COVID-19 subject HUP Q-0040

2021-04-17

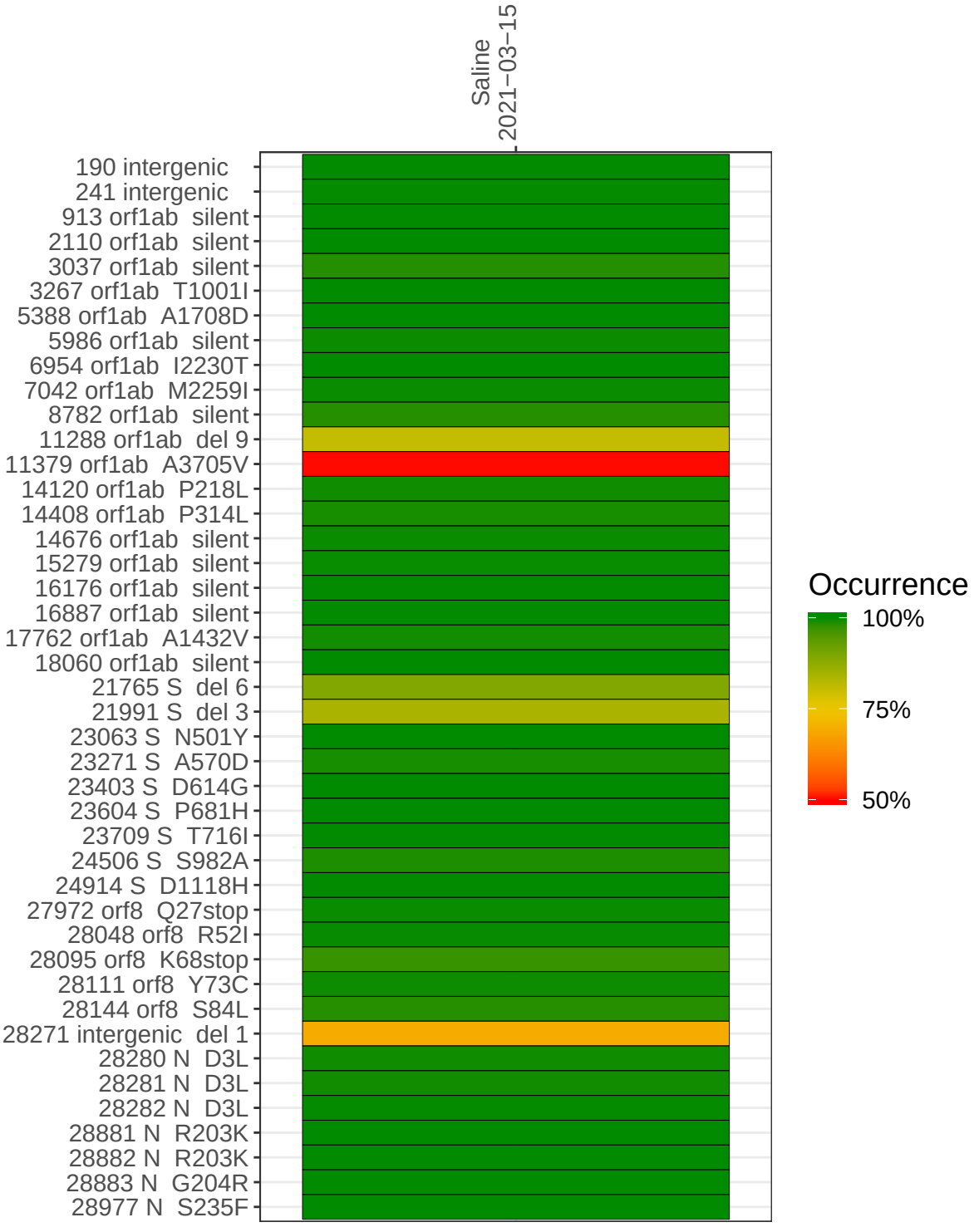
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

