# COVID-19 subject HUP Q-0093

*2021-04-17*

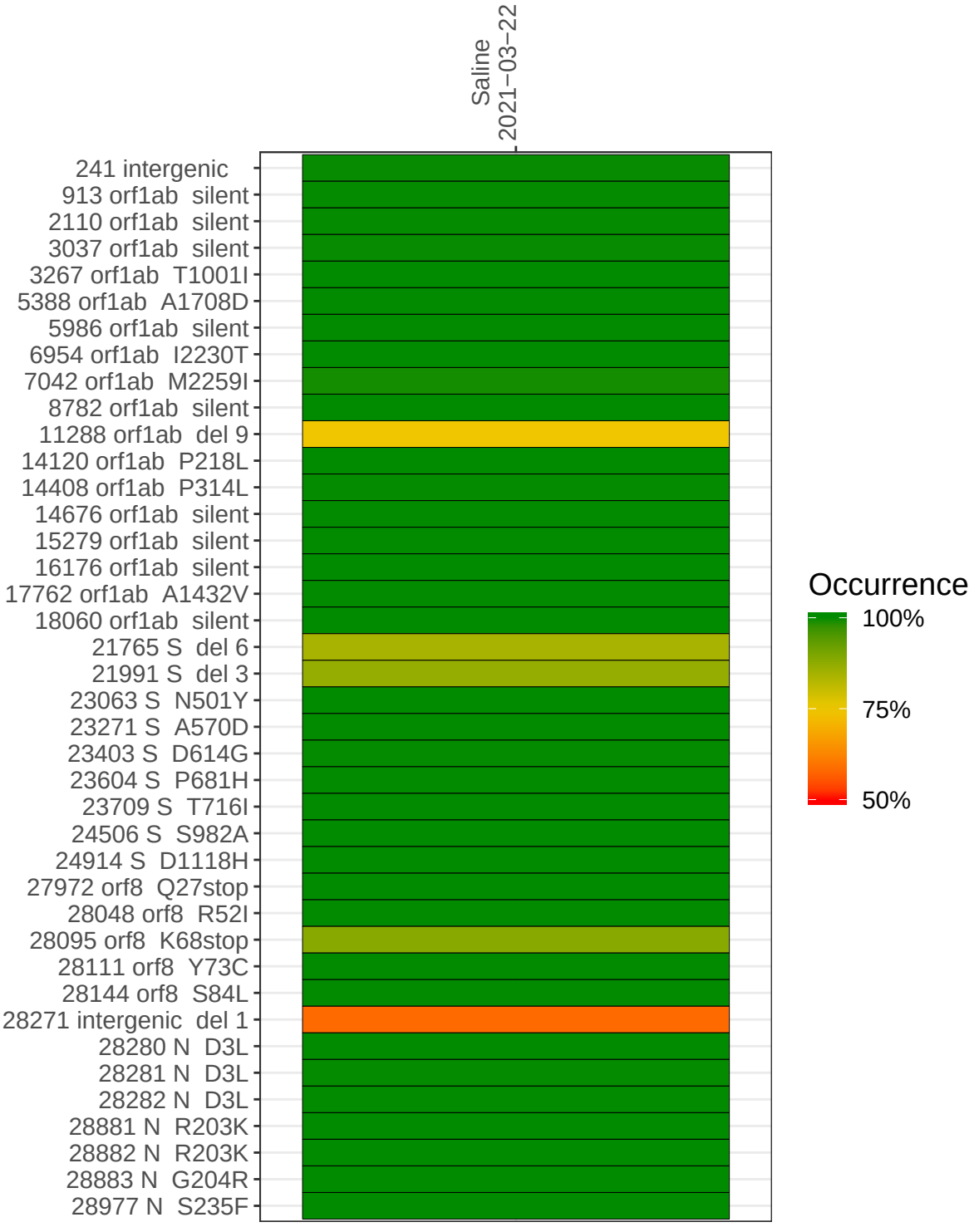
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

