COVID-19 subject HUP Q-0017

2021-04-17

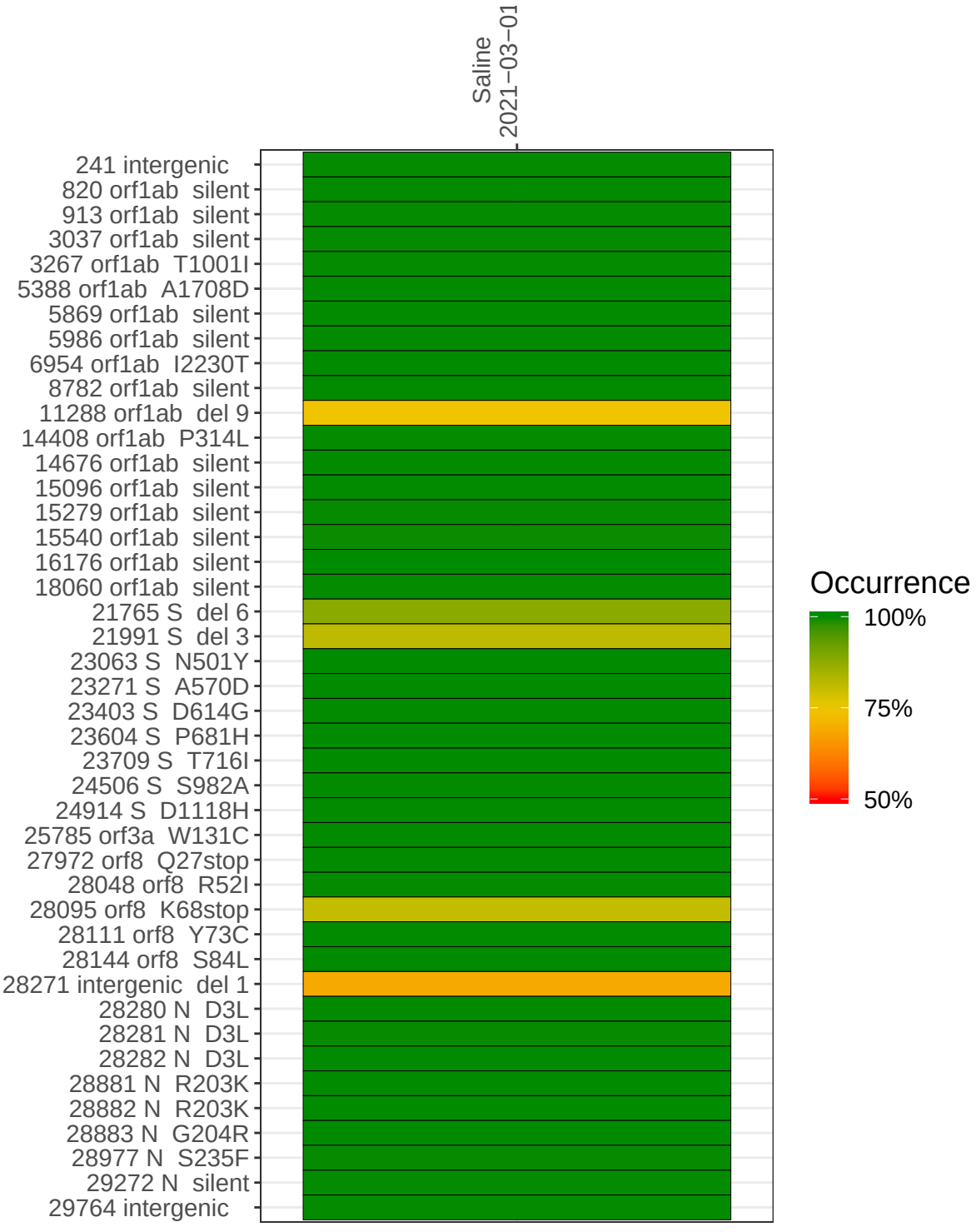
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