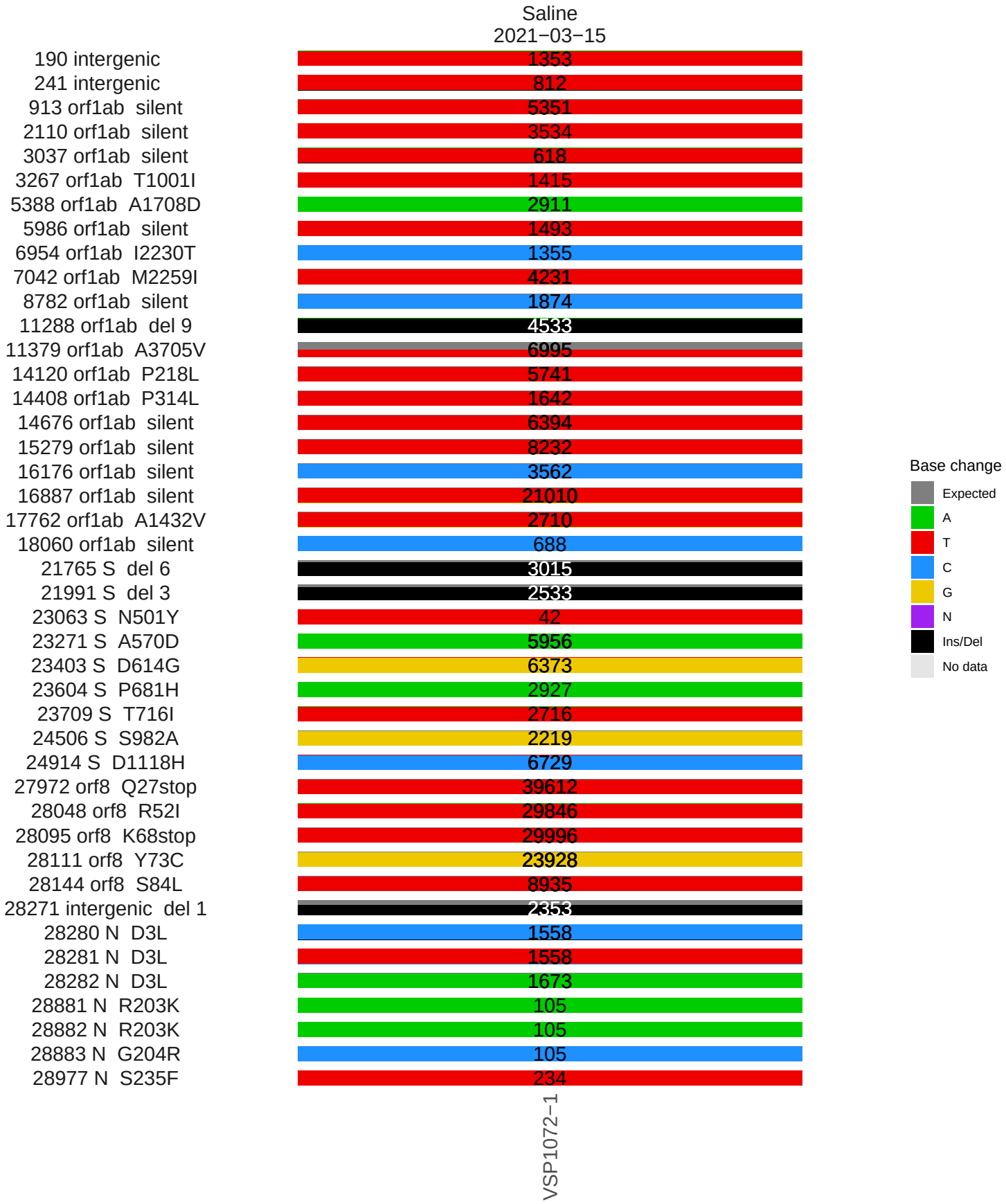
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1072-1	single experiment	NA	Saline	2021-03-15	29.84	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.

