COVID-19 subject UPHS-0332

2021-05-05

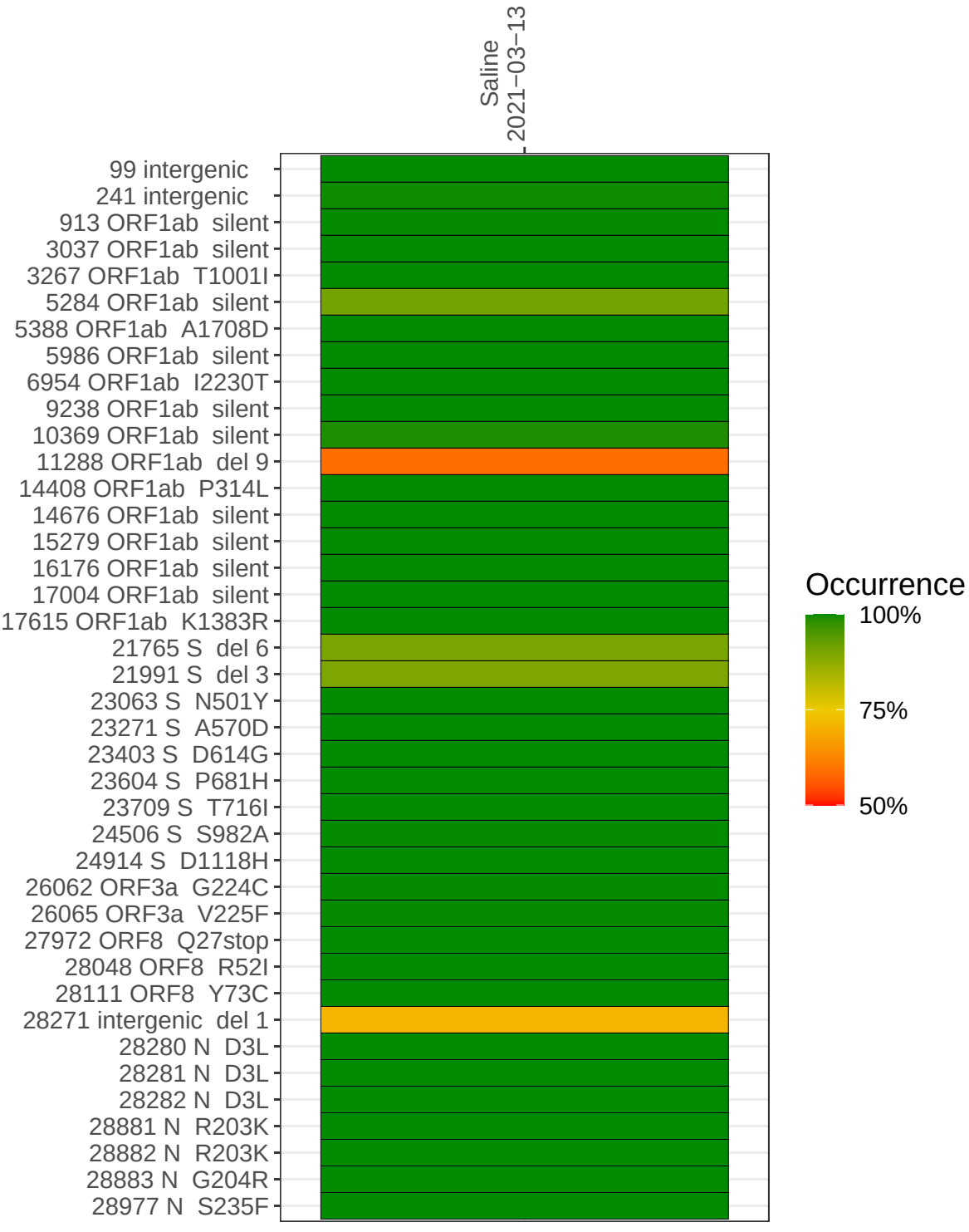
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

