COVID-19 subject UPHS-1639

2021-06-03

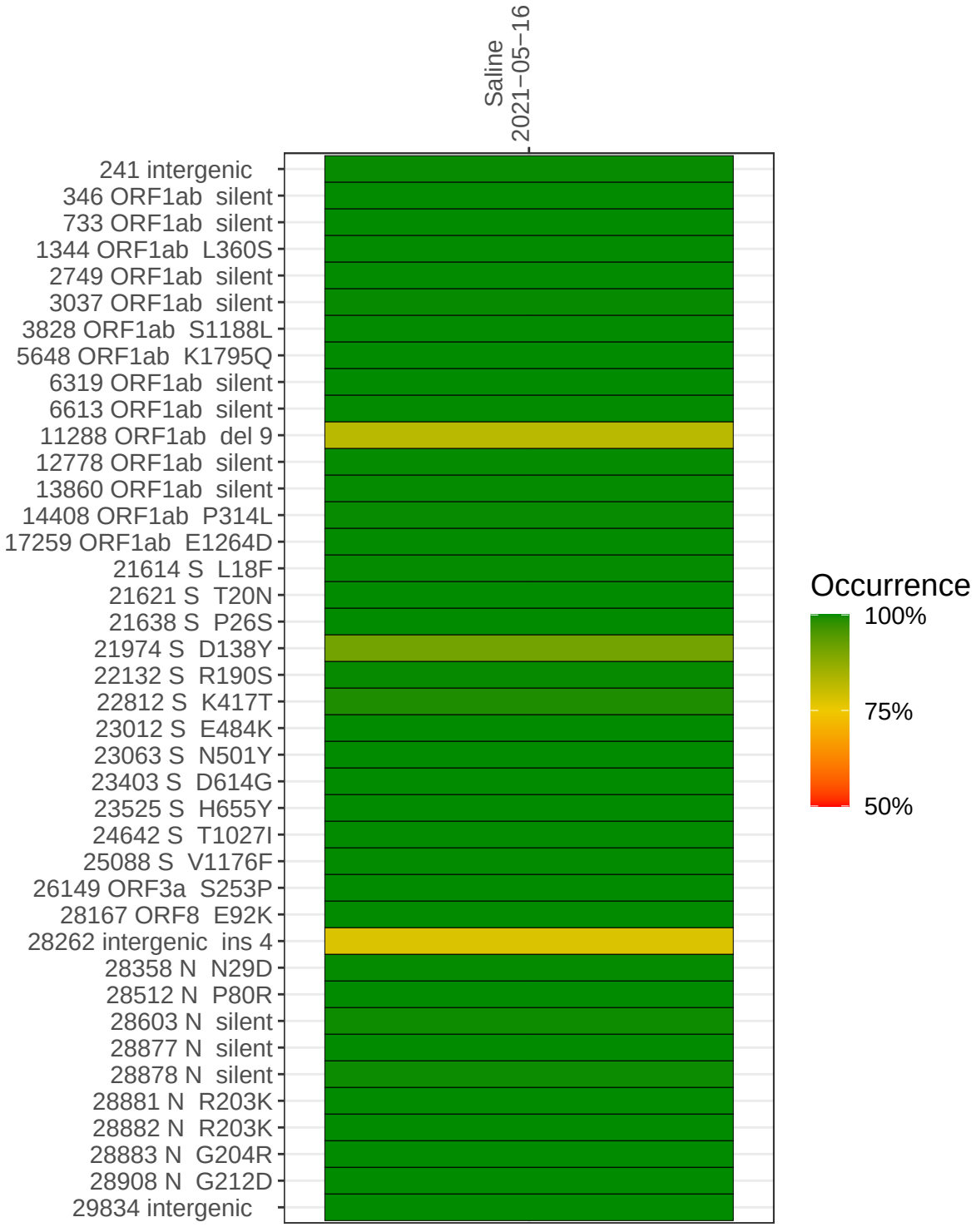
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

