

COVID-19 subject UPHS-0099

2021-04-17

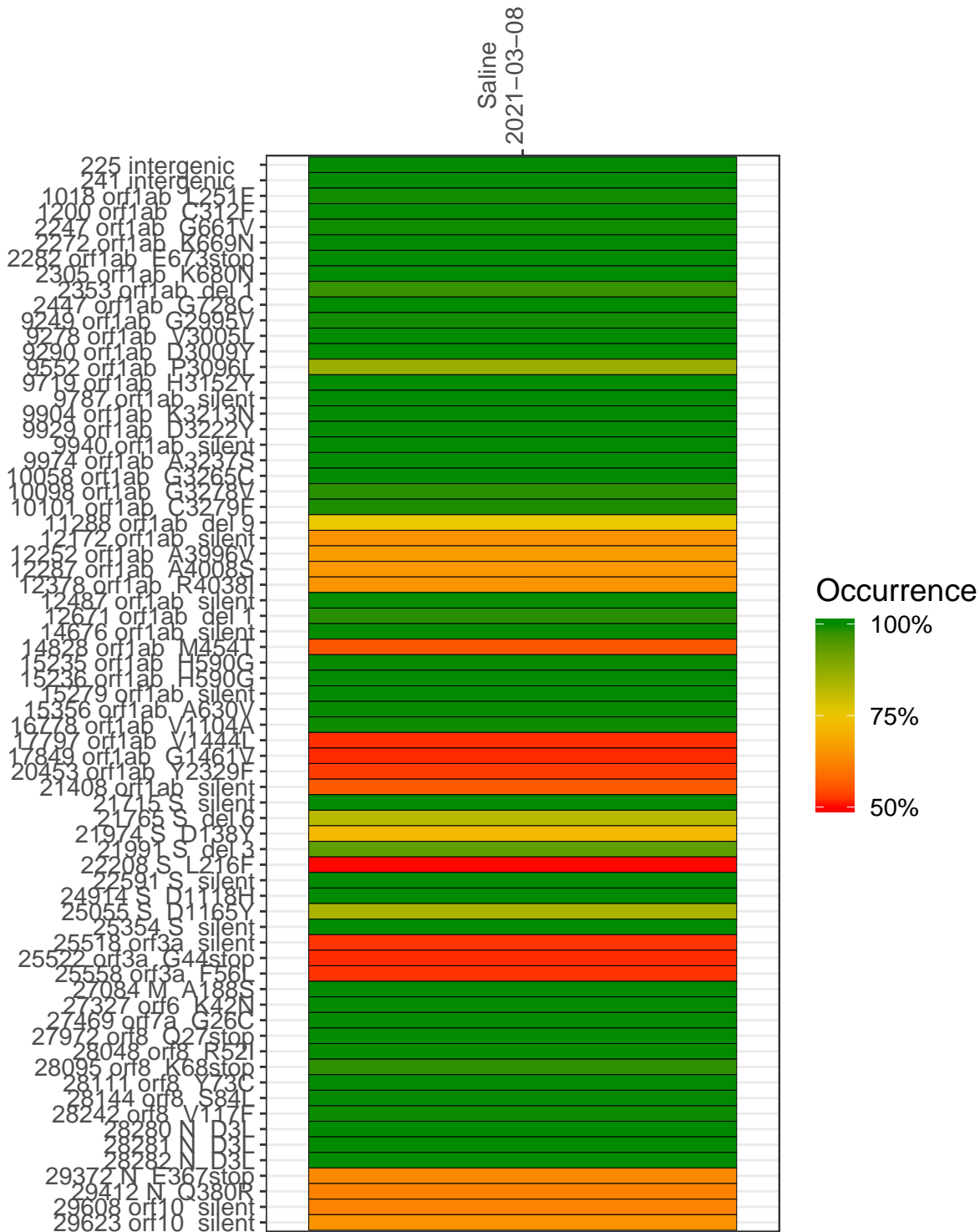
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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) |
|------------|-------------------|---------|-------------|-------------|---------------------|---------|-------------------------|---|
| VSP1030-1 | single experiment | NA | Saline | 2021-03-08 | 1.25 | NA | 38.2% | 36.9% |

