COVID-19 subject UPHS-0327

2021-04-17

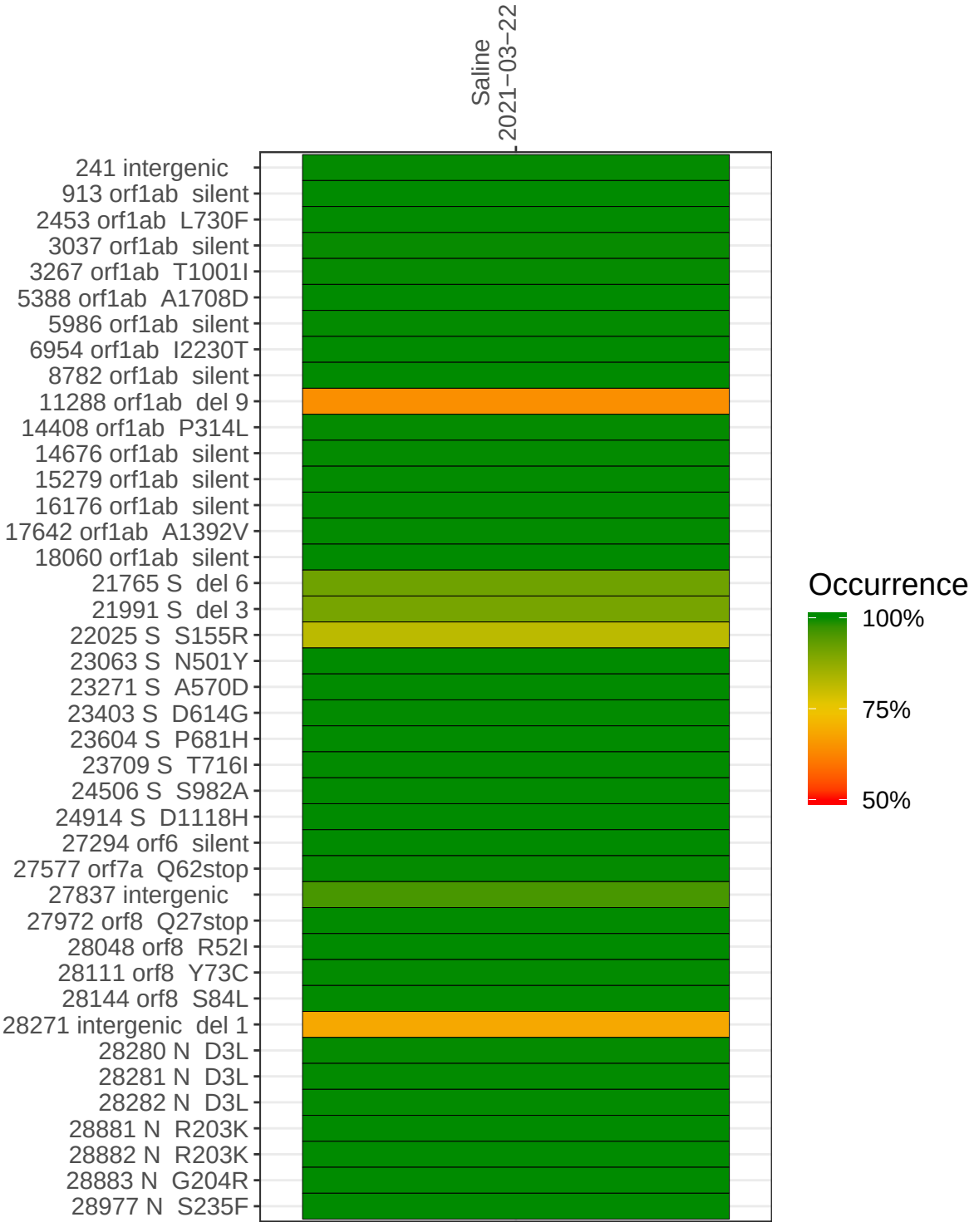
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

