# COVID-19 subject HUP Q-0052

*2021-06-23*

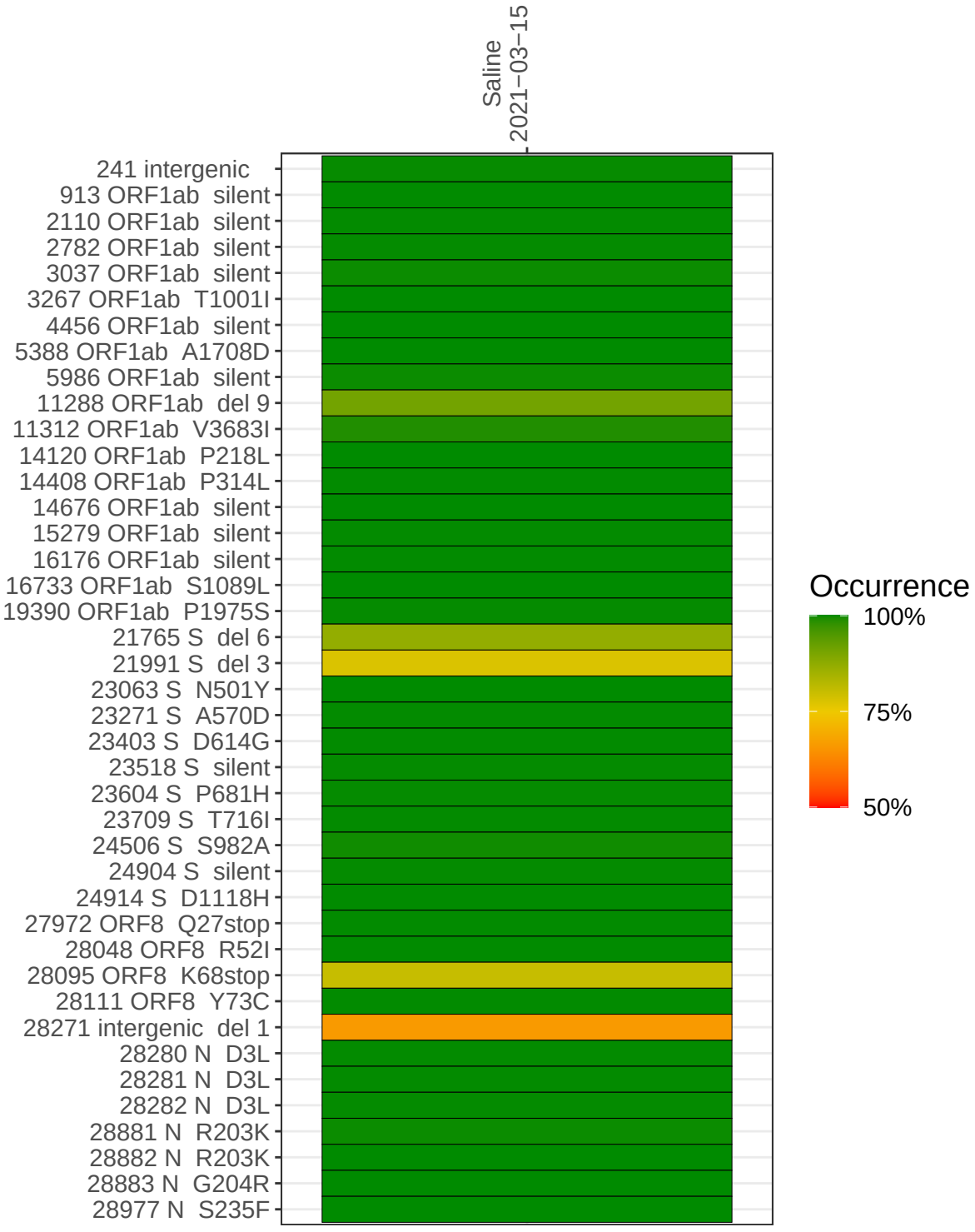
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

