# COVID-19 subject HUP Q-0105

*2021-04-17*

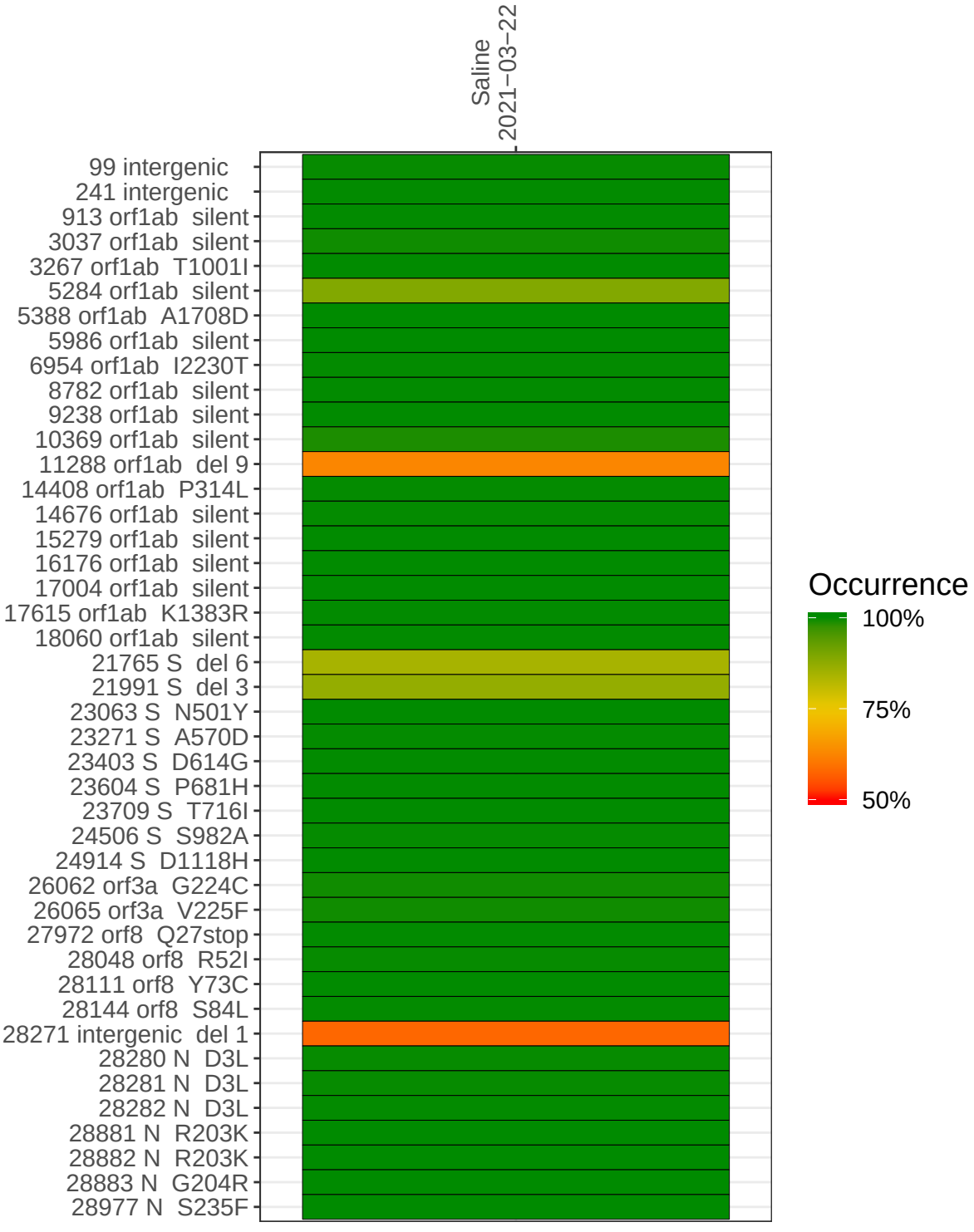
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

