COVID-19 subject HUP Q-0006

2021-04-17

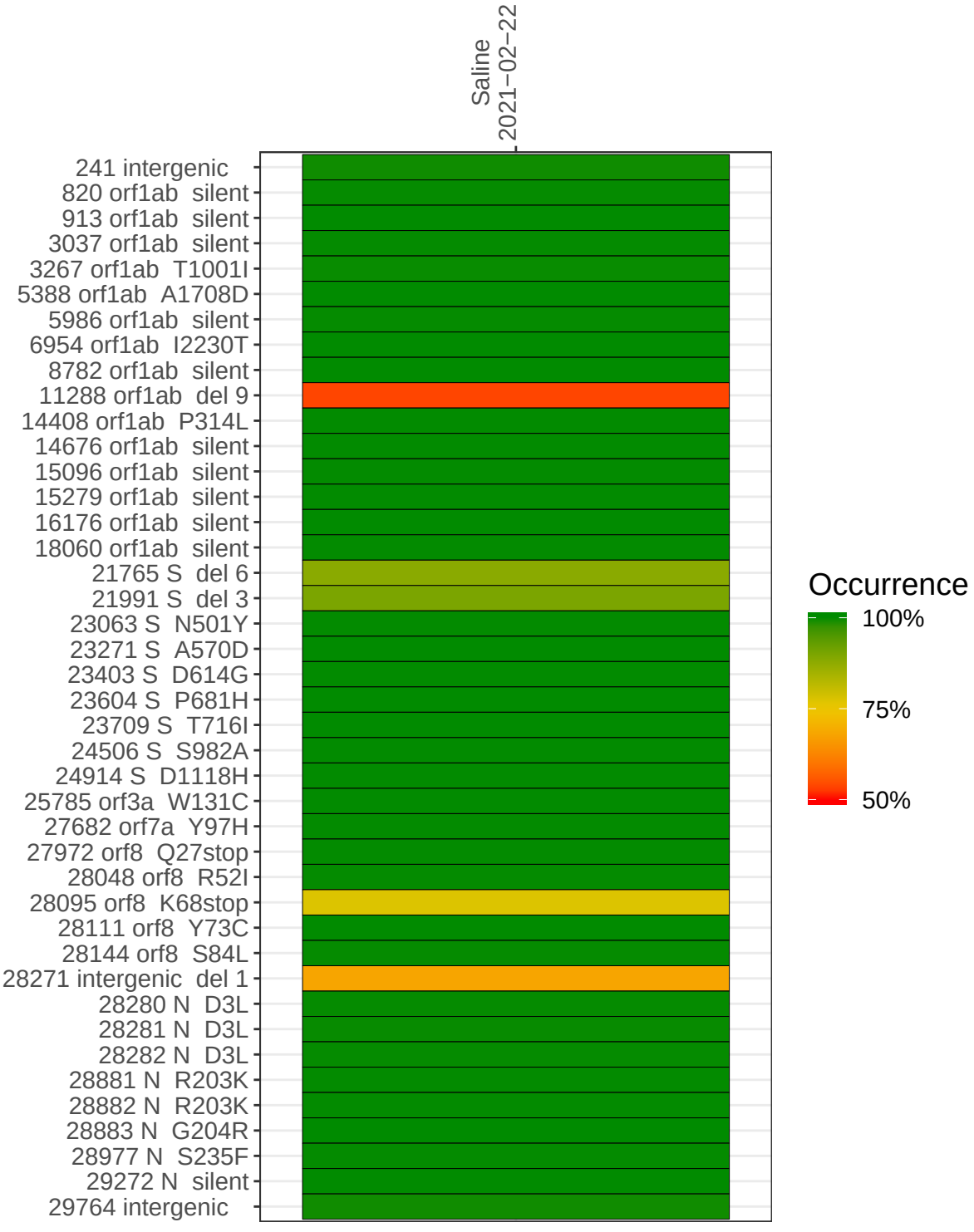
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

