COVID-19 subject UPHS-1027

2021-05-10

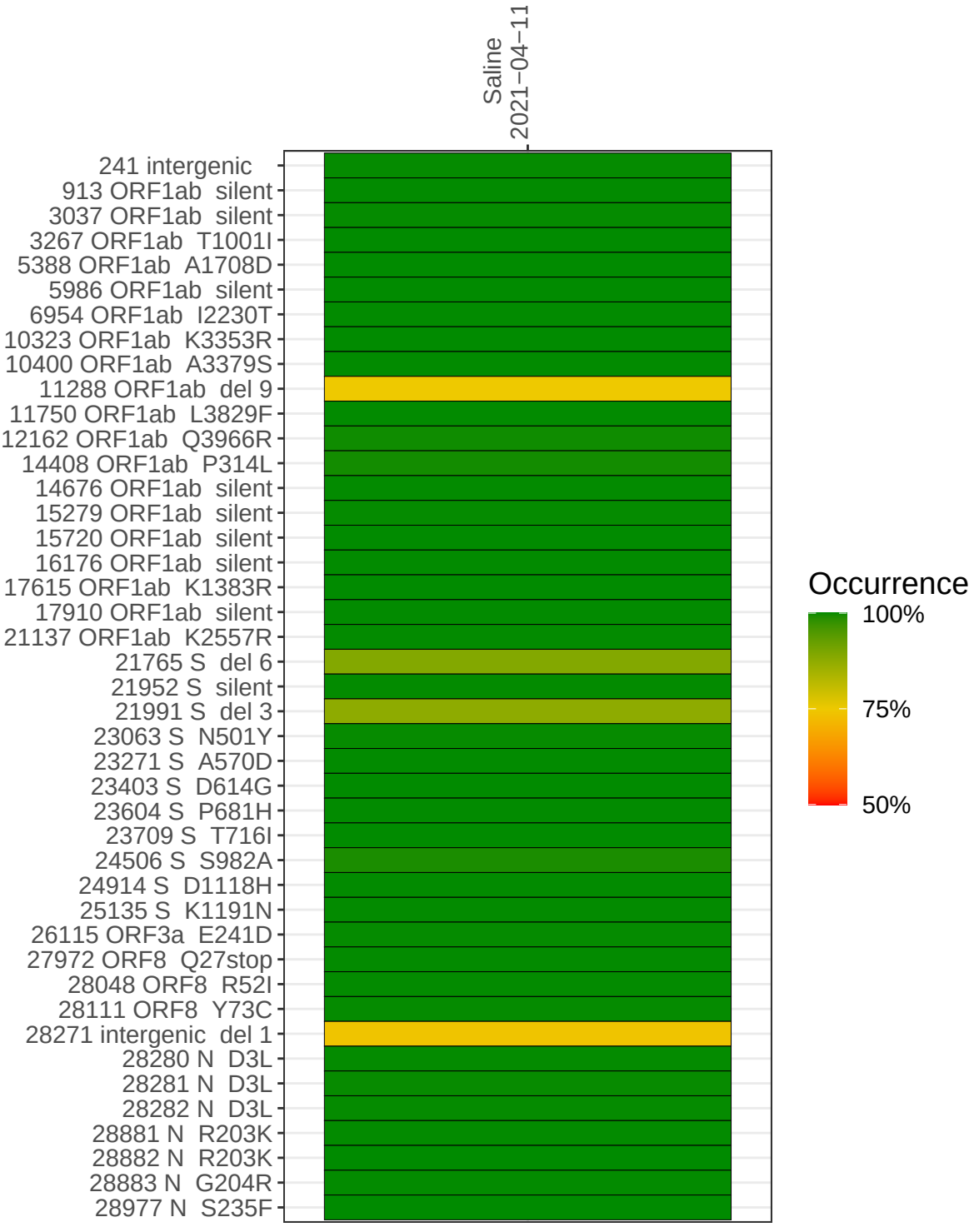
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