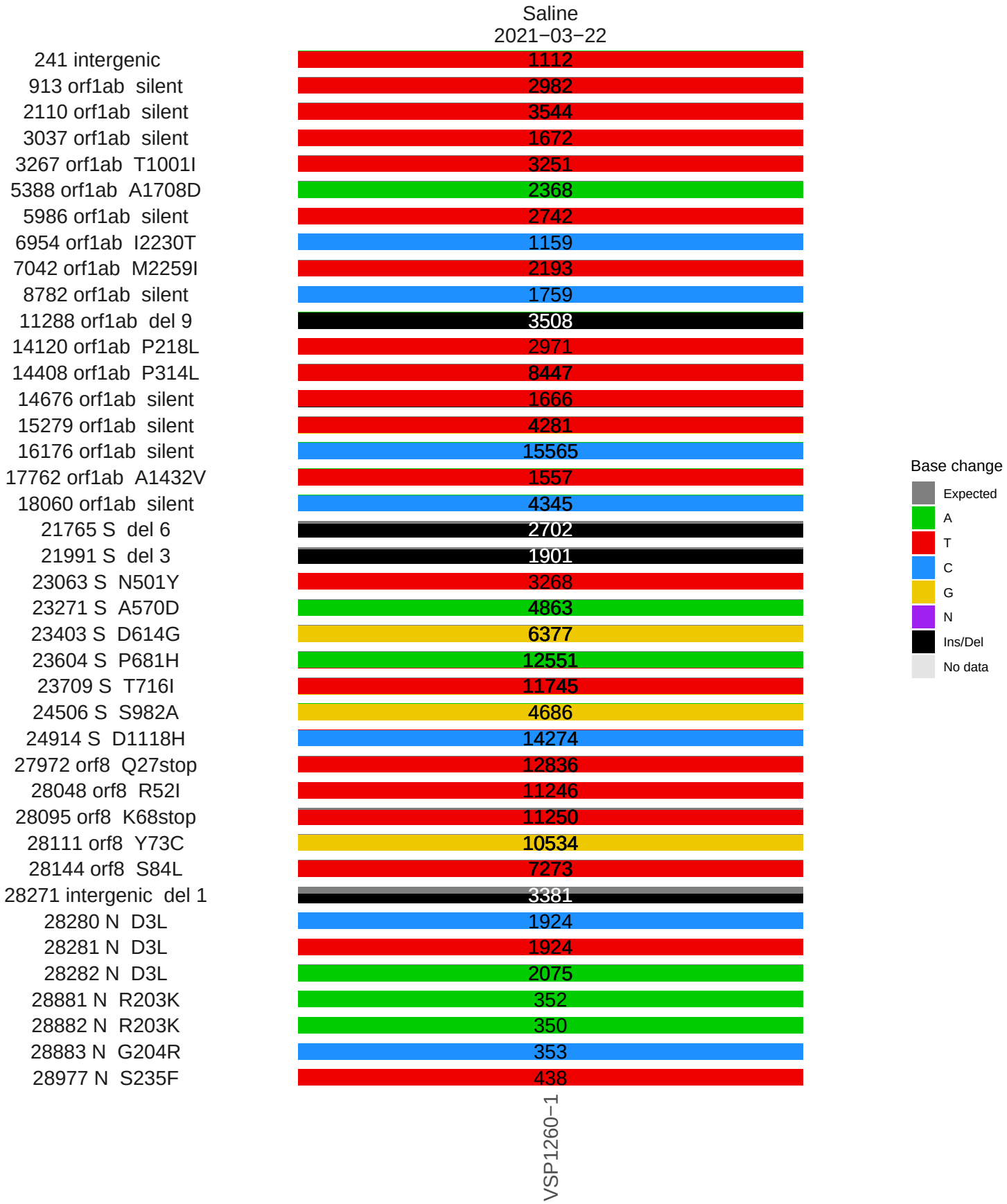
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1260-1 | single experiment | NA | Saline | 2021-03-22 | 29.84 | 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.