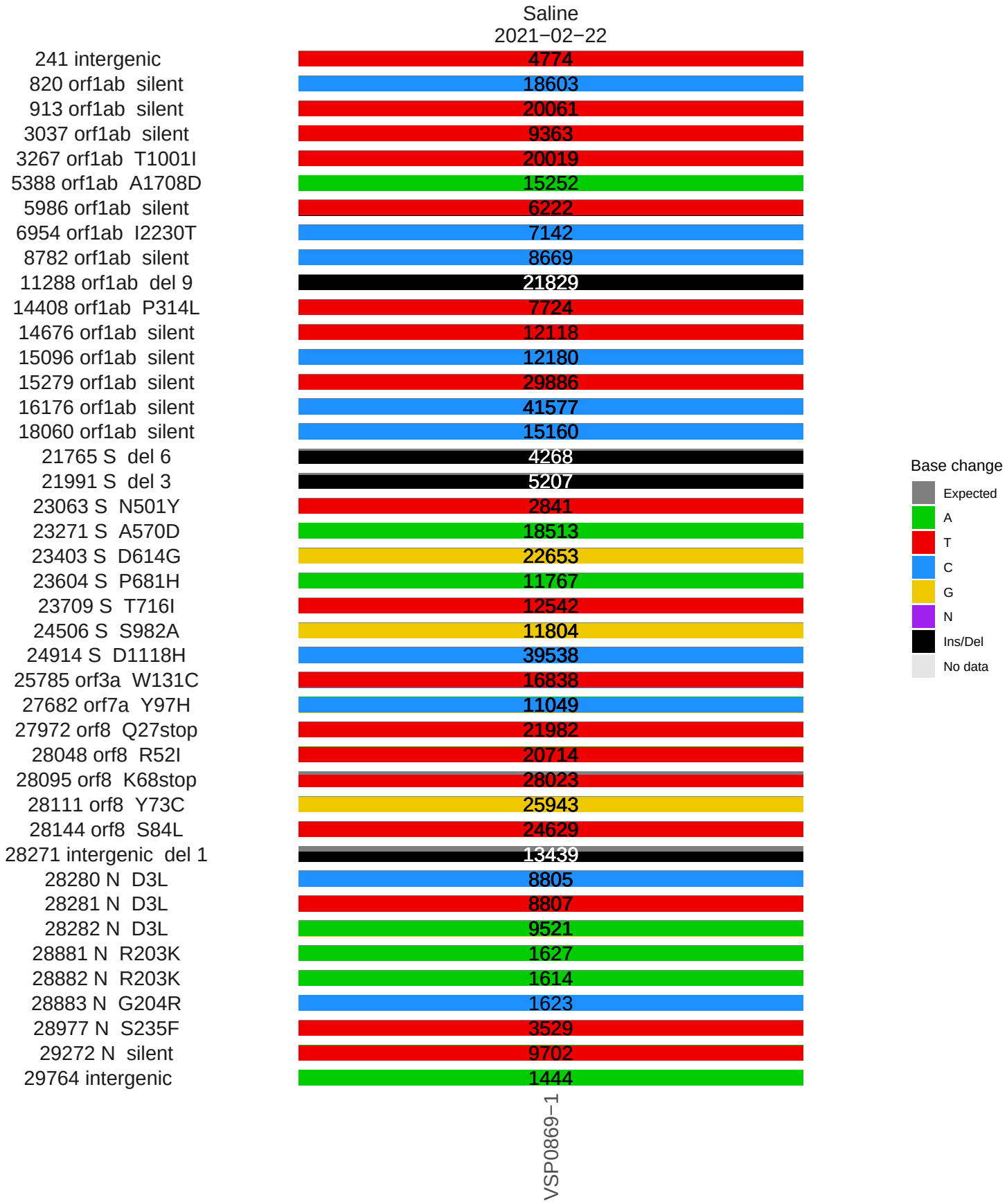
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0869-1	single experiment	NA	Saline	2021-02-22	29.88	B.1.1.7	99.9%	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.

