COVID-19 subject UPHS-1374

2021-05-21

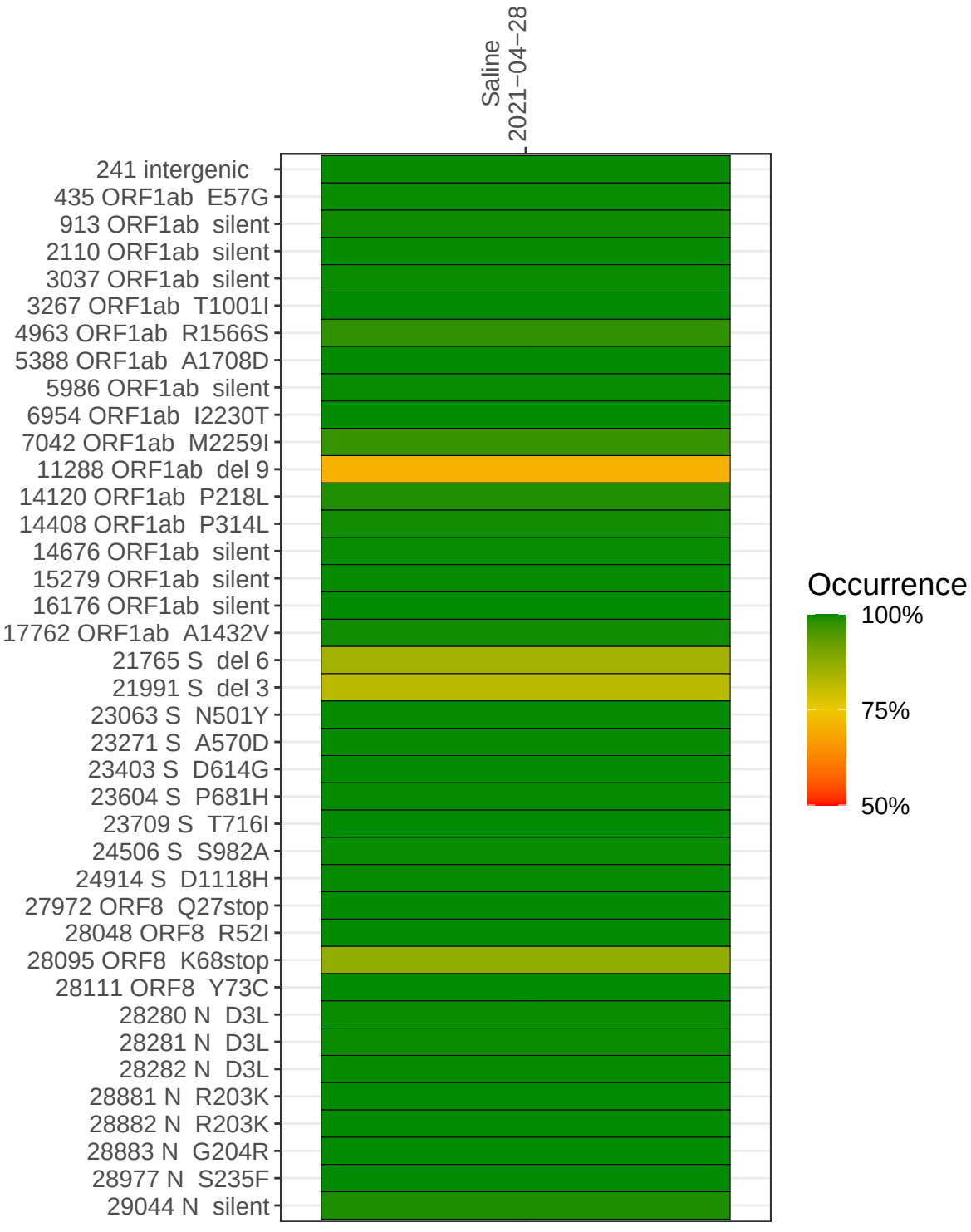
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