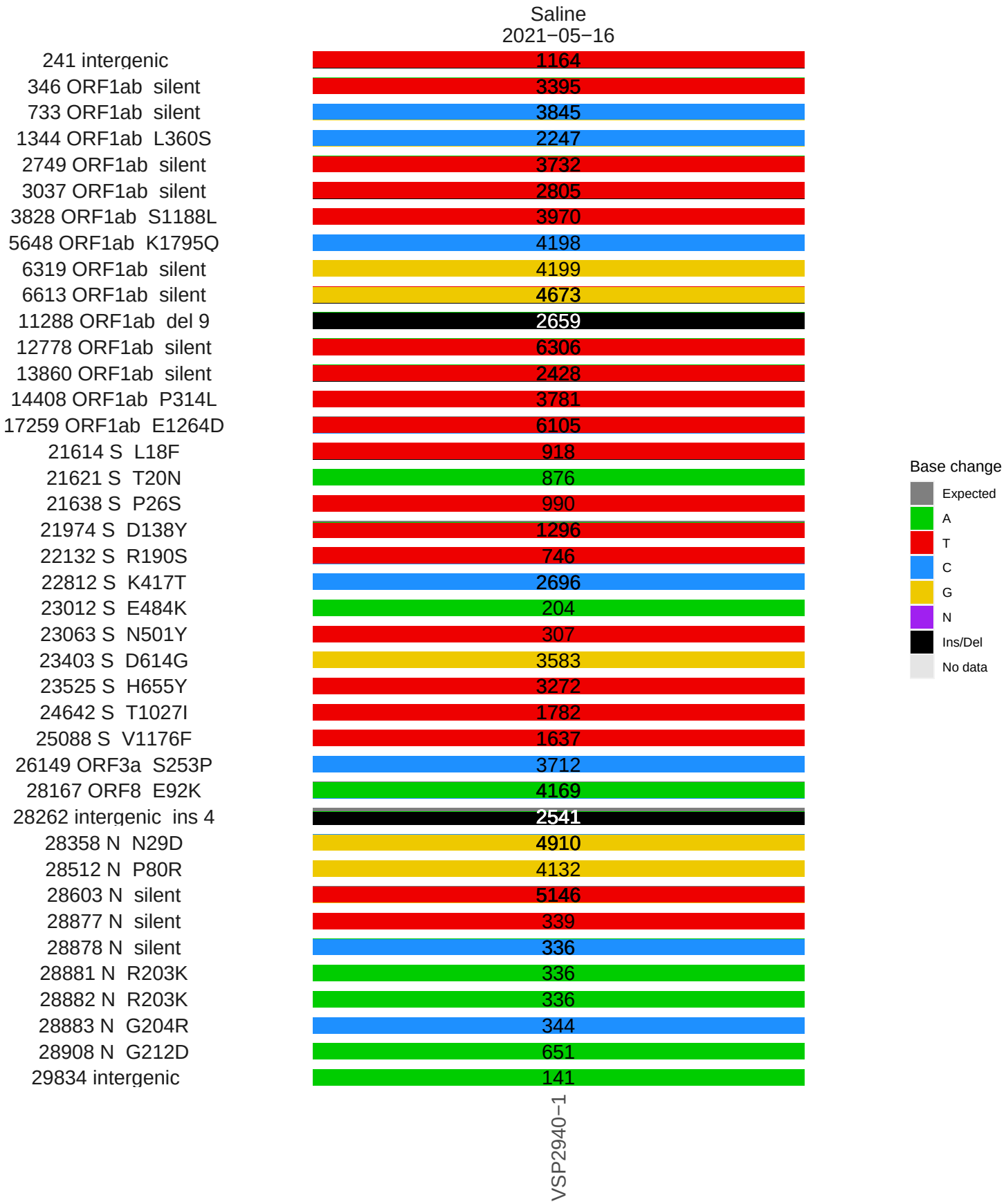
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2940-1	single experiment	NA	Saline	2021-05-16	29.87	P.1	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

