COVID-19 subject HUP Q-0010

2021-04-17

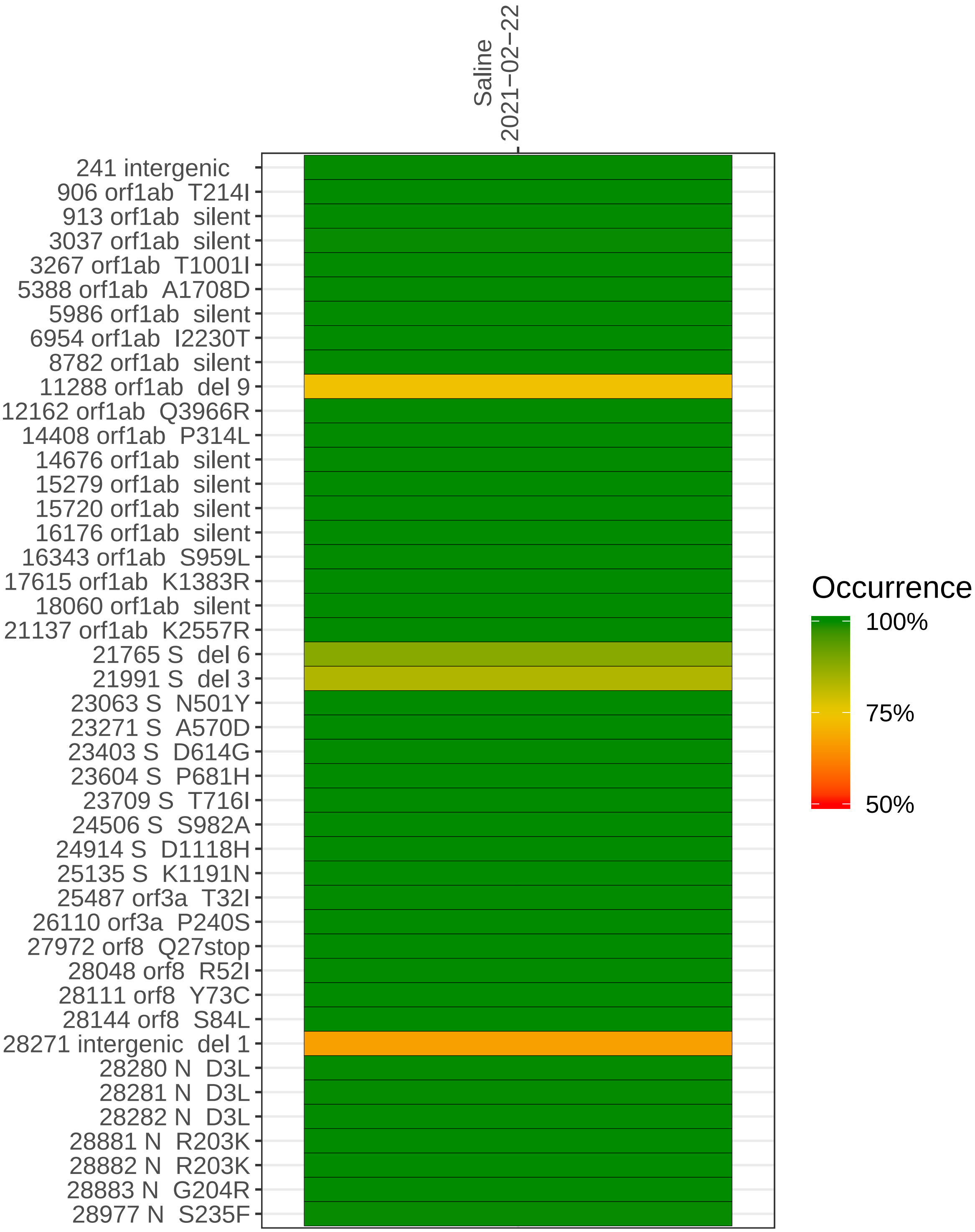
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