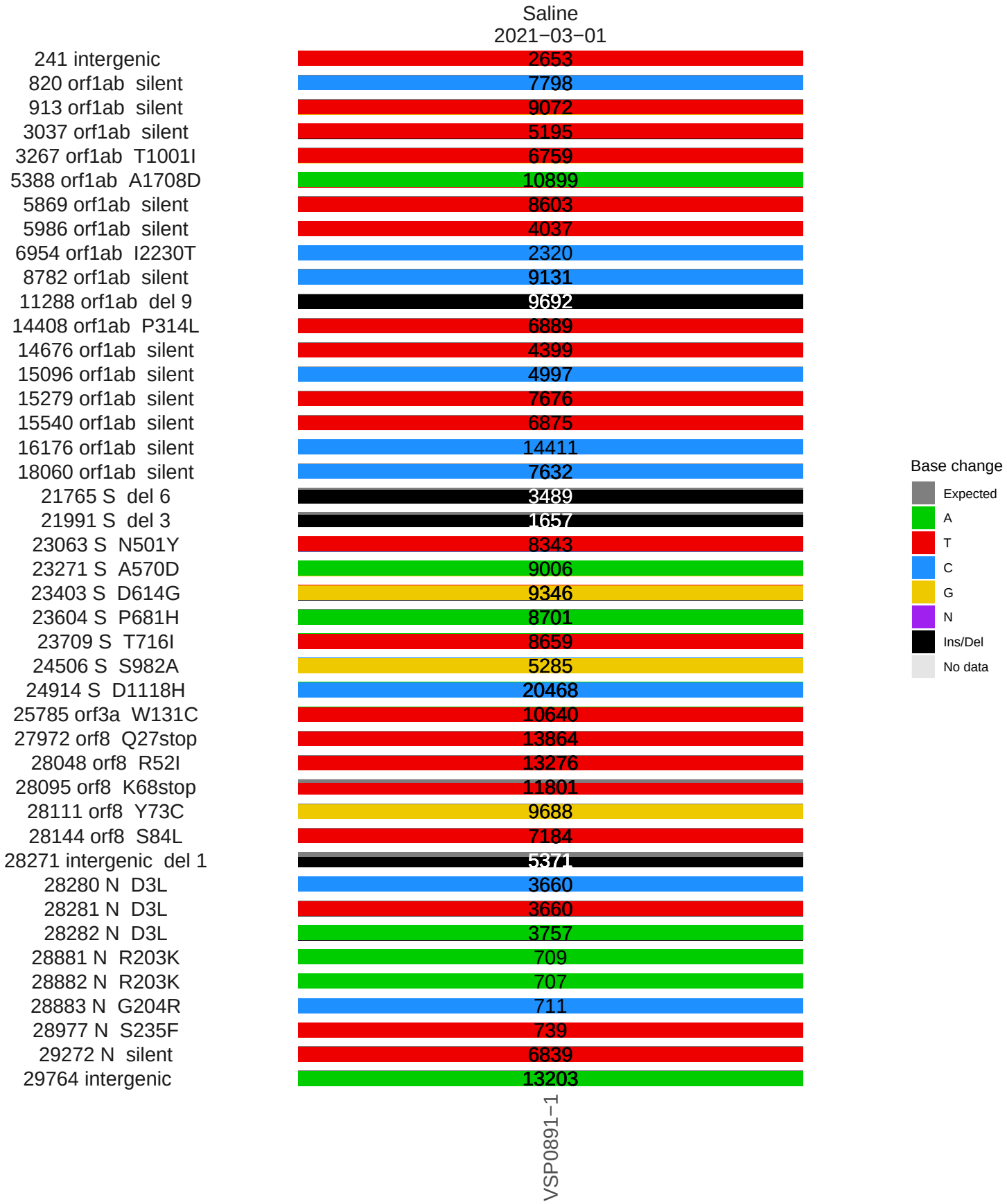
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0891-1	single experiment	NA	Saline	2021-03-01	29.82	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.

