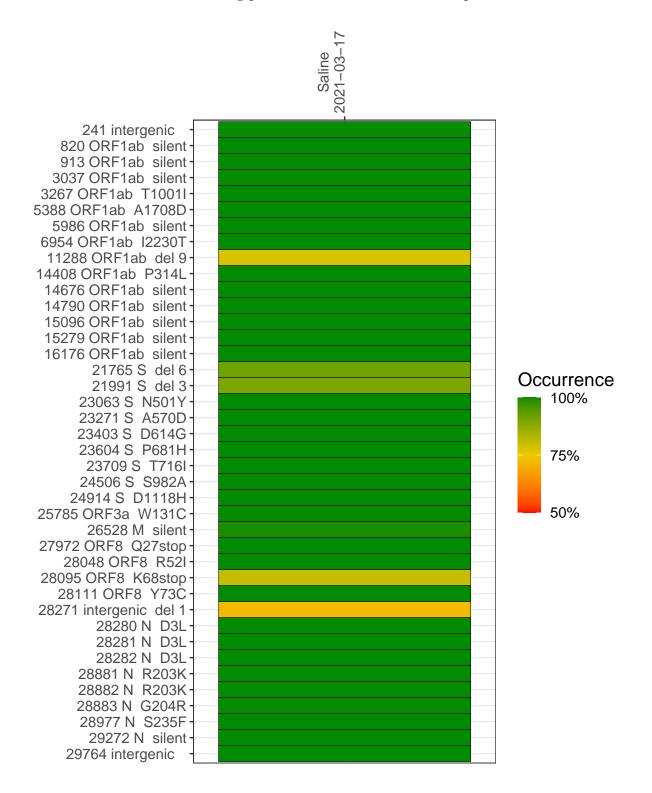
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1382-1	single experiment	NA	Saline	2021-03-17	29.78	B.1.1.7	99.8%	99.6%

#### 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.



#### Saline 2021-03-17

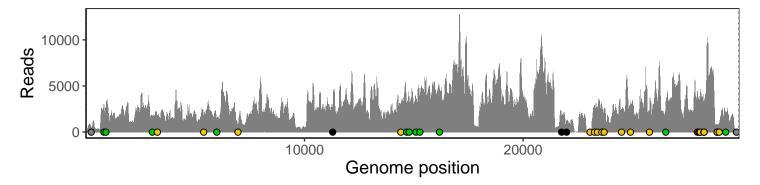
	2021-03-17
241 intergenic	522
820 ORF1ab silent	2953
913 ORF1ab silent	2476
3037 ORF1ab silent	1581
3267 ORF1ab T1001I	1851
5388 ORF1ab A1708D	1758
5986 ORF1ab silent	1437
6954 ORF1ab I2230T	630
11288 ORF1ab del 9	1731
14408 ORF1ab P314L	2785
14676 ORF1ab silent	2883
14790 ORF1ab silent	3434
15096 ORF1ab silent	3659
15279 ORF1ab silent	3621
16176 ORF1ab silent	4620
21765 S del 6	1489
21991 S del 3	1065
23063 S N501Y	199
23271 S A570D	2638
23403 S D614G	2635
23604 S P681H	2887
23709 S T716I	2404
24506 S S982A	2499
24914 S D1118H	3176
25785 ORF3a W131C	2269
26528 M silent	2155
27972 ORF8 Q27stop	4370
28048 ORF8 R52I	3168
28095 ORF8 K68stop	3902
28111 ORF8 Y73C	4171
28271 intergenic del 1	2902
28280 N D3L	1997
28281 N D3L	1997
28282 N D3L	2132
28881 N R203K	555
28882 N R203K	555
28883 N G204R	556
28977 N S235F	985
29272 N silent	2223
29764 intergenic	38
	382-1
	Ø.



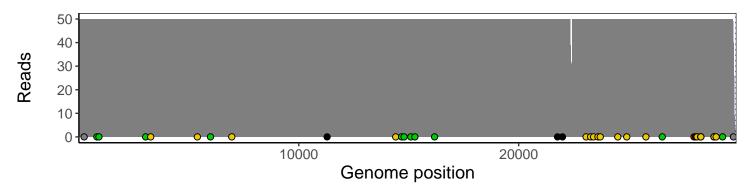
## Analyses of individual experiments and composite results

### VSP1382-1 | 2021-03-17 | Saline | UPHS-0337 | genomes | single experiment

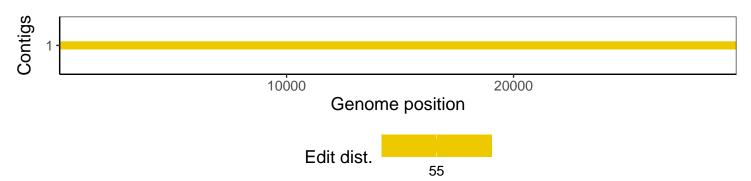
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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
${\bf Summarized Experiment}$	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