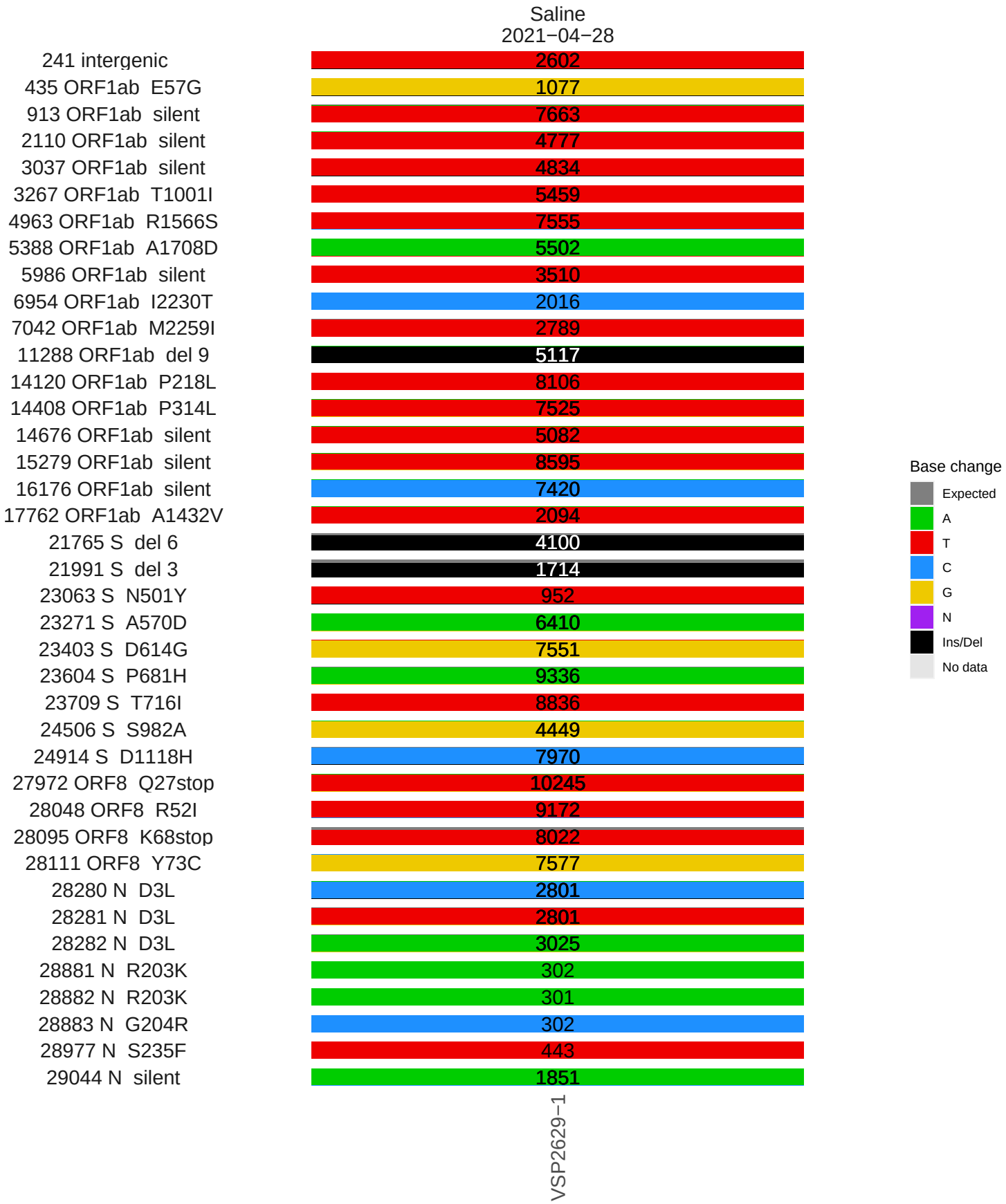
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2629-1	single experiment	NA	Saline	2021-04-28	29.88	B.1.1.7	99.9%	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.