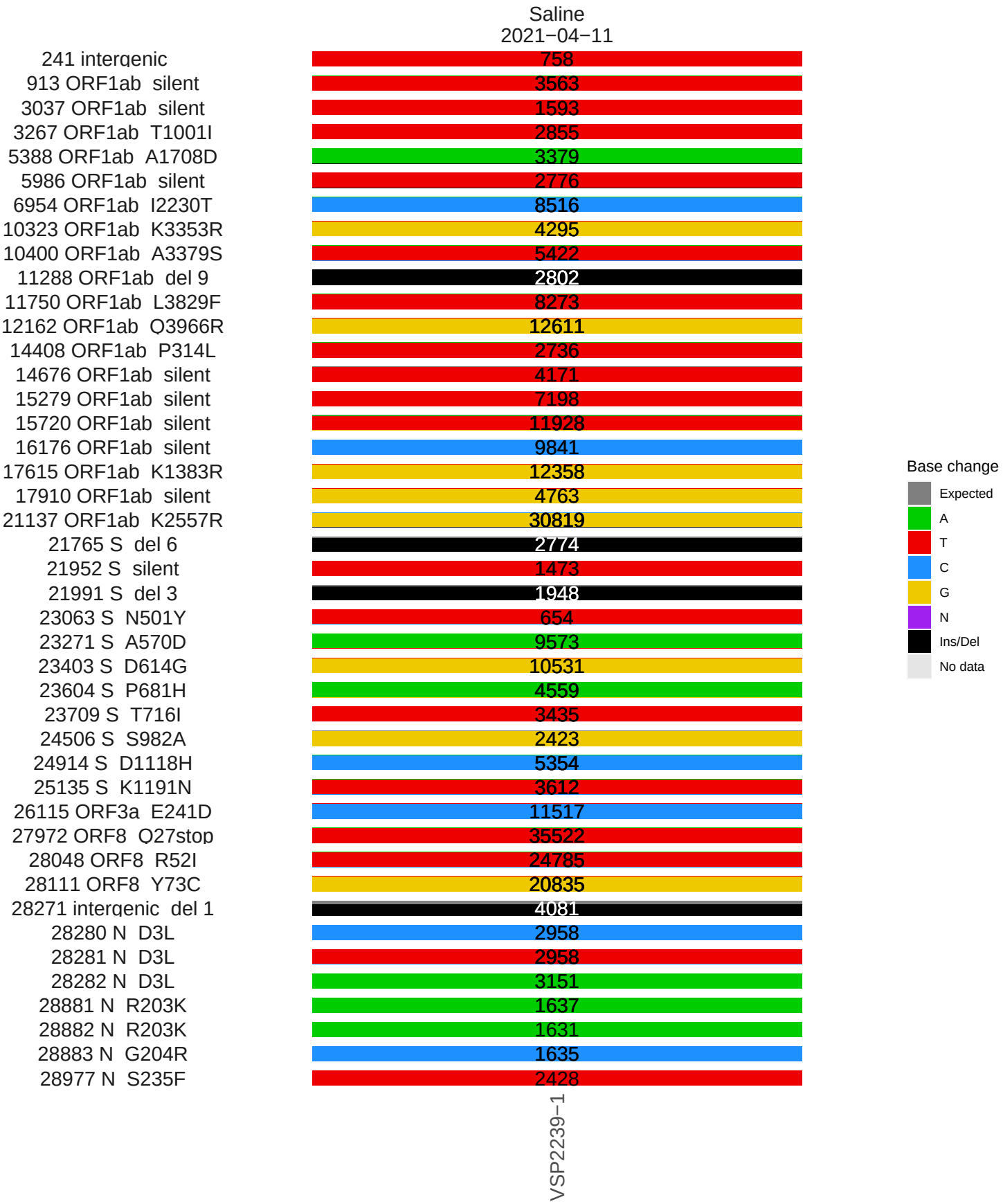
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2239-1	single experiment	NA	Saline	2021-04-11	29.80	B.1.1.7	99.7%	99.7%

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.

