COVID-19 subject UPHS-0068

2021-04-17

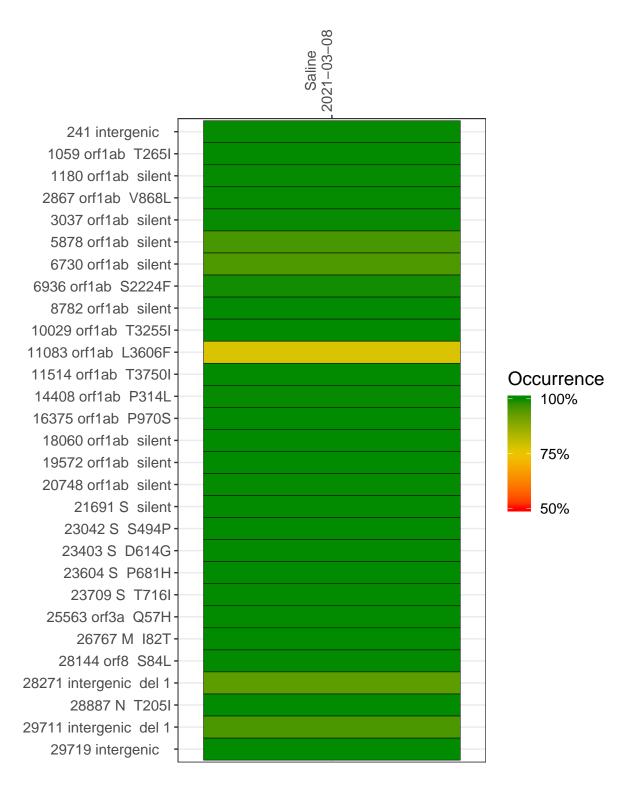
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1000-1	single experiment	NA	Saline	2021-03-08	29.93	B.1.575	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

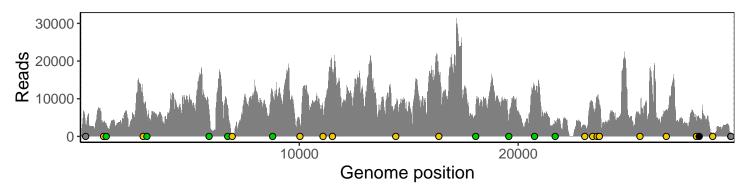
	2021 00 00
241 intergenic	3151
1059 orf1ab T265I	3745
1180 orf1ab silent	3019
2867 orf1ab V868L	10573
3037 orf1ab silent	5421
5878 orf1ab silent	7192
6730 orf1ab silent	8061
6936 orf1ab S2224F	207
8782 orf1ab silent	11372
10029 orf1ab T3255I	3520
11083 orf1ab L3606F	5643
11514 orf1ab T3750I	16759
14408 orf1ab P314L	8485
16375 orf1ab P970S	16814
18060 orf1ab silent	7640
19572 orf1ab silent	3375
20748 orf1ab silent	13425
21691 S silent	3954
23042 S S494P	3006
23403 S D614G	9374
23604 S P681H	10371
23709 S T716I	8712
25563 orf3a Q57H	5726
26767 M 182T	7091
28144 orf8 S84L	4243
28271 intergenic del 1	4742
28887 N T205I	887
29711 intergenic del 1	488
29719 intergenic	481
	1-0



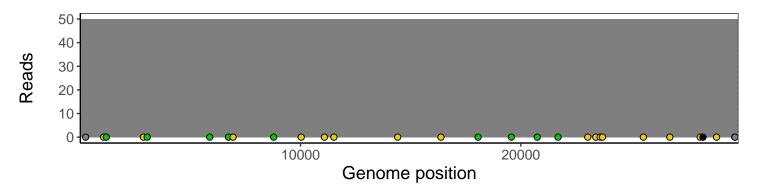
Analyses of individual experiments and composite results

VSP1000-1 | 2021-03-08 | Saline | UPHS-0068 | genomes | single experiment

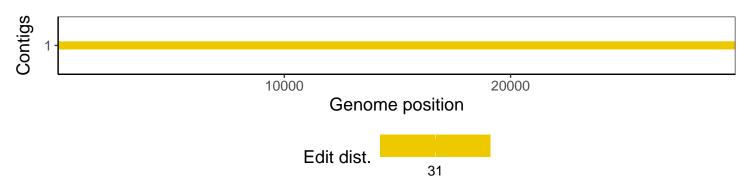
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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