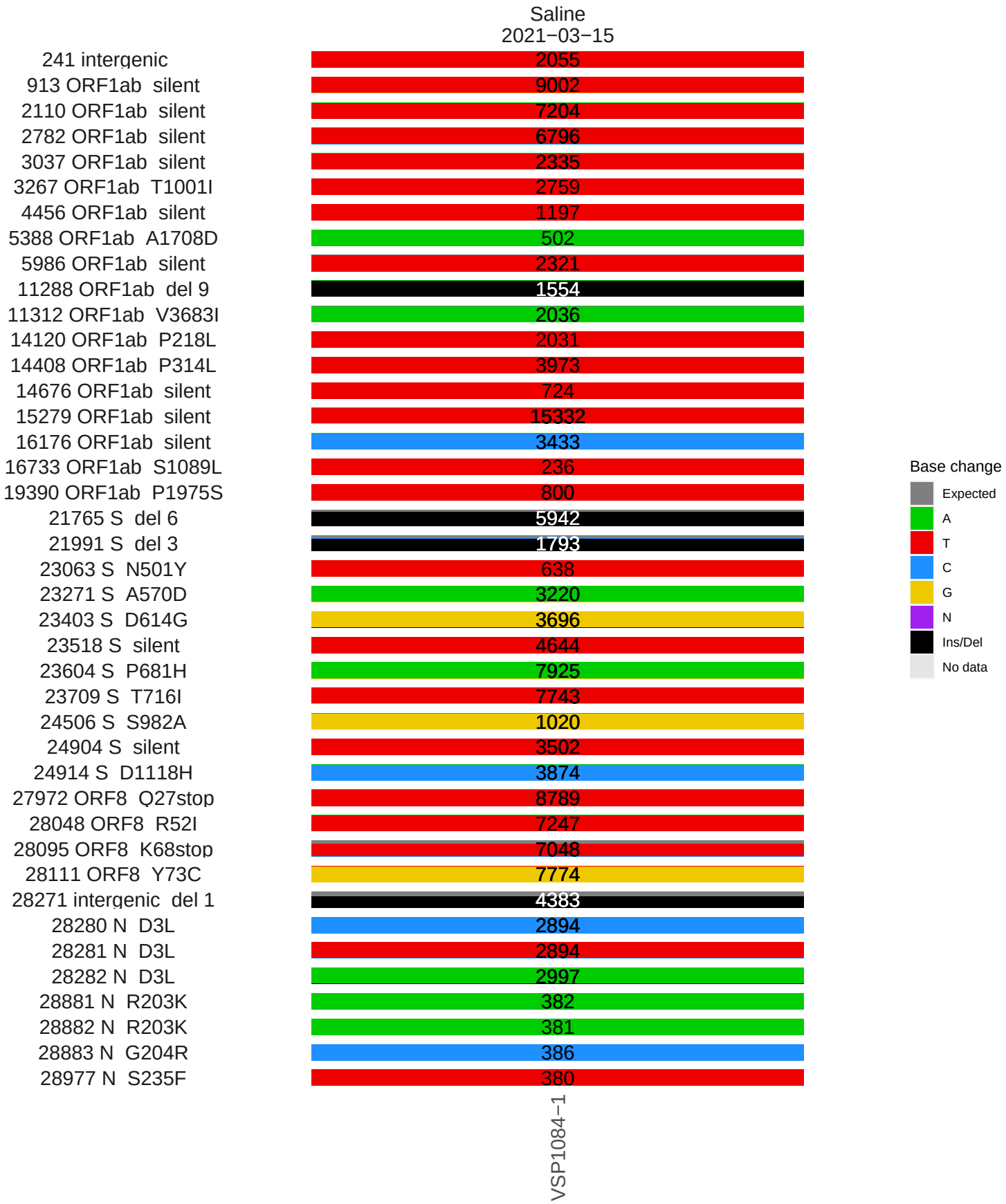
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1084-1 | single experiment | NA | Saline | 2021-03-15 | 29.81 | B.1.1.7 | 99.8% | 99.6% |

