

COVID-19 subject HUP-Q-0001

2021-06-23

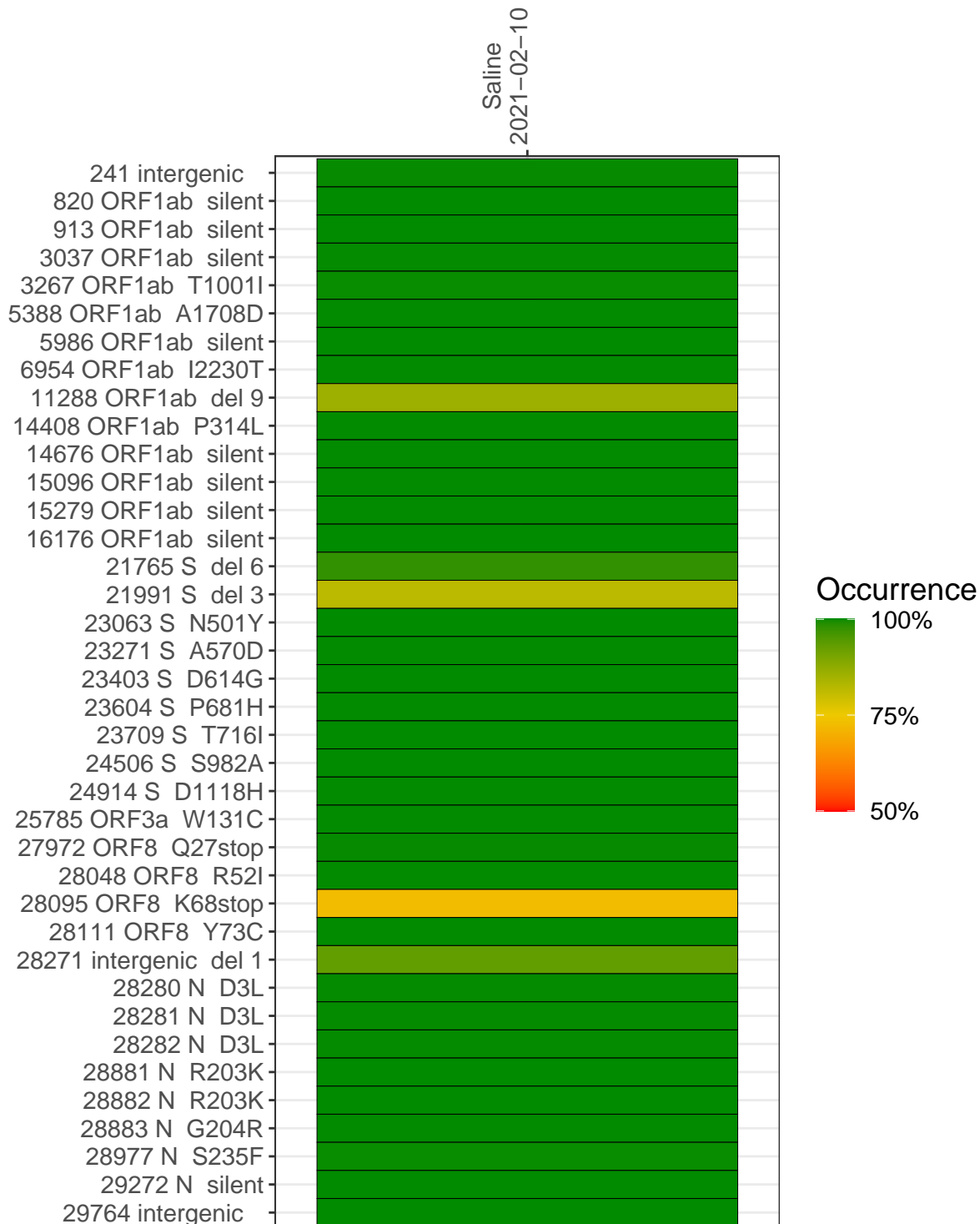
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 (≥ 5 reads)
VSP0813-1	single experiment	NA	Saline	2021-02-10	29.67	B.1.1.7	100.0%	99.7%

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 2021-02-10	
241 intergenic	8587	
820 ORF1ab silent	18140	
913 ORF1ab silent	16374	
3037 ORF1ab silent	13019	
3267 ORF1ab T1001I	11567	
5388 ORF1ab A1708D	14907	
5986 ORF1ab silent	6681	
6954 ORF1ab I2230T	12922	
11288 ORF1ab del 9	16882	
14408 ORF1ab P314L	13354	
14676 ORF1ab silent	17273	
15096 ORF1ab silent	10397	
15279 ORF1ab silent	16168	
16176 ORF1ab silent	11835	
21765 S del 6	3783	
21991 S del 3	1673	
23063 S N501Y	2948	
23271 S A570D	12737	
23403 S D614G	14821	
23604 S P681H	17024	
23709 S T716I	10355	
24506 S S982A	6535	
24914 S D1118H	19709	
25785 ORF3a W131C	18718	
27972 ORF8 Q27stop	9167	
28048 ORF8 R52I	7505	
28095 ORF8 K68stop	6467	
28111 ORF8 Y73C	6248	
28271 intergenic del 1	14078	
28280 N D3L	13056	
28281 N D3L	13056	
28282 N D3L	13096	
28881 N R203K	4590	
28882 N R203K	4587	
28883 N G204R	4594	
28977 N S235F	2065	
29272 N silent	11467	
29764 intergenic	1400	

