COVID-19 subject UPHS-0329

2021-05-05

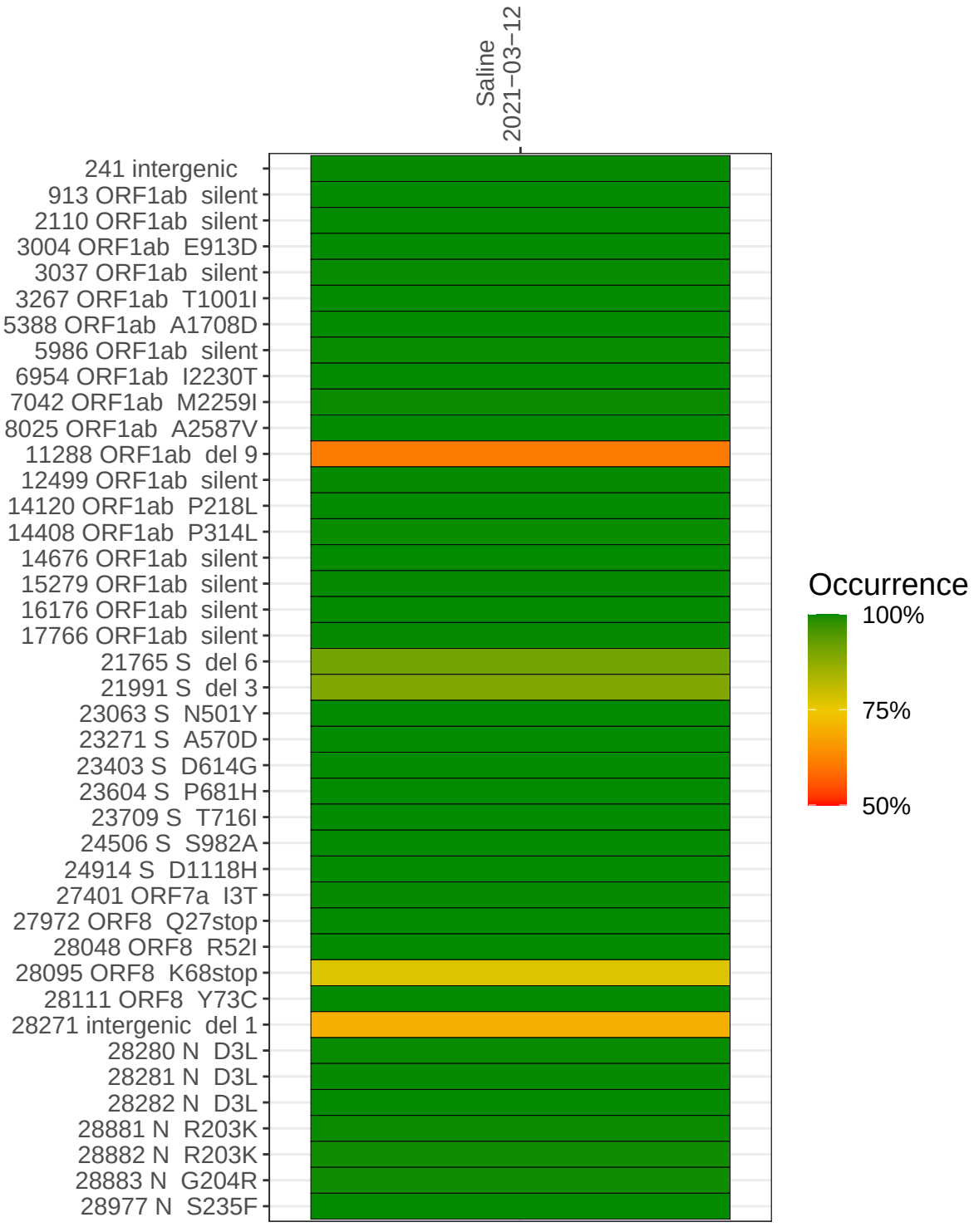
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