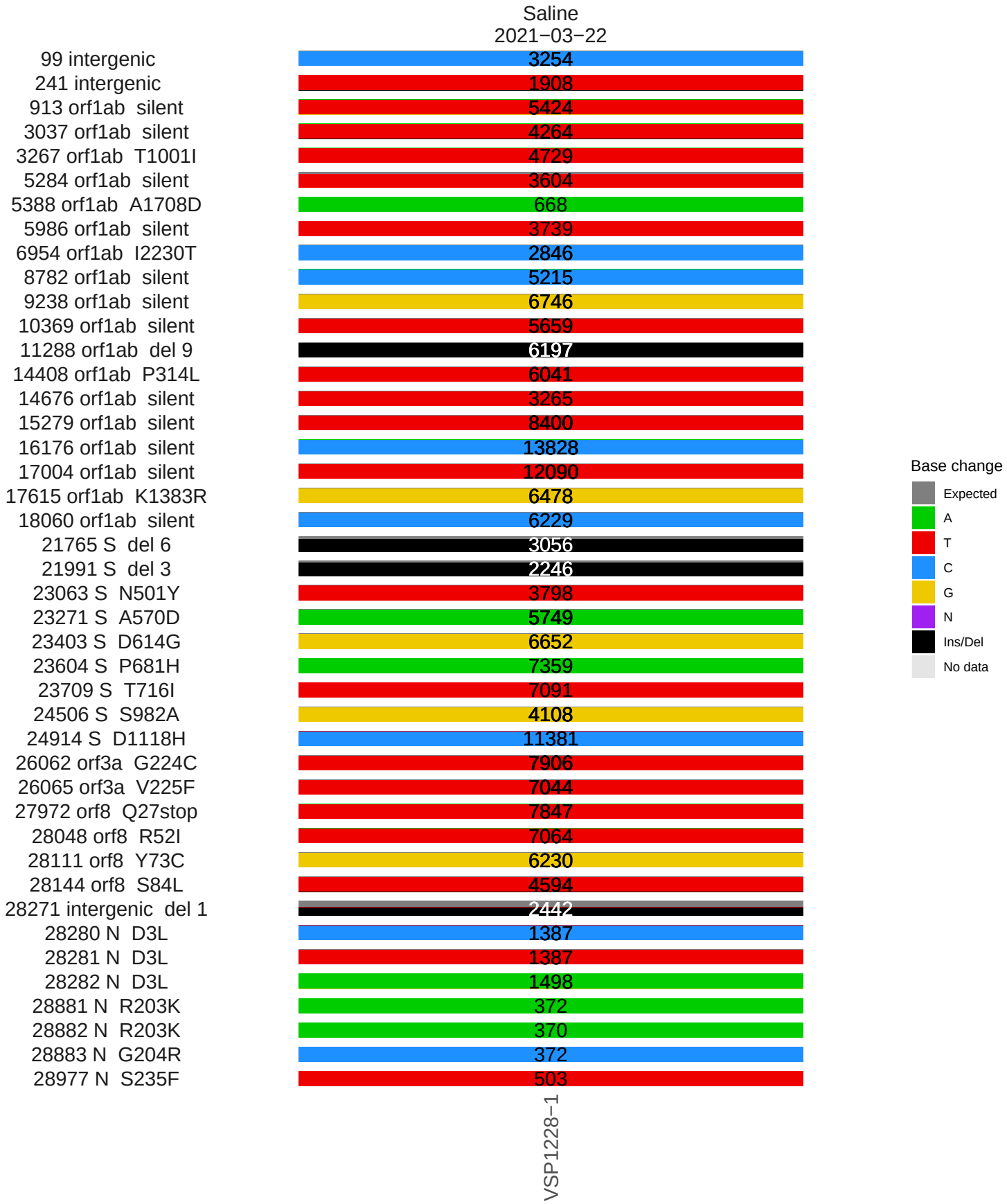
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1228-1 | single experiment | NA | Saline | 2021-03-22 | 29.87 | 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.

