COVID-19 subject HUP Q-0154

2021-06-23

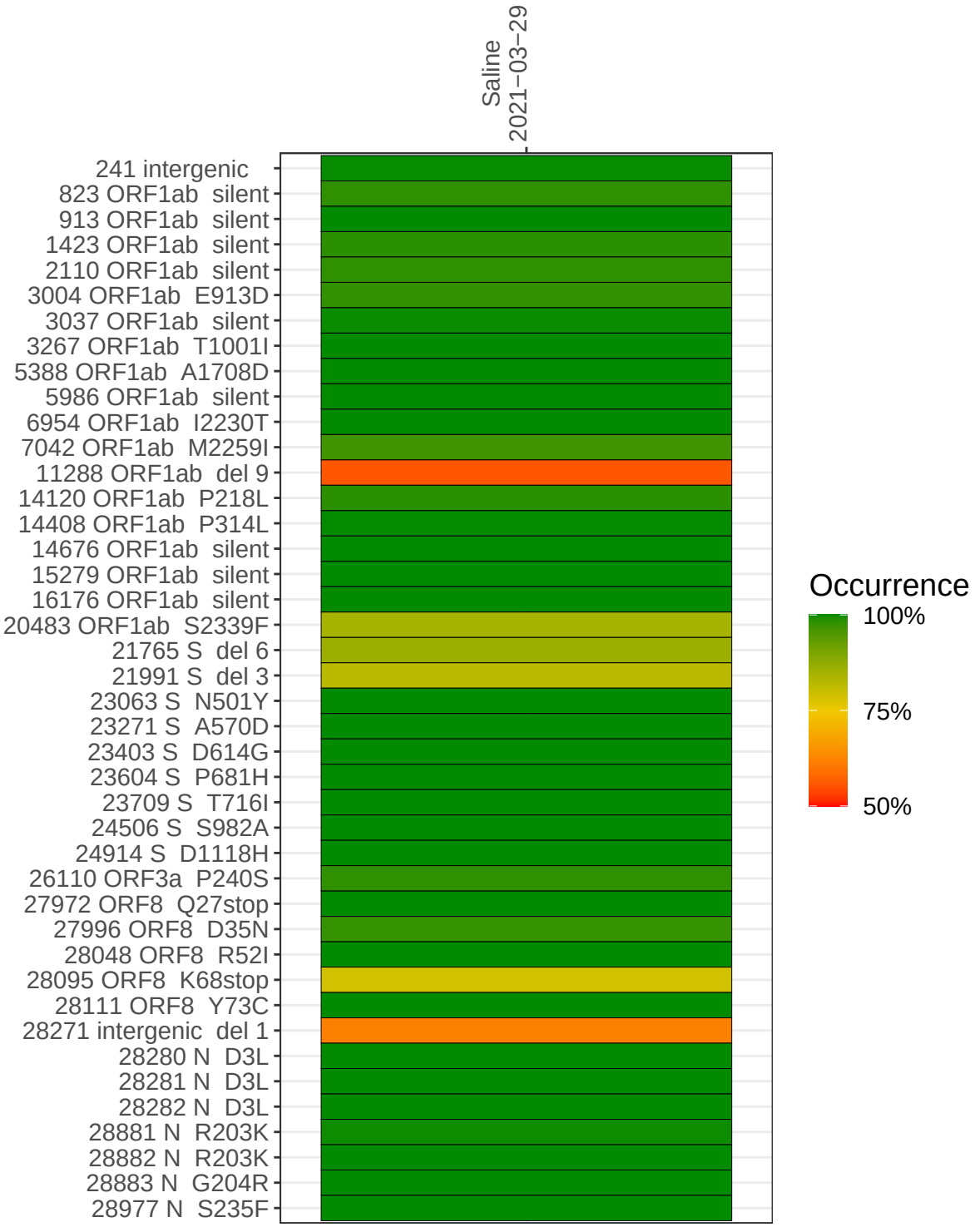
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

