COVID-19 subject HUP Q-0036

2021-04-17

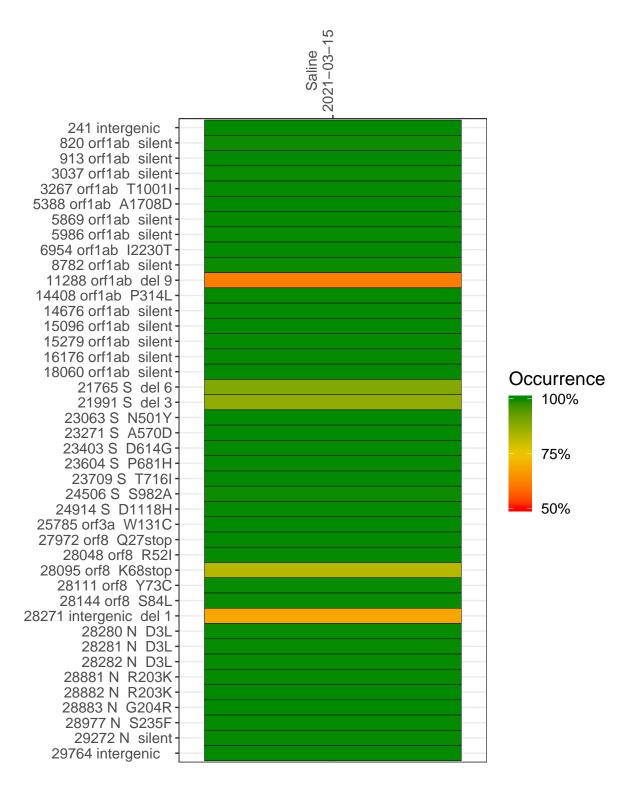
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1068-1	single experiment	NA	Saline	2021-03-15	29.82	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 2021-03-15

	2021-03-15
241 intergenic	1289
820 orf1ab silent	6530
913 orf1ab silent	6414
3037 orf1ab silent	3862
3267 orf1ab T1001I	5684
5388 orf1ab A1708D	8666
5869 orf1ab silent	4976
5986 orf1ab silent	4085
6954 orf1ab I2230T	1896
8782 orf1ab silent	5500
11288 orf1ab del 9	5754
14408 orf1ab P314L	4448
14676 orf1ab silent	5523
15096 orf1ab silent	7570
15279 orf1ab silent	9568
16176 orf1ab silent	12619
18060 orf1ab silent	5676
21765 S del 6	3354
21991 S del 3	2654
23063 S N501Y	595
23271 S A570D	7460
23403 S D614G	8013
23604 S P681H	7519
23709 S T716I	7051
24506 S S982A	5283
24914 S D1118H	12392
25785 orf3a W131C	5204
27972 orf8 Q27stop	8154
28048 orf8 R52I	6889
28095 orf8 K68stop	8761
28111 orf8 Y73C	8351
28144 orf8 S84L	6730
28271 intergenic del 1	4249
28280 N D3L	2830
28281 N D3L	2830
28282 N D3L	3087
28881 N R203K	1494
28882 N R203K	1484
28883 N G204R	1486
28977 N S235F	3202
29272 N silent	8171
29764 intergenic	1654
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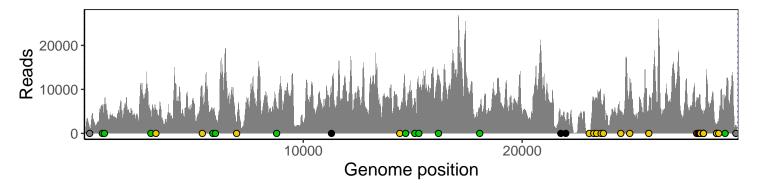


3P1068-1

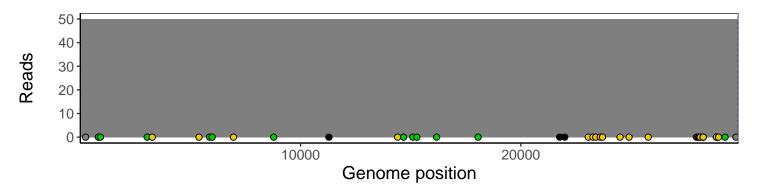
Analyses of individual experiments and composite results

VSP1068-1 | 2021-03-15 | Saline | HUP Q-0036 | genomes | single experiment

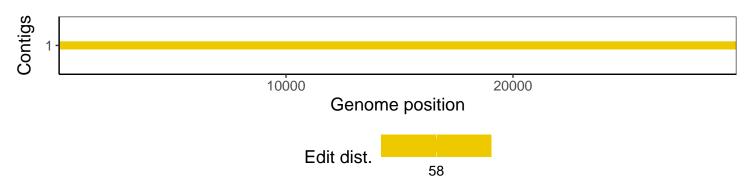
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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