

COVID-19 subject UPHS-0056

2021-03-25

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.

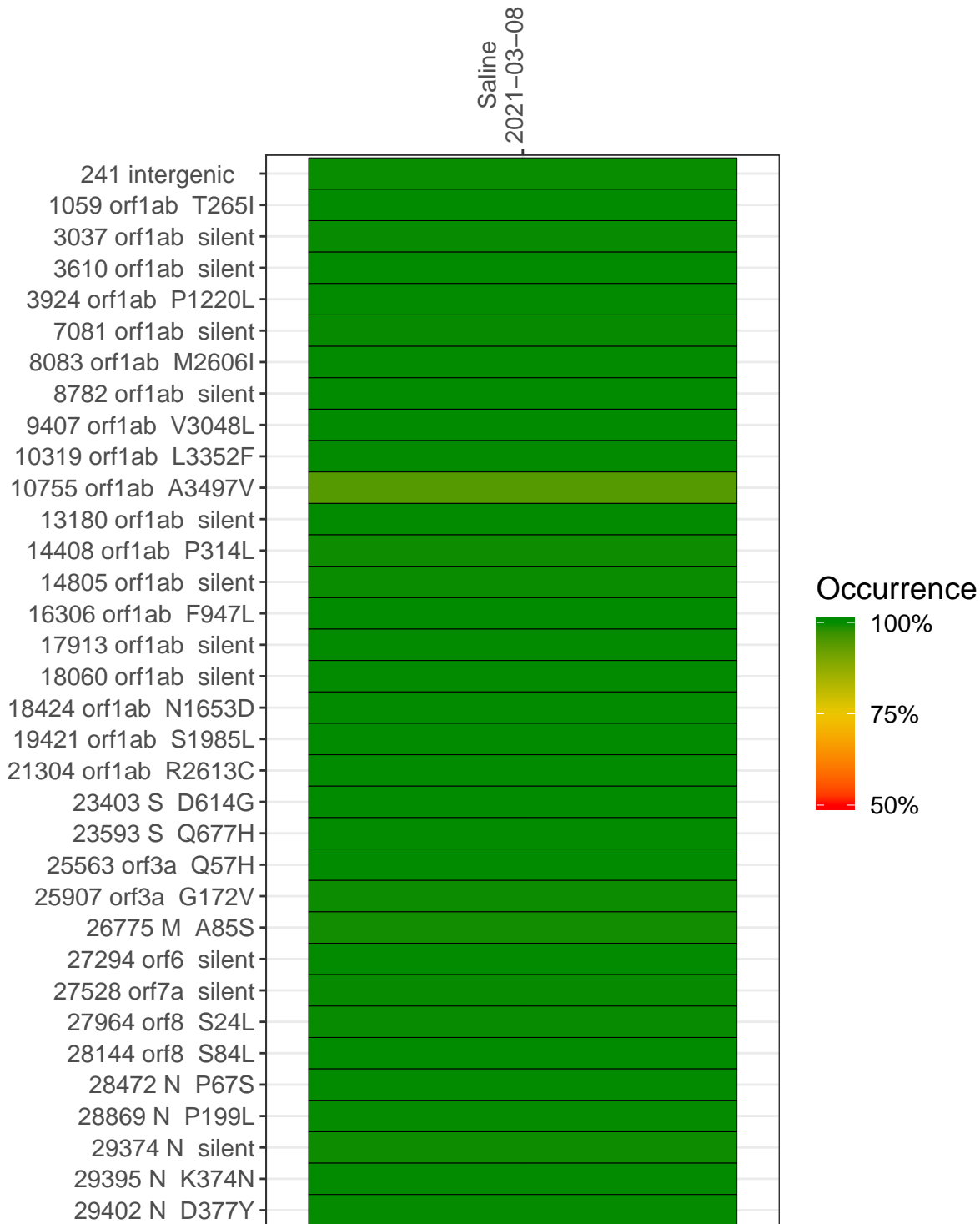
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0988-1	single experiment	NA	Saline	2021-03-08	27.53	B.1.2	99.9%	99.8%

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 2021-03-08	
241 intergenic	2705	
1059 orf1ab T265I	3772	
3037 orf1ab silent	4878	
3610 orf1ab silent	5390	
3924 orf1ab P1220L	2376	
7081 orf1ab silent	3254	
8083 orf1ab M2606I	9661	
8782 orf1ab silent	8494	
9407 orf1ab V3048L	15214	
10319 orf1ab L3352F	10711	
10755 orf1ab A3497V	7401	
13180 orf1ab silent	15598	
14408 orf1ab P314L	8038	
14805 orf1ab silent	10018	
16306 orf1ab F947L	14799	
17913 orf1ab silent	3334	
18060 orf1ab silent	6365	
18424 orf1ab N1653D	10818	
19421 orf1ab S1985L	8715	
21304 orf1ab R2613C	6760	
23403 S D614G	9786	
23593 S Q677H	10799	
25563 orf3a Q57H	6488	
25907 orf3a G172V	4187	
26775 M A85S	8235	
27294 orf6 silent	5153	
27528 orf7a silent	3466	
27964 orf8 S24L	7586	
28144 orf8 S84L	5287	
28472 N P67S	5598	
28869 N P199L	884	
29374 N silent	3738	
29395 N K374N	4393	
29402 N D377Y	4495	
	VSP0988-1	

