# COVID-19 subject HUP Q-0008

*2021-04-17*

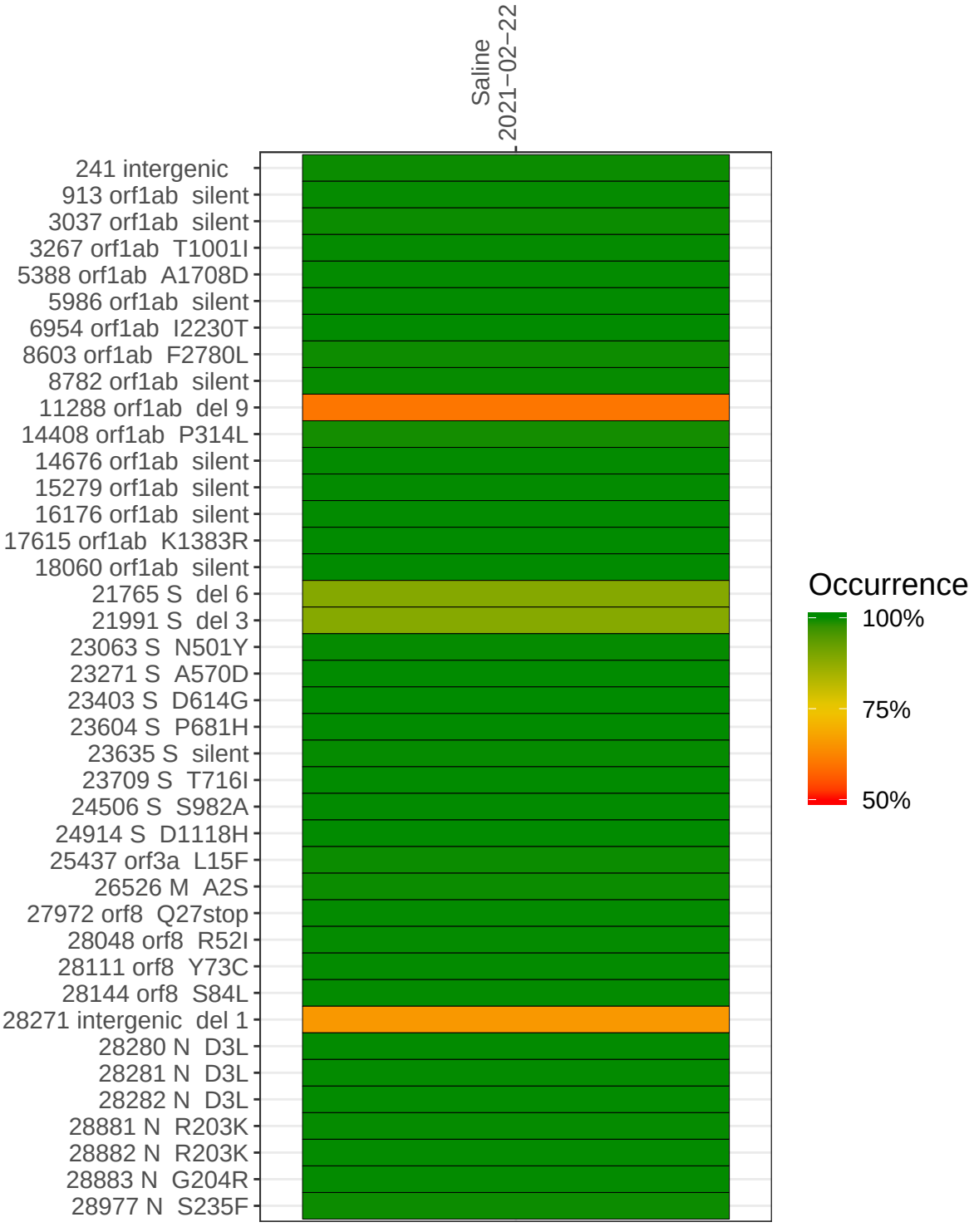
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

