

# COVID-19 subject UPHS-0863

*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.

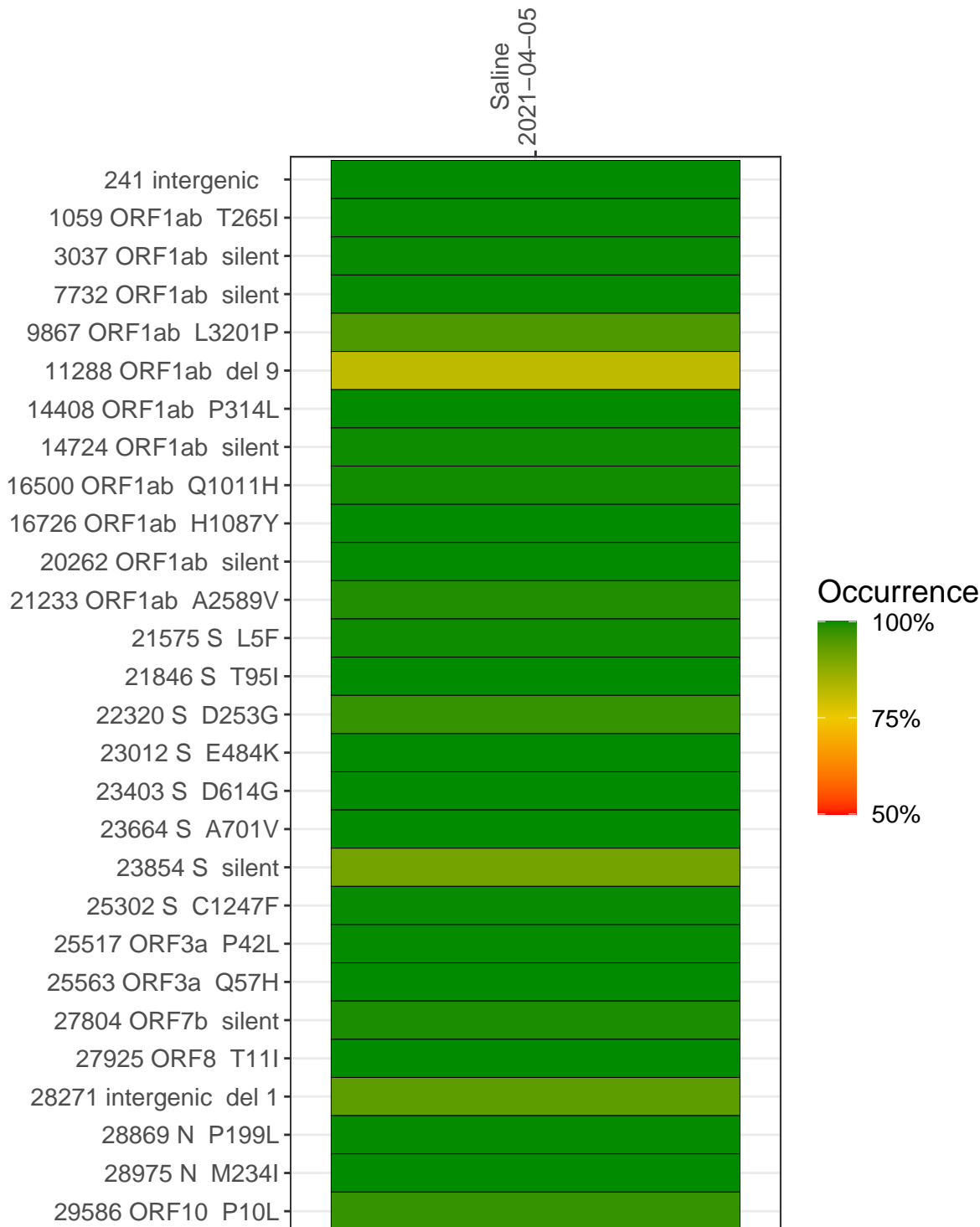
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP2077-2	single experiment	NA	Saline	2021-04-05	29.83	B.1.526	99.9%	99.8%

## 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 2021-04-05	
241 intergenic	219	
1059 ORF1ab T265I	969	
3037 ORF1ab silent	698	
7732 ORF1ab silent	3339	
9867 ORF1ab L3201P	928	
11288 ORF1ab del 9	1584	
14408 ORF1ab P314L	1604	
14724 ORF1ab silent	4213	
16500 ORF1ab Q1011H	5321	
16726 ORF1ab H1087Y	4340	
20262 ORF1ab silent	4227	
21233 ORF1ab A2589V	7482	
21575 S L5F	887	
21846 S T95I	1572	
22320 S D253G	519	
23012 S E484K	19	
23403 S D614G	3906	
23664 S A701V	815	
23854 S silent	1224	
25302 S C1247F	1231	
25517 ORF3a P42L	1769	
25563 ORF3a Q57H	2761	
27804 ORF7b silent	5268	
27925 ORF8 T11I	159	
28271 intergenic del 1	2184	
28869 N P199L	2006	
28975 N M234I	2392	
29586 ORF10 P10L	4083	
	VSP2077-2	