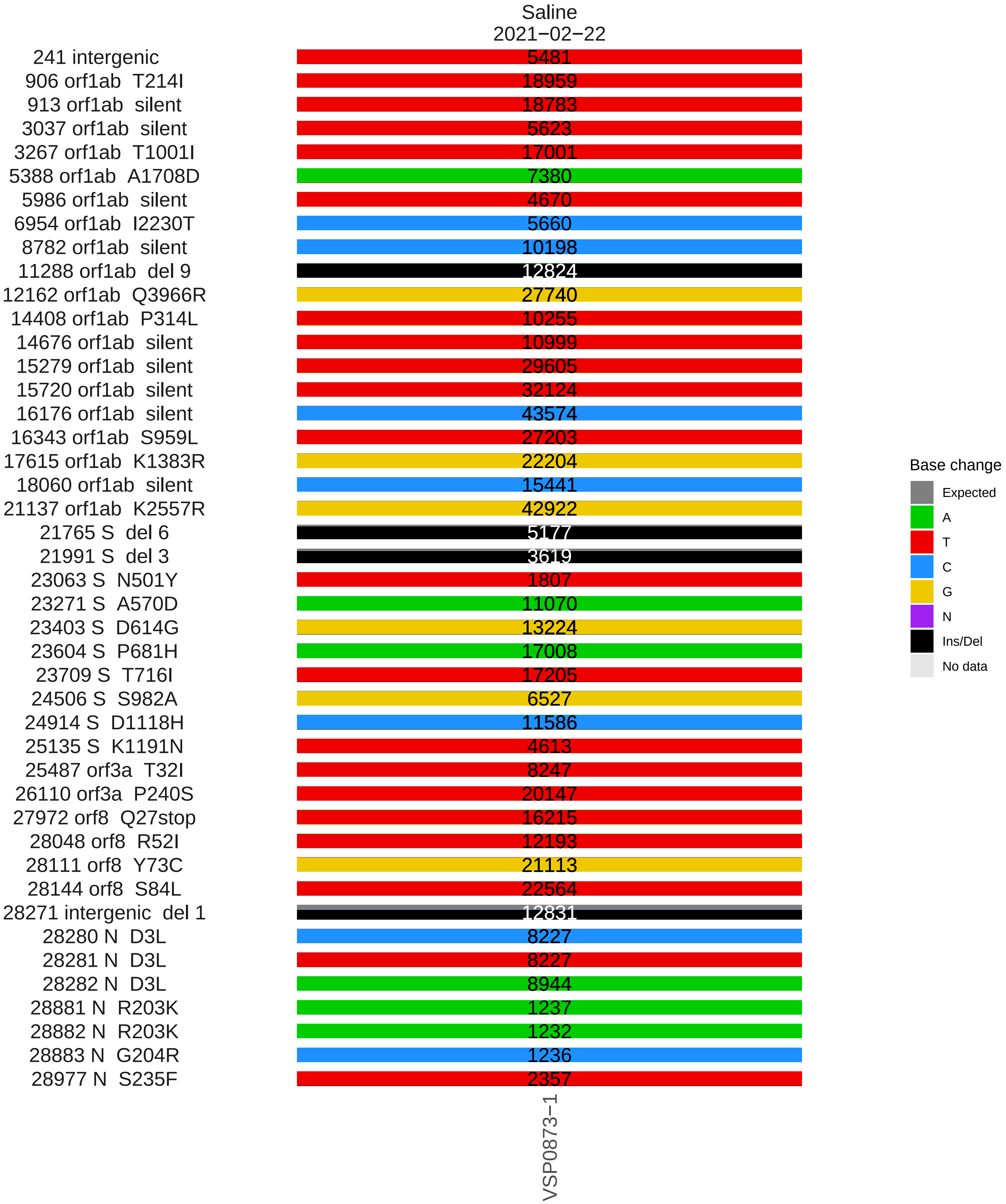
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0873-1	single experiment	NA	Saline	2021-02-22	29.71	B.1.1.7	99.3%	99.2%

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.



