

# COVID-19 subject HUP Q-0022

*2021-03-29*

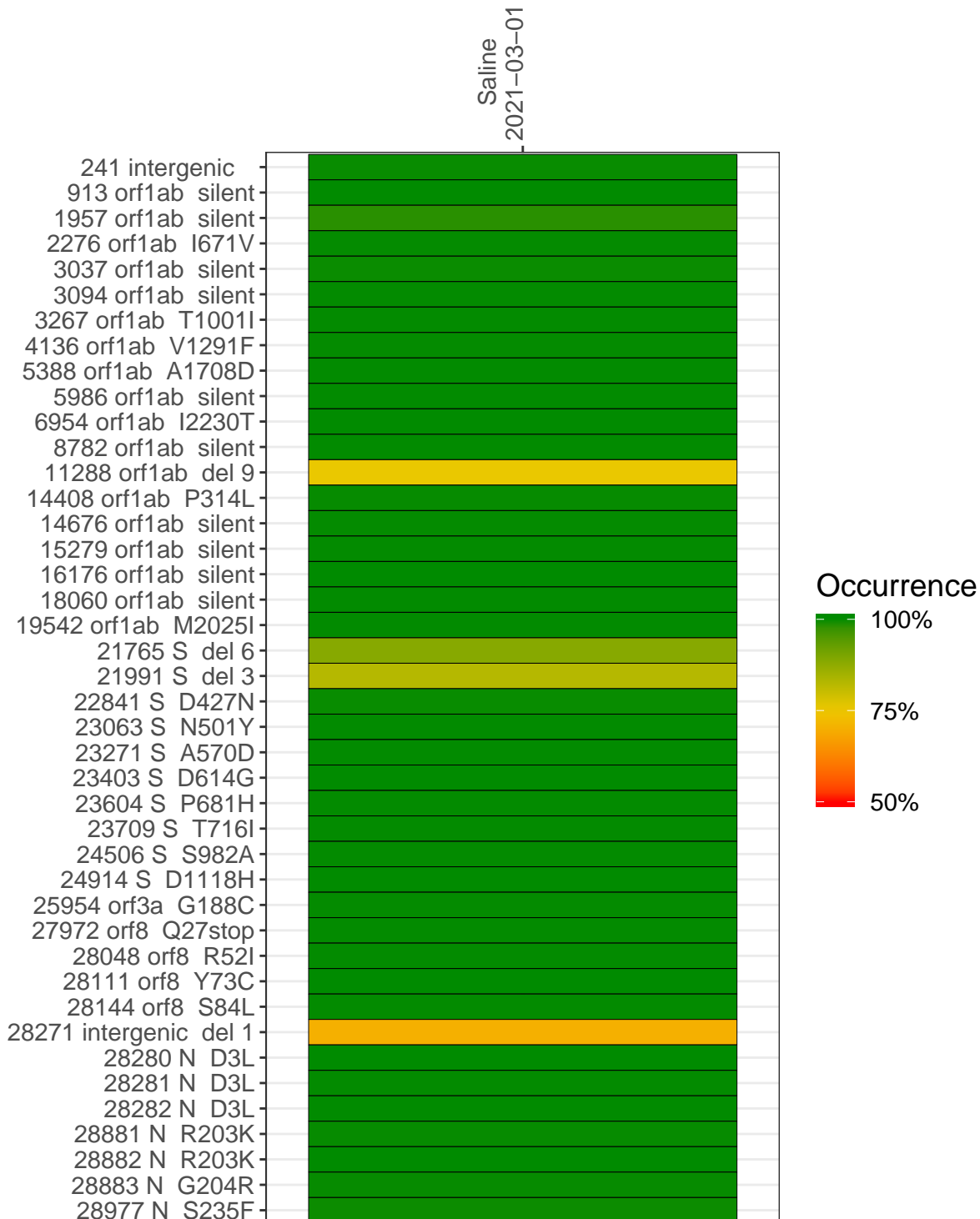
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0886-1	single experiment	NA	Saline	2021-03-01	29.92	B.1.1.7	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

241 intergenic	3110
913 orf1ab silent	9117
1957 orf1ab silent	5183
2276 orf1ab I671V	2940
3037 orf1ab silent	6015
3094 orf1ab silent	6465
3267 orf1ab T1001I	7989
4136 orf1ab V1291F	10198
5388 orf1ab A1708D	11722
5986 orf1ab silent	5349
6954 orf1ab I2230T	3568
8782 orf1ab silent	10309
11288 orf1ab del 9	11021
14408 orf1ab P314L	8933
14676 orf1ab silent	4905
15279 orf1ab silent	11076
16176 orf1ab silent	17108
18060 orf1ab silent	9019
19542 orf1ab M2025I	4249
21765 S del 6	4377
21991 S del 3	1894
22841 S D427N	4893
23063 S N501Y	7608
23271 S A570D	8919
23403 S D614G	9909
23604 S P681H	10245
23709 S T716I	9650
24506 S S982A	5491
24914 S D1118H	19729
25954 orf3a G188C	8132
27972 orf8 Q27stop	12366
28048 orf8 R52I	11170
28111 orf8 Y73C	8862
28144 orf8 S84L	6331
28271 intergenic del 1	4169
28280 N D3L	2890
28281 N D3L	2890
28282 N D3L	2964
28881 N R203K	718
28882 N R203K	715
28883 N G204R	720
28977 N S235F	671

