

# COVID-19 subject HUP PH-0021

*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.

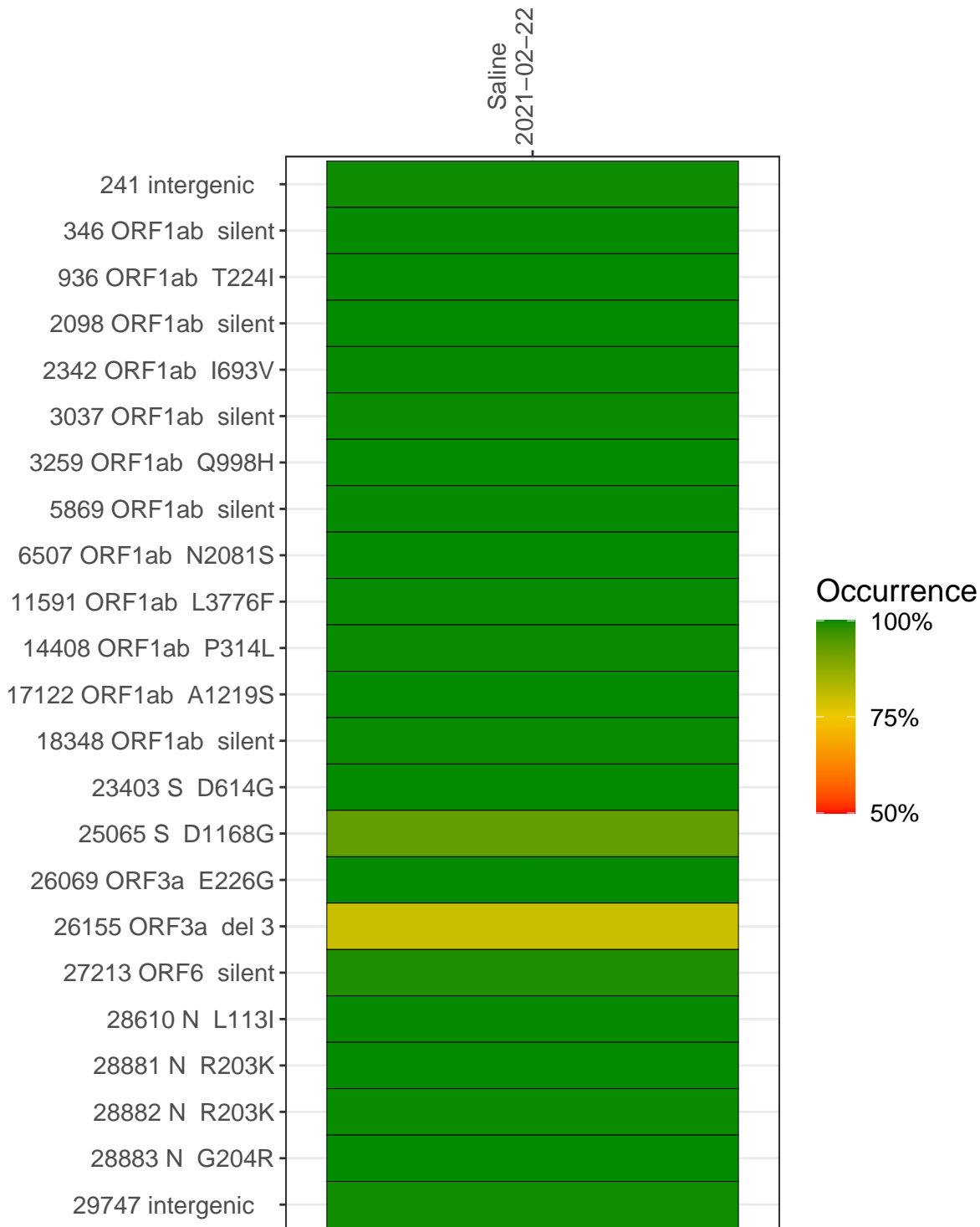
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP0865-1	single experiment	NA	Saline	2021-02-22	29.83	B.1.1.434	100.0%	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  
2021-02-22

241 intergenic	5089
346 ORF1ab silent	12060
936 ORF1ab T224I	17689
2098 ORF1ab silent	7963
2342 ORF1ab I693V	5797
3037 ORF1ab silent	9683
3259 ORF1ab Q998H	13604
5869 ORF1ab silent	16274
6507 ORF1ab N2081S	24744
11591 ORF1ab L3776F	36778
14408 ORF1ab P314L	11409
17122 ORF1ab A1219S	50706
18348 ORF1ab silent	12525
23403 S D614G	15073
25065 S D1168G	8486
26069 ORF3a E226G	26472
26155 ORF3a del 3	8283
27213 ORF6 silent	12904
28610 N L113I	9953
28881 N R203K	1264
28882 N R203K	1262
28883 N G204R	1266
29747 intergenic	1903

