# COVID-19 subject UPHS-0057

2021-04-17

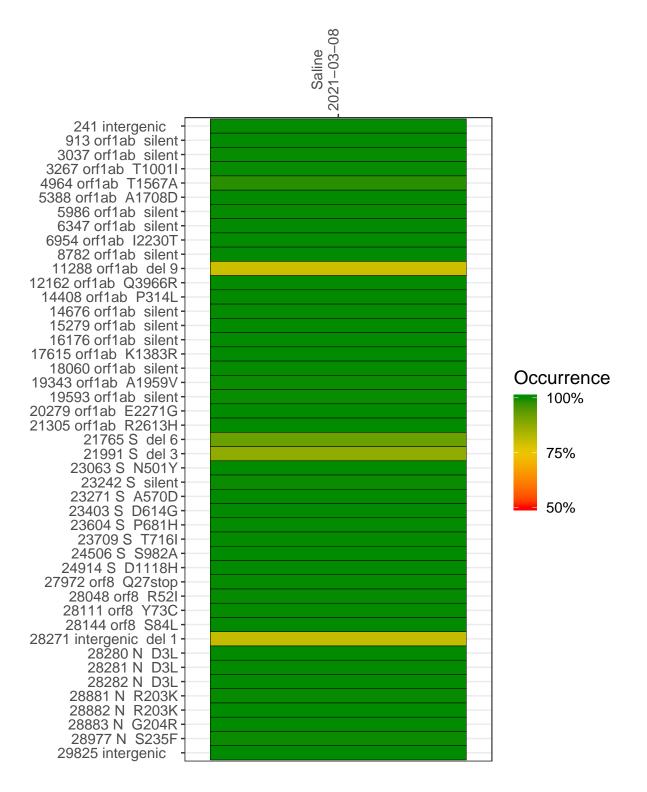
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0989-1	single experiment	NA	Saline	2021-03-08	29.98	B.1.1.7	99.9%	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.



#### Saline 2021-03-08

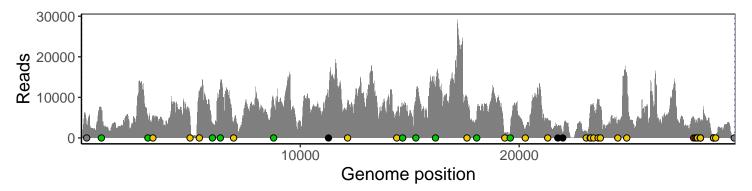
	2021-03-08
241 intergenic	3180
913 orf1ab silent	6899
3037 orf1ab silent	4587
3267 orf1ab T1001I	5541
4964 orf1ab T1567A	5297
5388 orf1ab A1708D	11097
5986 orf1ab silent	3473
6347 orf1ab silent	11921
6954 orf1ab I2230T	3770
8782 orf1ab silent	9027
11288 orf1ab del 9	8927
12162 orf1ab Q3966R	8334
14408 orf1ab P314L	6492
14676 orf1ab silent	7672
15279 orf1ab silent	9664
16176 orf1ab silent	12480
17615 orf1ab K1383R	10082
18060 orf1ab silent	6032
19343 orf1ab A1959V	1188
19593 orf1ab silent	2526
20279 orf1ab E2271G	2246
21305 orf1ab R2613H	4846
21765 S del 6	2499
21991 S del 3	1414
23063 S N501Y	1521
23242 S silent	7698
23271 S A570D	7574
23403 S D614G	8323
23604 S P681H	9448
23709 S T716I	7366
24506 S S982A	4129
24914 S D1118H	16045
27972 orf8 Q27stop	5028
28048 orf8 R52I	3826
28111 orf8 Y73C	4323
28144 orf8 S84L	3845
28271 intergenic del 1	
28280 N D3L	3866 3083
28281 N D3L	
	3083
28282 N D3L	3114
28881 N R203K	682
28882 N R203K	681
28883 N G204R	683
28977 N S235F	731
29825 intergenic	148
	<u></u>



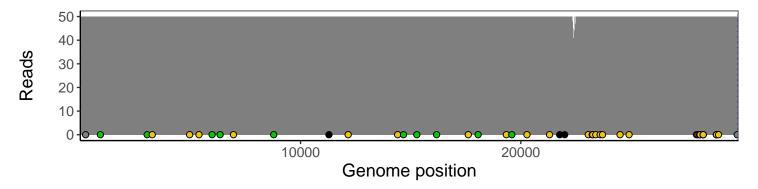
### Analyses of individual experiments and composite results

#### $VSP0989\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0057 \mid genomes \mid single \ experiment$

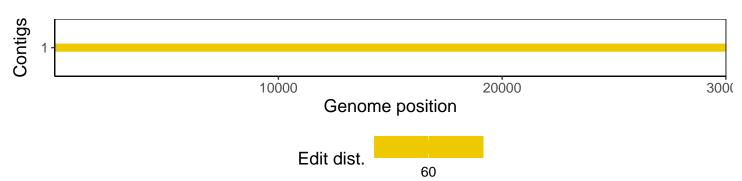
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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
${\it Genomic Alignments}$	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
$\operatorname{GenomeInfoDb}$	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