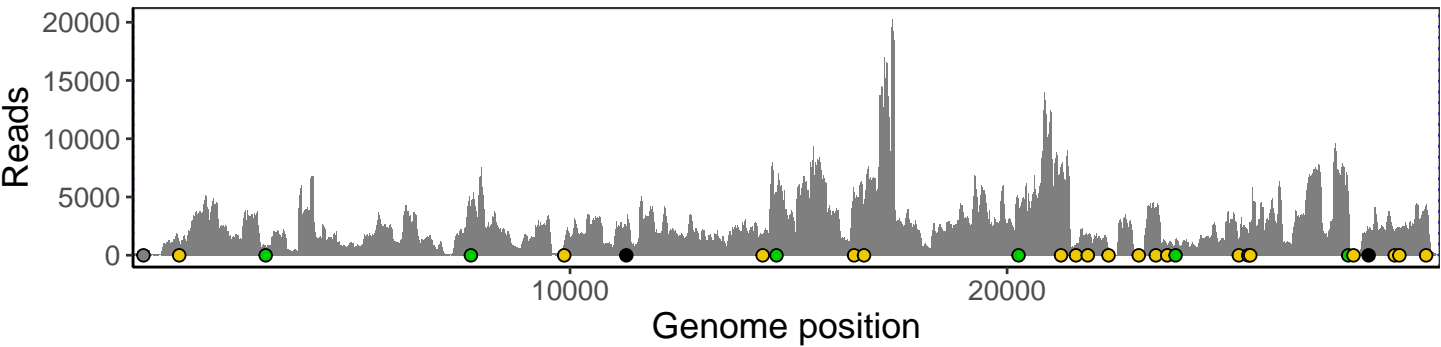
Base change

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

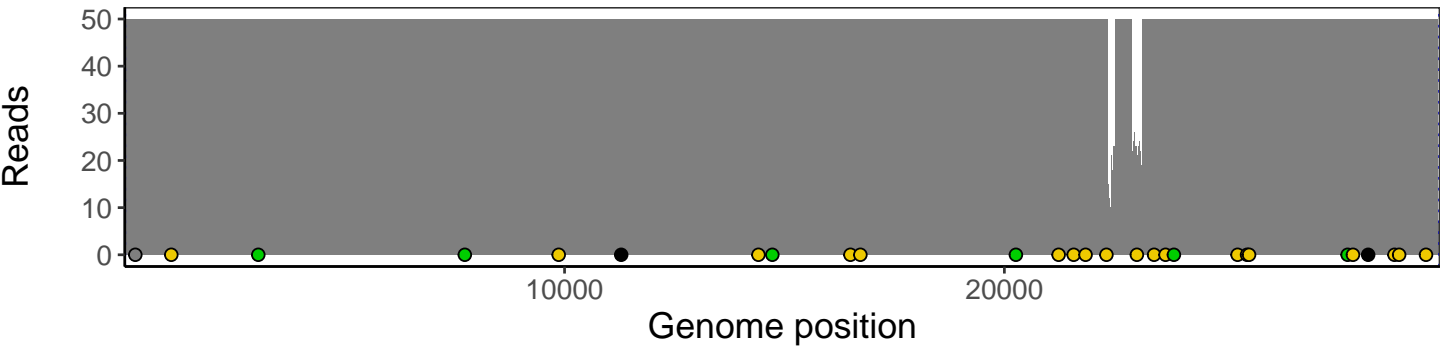
# Analyses of individual experiments and composite results

VSP2077-2 | 2021-04-05 | Saline | UPHS-0863 | genomes | single experiment

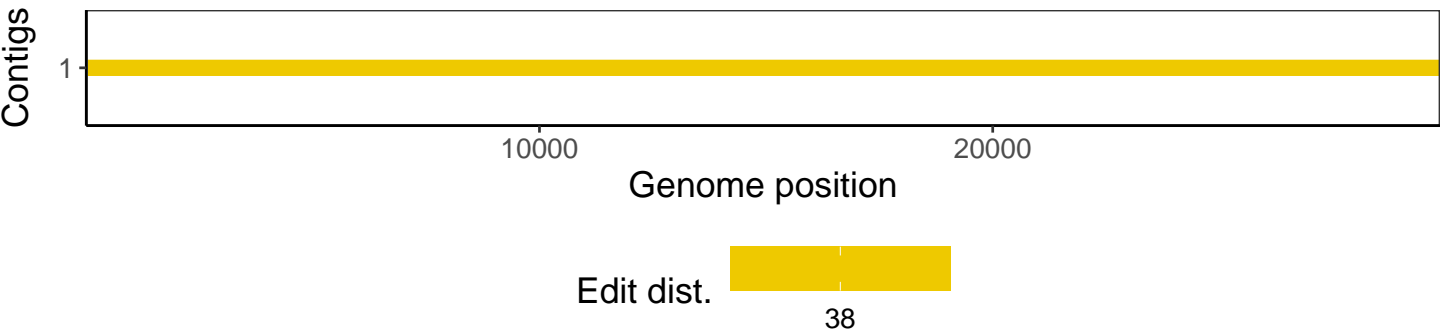
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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
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