COVID-19 subject UPHS-1040

2021-06-23

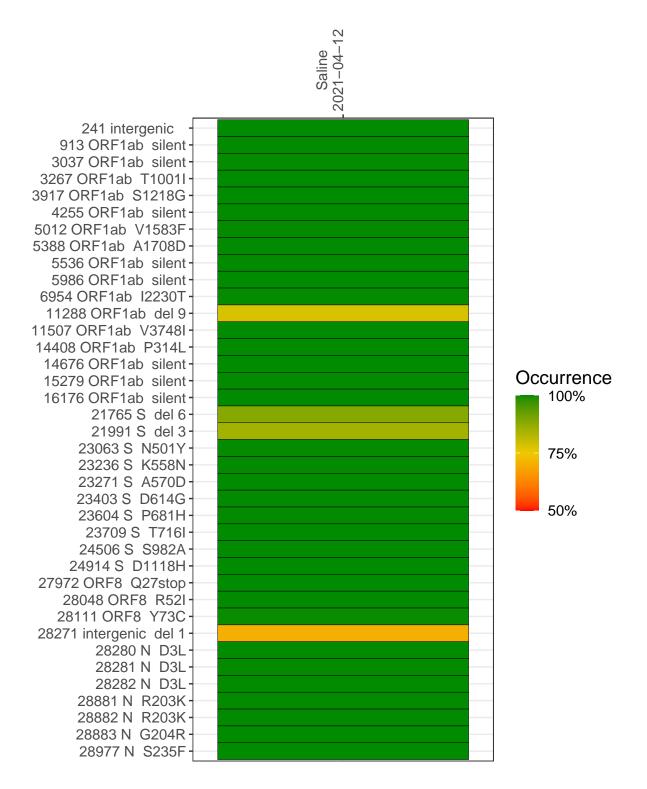
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2252-1	single experiment	NA	Saline	2021-04-12	29.80	B.1.1.7	99.8%	99.7%

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 2021-04-12

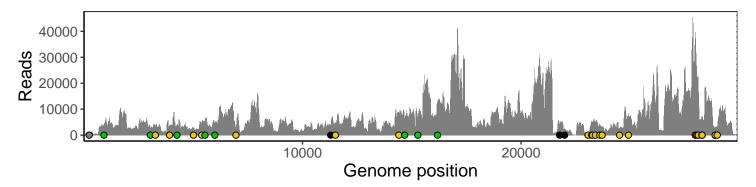
	2021-04-12
241 intergenic	656
913 ORF1ab silent	3613
3037 ORF1ab silent	2884
3267 ORF1ab T1001I	3711
3917 ORF1ab S1218G	3625
4255 ORF1ab silent	3274
5012 ORF1ab V1583F	2510
5388 ORF1ab A1708D	4376
5536 ORF1ab silent	5153
5986 ORF1ab silent	4385
6954 ORF1ab I2230T	2964
11288 ORF1ab del 9	2417
11507 ORF1ab V3748I	4697
14408 ORF1ab P314L	7712
14676 ORF1ab silent	5735
15279 ORF1ab silent	6696
16176 ORF1ab silent	12632
21765 S del 6	3363
21991 S del 3	2267
23063 S N501Y	1087
23236 S K558N	4801
23271 S A570D	4705
23403 S D614G	5066
23604 S P681H	3931
23709 S T716I	3131
24506 S S982A	2761
24914 S D1118H	8057
27972 ORF8 Q27stop	38301
28048 ORF8 R52I	20702
28111 ORF8 Y73C	18626
28271 intergenic del 1	5880
28280 N D3L	3958
28281 N D3L	3958
28282 N D3L	4208
28881 N R203K	2091
28882 N R203K	2080
28883 N G204R	2086
28977 N S235F	3256



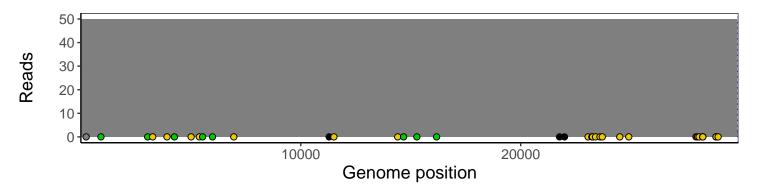
Analyses of individual experiments and composite results

$VSP2252\text{-}1 \mid 2021\text{-}04\text{-}12 \mid Saline \mid UPHS\text{-}1040 \mid genomes \mid single \ experiment$

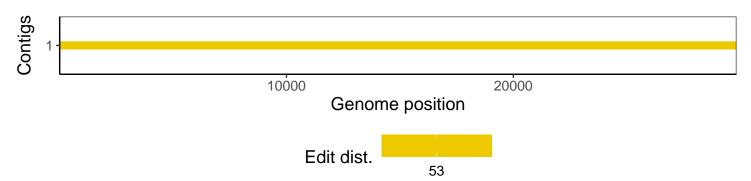
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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				