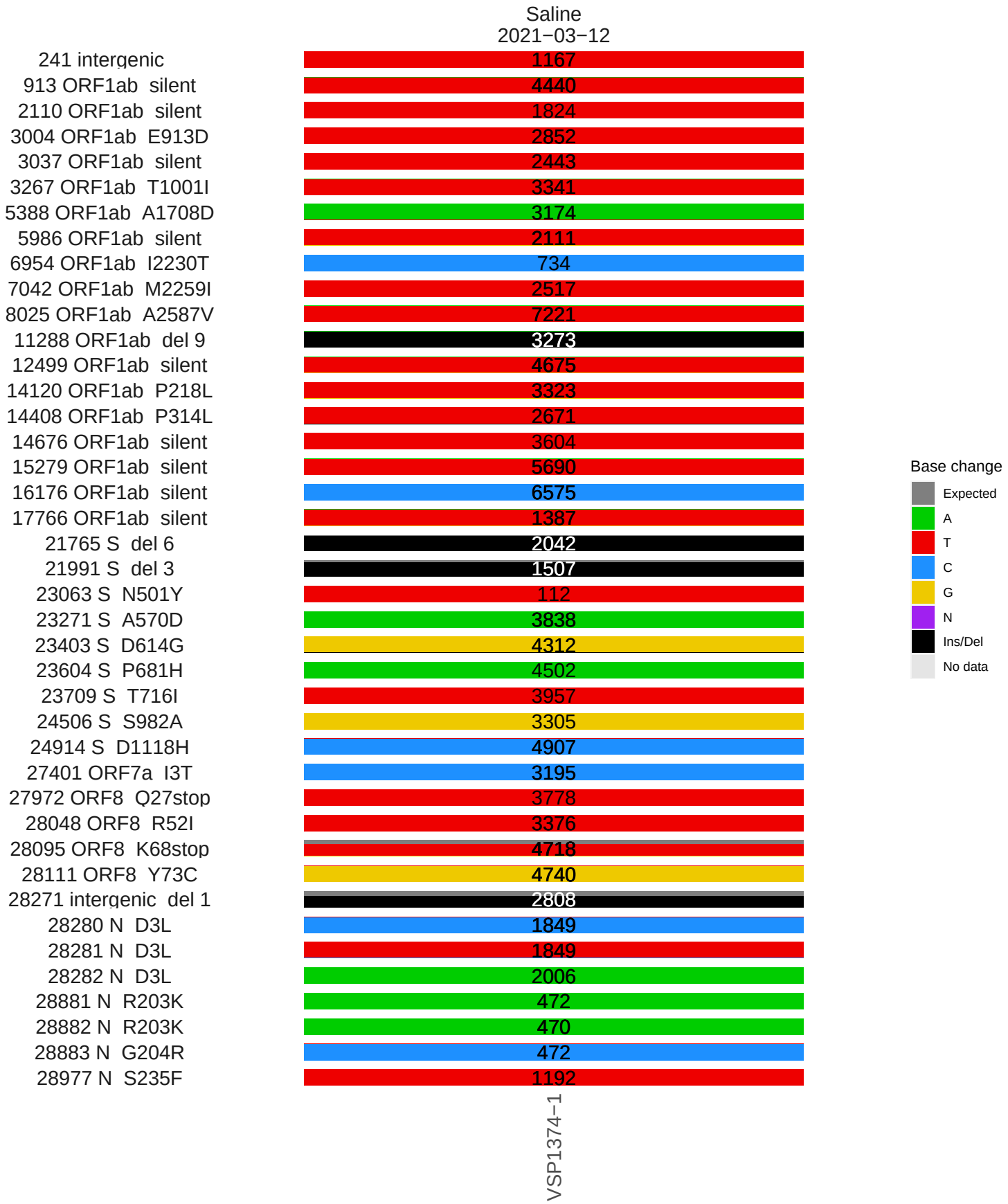
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1374-1	single experiment	NA	Saline	2021-03-12	29.87	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/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.