Base change

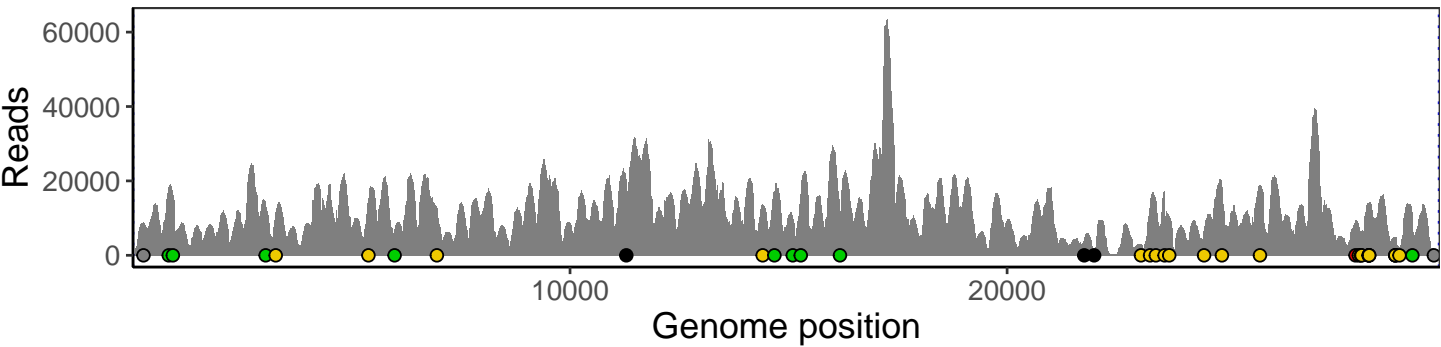
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP0813-1

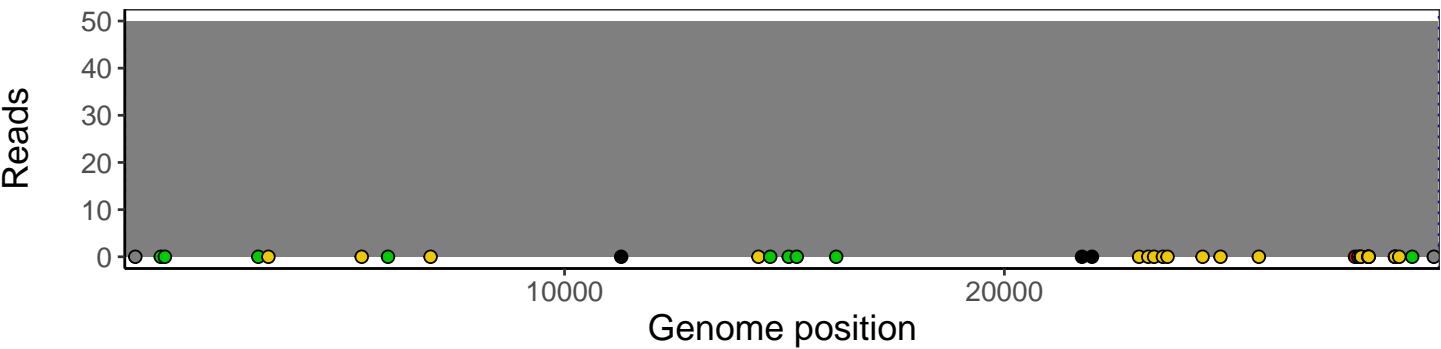
Analyses of individual experiments and composite results

VSP0813-1 | 2021-02-10 | Saline | HUP-Q-0001 | genomes | single experiment

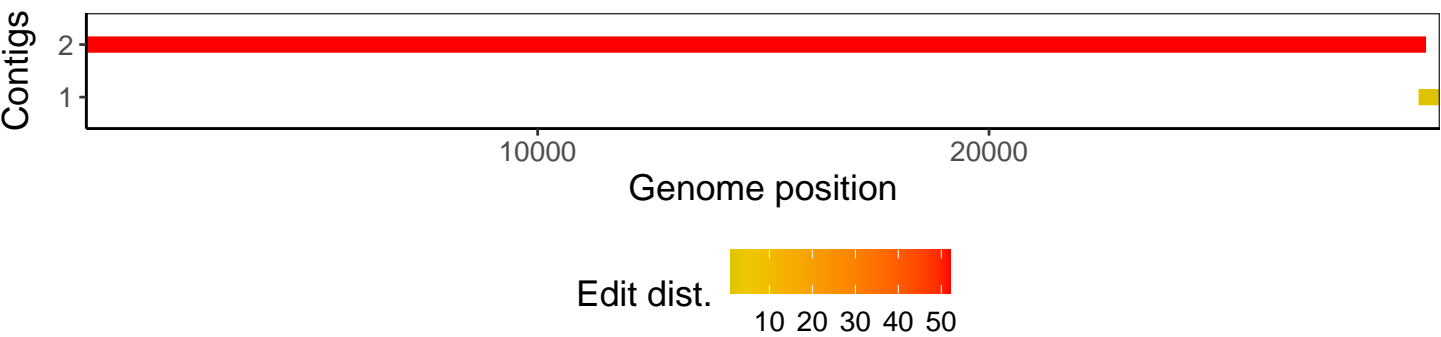
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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