COVID-19 subject HUP Q-0038

2021-03-31

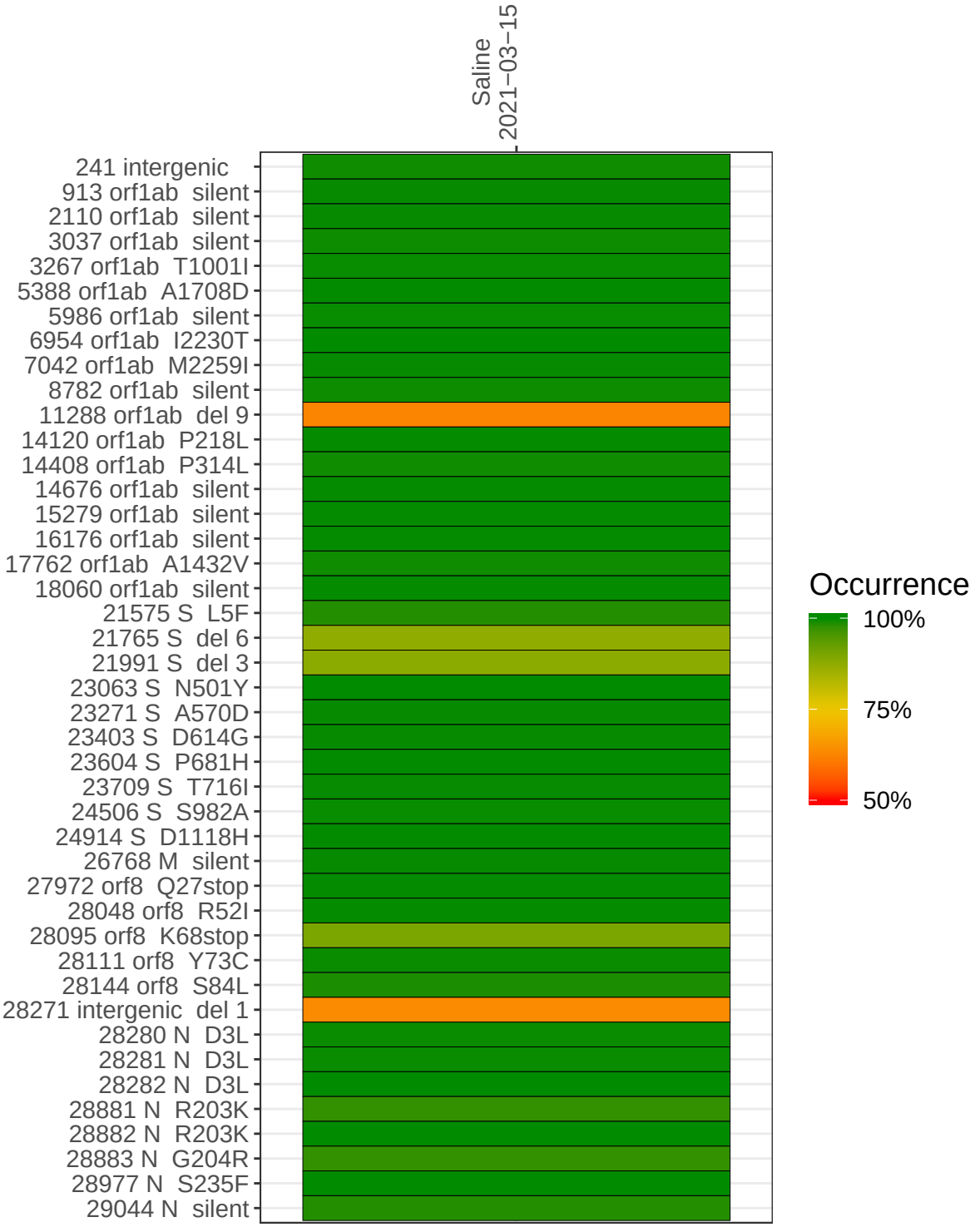
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

