COVID-19 subject HUP Q-0241

2021-06-03

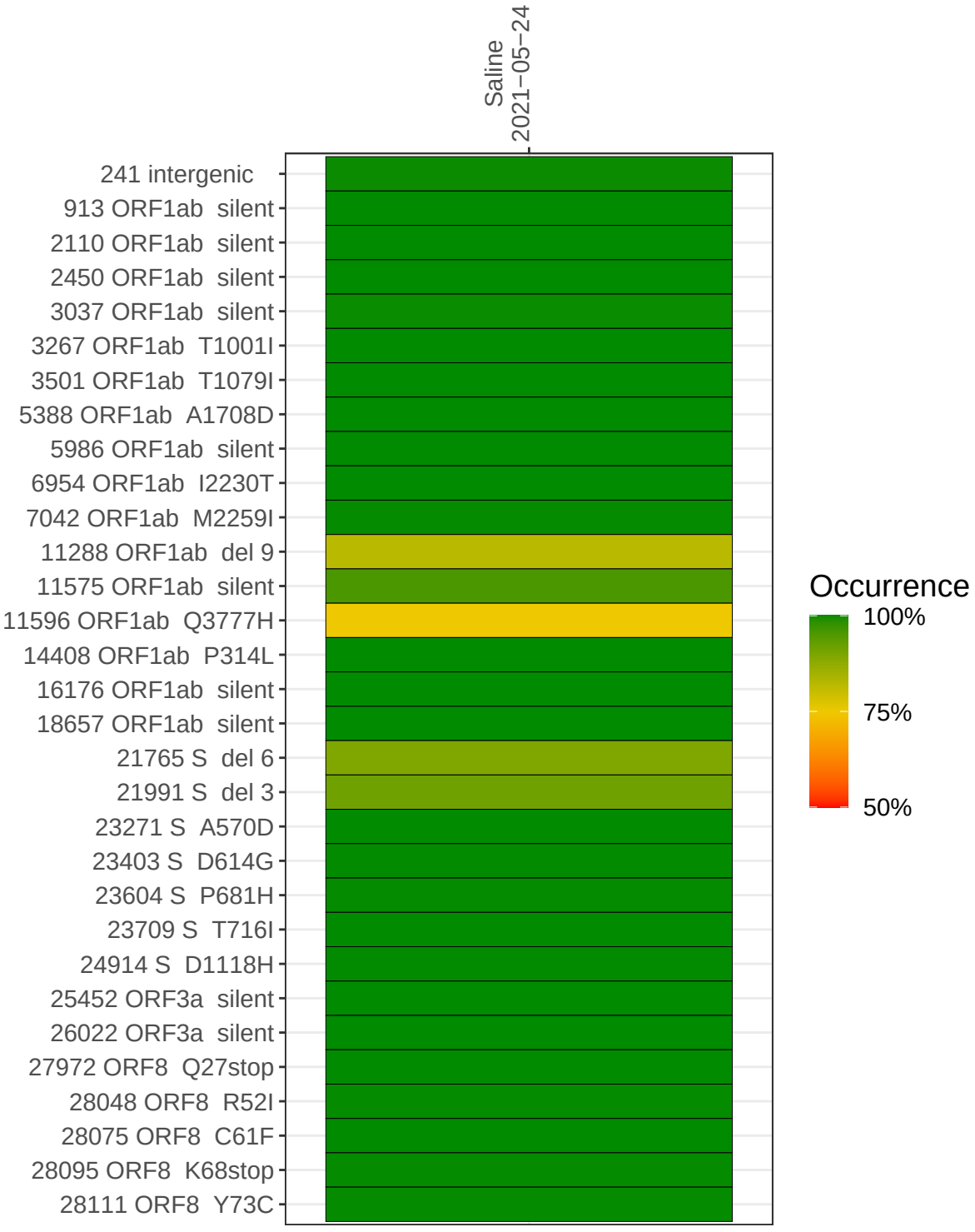
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