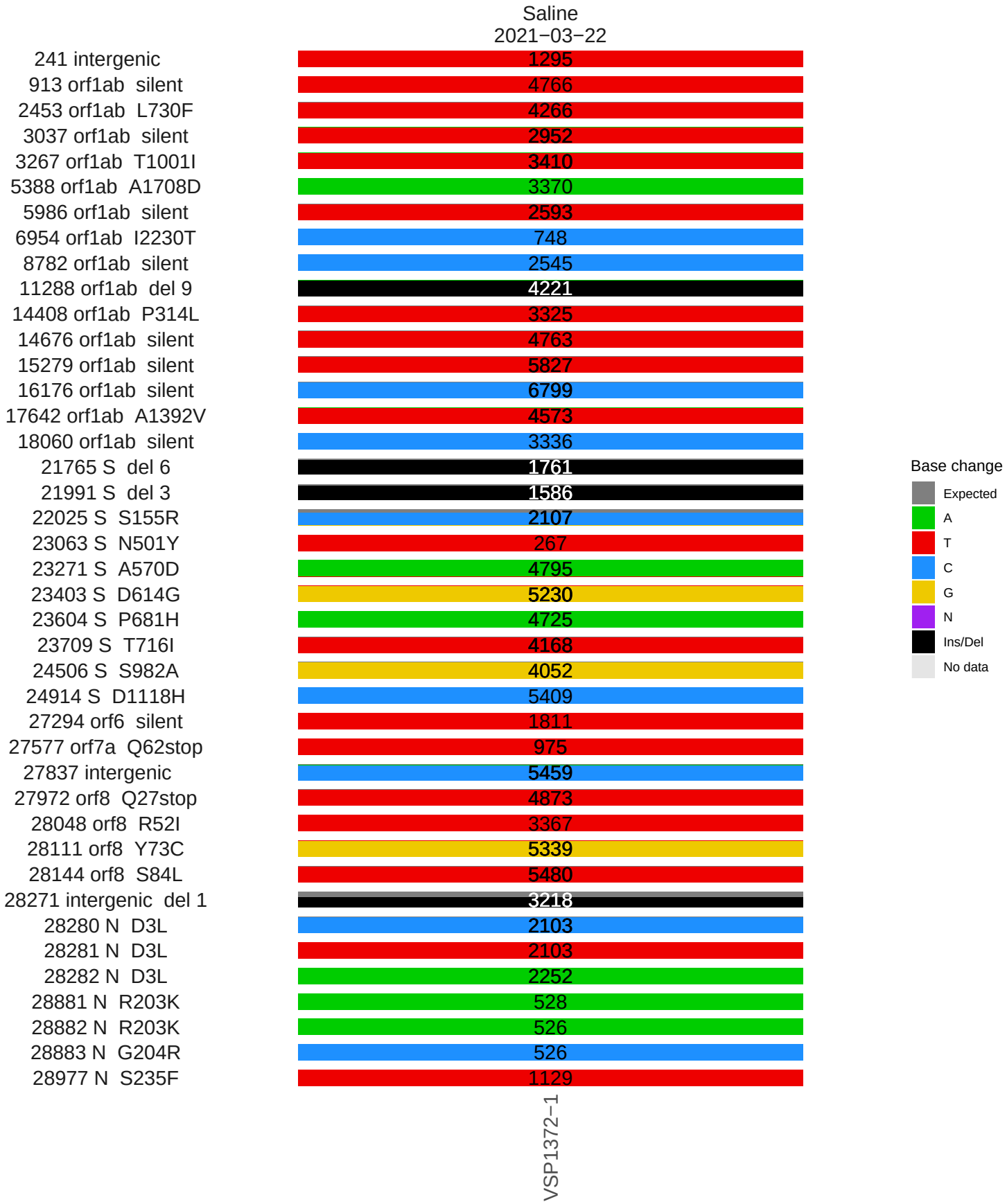
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1372-1	single experiment	NA	Saline	2021-03-22	29.81	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/USA-WA1-2020) 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.