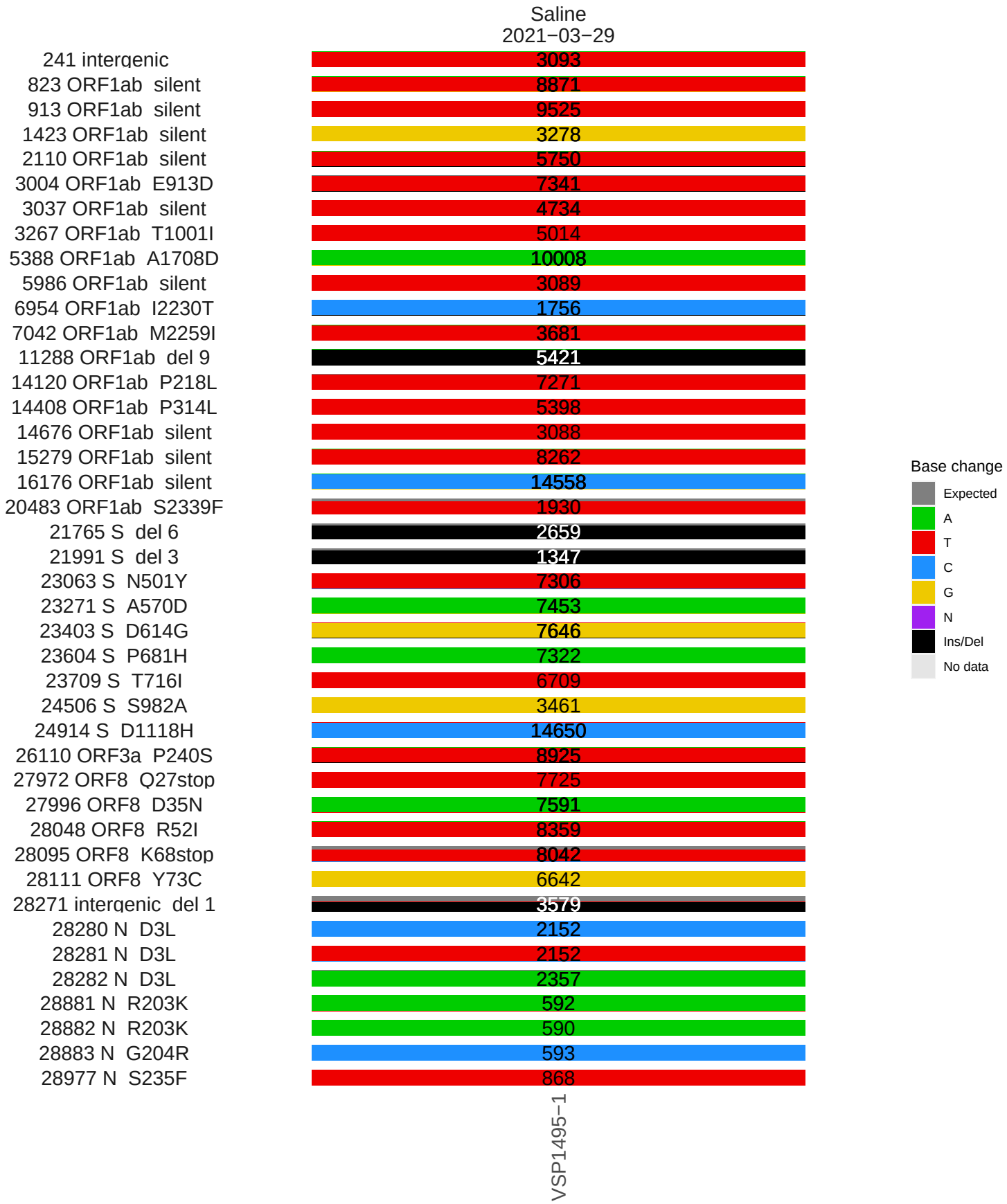
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1495-1	single experiment	NA	Saline	2021-03-29	29.82	B.1.1.7	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