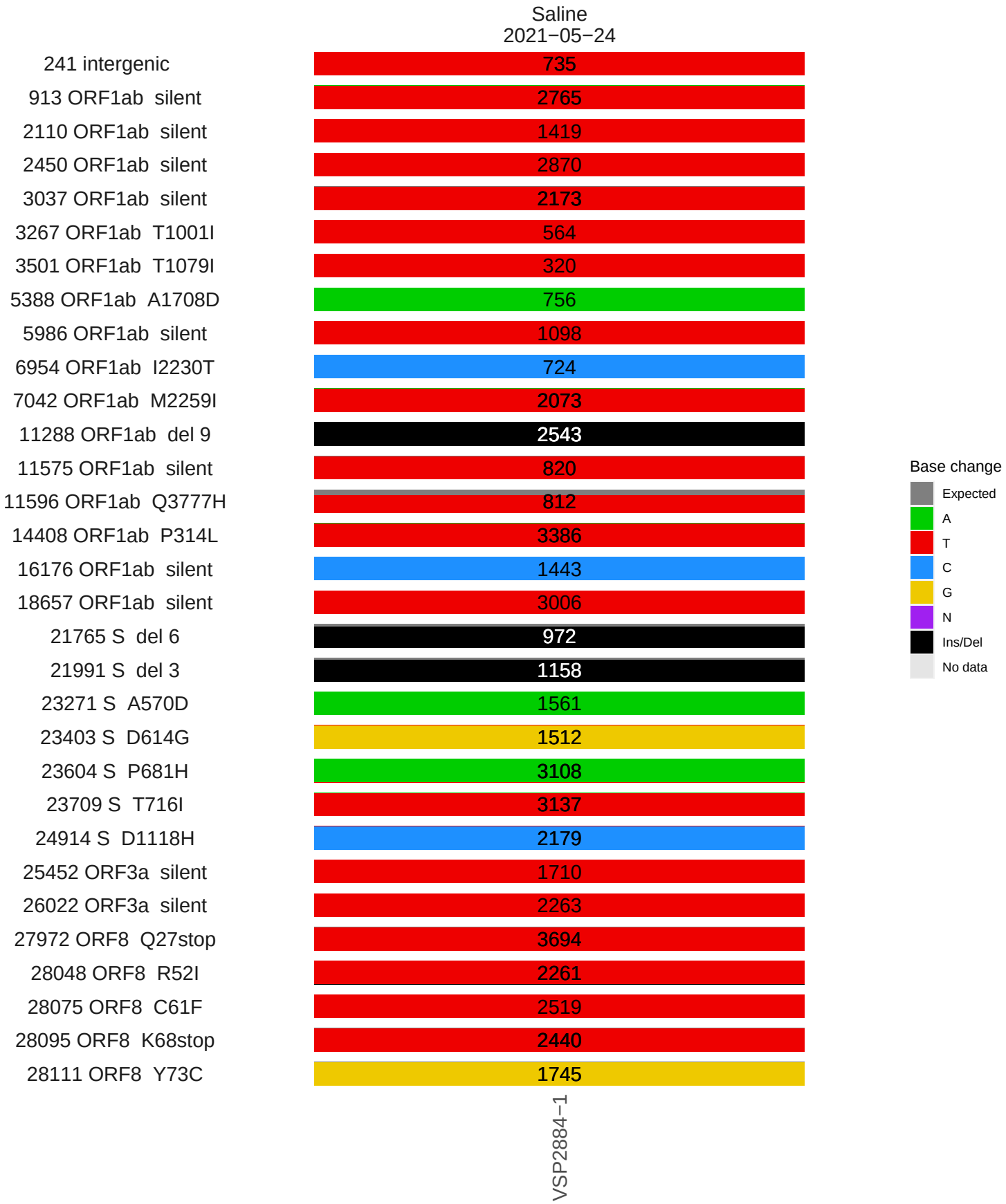
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2884-1	single experiment	NA	Saline	2021-05-24	4.39	NA	78.7%	77.9%

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.