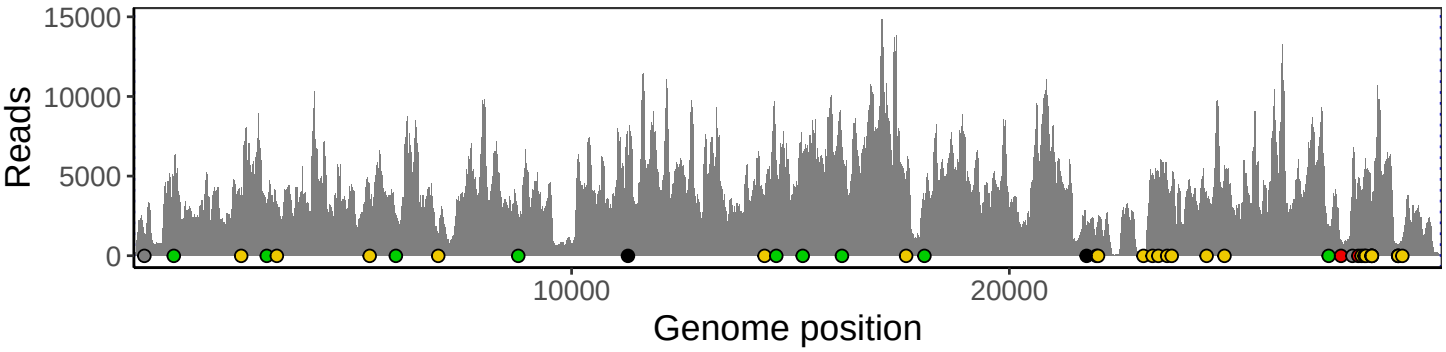



Saline
2021−03−22
241 intergenic 1295
913 orf1ab silent 4766
2453 orf1ab L730F 4266
3037 orf1ab silent 2952
3267 orf1ab T1001I 3410
5388 orf1ab A1708D 3370
5986 orf1ab silent 2593
6954 orf1ab I2230T 748
8782 orf1ab silent 2545
11288 orf1ab del 9 4221
14408 orf1ab P314L 3325
14676 orf1ab silent 4763
15279 orf1ab silent 5827
16176 orf1ab silent 6799
17642 orf1ab A1392V 4573
18060 orf1ab silent 3336
21765 S del 6 1761
21991 S del 3 1586
22025 S S155R 2107
23063 S N501Y 267
23271 S A570D 4795
23403 S D614G 5230
23604 S P681H 4725
23709 S T716I 4168
24506 S S982A 4052
24914 S D1118H 5409
27294 orf6 silent 1811
27577 orf7a Q62stop 975
27837 intergenic 5459
27972 orf8 Q27stop 4873
28048 orf8 R52I 3367
28111 orf8 Y73C 5339
28144 orf8 S84L 5480
28271 intergenic del 1 3218
28280 N D3L 2103
28281 N D3L 2103
28282 N D3L 2252
28881 N R203K 528
28882 N R203K 526
28883 N G204R 526
28977 N S235F 1129
VSP1372−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

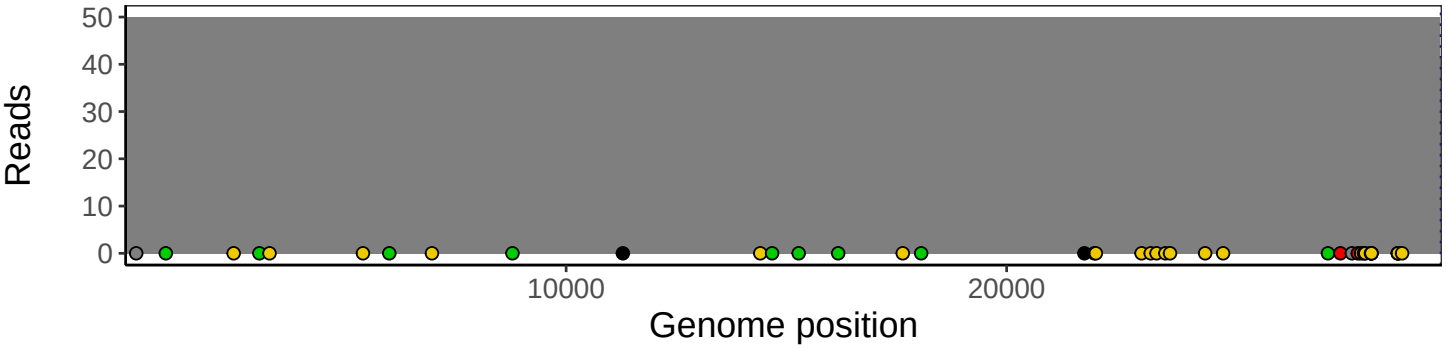
Analyses of individual experiments and composite results

VSP1372-1 | 2021-03-22 | Saline | UPHS-0327 | genomes | single experiment

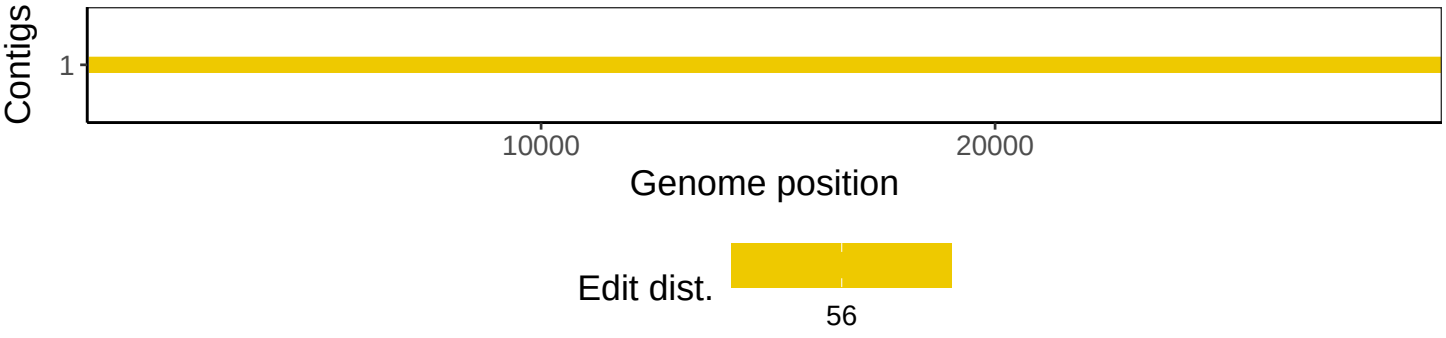
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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