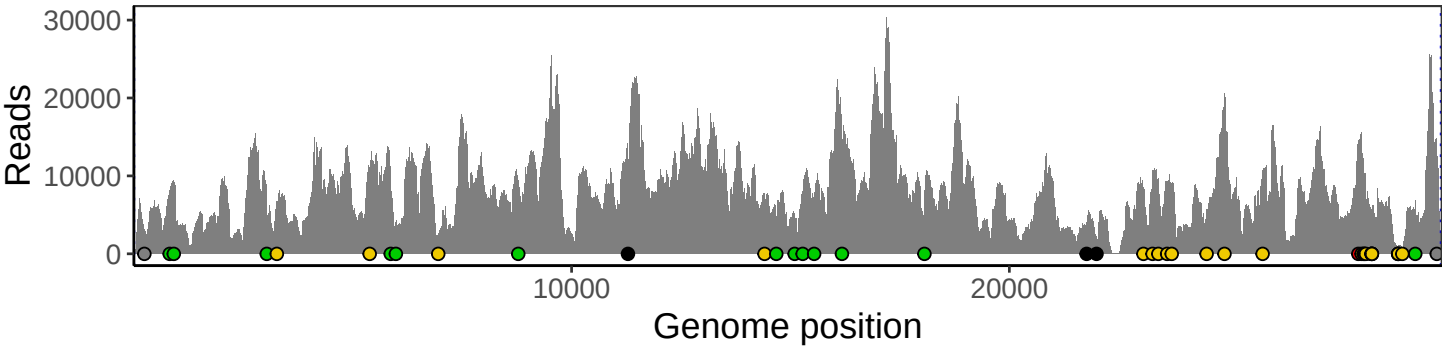



Saline
2021−03−01
241 intergenic 2653
820 orf1ab silent 7798
913 orf1ab silent 9072
3037 orf1ab silent 5195
3267 orf1ab T1001I 6759
5388 orf1ab A1708D 10899
5869 orf1ab silent 8603
5986 orf1ab silent 4037
6954 orf1ab I2230T 2320
8782 orf1ab silent 9131
11288 orf1ab del 9 9692
14408 orf1ab P314L 6889
14676 orf1ab silent 4399
15096 orf1ab silent 4997
15279 orf1ab silent 7676
15540 orf1ab silent 6875
16176 orf1ab silent 14411
18060 orf1ab silent 7632
21765 S del 6 3489
21991 S del 3 1657
23063 S N501Y 8343
23271 S A570D 9006
23403 S D614G 9346
23604 S P681H 8701
23709 S T716I 8659
24506 S S982A 5285
24914 S D1118H 20468
25785 orf3a W131C 10640
27972 orf8 Q27stop 13864
28048 orf8 R52I 13276
28095 orf8 K68stop 11801
28111 orf8 Y73C 9688
28144 orf8 S84L 7184
28271 intergenic del 1 5371
28280 N D3L 3660
28281 N D3L 3660
28282 N D3L 3757
28881 N R203K 709
28882 N R203K 707
28883 N G204R 711
28977 N S235F 739
29272 N silent 6839
29764 intergenic 13203
VSP0891−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

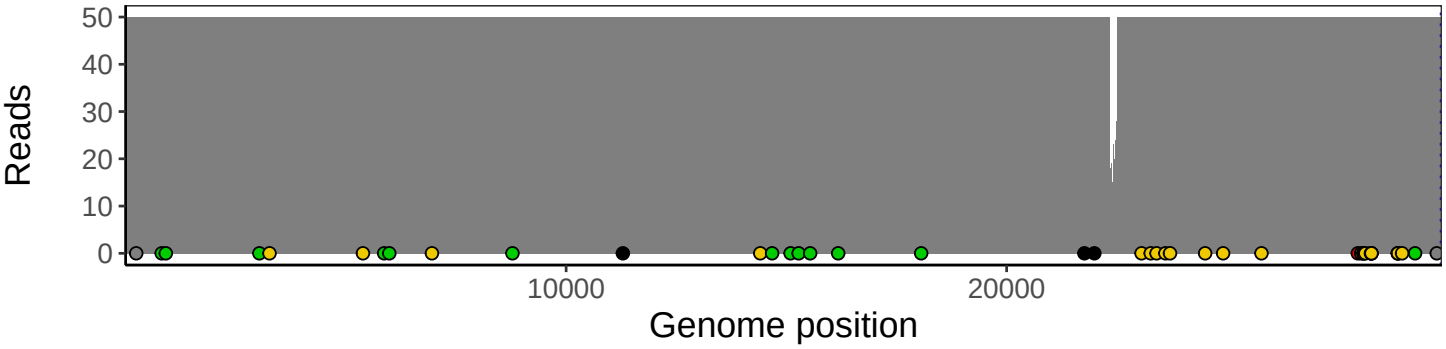
Analyses of individual experiments and composite results

VSP0891-1 | 2021-03-01 | Saline | HUP Q-0017 | genomes | single experiment

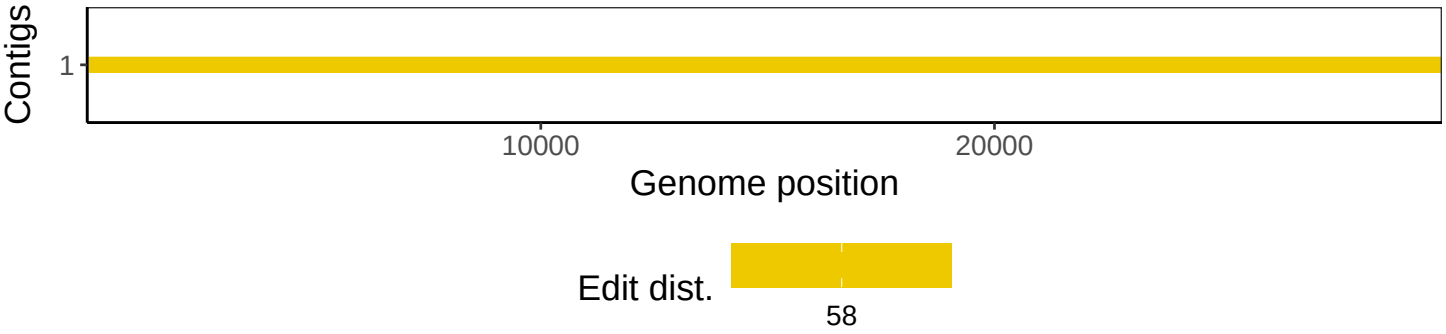
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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