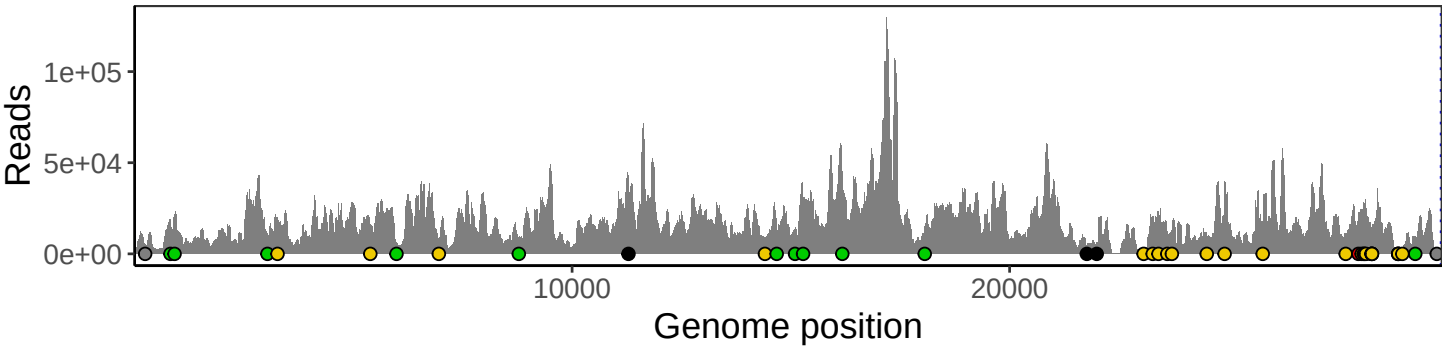



Saline
2021−02−22
241 intergenic 4774
820 orf1ab silent 18603
913 orf1ab silent 20061
3037 orf1ab silent 9363
3267 orf1ab T1001I 20019
5388 orf1ab A1708D 15252
5986 orf1ab silent 6222
6954 orf1ab I2230T 7142
8782 orf1ab silent 8669
11288 orf1ab del 9 21829
14408 orf1ab P314L 7724
14676 orf1ab silent 12118
15096 orf1ab silent 12180
15279 orf1ab silent 29886
16176 orf1ab silent 41577
18060 orf1ab silent 15160
21765 S del 6 4268
21991 S del 3 5207
23063 S N501Y 2841
23271 S A570D 18513
23403 S D614G 22653
23604 S P681H 11767
23709 S T716I 12542
24506 S S982A 11804
24914 S D1118H 39538
25785 orf3a W131C 16838
27682 orf7a Y97H 11049
27972 orf8 Q27stop 21982
28048 orf8 R52I 20714
28095 orf8 K68stop 28023
28111 orf8 Y73C 25943
28144 orf8 S84L 24629
28271 intergenic del 1 13439
28280 N D3L 8805
28281 N D3L 8807
28282 N D3L 9521
28881 N R203K 1627
28882 N R203K 1614
28883 N G204R 1623
28977 N S235F 3529
29272 N silent 9702
29764 intergenic 1444
VSP0869−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

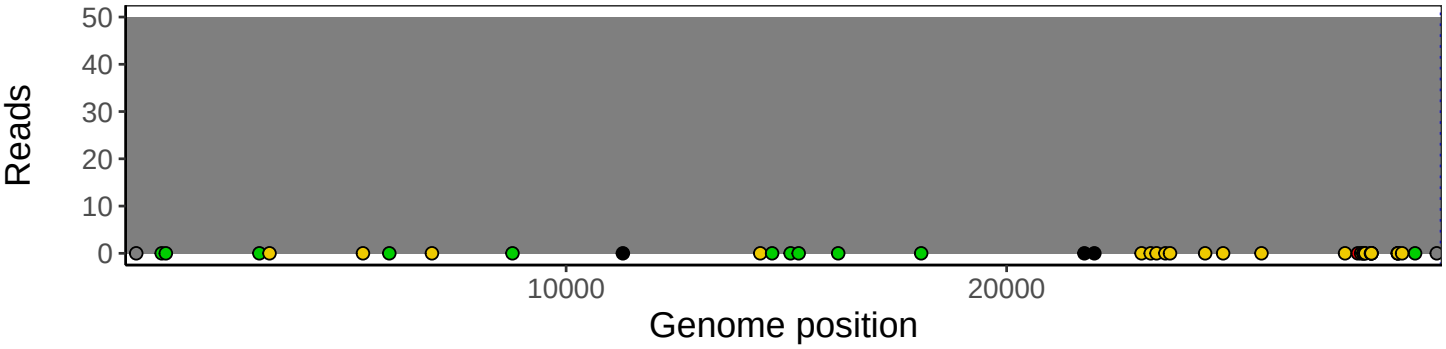
Analyses of individual experiments and composite results

VSP0869-1 | 2021-02-22 | Saline | HUP-Q-0006 | genomes | single experiment

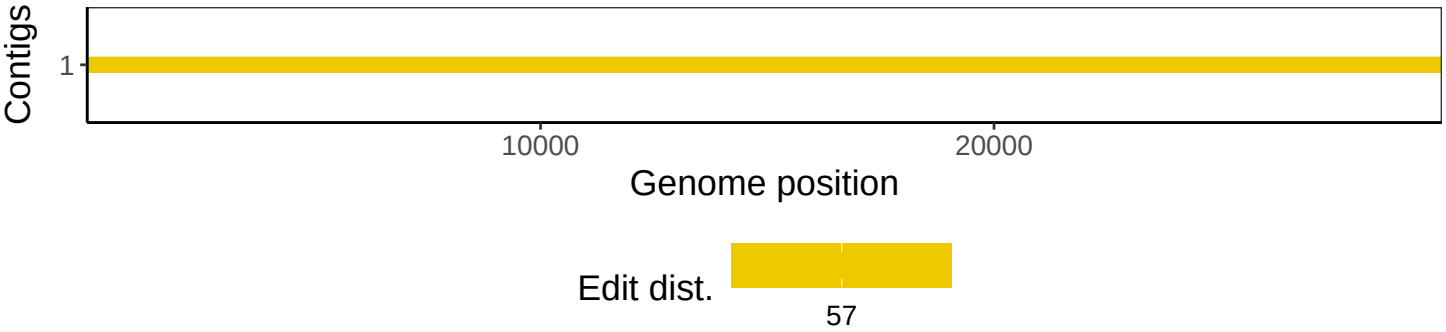
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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