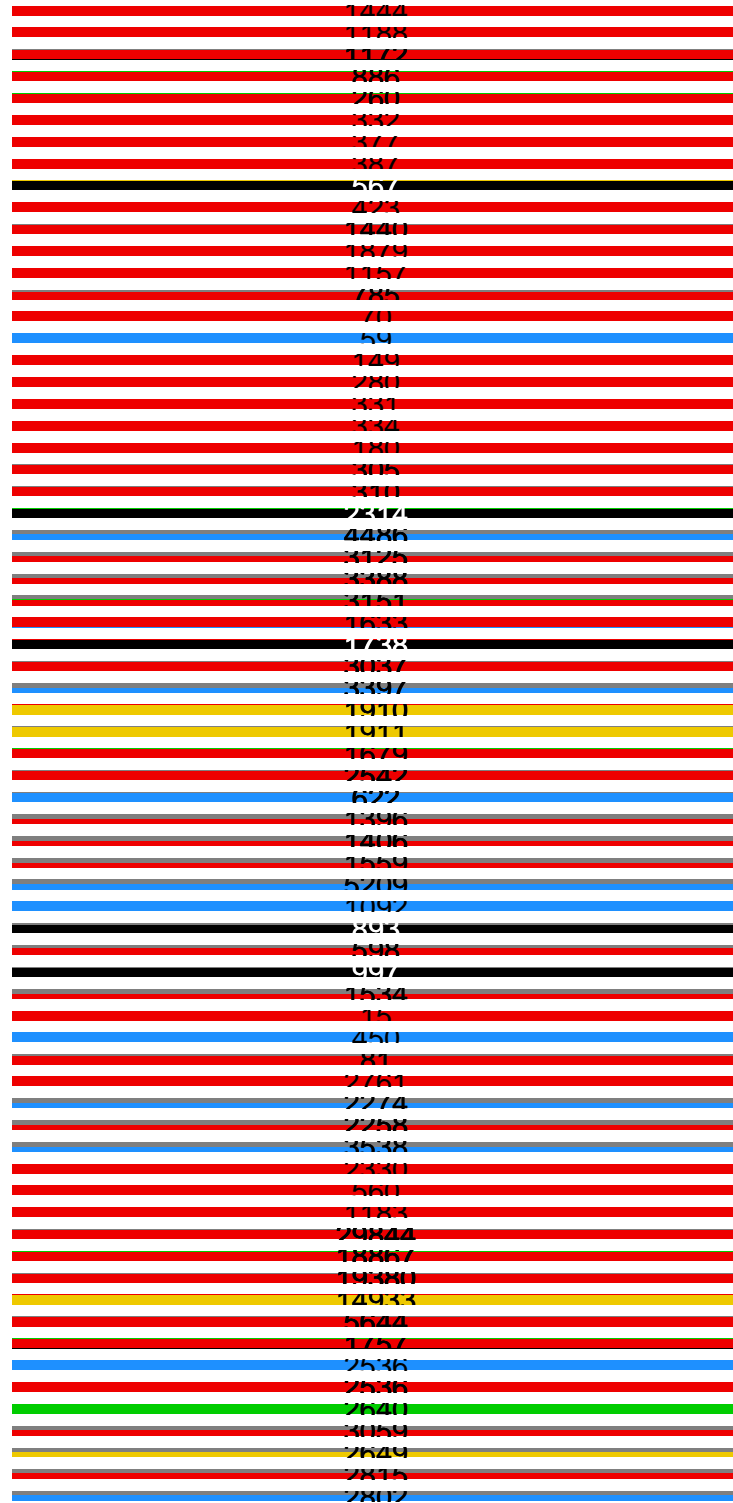
Variants shared across samples

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
2021-03-08

225 intergenic
241 intergenic
1018 orf1ab L251F
1200 orf1ab C312F
2247 orf1ab G661V
2272 orf1ab K669N
2282 orf1ab E673stop
2305 orf1ab K680N
2353 orf1ab del 1
2447 orf1ab G728C
9249 orf1ab G2995V
9278 orf1ab V3005L
9290 orf1ab D3009Y
9552 orf1ab P3096L
9719 orf1ab H3152Y
9787 orf1ab silent
9904 orf1ab K3213N
9929 orf1ab D3222Y
9940 orf1ab silent
9974 orf1ab A3237S
10058 orf1ab G3265C
10098 orf1ab G3278V
10101 orf1ab C3279F
11288 orf1ab del 9
12172 orf1ab silent
12252 orf1ab A3996V
12287 orf1ab A4008S
12378 orf1ab R4038I
12487 orf1ab silent
12671 orf1ab del 1
14676 orf1ab silent
14828 orf1ab M454T
15235 orf1ab H590G
15236 orf1ab H590G
15279 orf1ab silent
15356 orf1ab A630V
16778 orf1ab V1104A
17797 orf1ab V1444L
17849 orf1ab G1461V
20453 orf1ab Y2329F
21408 orf1ab silent
21715 S silent
21765 S del 6
21974 S D138Y
21991 S del 3
22208 S L216F
22591 S silent
24914 S D1118H
25055 S D1165Y
25354 S silent
25518 orf3a silent
25522 orf3a G44stop
25558 orf3a F56L
27084 M A188S
27327 orf6 K42N
27469 orf7a G26C
27972 orf8 Q27stop
28048 orf8 R52I
28095 orf8 K68stop
28111 orf8 Y73C
28144 orf8 S84L
28242 orf8 V117F
28280 N D3L
28281 N D3L
28282 N D3L
29372 N E367stop
29412 N Q380R
29608 orf10 silent
29623 orf10 silent