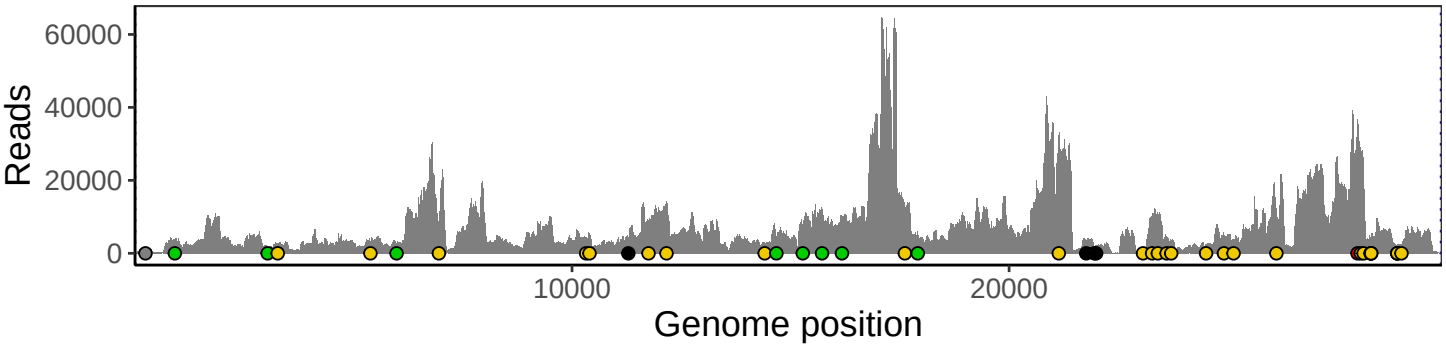



Saline
2021−04−11
241 intergenic 758
913 ORF1ab silent 3563
3037 ORF1ab silent 1593
3267 ORF1ab T1001I 2855
5388 ORF1ab A1708D 3379
5986 ORF1ab silent 2776
6954 ORF1ab I2230T 8516
10323 ORF1ab K3353R 4295
10400 ORF1ab A3379S 5422
11288 ORF1ab del 9 2802
11750 ORF1ab L3829F 8273
12162 ORF1ab Q3966R 12611
14408 ORF1ab P314L 2736
14676 ORF1ab silent 4171
15279 ORF1ab silent 7198
15720 ORF1ab silent 11928
16176 ORF1ab silent 9841
17615 ORF1ab K1383R 12358
17910 ORF1ab silent 4763
21137 ORF1ab K2557R 30819
21765 S del 6 2774
21952 S silent 1473
21991 S del 3 1948
23063 S N501Y 654
23271 S A570D 9573
23403 S D614G 10531
23604 S P681H 4559
23709 S T716I 3435
24506 S S982A 2423
24914 S D1118H 5354
25135 S K1191N 3612
26115 ORF3a E241D 11517
27972 ORF8 Q27stop 35522
28048 ORF8 R52I 24785
28111 ORF8 Y73C 20835
28271 intergenic del 1 4081
28280 N D3L 2958
28281 N D3L 2958
28282 N D3L 3151
28881 N R203K 1637
28882 N R203K 1631
28883 N G204R 1635
28977 N S235F 2428
VSP2239−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

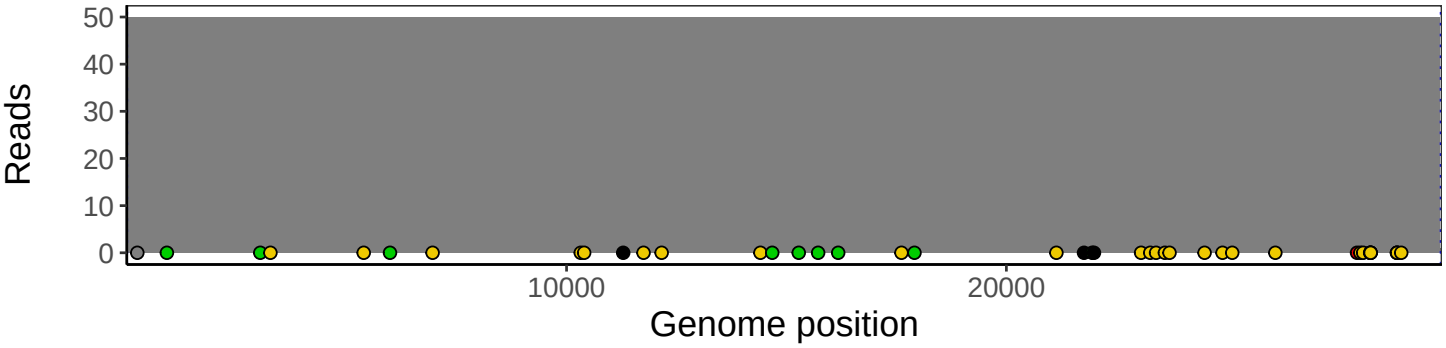
Analyses of individual experiments and composite results

VSP2239-1 | 2021-04-11 | Saline | UPHS-1027 | genomes | single experiment

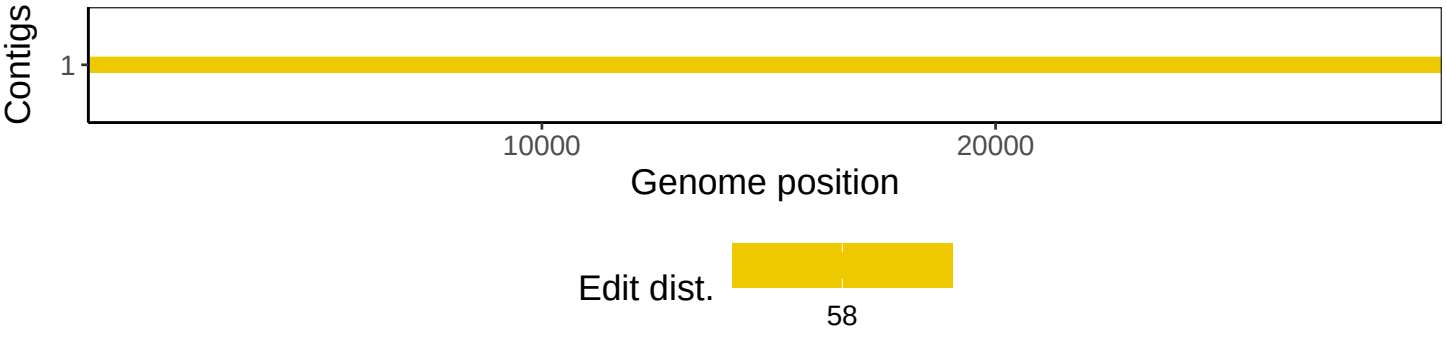
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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