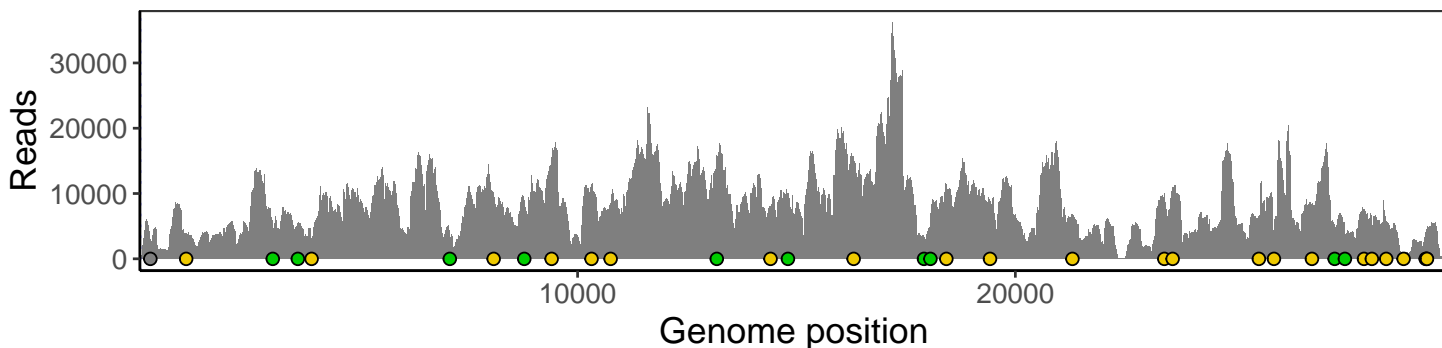
Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

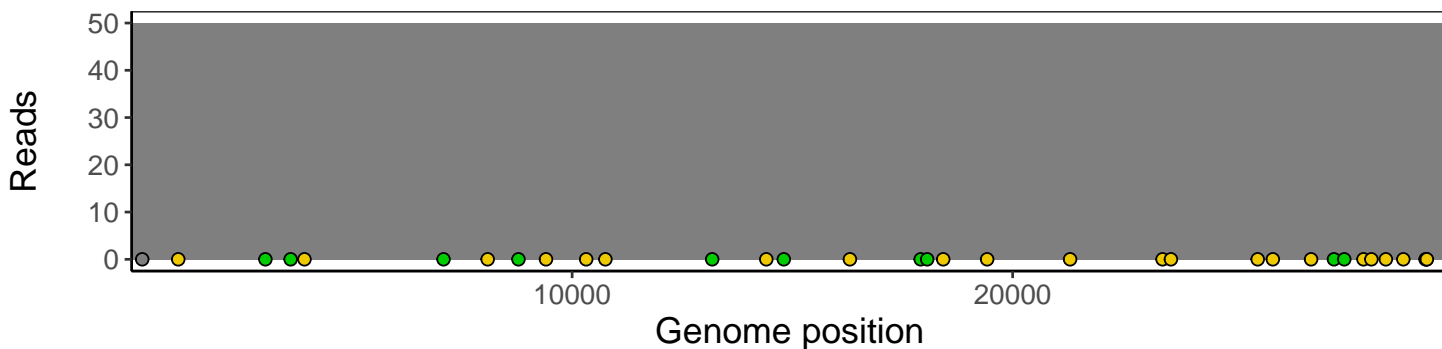
Analyses of individual experiments and composite results

VSP0988-1 | 2021-03-08 | Saline | UPHS-0056 | genomes | single experiment

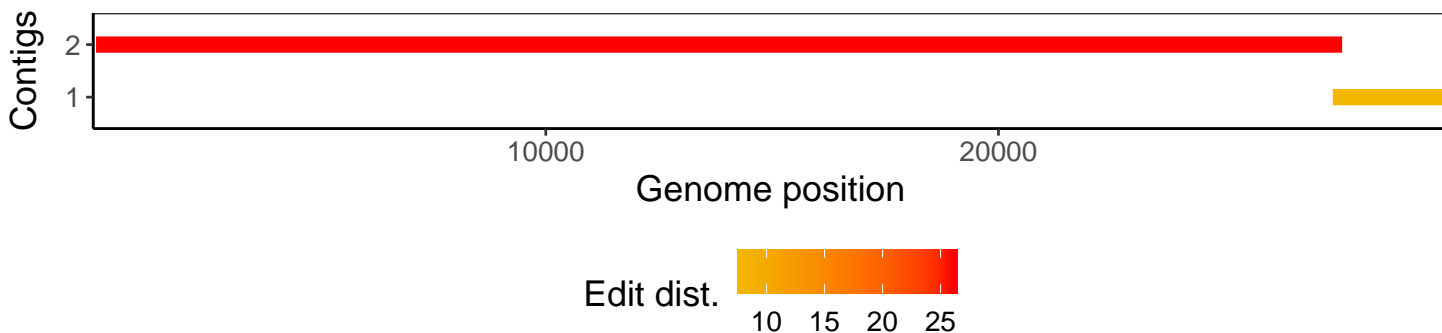
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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
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
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