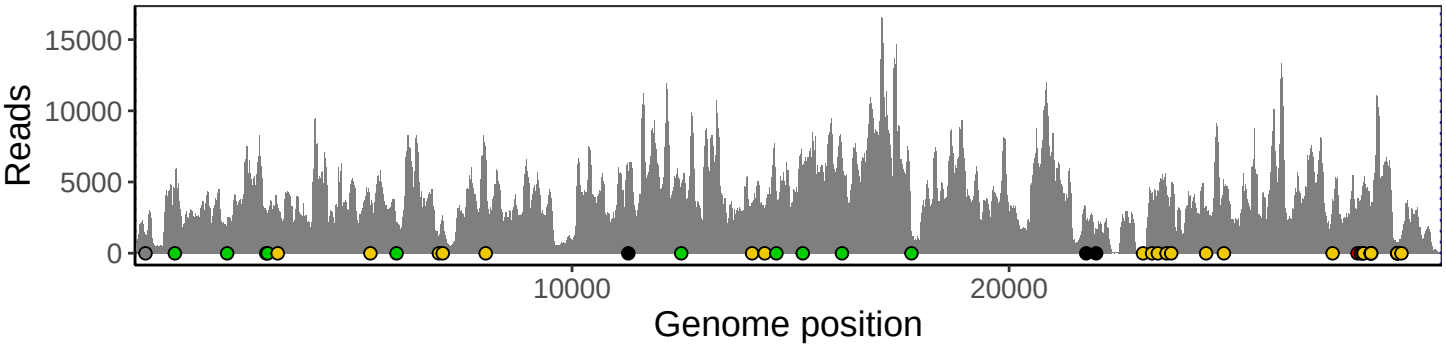



Saline
2021−03−12
241 intergenic 1167
913 ORF1ab silent 4440
2110 ORF1ab silent 1824
3004 ORF1ab E913D 2852
3037 ORF1ab silent 2443
3267 ORF1ab T1001I 3341
5388 ORF1ab A1708D 3174
5986 ORF1ab silent 2111
6954 ORF1ab I2230T 734
7042 ORF1ab M2259I 2517
8025 ORF1ab A2587V 7221
11288 ORF1ab del 9 3273
12499 ORF1ab silent 4675
14120 ORF1ab P218L 3323
14408 ORF1ab P314L 2671
14676 ORF1ab silent 3604
15279 ORF1ab silent 5690
16176 ORF1ab silent 6575
17766 ORF1ab silent 1387
21765 S del 6 2042
21991 S del 3 1507
23063 S N501Y 112
23271 S A570D 3838
23403 S D614G 4312
23604 S P681H 4502
23709 S T716I 3957
24506 S S982A 3305
24914 S D1118H 4907
27401 ORF7a I3T 3195
27972 ORF8 Q27stop 3778
28048 ORF8 R52I 3376
28095 ORF8 K68stop 4718
28111 ORF8 Y73C 4740
28271 intergenic del 1 2808
28280 N D3L 1849
28281 N D3L 1849
28282 N D3L 2006
28881 N R203K 472
28882 N R203K 470
28883 N G204R 472
28977 N S235F 1192
VSP1374−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

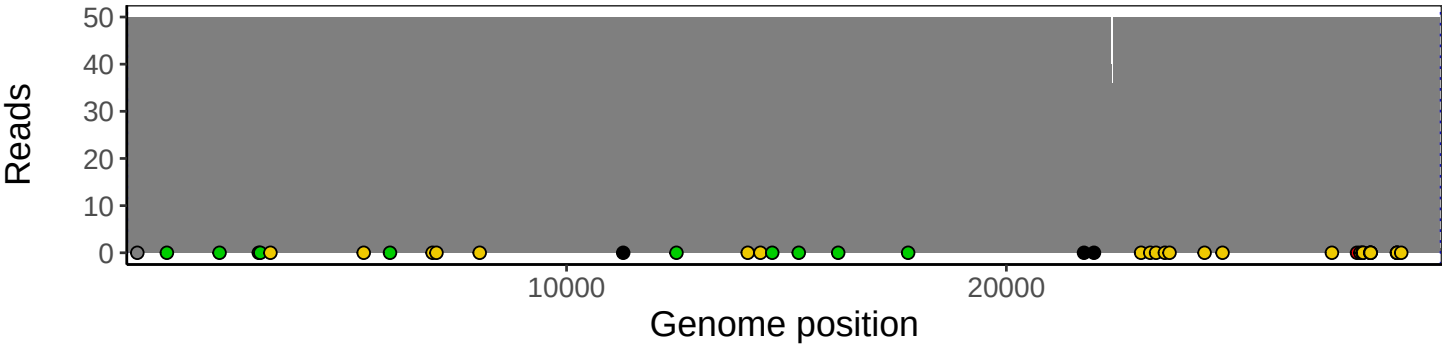
Analyses of individual experiments and composite results

VSP1374-1 | 2021-03-12 | Saline | UPHS-0329 | genomes | single experiment

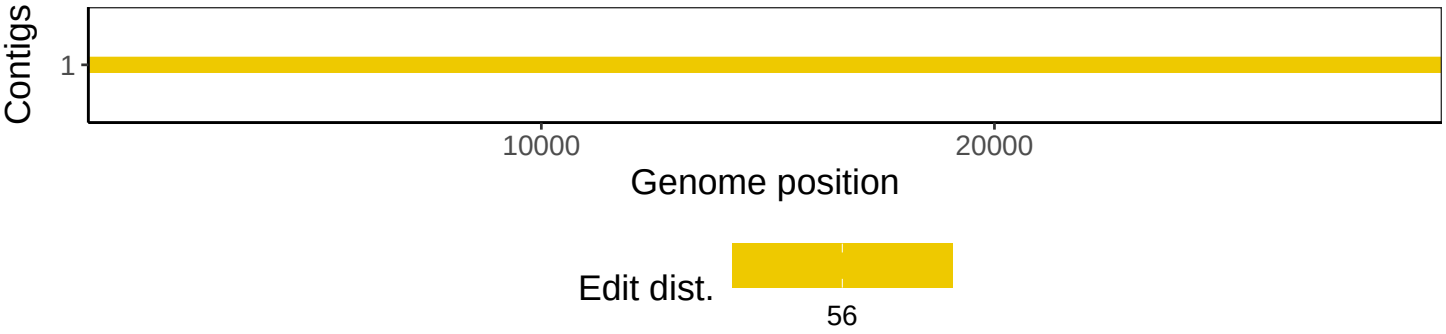
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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