

COVID-19 subject HUP Q-0011

2021-04-17

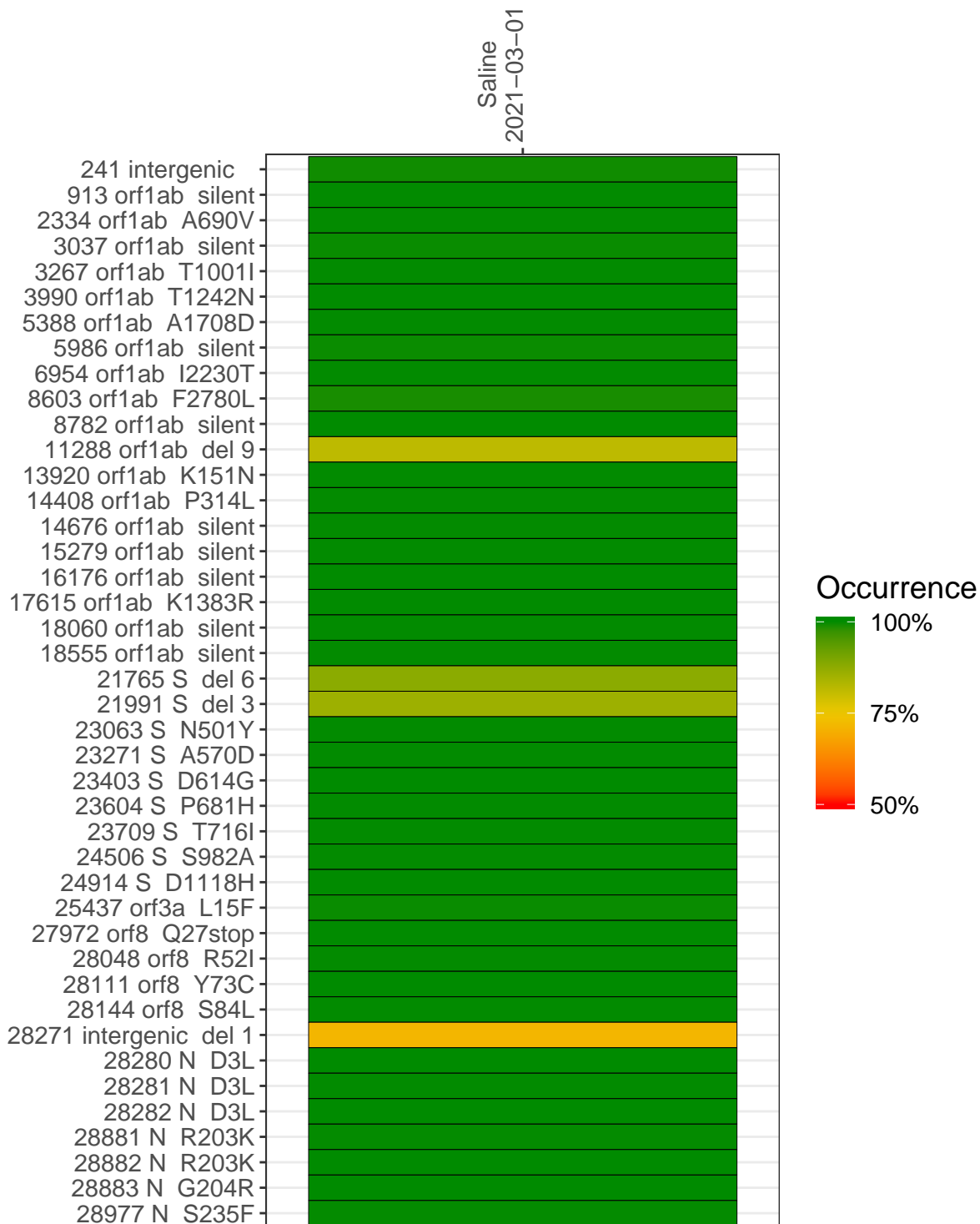
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0879-1	single experiment	NA	Saline	2021-03-01	29.82	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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 2021-03-01	
241 intergenic	2485	
913 orf1ab silent	8920	
2334 orf1ab A690V	3131	
3037 orf1ab silent	5767	
3267 orf1ab T1001I	7137	
3990 orf1ab T1242N	5837	
5388 orf1ab A1708D	12193	
5986 orf1ab silent	4711	
6954 orf1ab I2230T	2737	
8603 orf1ab F2780L	4951	
8782 orf1ab silent	9912	
11288 orf1ab del 9	9524	
13920 orf1ab K151N	8392	
14408 orf1ab P314L	8499	
14676 orf1ab silent	5054	
15279 orf1ab silent	11036	
16176 orf1ab silent	15810	
17615 orf1ab K1383R	10539	
18060 orf1ab silent	8261	
18555 orf1ab silent	7677	
21765 S del 6	4334	
21991 S del 3	2035	
23063 S N501Y	8771	
23271 S A570D	7755	
23403 S D614G	8679	
23604 S P681H	9508	
23709 S T716I	8799	
24506 S S982A	5144	
24914 S D1118H	15666	
25437 orf3a L15F	5889	
27972 orf8 Q27stop	12639	
28048 orf8 R52I	10959	
28111 orf8 Y73C	9276	
28144 orf8 S84L	6735	
28271 intergenic del 1	4784	
28280 N D3L	3388	
28281 N D3L	3388	
28282 N D3L	3472	
28881 N R203K	1048	
28882 N R203K	1039	
28883 N G204R	1045	
28977 N S235F	1133	