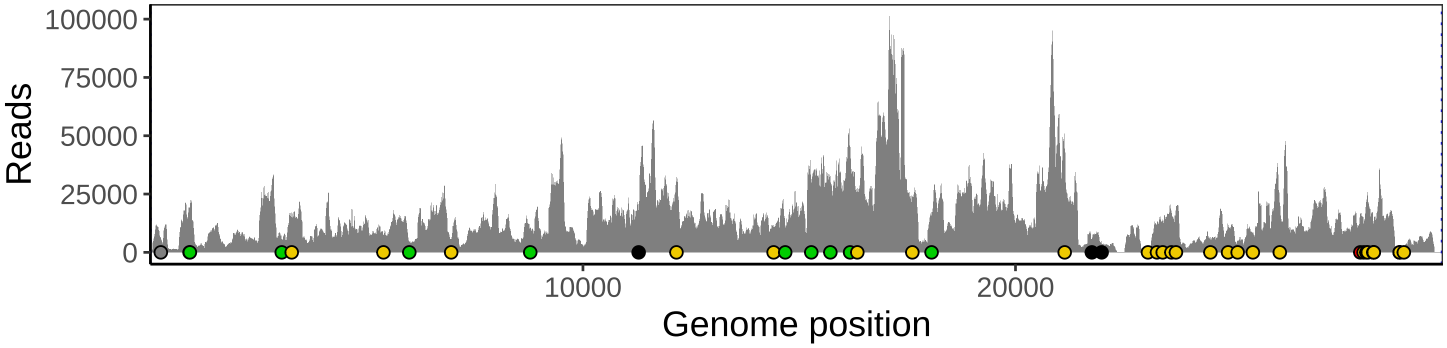


Saline
2021−02−22
241 intergenic
5481
906 orf1ab T214I
18959
913 orf1ab silent
18783
3037 orf1ab silent
5623
3267 orf1ab T1001I
17001
5388 orf1ab A1708D
7380
5986 orf1ab silent
4670
6954 orf1ab I2230T
5660
8782 orf1ab silent
10198
11288 orf1ab del 9
12824
12162 orf1ab Q3966R
27740
14408 orf1ab P314L
10255
14676 orf1ab silent
10999
15279 orf1ab silent
29605
15720 orf1ab silent
32124
16176 orf1ab silent
43574
16343 orf1ab S959L
27203
17615 orf1ab K1383R
22204
18060 orf1ab silent
15441
21137 orf1ab K2557R
42922
21765 S del 6
5177
21991 S del 3
3619
23063 S N501Y
1807
23271 S A570D
11070
23403 S D614G
13224
23604 S P681H
17008
23709 S T716I
17205
24506 S S982A
6527
24914 S D1118H
11586
25135 S K1191N
4613
25487 orf3a T32I
8247
26110 orf3a P240S
20147
27972 orf8 Q27stop
16215
28048 orf8 R52I
12193
28111 orf8 Y73C
21113
28144 orf8 S84L
22564
28271 intergenic del 1
12831
28280 N D3L
8227
28281 N D3L
8227
28282 N D3L
8944
28881 N R203K
1237
28882 N R203K
1232
28883 N G204R
1236
28977 N S235F
2357
VSP0873−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

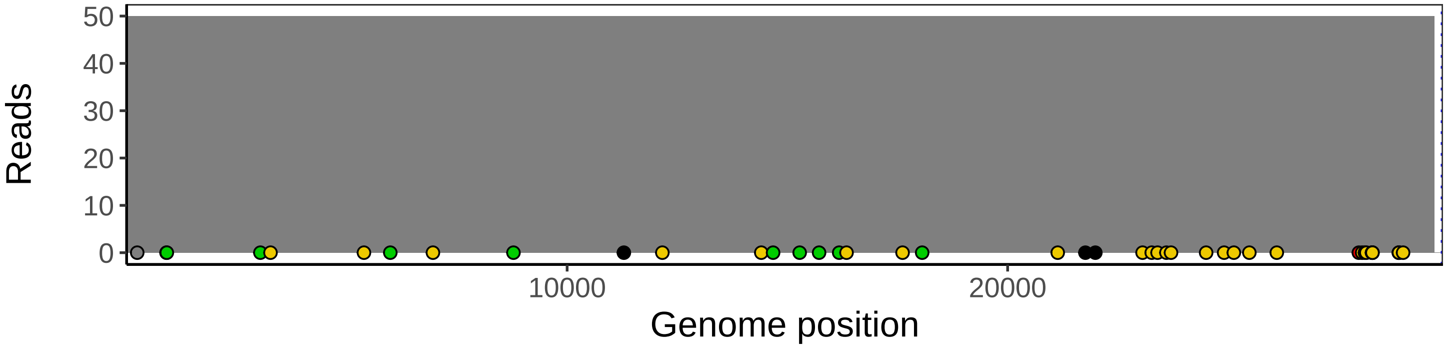
Analyses of individual experiments and composite results

VSP0873-1 | 2021-02-22 | Saline | HUP-Q-0010 | genomes | single experiment

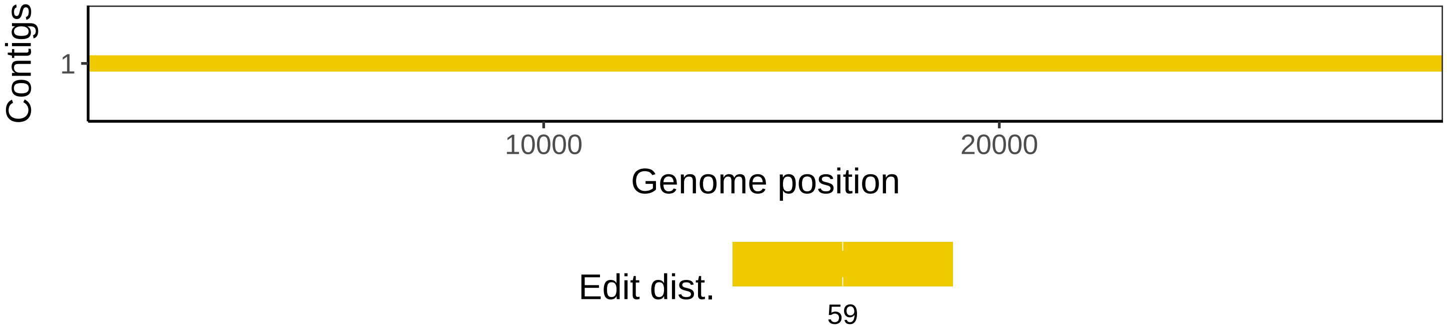
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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