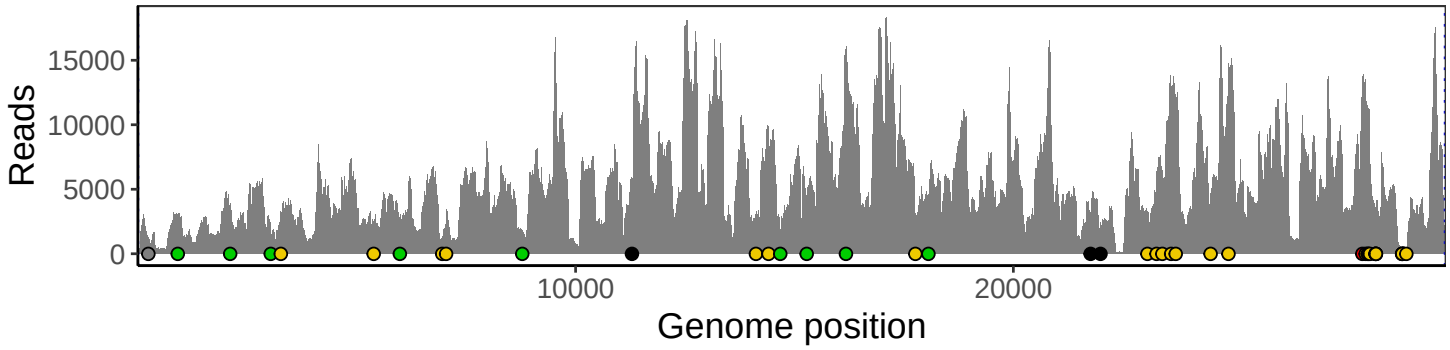



Saline
2021−03−22
241 intergenic 1112
913 orf1ab silent 2982
2110 orf1ab silent 3544
3037 orf1ab silent 1672
3267 orf1ab T1001I 3251
5388 orf1ab A1708D 2368
5986 orf1ab silent 2742
6954 orf1ab I2230T 1159
7042 orf1ab M2259I 2193
8782 orf1ab silent 1759
11288 orf1ab del 9 3508
14120 orf1ab P218L 2971
14408 orf1ab P314L 8447
14676 orf1ab silent 1666
15279 orf1ab silent 4281
16176 orf1ab silent 15565
17762 orf1ab A1432V 1557
18060 orf1ab silent 4345
21765 S del 6 2702
21991 S del 3 1901
23063 S N501Y 3268
23271 S A570D 4863
23403 S D614G 6377
23604 S P681H 12551
23709 S T716I 11745
24506 S S982A 4686
24914 S D1118H 14274
27972 orf8 Q27stop 12836
28048 orf8 R52I 11246
28095 orf8 K68stop 11250
28111 orf8 Y73C 10534
28144 orf8 S84L 7273
28271 intergenic del 1 3381
28280 N D3L 1924
28281 N D3L 1924
28282 N D3L 2075
28881 N R203K 352
28882 N R203K 350
28883 N G204R 353
28977 N S235F 438
VSP1260−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

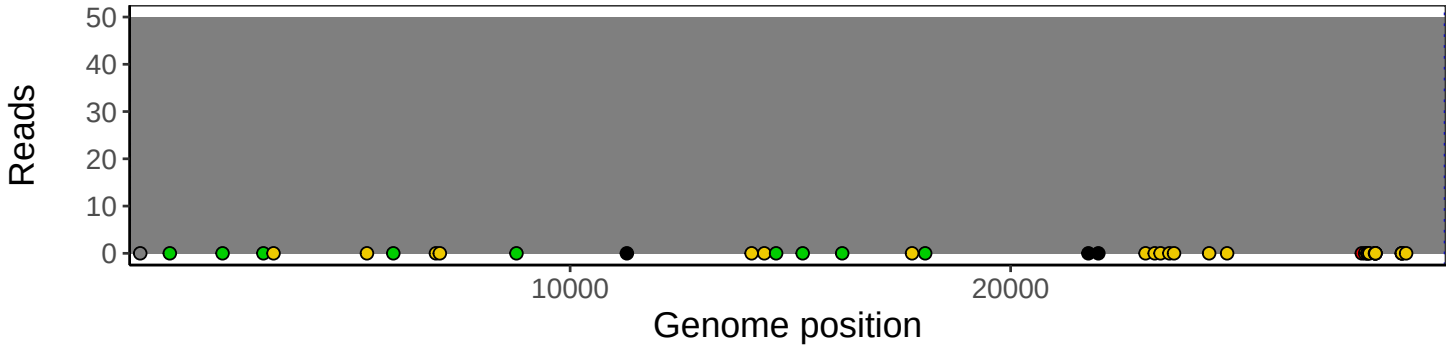
## Analyses of individual experiments and composite results

### VSP1260-1 | 2021-03-22 | Saline | HUP Q-0093 | genomes | single experiment

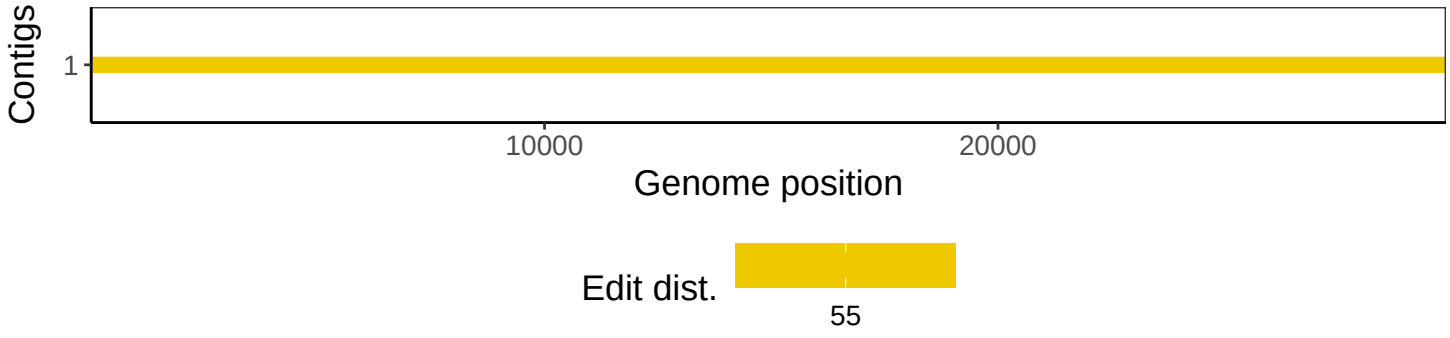
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 htslib 1.10 |
| bcftools | 1.10.2-34-g1a12af0-dirty Using htslib 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 |