Base change

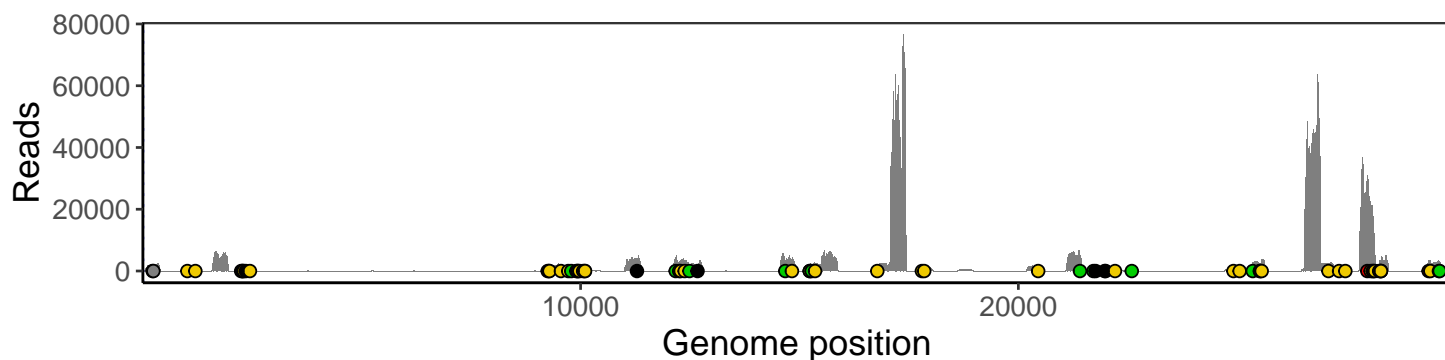
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP1030-1

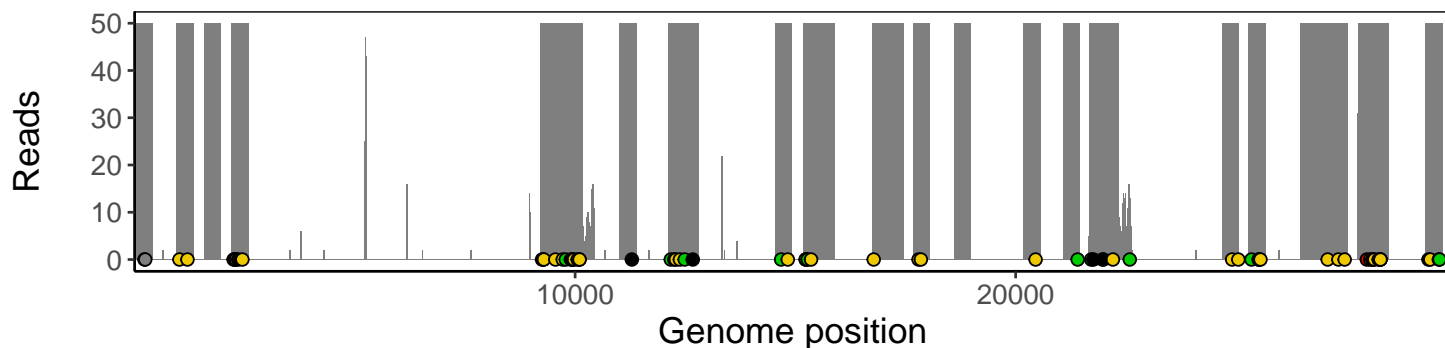
Analyses of individual experiments and composite results

VSP1030-1 | 2021-03-08 | Saline | UPHS-0099 | genomes | single experiment

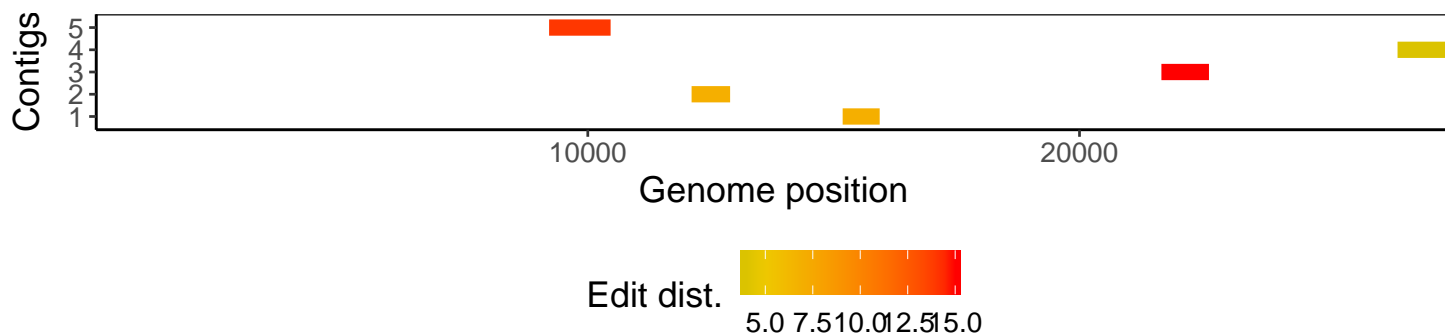
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 |