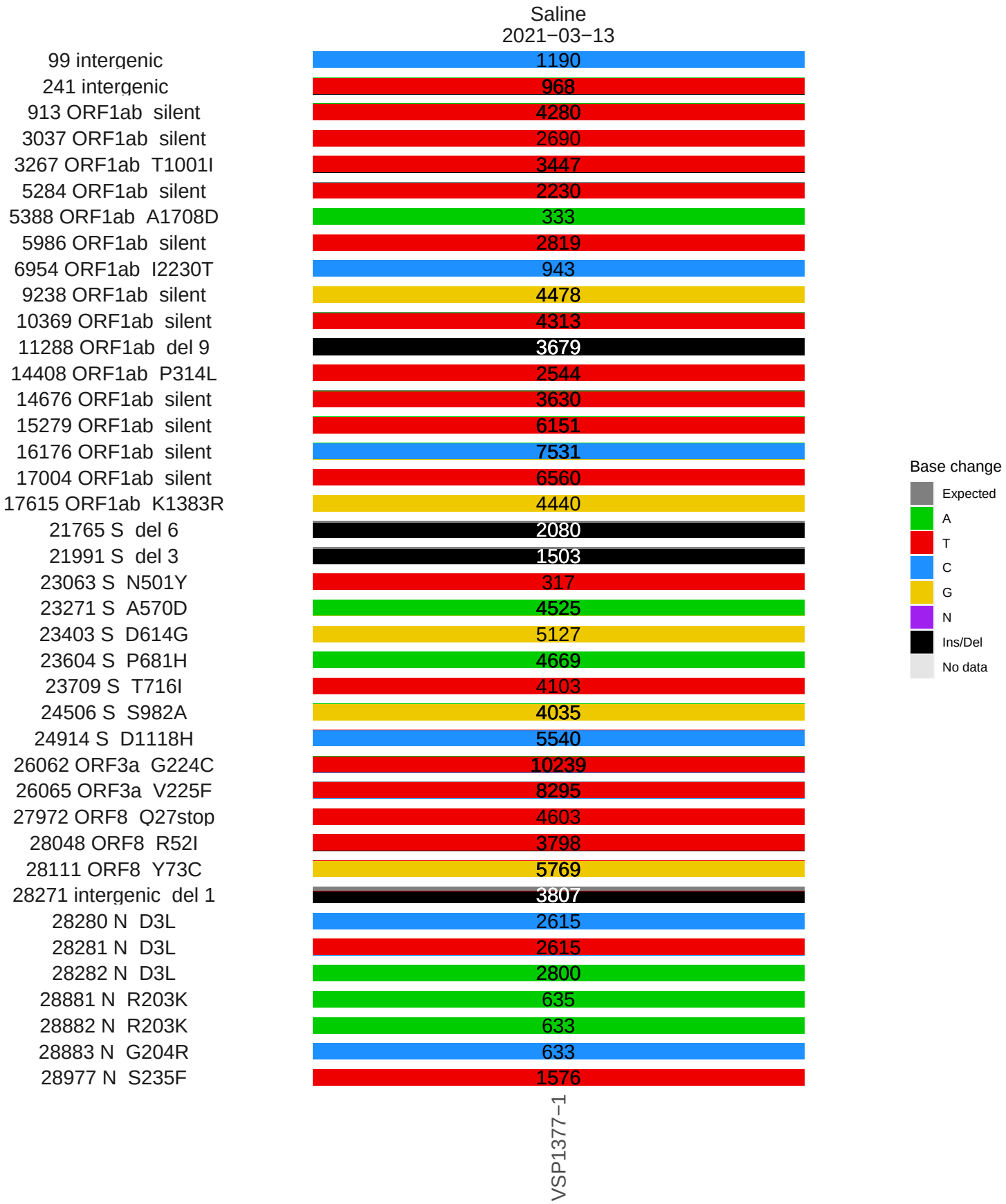
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1377-1	single experiment	NA	Saline	2021-03-13	29.86	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.