**Variants shared across samples**

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

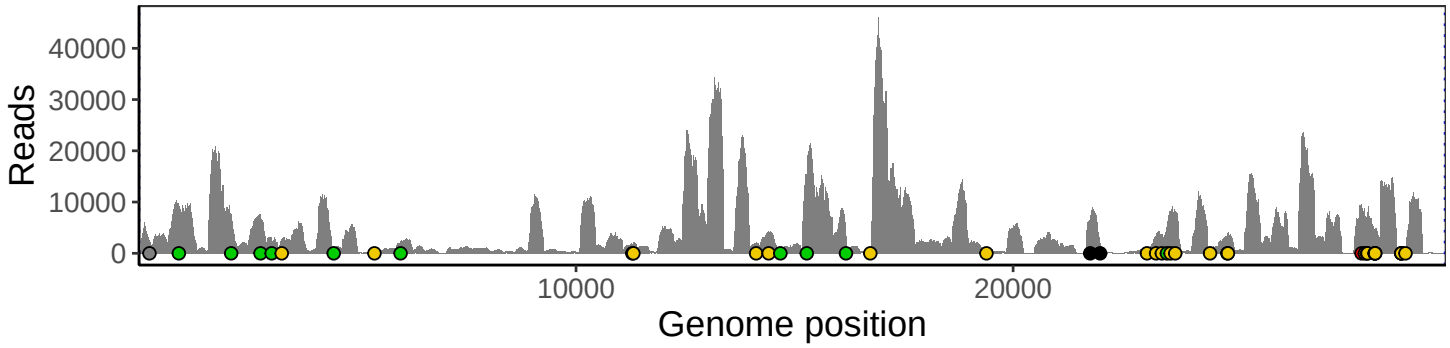



Saline
2021−03−15
241 intergenic 2055
913 ORF1ab silent 9002
2110 ORF1ab silent 7204
2782 ORF1ab silent 6796
3037 ORF1ab silent 2335
3267 ORF1ab T1001I 2759
4456 ORF1ab silent 1197
5388 ORF1ab A1708D 502
5986 ORF1ab silent 2321
11288 ORF1ab del 9 1554
11312 ORF1ab V3683I 2036
14120 ORF1ab P218L 2031
14408 ORF1ab P314L 3973
14676 ORF1ab silent 724
15279 ORF1ab silent 15332
16176 ORF1ab silent 3433
16733 ORF1ab S1089L 236
19390 ORF1ab P1975S 800
21765 S del 6 5942
21991 S del 3 1793
23063 S N501Y 638
23271 S A570D 3220
23403 S D614G 3696
23518 S silent 4644
23604 S P681H 7925
23709 S T716I 7743
24506 S S982A 1020
24904 S silent 3502
24914 S D1118H 3874
27972 ORF8 Q27stop 8789
28048 ORF8 R52I 7247
28095 ORF8 K68stop 7048
28111 ORF8 Y73C 7774
28271 intergenic del 1 4383
28280 N D3L 2894
28281 N D3L 2894
28282 N D3L 2997
28881 N R203K 382
28882 N R203K 381
28883 N G204R 386
28977 N S235F 380
VSP1084−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

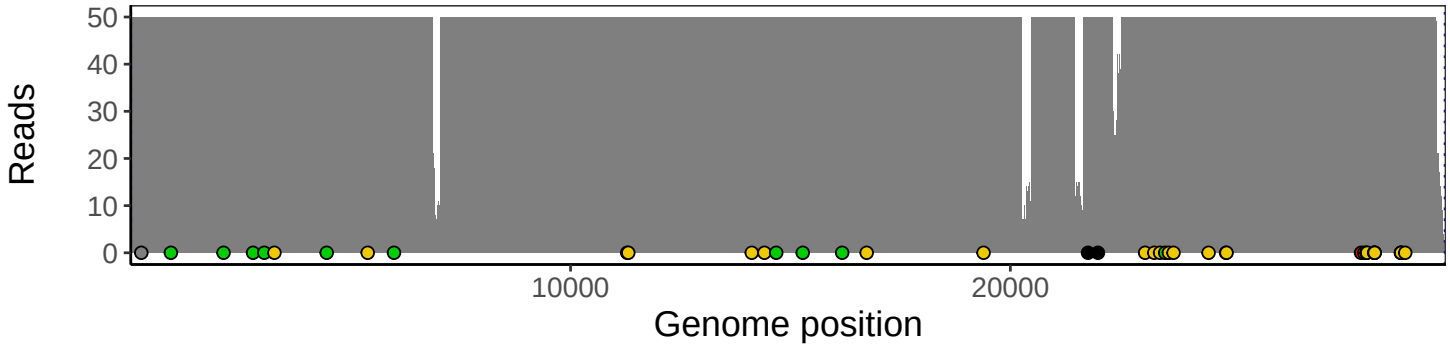
## Analyses of individual experiments and composite results

### VSP1084-1 | 2021-03-15 | Saline | HUP Q-0052 | genomes | single experiment

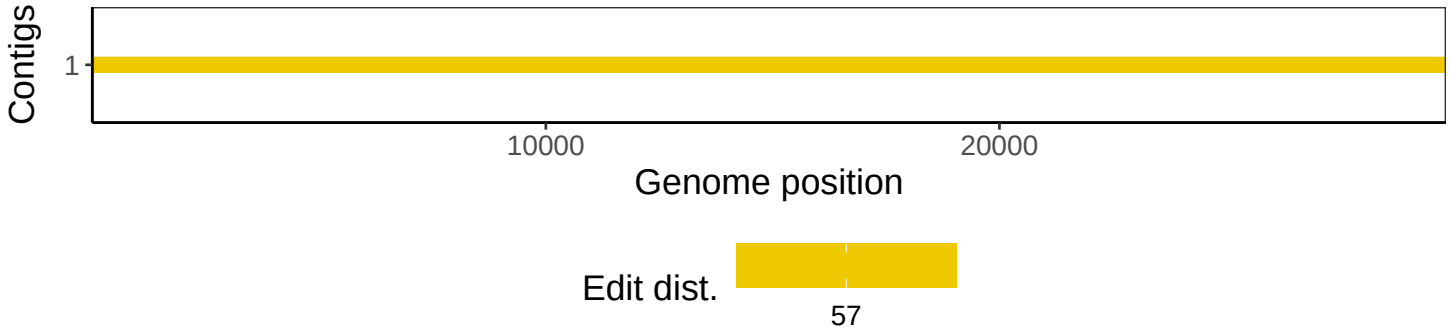
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 3.1.3 |
| 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 | 3.3.3 |
| 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 |