Base change

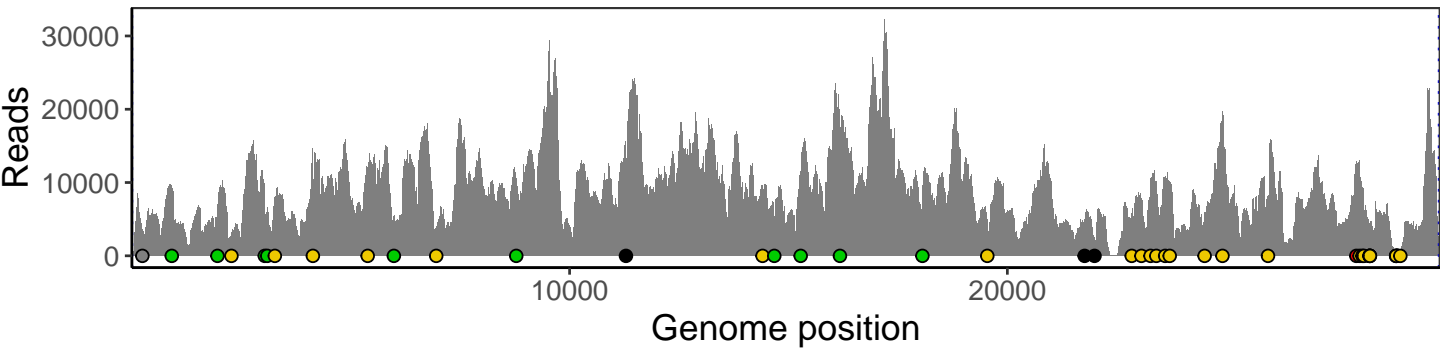
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP0886-1

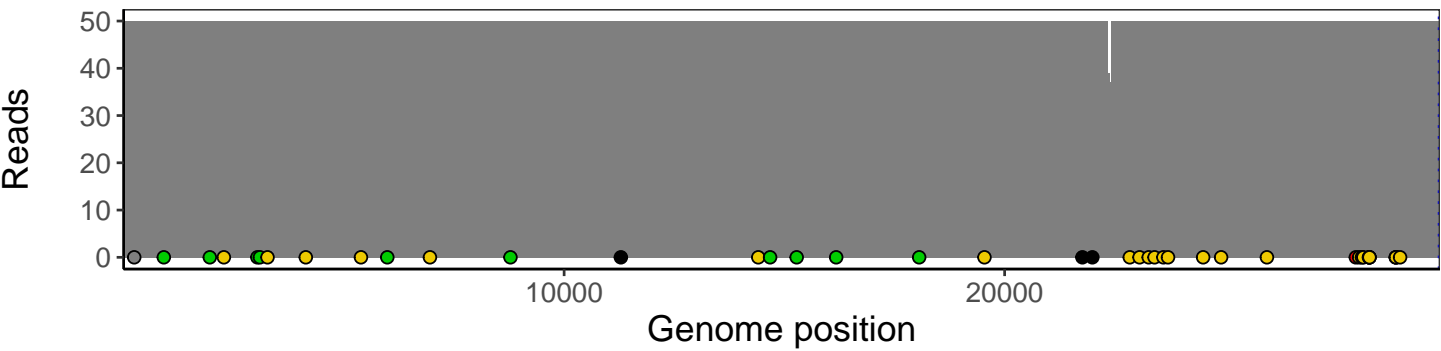
# Analyses of individual experiments and composite results

VSP0886-1 | 2021-03-01 | Saline | HUP Q-0022 | genomes | single experiment

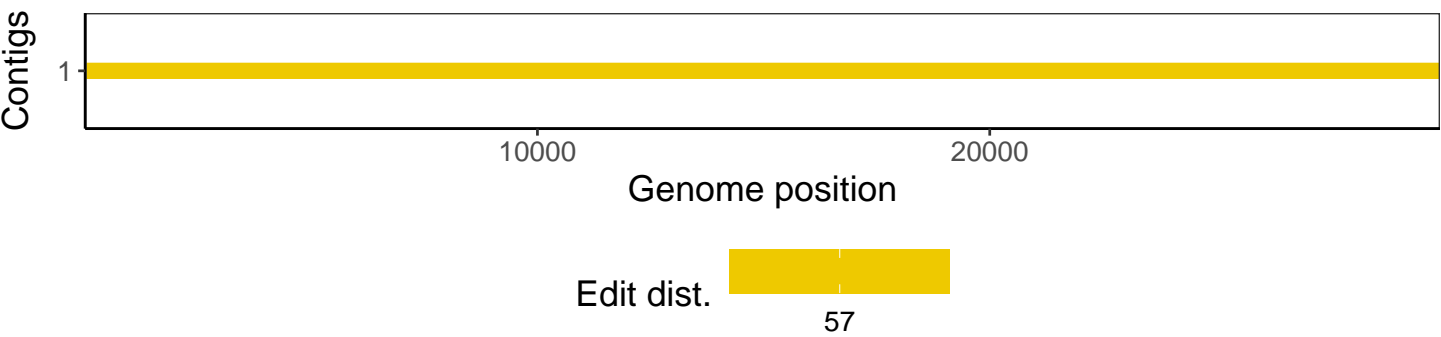
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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