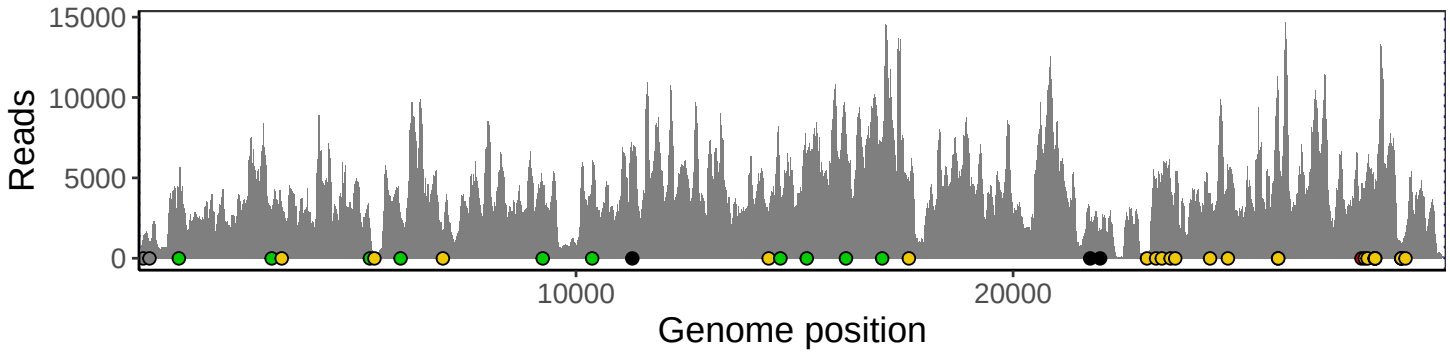



Saline
2021−03−13
99 intergenic 1190
241 intergenic 968
913 ORF1ab silent 4280
3037 ORF1ab silent 2690
3267 ORF1ab T1001I 3447
5284 ORF1ab silent 2230
5388 ORF1ab A1708D 333
5986 ORF1ab silent 2819
6954 ORF1ab I2230T 943
9238 ORF1ab silent 4478
10369 ORF1ab silent 4313
11288 ORF1ab del 9 3679
14408 ORF1ab P314L 2544
14676 ORF1ab silent 3630
15279 ORF1ab silent 6151
16176 ORF1ab silent 7531
17004 ORF1ab silent 6560
17615 ORF1ab K1383R 4440
21765 S del 6 2080
21991 S del 3 1503
23063 S N501Y 317
23271 S A570D 4525
23403 S D614G 5127
23604 S P681H 4669
23709 S T716I 4103
24506 S S982A 4035
24914 S D1118H 5540
26062 ORF3a G224C 10239
26065 ORF3a V225F 8295
27972 ORF8 Q27stop 4603
28048 ORF8 R52I 3798
28111 ORF8 Y73C 5769
28271 intergenic del 1 3807
28280 N D3L 2615
28281 N D3L 2615
28282 N D3L 2800
28881 N R203K 635
28882 N R203K 633
28883 N G204R 633
28977 N S235F 1576
VSP1377−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

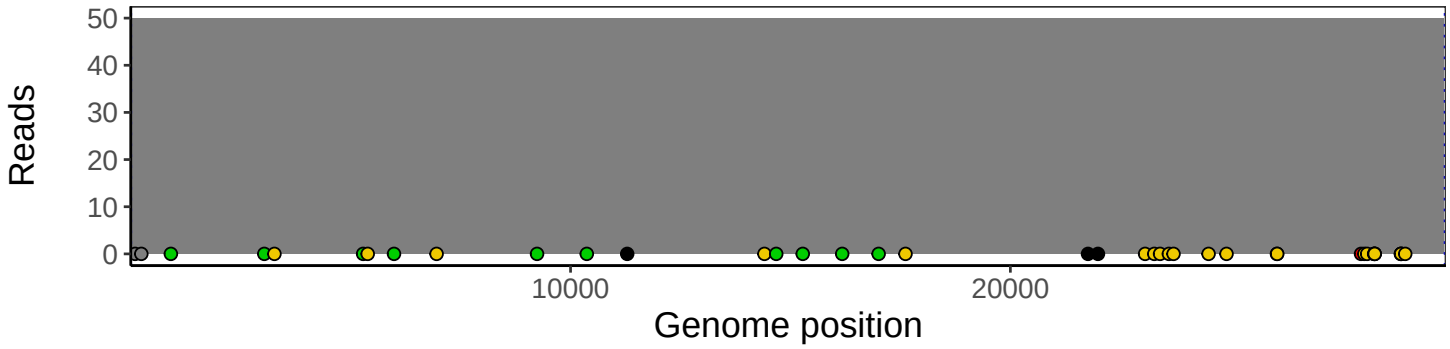
Analyses of individual experiments and composite results

VSP1377-1 | 2021-03-13 | Saline | UPHS-0332 | genomes | single experiment

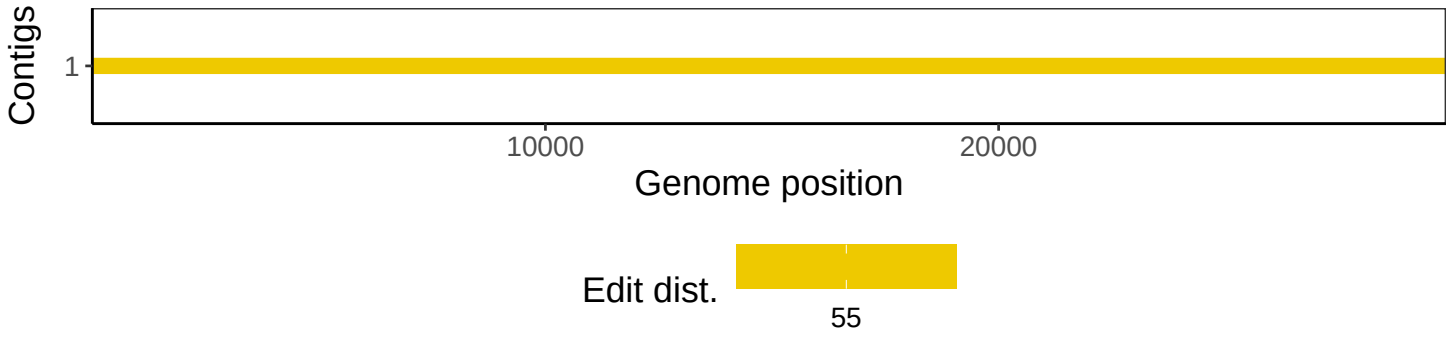
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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