

COVID-19 subject HUP Q-0006

2021-06-23

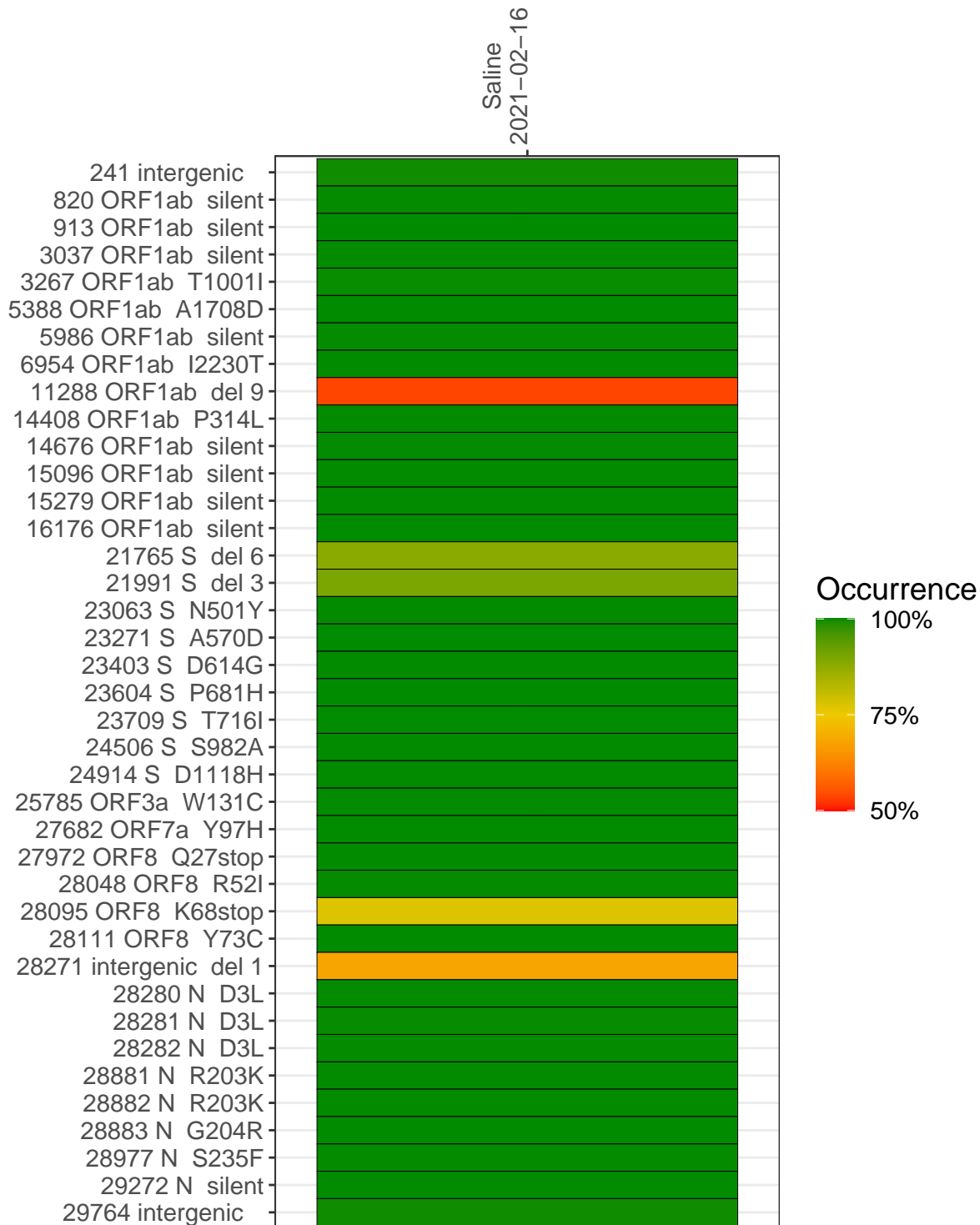
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0869-1	single experiment	NA	Saline	2021-02-16	29.88	B.1.1.7	99.9%	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 2021-02-16	
241 intergenic	4774	
820 ORF1ab silent	18603	
913 ORF1ab silent	20061	
3037 ORF1ab silent	9363	
3267 ORF1ab T1001I	20019	
5388 ORF1ab A1708D	15252	
5986 ORF1ab silent	6222	
6954 ORF1ab I2230T	7142	
11288 ORF1ab del 9	21829	
14408 ORF1ab P314L	7724	
14676 ORF1ab silent	12118	
15096 ORF1ab silent	12180	
15279 ORF1ab silent	29886	
16176 ORF1ab silent	41577	
21765 S del 6	4268	
21991 S del 3	5207	
23063 S N501Y	2841	
23271 S A570D	18513	
23403 S D614G	22653	
23604 S P681H	11767	
23709 S T716I	12542	
24506 S S982A	11804	
24914 S D1118H	39538	
25785 ORF3a W131C	16838	
27682 ORF7a Y97H	11049	
27972 ORF8 Q27stop	21985	
28048 ORF8 R52I	20715	
28095 ORF8 K68stop	28024	
28111 ORF8 Y73C	25945	
28271 intergenic del 1	13441	
28280 N D3L	8805	
28281 N D3L	8807	
28282 N D3L	9521	
28881 N R203K	1627	
28882 N R203K	1614	
28883 N G204R	1623	
28977 N S235F	3529	
29272 N silent	9702	
29764 intergenic	1445	