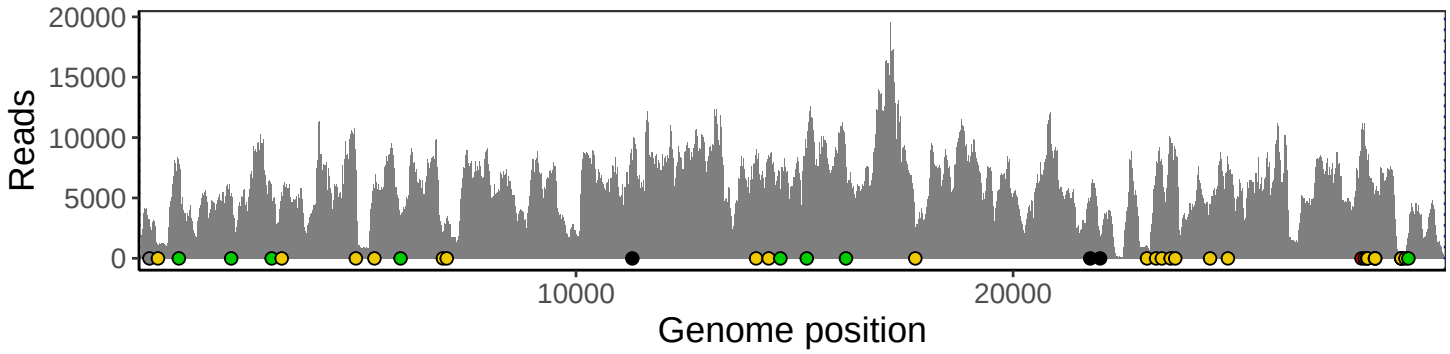



Saline
2021−04−28
241 intergenic 2602
435 ORF1ab E57G 1077
913 ORF1ab silent 7663
2110 ORF1ab silent 4777
3037 ORF1ab silent 4834
3267 ORF1ab T1001I 5459
4963 ORF1ab R1566S 7555
5388 ORF1ab A1708D 5502
5986 ORF1ab silent 3510
6954 ORF1ab I2230T 2016
7042 ORF1ab M2259I 2789
11288 ORF1ab del 9 5117
14120 ORF1ab P218L 8106
14408 ORF1ab P314L 7525
14676 ORF1ab silent 5082
15279 ORF1ab silent 8595
16176 ORF1ab silent 7420
17762 ORF1ab A1432V 2094
21765 S del 6 4100
21991 S del 3 1714
23063 S N501Y 952
23271 S A570D 6410
23403 S D614G 7551
23604 S P681H 9336
23709 S T716I 8836
24506 S S982A 4449
24914 S D1118H 7970
27972 ORF8 Q27stop 10245
28048 ORF8 R52I 9172
28095 ORF8 K68stop 8022
28111 ORF8 Y73C 7577
28280 N D3L 2801
28281 N D3L 2801
28282 N D3L 3025
28881 N R203K 302
28882 N R203K 301
28883 N G204R 302
28977 N S235F 443
29044 N silent 1851
VSP2629−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

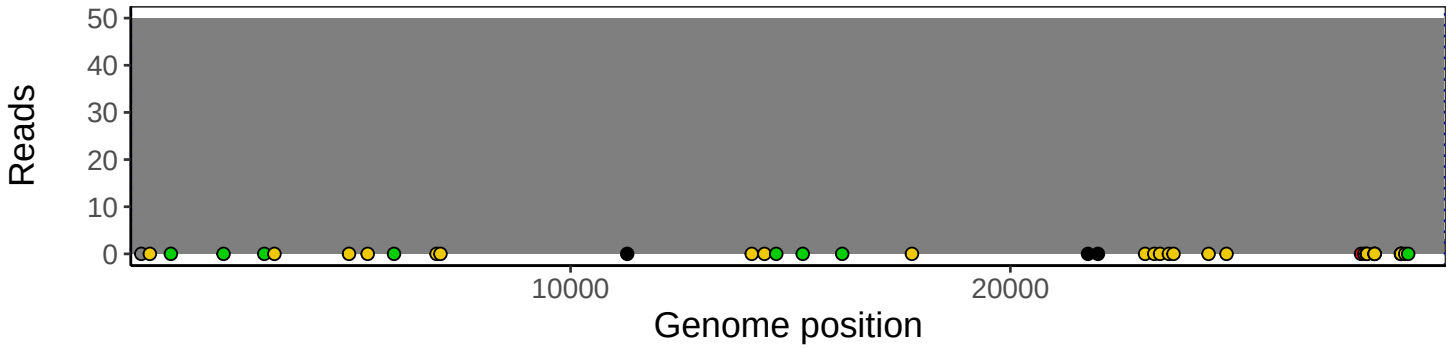
Analyses of individual experiments and composite results

VSP2629-1 | 2021-04-28 | Saline | UPHS-1374 | genomes | single experiment

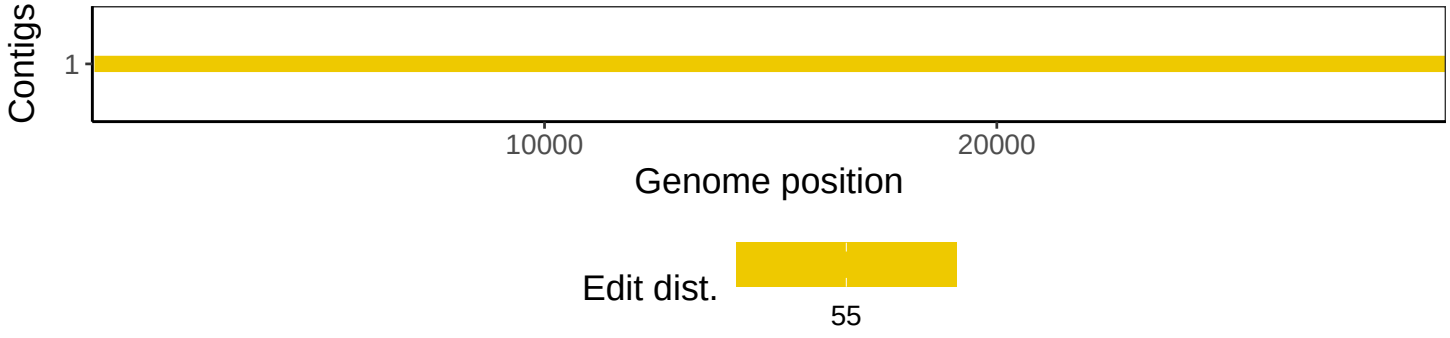
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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