COVID-19 subject HUP-Q-0003

2021-03-01

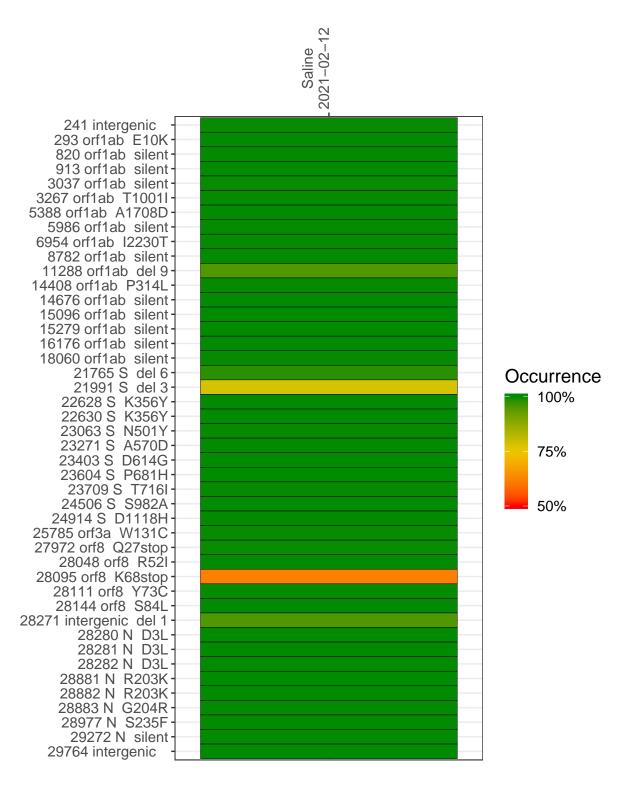
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0814-1	single experiment	NA	Saline	2021-02-12	28.62	B.1.1.7	99.8%	99.1%

Variants shared across samples

The heat map below shows how variants (reference genome 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 2021-02-12

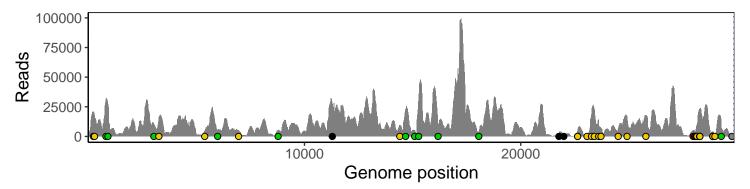
	2021–02–12
241 intergenic	20411
293 orf1ab E10K	17835
820 orf1ab silent	31101
913 orf1ab silent	27377
3037 orf1ab silent	10086
3267 orf1ab T1001I	16041
5388 orf1ab A1708D	4816
5986 orf1ab silent	5750
6954 orf1ab I2230T	5149
8782 orf1ab silent	5348
11288 orf1ab del 9	25931
14408 orf1ab P314L	9206
14676 orf1ab silent	22632
15096 orf1ab silent	5115
15279 orf1ab silent	32509
16176 orf1ab silent	10365
18060 orf1ab silent	3906
21765 S del 6	2898
21991 S del 3	933
22628 S K356Y	4350
22630 S K356Y	4359
23063 S N501Y	1435
23271 S A570D	18598
23403 S D614G	23068
23604 S P681H	13848
23709 S T716I	7052
24506 S S982A	6794
24914 S D1118H	16921
25785 orf3a W131C	17962
27972 orf8 Q27stop	5229
28048 orf8 R52I	4372
28095 orf8 K68stop	4932
28111 orf8 Y73C	7430
28144 orf8 S84L	9802
28271 intergenic del 1	22978
28280 N D3L	21872
28281 N D3L 28282 N D3L	21872
28282 N D3L 28881 N R203K	21960
28882 N R203K	3656 3653
28883 N G204R	3653 3653
28977 N S235F	3653 1392
29272 N silent	1392
29764 intergenic	106
29704 IIIIGIGGIIIC	
	1-1



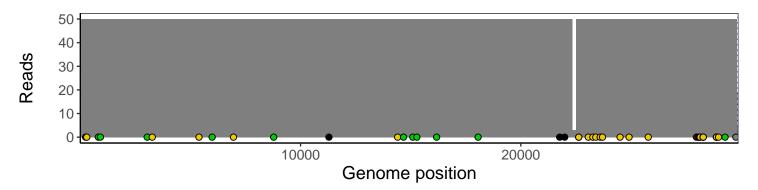
Analyses of individual experiments and composite results

$VSP0814-1 \mid 2021-02-12 \mid Saline \mid HUP-Q-0003 \mid genomes \mid single \; experiment$

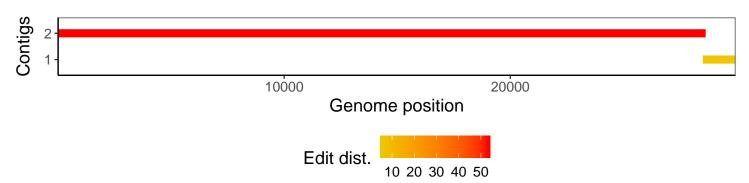
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
$\operatorname{GenomicAlignments}$	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
$\operatorname{GenomeInfoDb}$	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