Base change

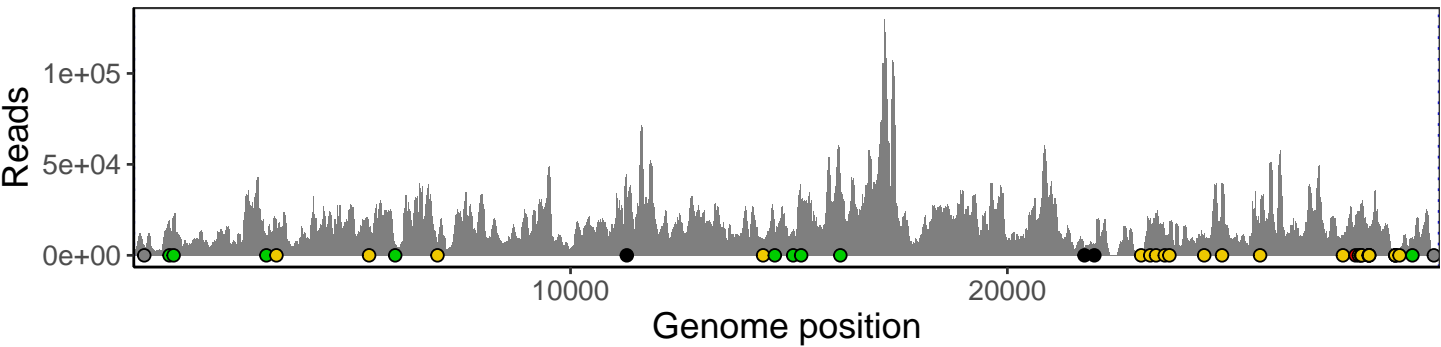
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP0869-1

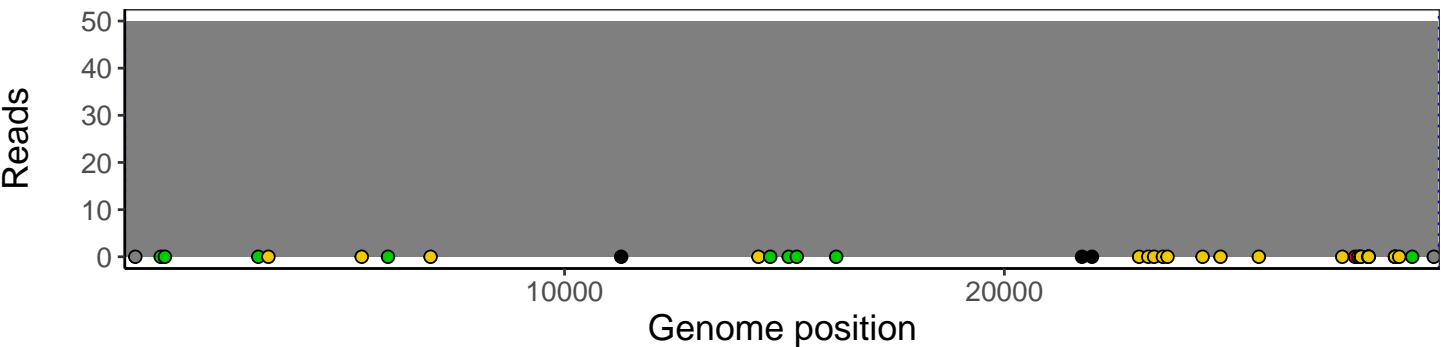
Analyses of individual experiments and composite results

VSP0869-1 | 2021-02-16 | Saline | HUP-Q-0006 | genomes | single experiment

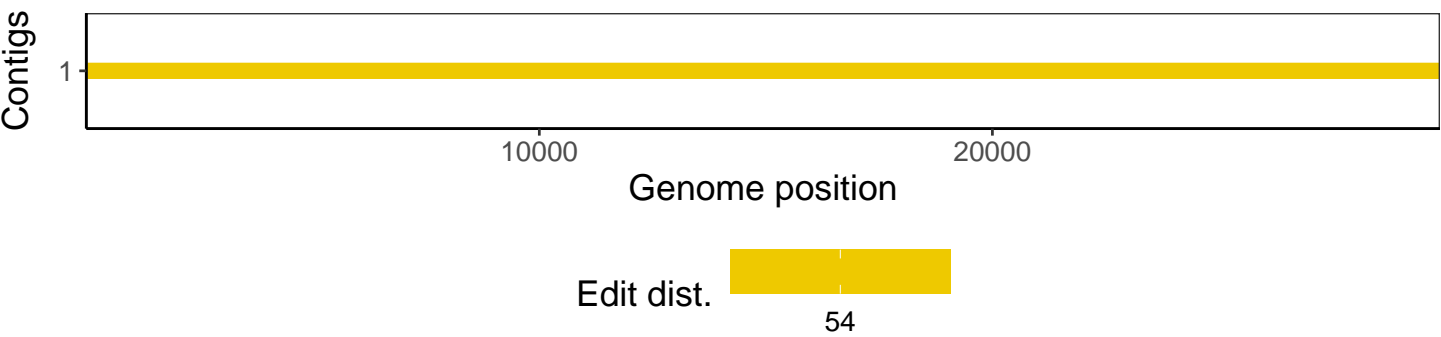
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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