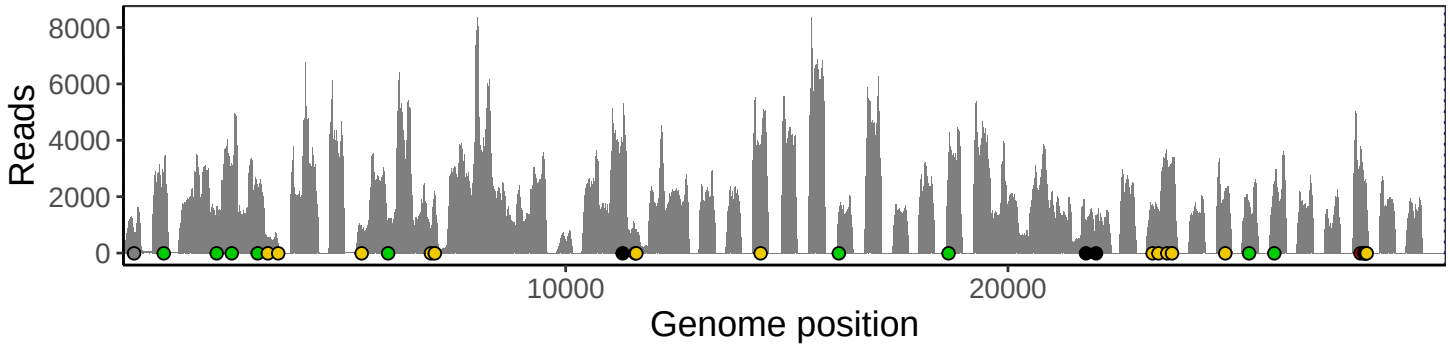



Saline
2021−05−24
241 intergenic
913 ORF1ab silent
2110 ORF1ab silent
2450 ORF1ab silent
3037 ORF1ab silent
3267 ORF1ab T1001I
3501 ORF1ab T1079I
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
7042 ORF1ab M2259I
11288 ORF1ab del 9
11575 ORF1ab silent
11596 ORF1ab Q3777H
14408 ORF1ab P314L
16176 ORF1ab silent
18657 ORF1ab silent
21765 S del 6
21991 S del 3
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24914 S D1118H
25452 ORF3a silent
26022 ORF3a silent
27972 ORF8 Q27stop
28048 ORF8 R52I
28075 ORF8 C61F
28095 ORF8 K68stop
28111 ORF8 Y73C
735
2765
1419
2870
2173
564
320
756
1098
724
2073
2543
820
812
3386
1443
3006
972
1158
1561
1512
3108
3137
2179
1710
2263
3694
2261
2519
2440
1745
VSP2884−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

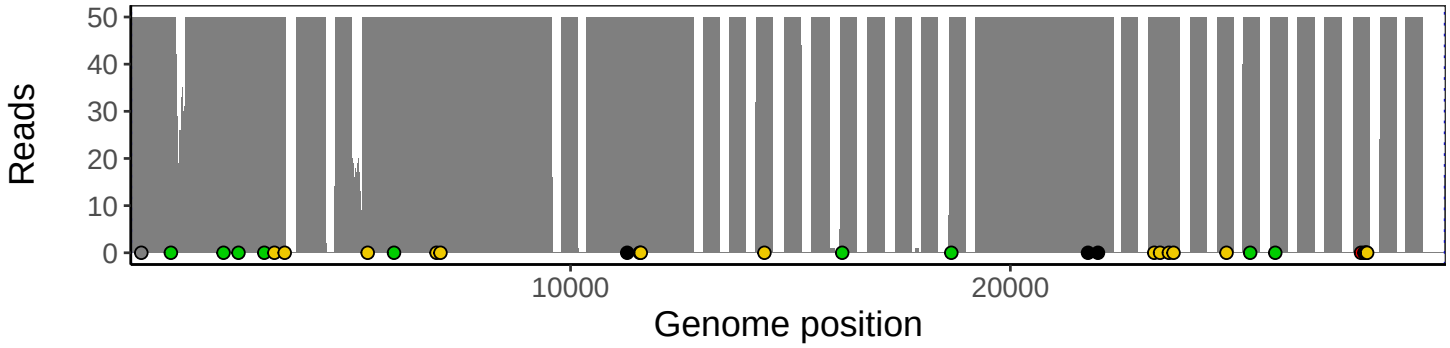
Analyses of individual experiments and composite results

VSP2884-1 | 2021-05-24 | Saline | HUP Q-0241 | genomes | single experiment

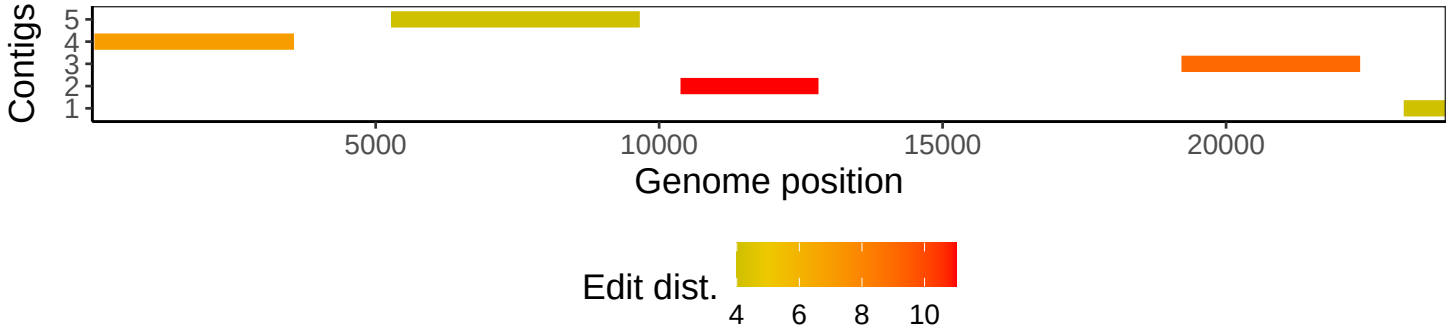
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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