Base change

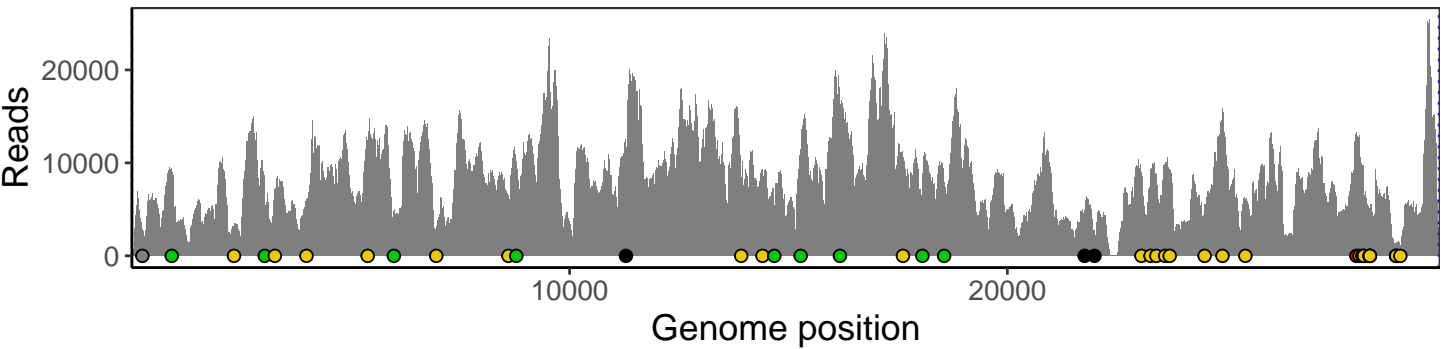
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP0879-1

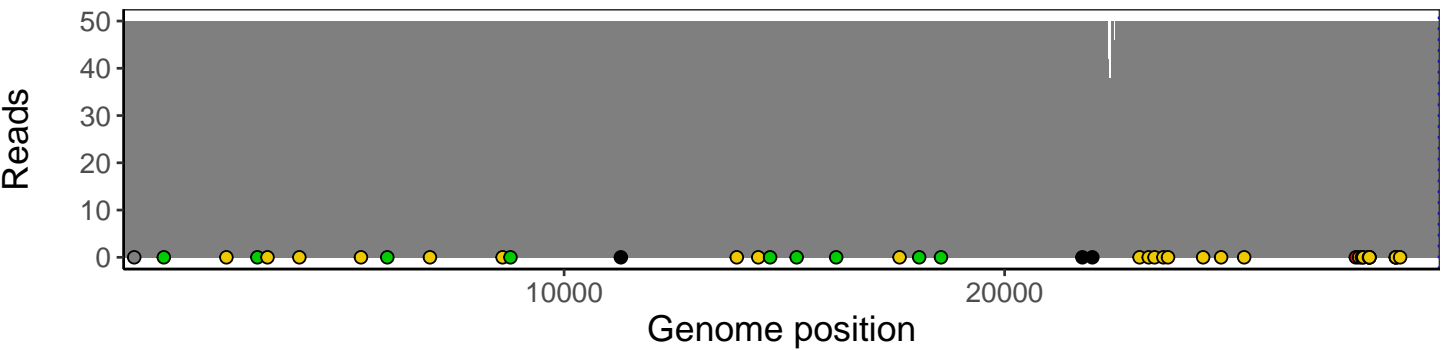
Analyses of individual experiments and composite results

VSP0879-1 | 2021-03-01 | Saline | HUP Q-0011 | genomes | single experiment

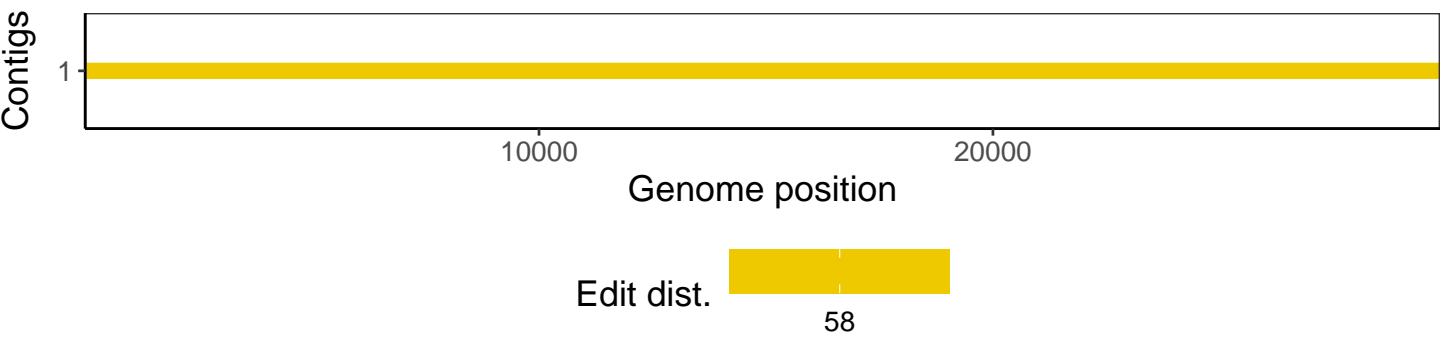
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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