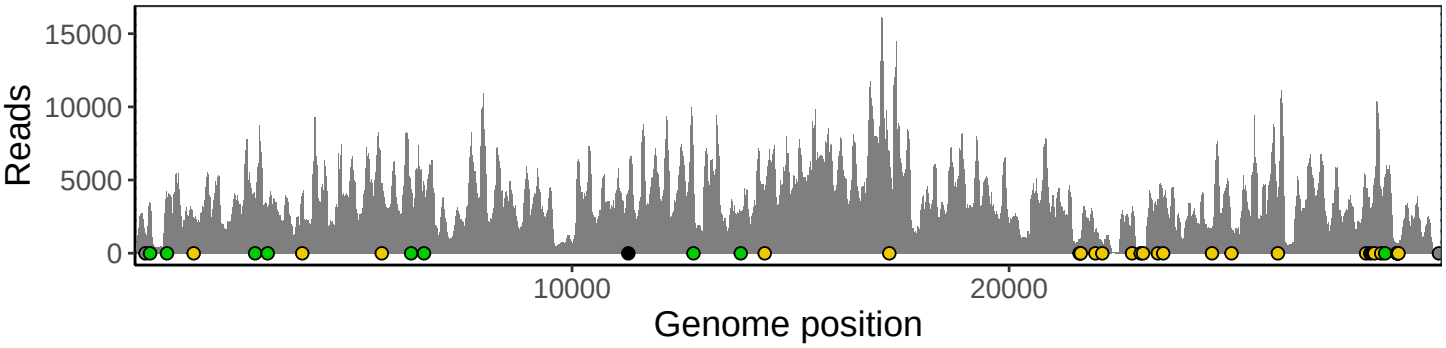



Saline
2021−05−16
241 intergenic 1164
346 ORF1ab silent 3395
733 ORF1ab silent 3845
1344 ORF1ab L360S 2247
2749 ORF1ab silent 3732
3037 ORF1ab silent 2805
3828 ORF1ab S1188L 3970
5648 ORF1ab K1795Q 4198
6319 ORF1ab silent 4199
6613 ORF1ab silent 4673
11288 ORF1ab del 9 2659
12778 ORF1ab silent 6306
13860 ORF1ab silent 2428
14408 ORF1ab P314L 3781
17259 ORF1ab E1264D 6105
21614 S L18F 918
21621 S T20N 876
21638 S P26S 990
21974 S D138Y 1296
22132 S R190S 746
22812 S K417T 2696
23012 S E484K 204
23063 S N501Y 307
23403 S D614G 3583
23525 S H655Y 3272
24642 S T1027I 1782
25088 S V1176F 1637
26149 ORF3a S253P 3712
28167 ORF8 E92K 4169
28262 intergenic ins 4 2541
28358 N N29D 4910
28512 N P80R 4132
28603 N silent 5146
28877 N silent 339
28878 N silent 336
28881 N R203K 336
28882 N R203K 336
28883 N G204R 344
28908 N G212D 651
29834 intergenic 141
VSP2940−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

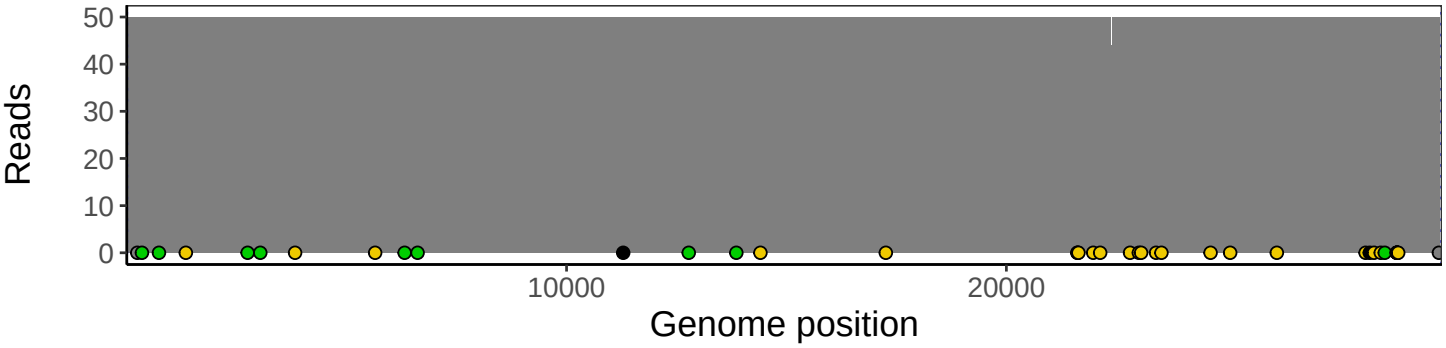
Analyses of individual experiments and composite results

VSP2940-1 | 2021-05-16 | Saline | UPHS-1639 | genomes | single experiment

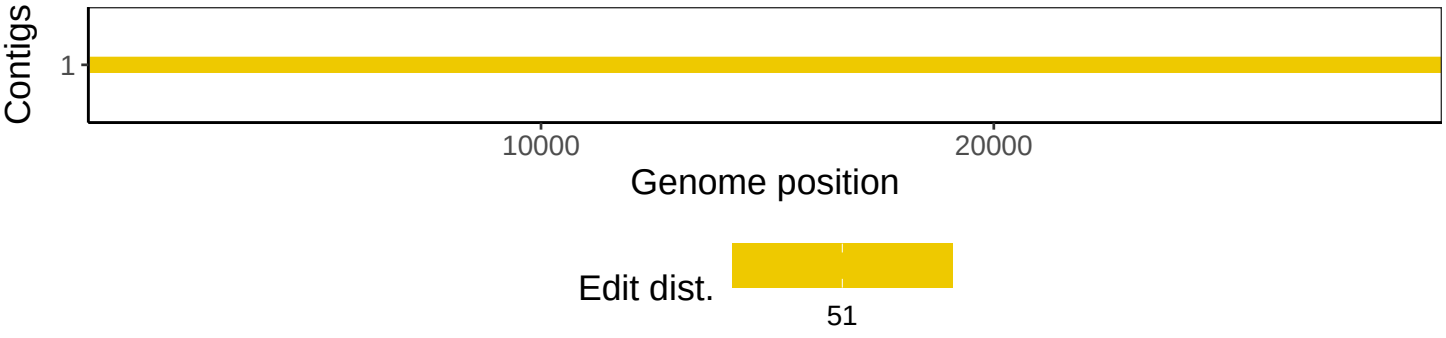
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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