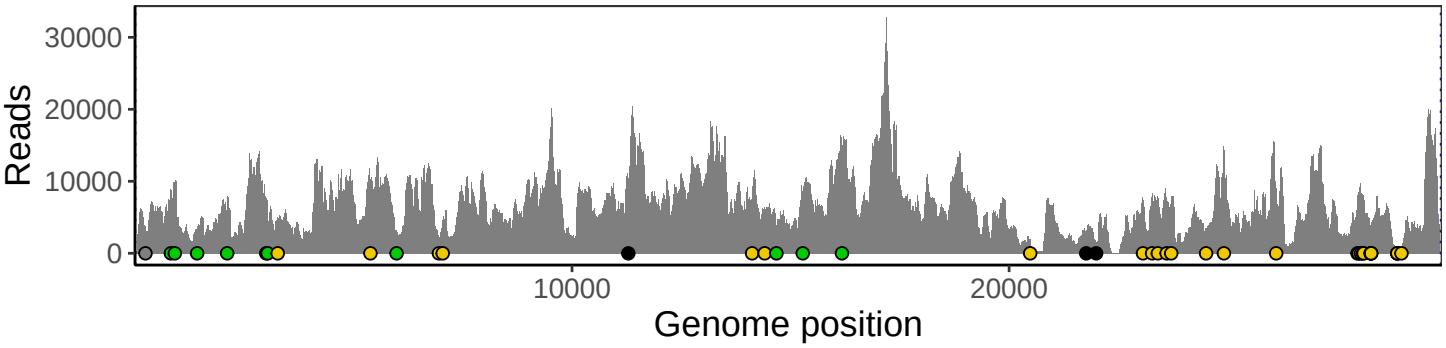



Saline
2021−03−29
241 intergenic 3093
823 ORF1ab silent 8871
913 ORF1ab silent 9525
1423 ORF1ab silent 3278
2110 ORF1ab silent 5750
3004 ORF1ab E913D 7341
3037 ORF1ab silent 4734
3267 ORF1ab T1001I 5014
5388 ORF1ab A1708D 10008
5986 ORF1ab silent 3089
6954 ORF1ab I2230T 1756
7042 ORF1ab M2259I 3681
11288 ORF1ab del 9 5421
14120 ORF1ab P218L 7271
14408 ORF1ab P314L 5398
14676 ORF1ab silent 3088
15279 ORF1ab silent 8262
16176 ORF1ab silent 14558
20483 ORF1ab S2339F 1930
21765 S del 6 2659
21991 S del 3 1347
23063 S N501Y 7306
23271 S A570D 7453
23403 S D614G 7646
23604 S P681H 7322
23709 S T716I 6709
24506 S S982A 3461
24914 S D1118H 14650
26110 ORF3a P240S 8925
27972 ORF8 Q27stop 7725
27996 ORF8 D35N 7591
28048 ORF8 R52I 8359
28095 ORF8 K68stop 8042
28111 ORF8 Y73C 6642
28271 intergenic del 1 3579
28280 N D3L 2152
28281 N D3L 2152
28282 N D3L 2357
28881 N R203K 592
28882 N R203K 590
28883 N G204R 593
28977 N S235F 868
VSP1495−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

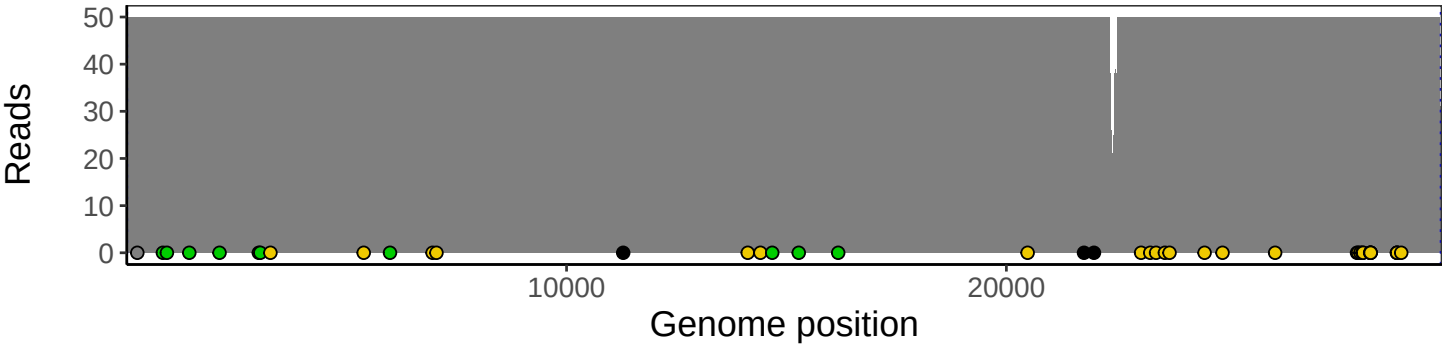
Analyses of individual experiments and composite results

VSP1495-1 | 2021-03-29 | Saline | HUP Q-0154 | genomes | single experiment

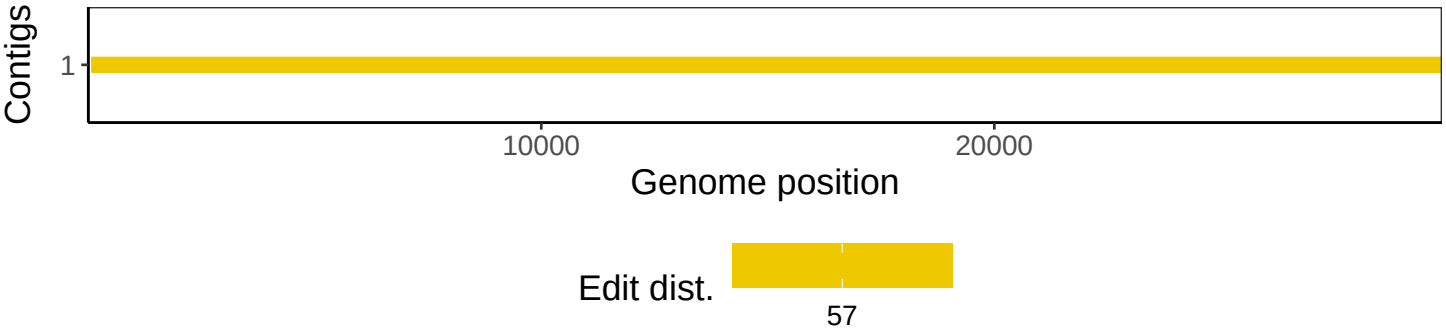
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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