Base change

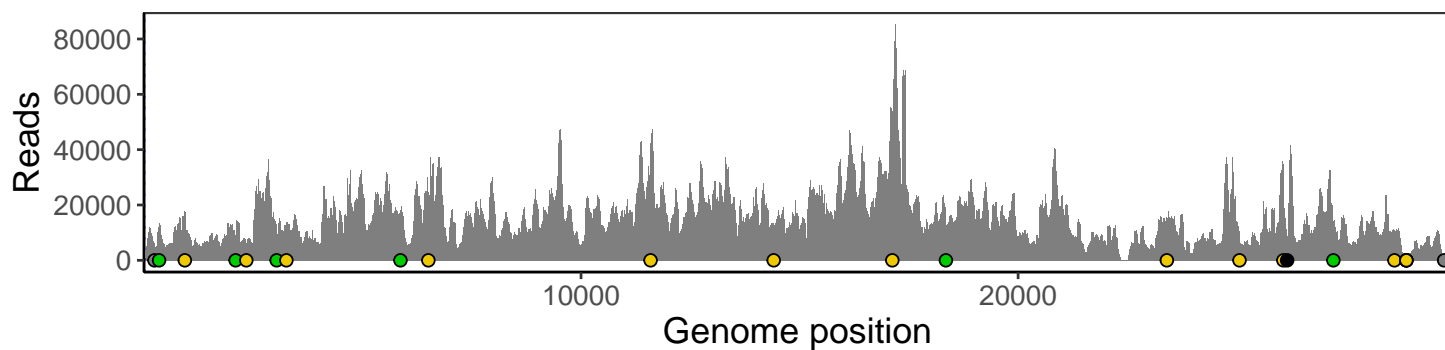


VSP0865-1

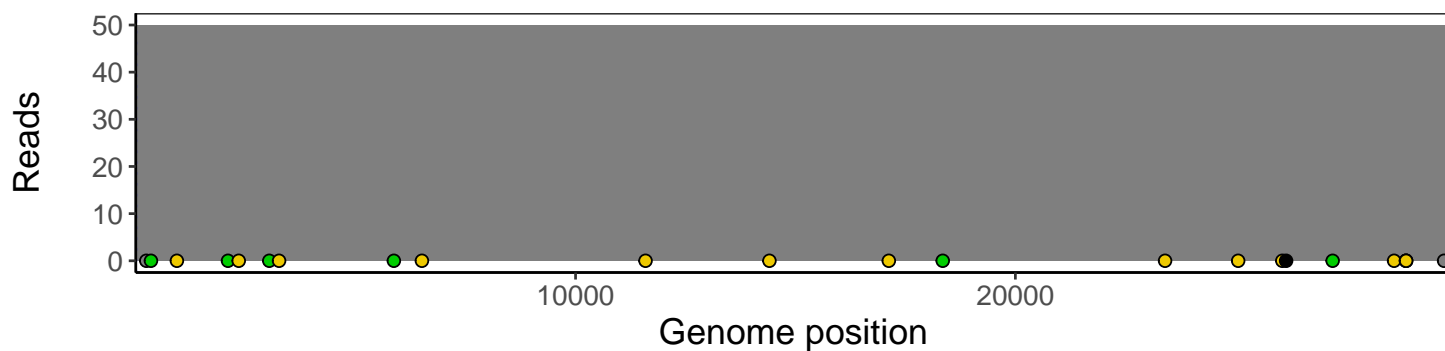
## Analyses of individual experiments and composite results

VSP0865-1 | 2021-02-22 | Saline | HUP-PH-0021 | genomes | single experiment

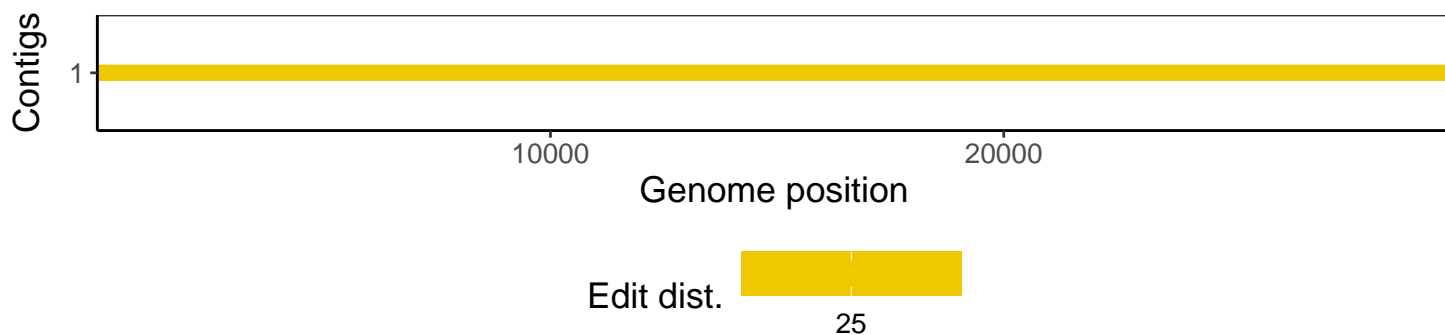
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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