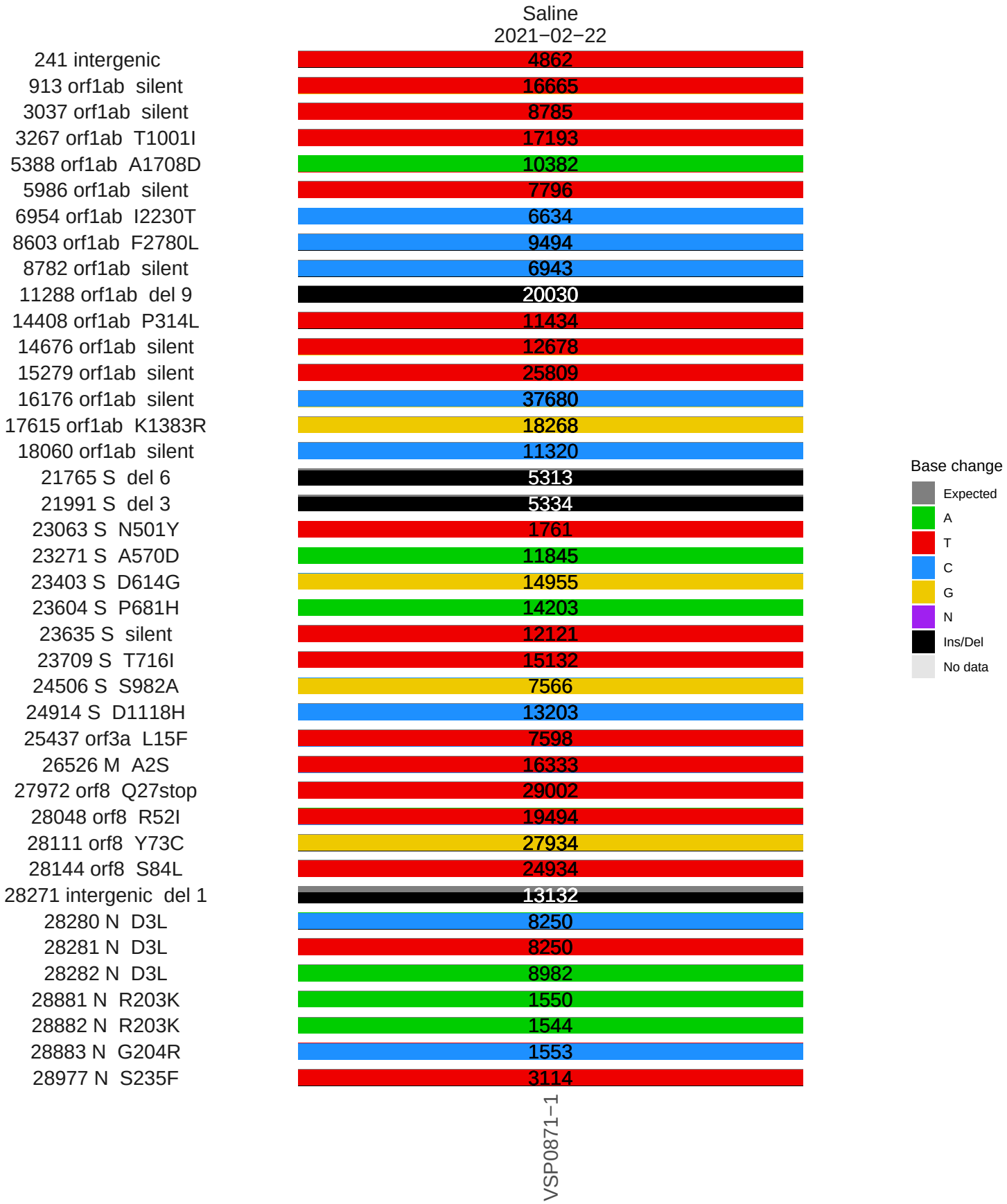
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP0871-1 | single experiment | NA | Saline | 2021-02-22 | 29.97 | B.1.1.7 | 99.9% | 99.9% |