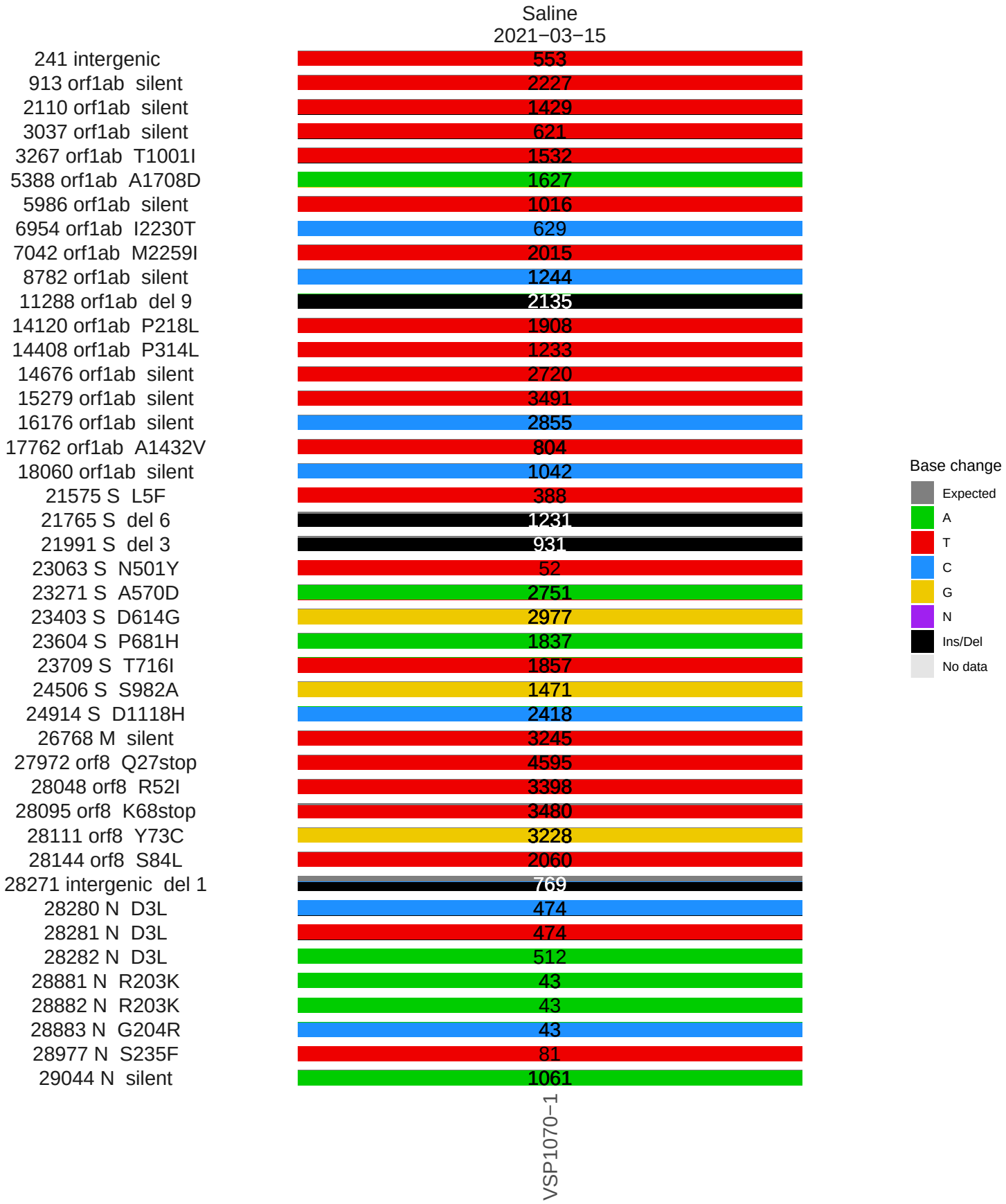
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1070-1	single experiment	NA	Saline	2021-03-15	29.82	B.1.1.7	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