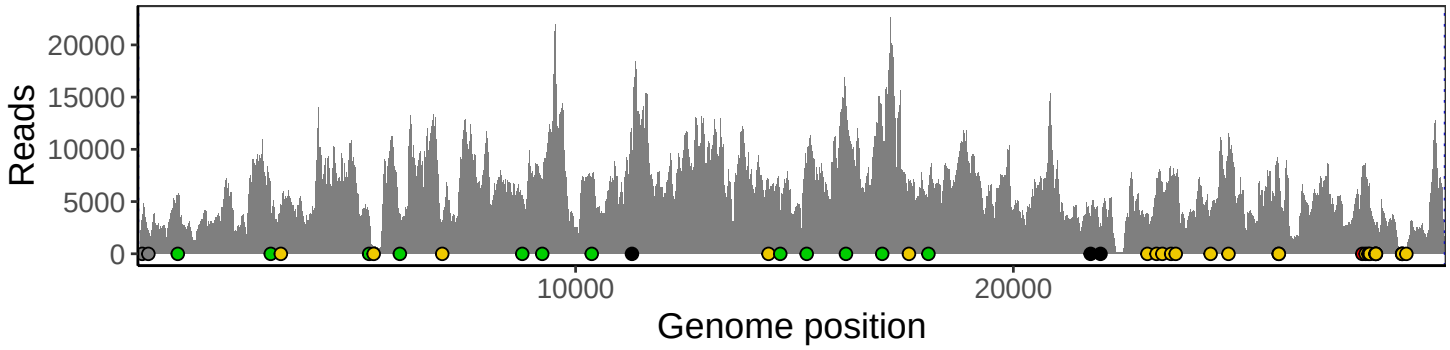



Saline
2021−03−22
99 intergenic 3254
241 intergenic 1908
913 orf1ab silent 5424
3037 orf1ab silent 4264
3267 orf1ab T1001I 4729
5284 orf1ab silent 3604
5388 orf1ab A1708D 668
5986 orf1ab silent 3739
6954 orf1ab I2230T 2846
8782 orf1ab silent 5215
9238 orf1ab silent 6746
10369 orf1ab silent 5659
11288 orf1ab del 9 6197
14408 orf1ab P314L 6041
14676 orf1ab silent 3265
15279 orf1ab silent 8400
16176 orf1ab silent 13828
17004 orf1ab silent 12090
17615 orf1ab K1383R 6478
18060 orf1ab silent 6229
21765 S del 6 3056
21991 S del 3 2246
23063 S N501Y 3798
23271 S A570D 5749
23403 S D614G 6652
23604 S P681H 7359
23709 S T716I 7091
24506 S S982A 4108
24914 S D1118H 11381
26062 orf3a G224C 7906
26065 orf3a V225F 7044
27972 orf8 Q27stop 7847
28048 orf8 R52I 7064
28111 orf8 Y73C 6230
28144 orf8 S84L 4594
28271 intergenic del 1 2442
28280 N D3L 1387
28281 N D3L 1387
28282 N D3L 1498
28881 N R203K 372
28882 N R203K 370
28883 N G204R 372
28977 N S235F 503
VSP1228−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

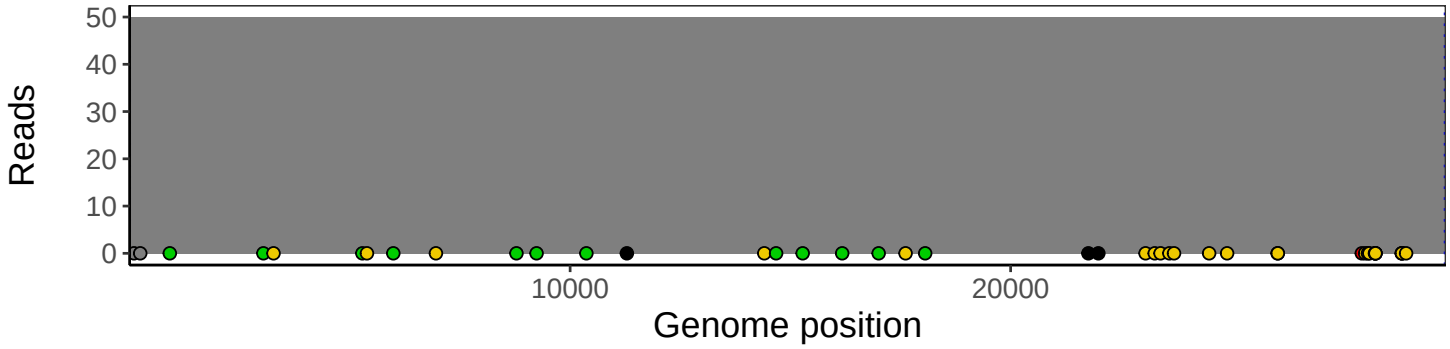
## Analyses of individual experiments and composite results

### VSP1228-1 | 2021-03-22 | Saline | HUP Q-0105 | genomes | single experiment

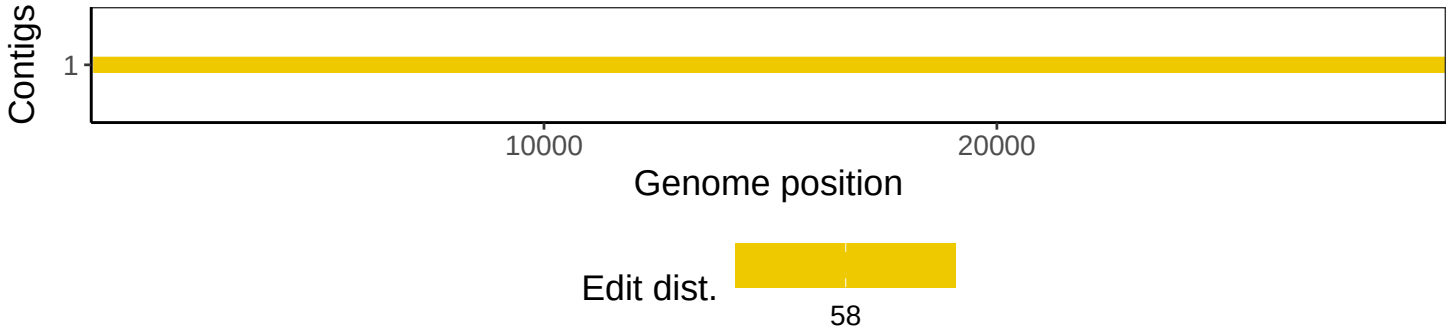
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |