COVID-19 subject HUP Q-0140

2021-05-05

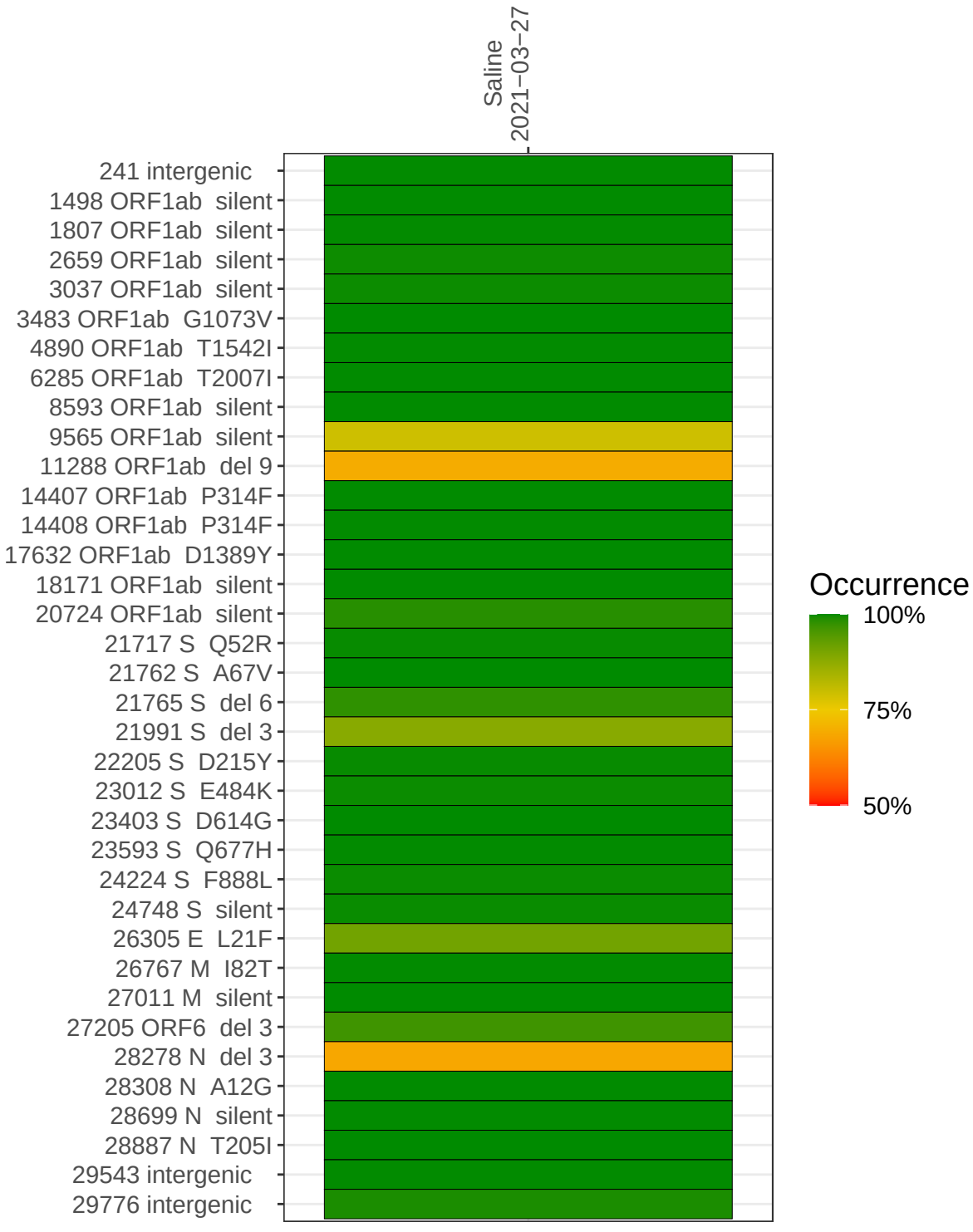
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

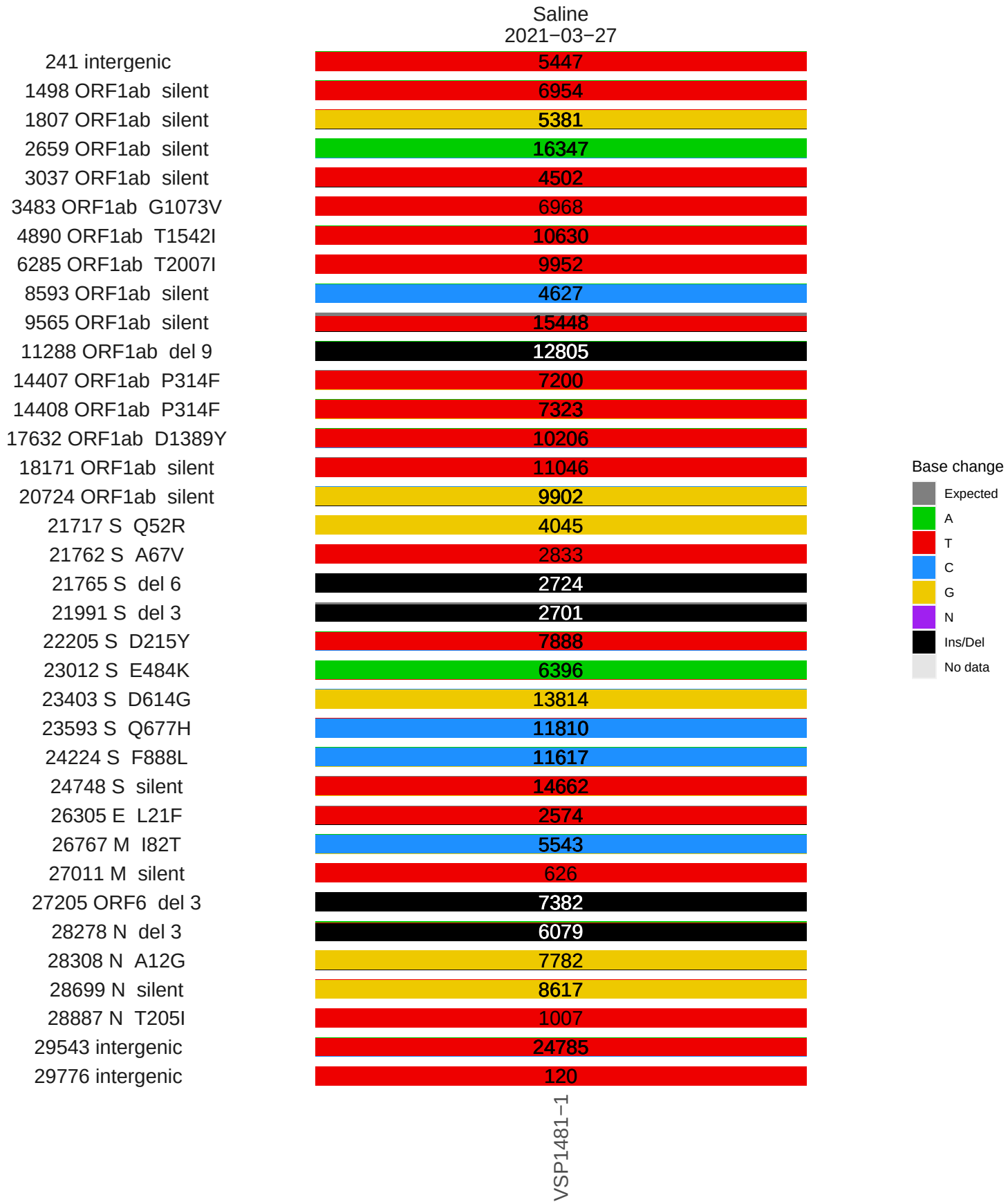
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1481-1	single experiment	NA	Saline	2021-03-27	29.82	B.1.525	99.7%	99.6%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

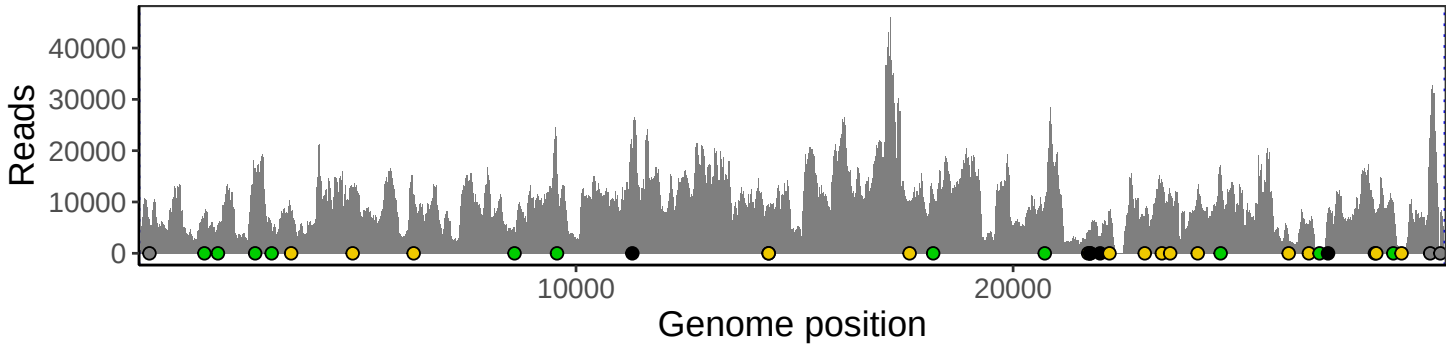



Saline
2021−03−27
241 intergenic
1498 ORF1ab silent
1807 ORF1ab silent
2659 ORF1ab silent
3037 ORF1ab silent
3483 ORF1ab G1073V
4890 ORF1ab T1542I
6285 ORF1ab T2007I
8593 ORF1ab silent
9565 ORF1ab silent
11288 ORF1ab del 9
14407 ORF1ab P314F
14408 ORF1ab P314F
17632 ORF1ab D1389Y
18171 ORF1ab silent
20724 ORF1ab silent
21717 S Q52R
21762 S A67V
21765 S del 6
21991 S del 3
22205 S D215Y
23012 S E484K
23403 S D614G
23593 S Q677H
24224 S F888L
24748 S silent
26305 E L21F
26767 M I82T
27011 M silent
27205 ORF6 del 3
28278 N del 3
28308 N A12G
28699 N silent
28887 N T205I
29543 intergenic
29776 intergenic
5447
6954
5381
16347
4502
6968
10630
9952
4627
15448
12805
7200
7323
10206
11046
9902
4045
2833
2724
2701
7888
6396
13814
11810
11617
14662
2574
5543
626
7382
6079
7782
8617
1007
24785
120
VSP1481−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

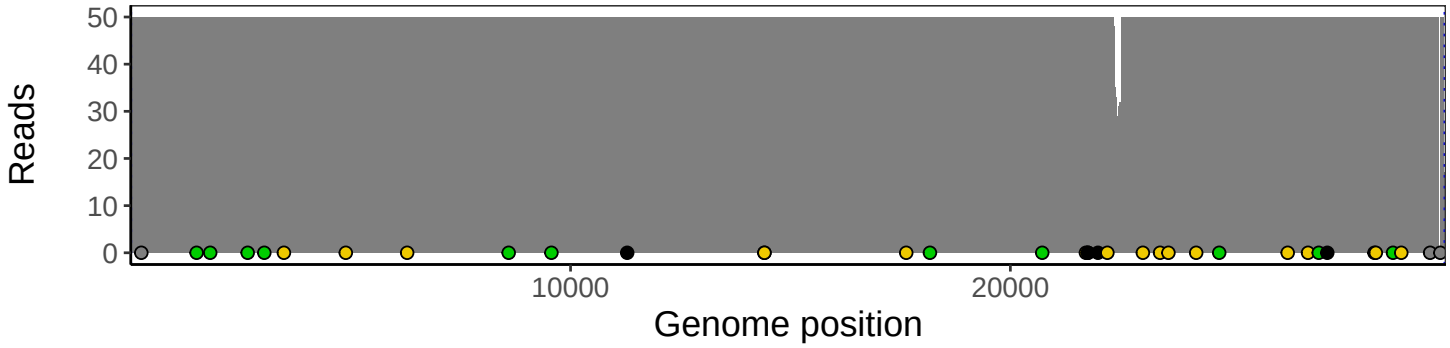
Analyses of individual experiments and composite results

VSP1481-1 | 2021-03-27 | Saline | HUP Q-0140 | genomes | single experiment

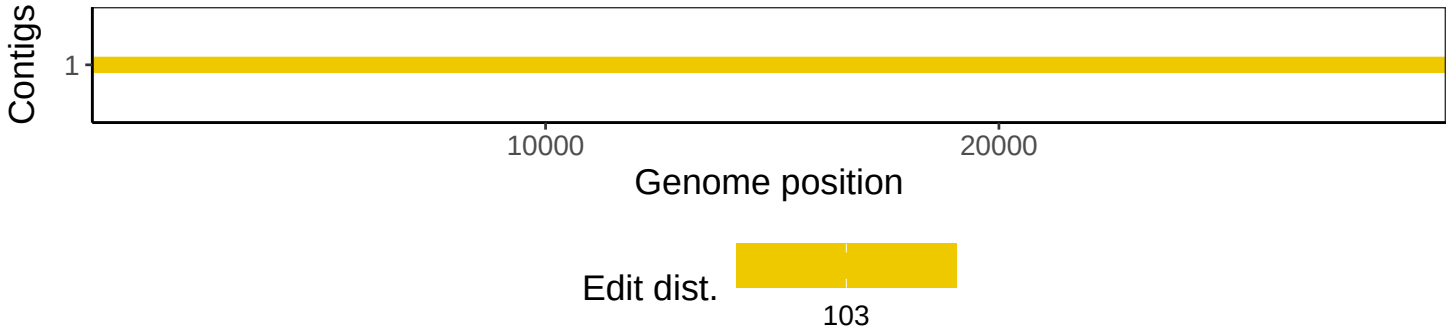
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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