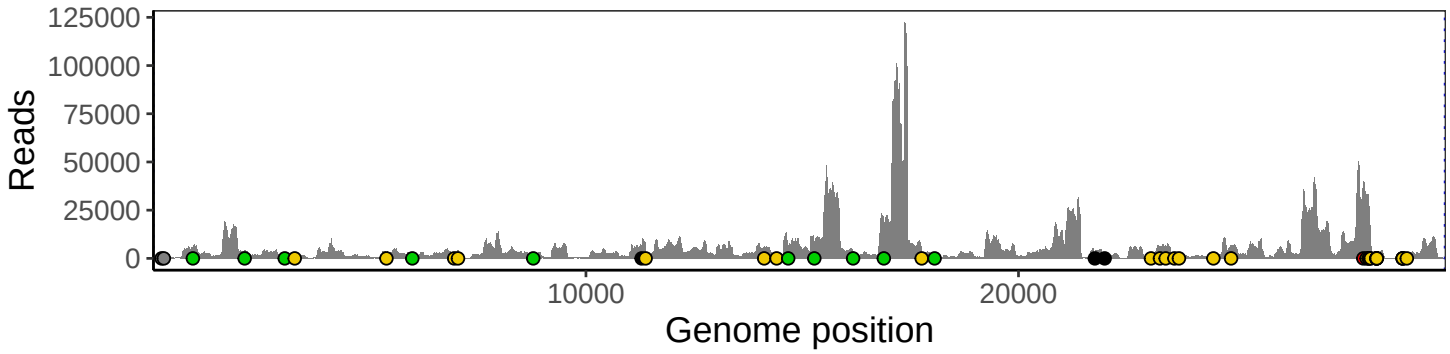



Saline
2021−03−15
190 intergenic 1353
241 intergenic 812
913 orf1ab silent 5351
2110 orf1ab silent 3534
3037 orf1ab silent 618
3267 orf1ab T1001I 1415
5388 orf1ab A1708D 2911
5986 orf1ab silent 1493
6954 orf1ab I2230T 1355
7042 orf1ab M2259I 4231
8782 orf1ab silent 1874
11288 orf1ab del 9 4533
11379 orf1ab A3705V 6995
14120 orf1ab P218L 5741
14408 orf1ab P314L 1642
14676 orf1ab silent 6394
15279 orf1ab silent 8232
16176 orf1ab silent 3562
16887 orf1ab silent 21010
17762 orf1ab A1432V 2710
18060 orf1ab silent 688
21765 S del 6 3015
21991 S del 3 2533
23063 S N501Y 42
23271 S A570D 5956
23403 S D614G 6373
23604 S P681H 2927
23709 S T716I 2716
24506 S S982A 2219
24914 S D1118H 6729
27972 orf8 Q27stop 39612
28048 orf8 R52I 29846
28095 orf8 K68stop 29996
28111 orf8 Y73C 23928
28144 orf8 S84L 8935
28271 intergenic del 1 2353
28280 N D3L 1558
28281 N D3L 1558
28282 N D3L 1673
28881 N R203K 105
28882 N R203K 105
28883 N G204R 105
28977 N S235F 234
VSP1072−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

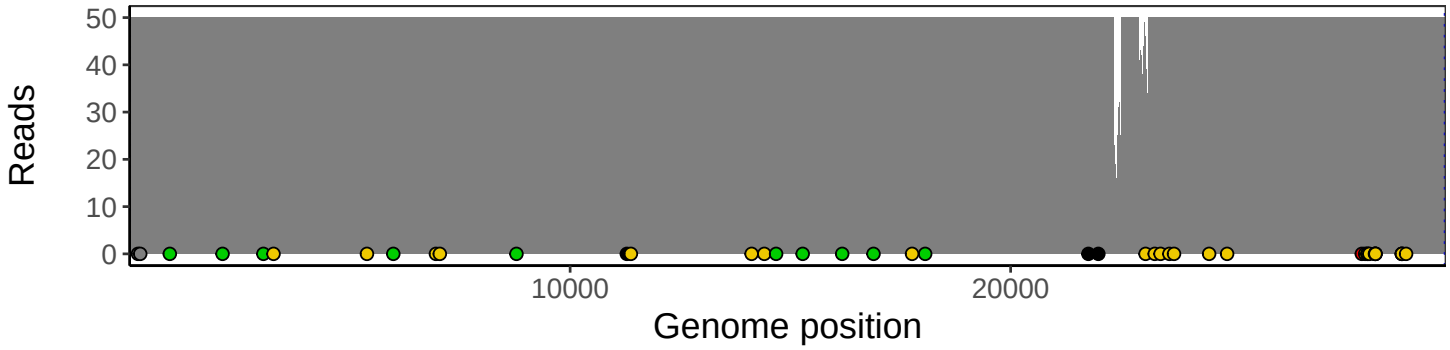
Analyses of individual experiments and composite results

VSP1072-1 | 2021-03-15 | Saline | HUP Q-0040 | genomes | single experiment

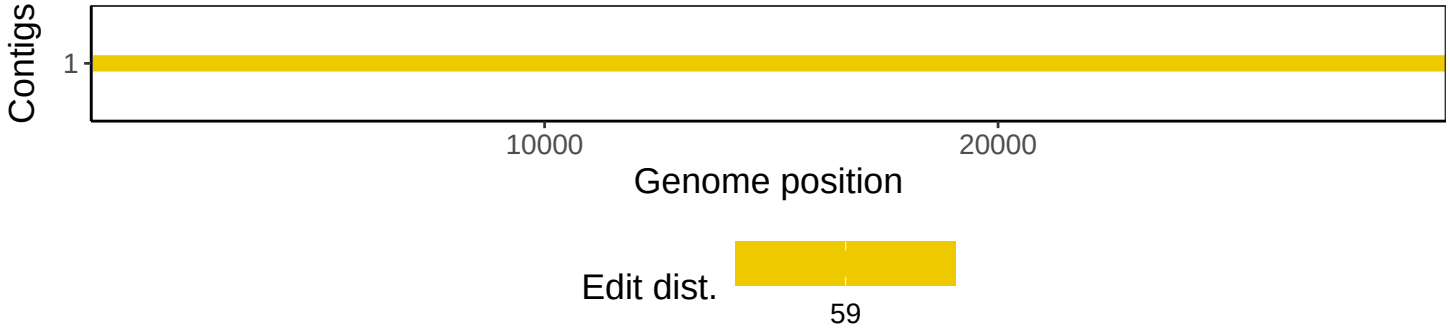
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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