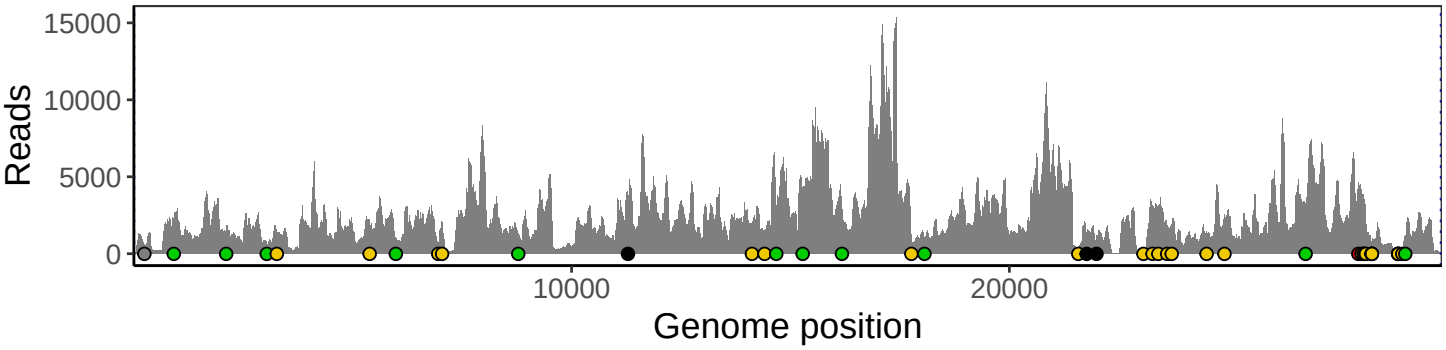



Saline
2021−03−15
241 intergenic 553
913 orf1ab silent 2227
2110 orf1ab silent 1429
3037 orf1ab silent 621
3267 orf1ab T1001I 1532
5388 orf1ab A1708D 1627
5986 orf1ab silent 1016
6954 orf1ab I2230T 629
7042 orf1ab M2259I 2015
8782 orf1ab silent 1244
11288 orf1ab del 9 2135
14120 orf1ab P218L 1908
14408 orf1ab P314L 1233
14676 orf1ab silent 2720
15279 orf1ab silent 3491
16176 orf1ab silent 2855
17762 orf1ab A1432V 804
18060 orf1ab silent 1042
21575 S L5F 388
21765 S del 6 1231
21991 S del 3 931
23063 S N501Y 52
23271 S A570D 2751
23403 S D614G 2977
23604 S P681H 1837
23709 S T716I 1857
24506 S S982A 1471
24914 S D1118H 2418
26768 M silent 3245
27972 orf8 Q27stop 4595
28048 orf8 R52I 3398
28095 orf8 K68stop 3480
28111 orf8 Y73C 3228
28144 orf8 S84L 2060
28271 intergenic del 1 769
28280 N D3L 474
28281 N D3L 474
28282 N D3L 512
28881 N R203K 43
28882 N R203K 43
28883 N G204R 43
28977 N S235F 81
29044 N silent 1061
VSP1070−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

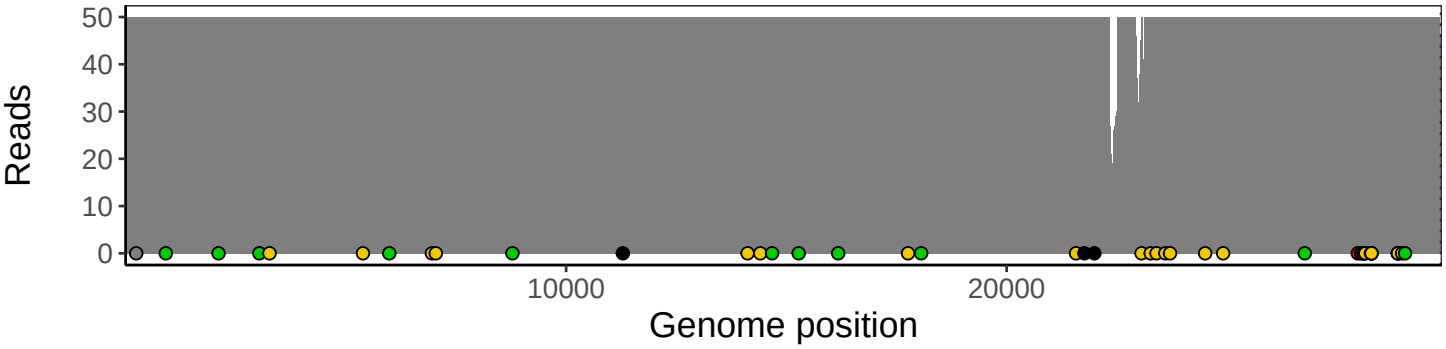
Analyses of individual experiments and composite results

VSP1070-1 | 2021-03-15 | Saline | HUP Q-0038 | genomes | single experiment

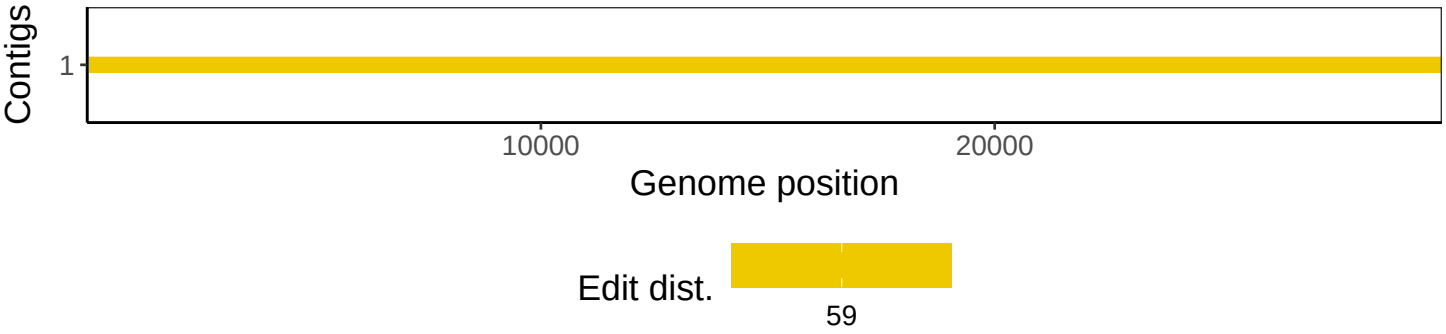
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
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