**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.

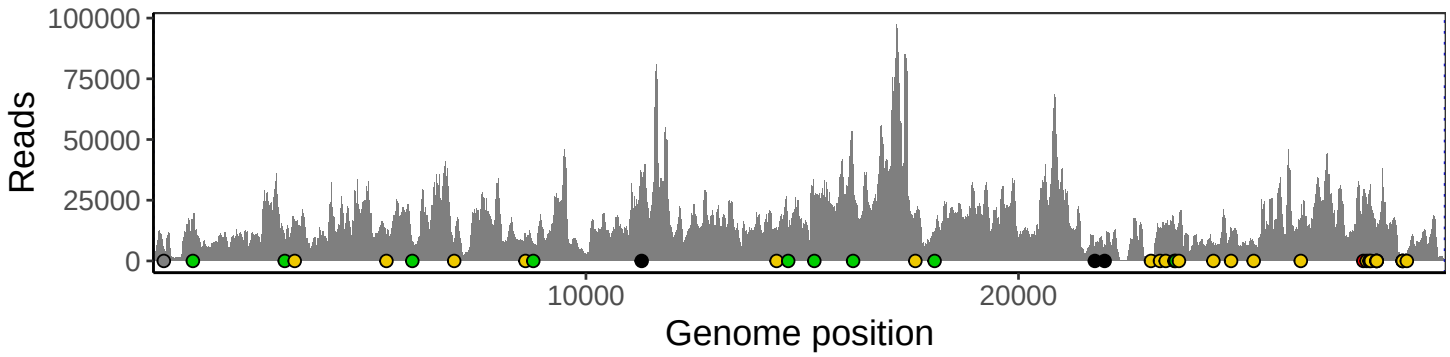



Saline
2021−02−22
241 intergenic 4862
913 orf1ab silent 16665
3037 orf1ab silent 8785
3267 orf1ab T1001I 17193
5388 orf1ab A1708D 10382
5986 orf1ab silent 7796
6954 orf1ab I2230T 6634
8603 orf1ab F2780L 9494
8782 orf1ab silent 6943
11288 orf1ab del 9 20030
14408 orf1ab P314L 11434
14676 orf1ab silent 12678
15279 orf1ab silent 25809
16176 orf1ab silent 37680
17615 orf1ab K1383R 18268
18060 orf1ab silent 11320
21765 S del 6 5313
21991 S del 3 5334
23063 S N501Y 1761
23271 S A570D 11845
23403 S D614G 14955
23604 S P681H 14203
23635 S silent 12121
23709 S T716I 15132
24506 S S982A 7566
24914 S D1118H 13203
25437 orf3a L15F 7598
26526 M A2S 16333
27972 orf8 Q27stop 29002
28048 orf8 R52I 19494
28111 orf8 Y73C 27934
28144 orf8 S84L 24934
28271 intergenic del 1 13132
28280 N D3L 8250
28281 N D3L 8250
28282 N D3L 8982
28881 N R203K 1550
28882 N R203K 1544
28883 N G204R 1553
28977 N S235F 3114
VSP0871−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

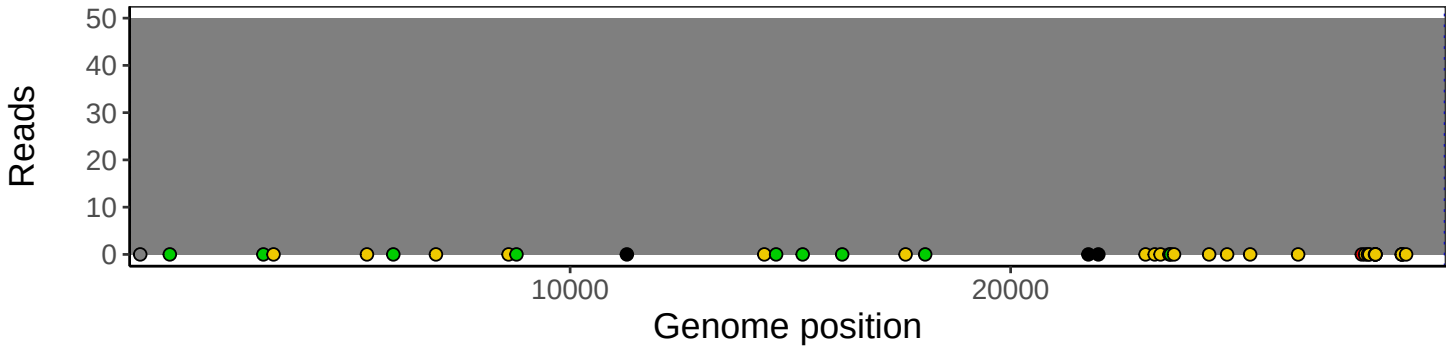
## Analyses of individual experiments and composite results

### VSP0871-1 | 2021-02-22 | Saline | HUP-Q-0008 | genomes | single experiment

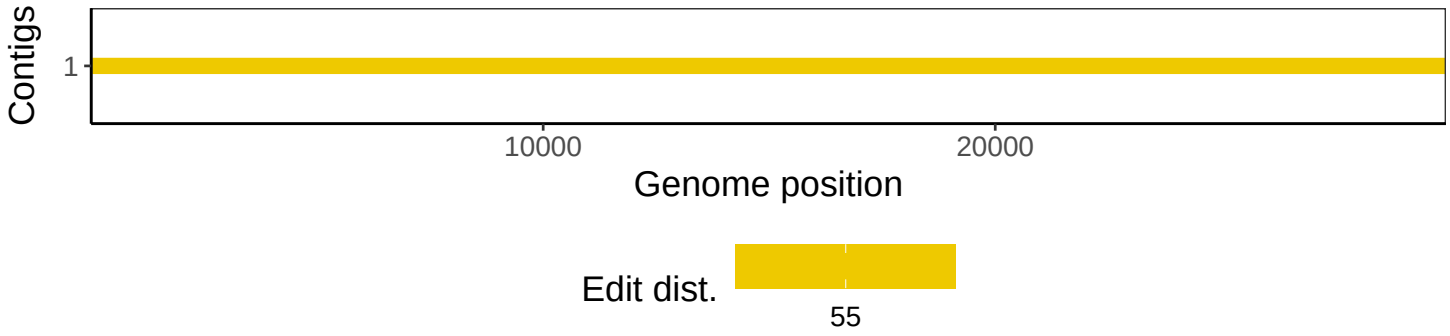
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |