COVID-19 subject UPHS-1635

2021-06-23

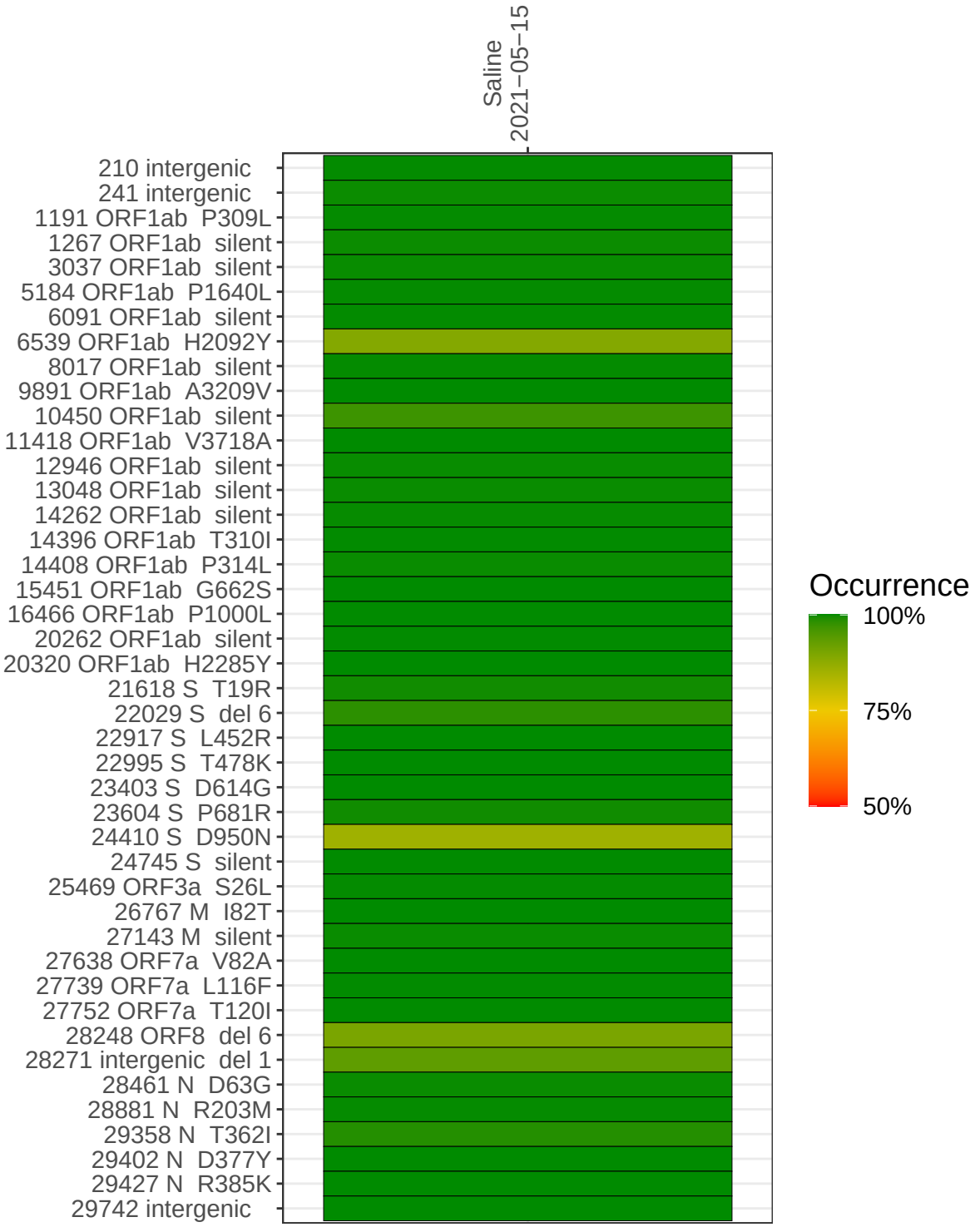
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

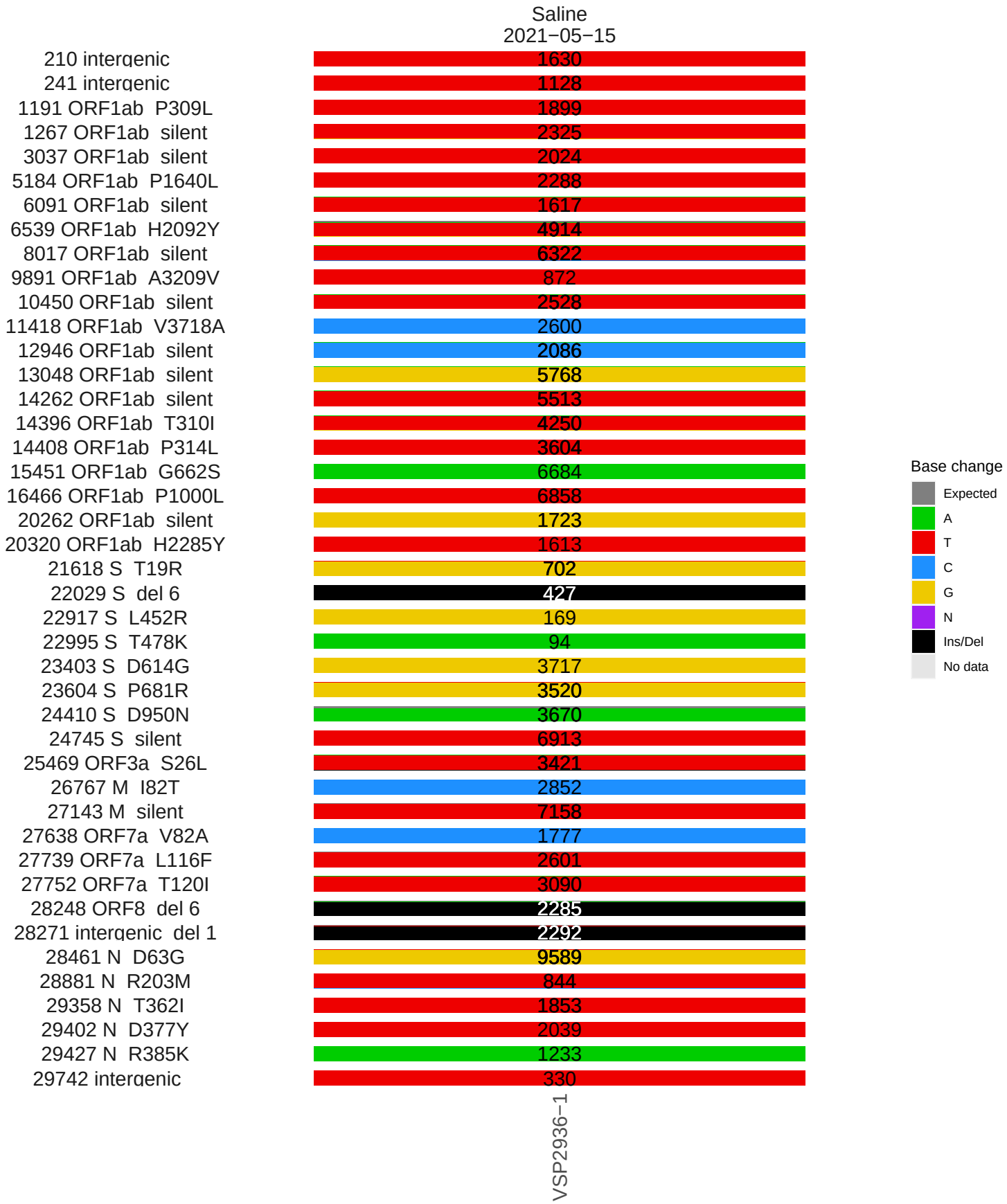
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2936-1	single experiment	NA	Saline	2021-05-15	29.88	B.1.617.2	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.

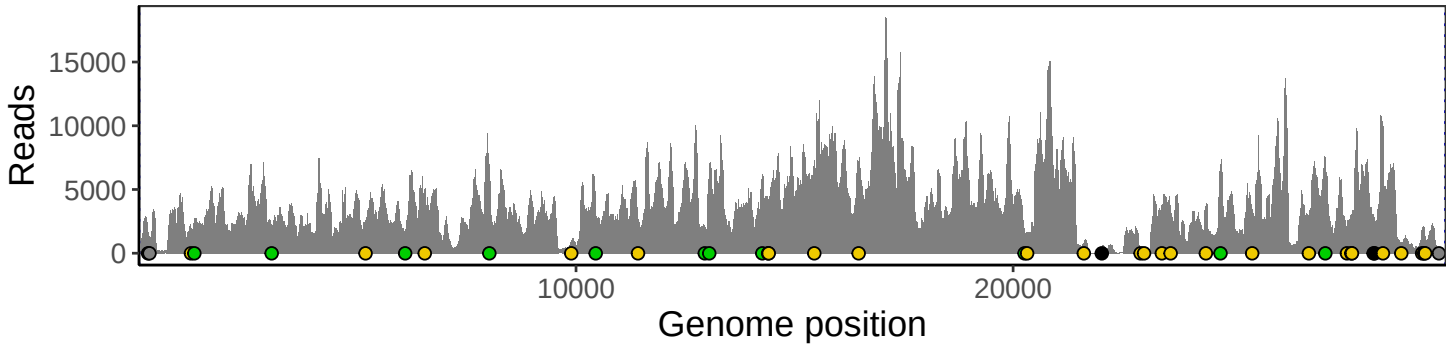



Saline
2021−05−15
210 intergenic 1630
241 intergenic 1128
1191 ORF1ab P309L 1899
1267 ORF1ab silent 2325
3037 ORF1ab silent 2024
5184 ORF1ab P1640L 2288
6091 ORF1ab silent 1617
6539 ORF1ab H2092Y 4914
8017 ORF1ab silent 6322
9891 ORF1ab A3209V 872
10450 ORF1ab silent 2528
11418 ORF1ab V3718A 2600
12946 ORF1ab silent 2086
13048 ORF1ab silent 5768
14262 ORF1ab silent 5513
14396 ORF1ab T310I 4250
14408 ORF1ab P314L 3604
15451 ORF1ab G662S 6684
16466 ORF1ab P1000L 6858
20262 ORF1ab silent 1723
20320 ORF1ab H2285Y 1613
21618 S T19R 702
22029 S del 6 427
22917 S L452R 169
22995 S T478K 94
23403 S D614G 3717
23604 S P681R 3520
24410 S D950N 3670
24745 S silent 6913
25469 ORF3a S26L 3421
26767 M I82T 2852
27143 M silent 7158
27638 ORF7a V82A 1777
27739 ORF7a L116F 2601
27752 ORF7a T120I 3090
28248 ORF8 del 6 2285
28271 intergenic del 1 2292
28461 N D63G 9589
28881 N R203M 844
29358 N T362I 1853
29402 N D377Y 2039
29427 N R385K 1233
29742 intergenic 330
VSP2936−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

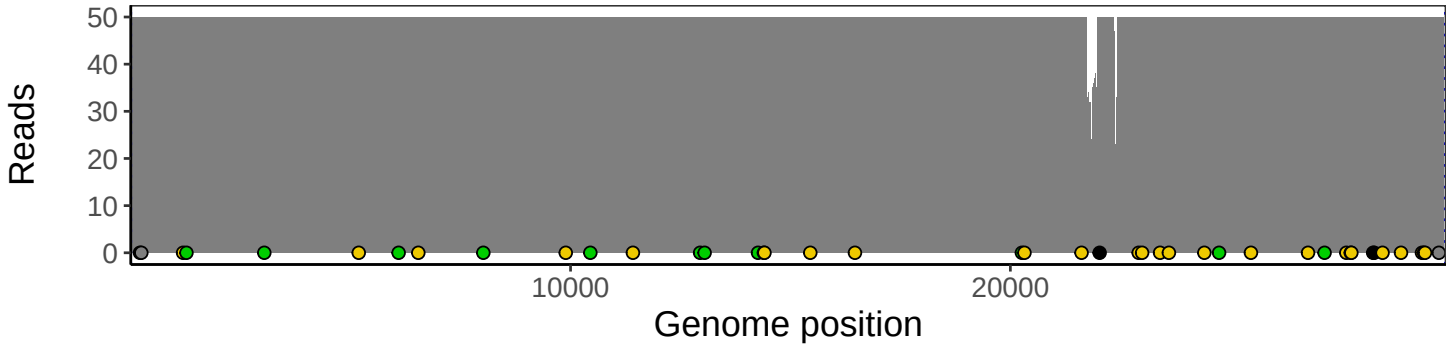
Analyses of individual experiments and composite results

VSP2936-1 | 2021-05-15 | Saline | UPHS-1635 | genomes | single experiment

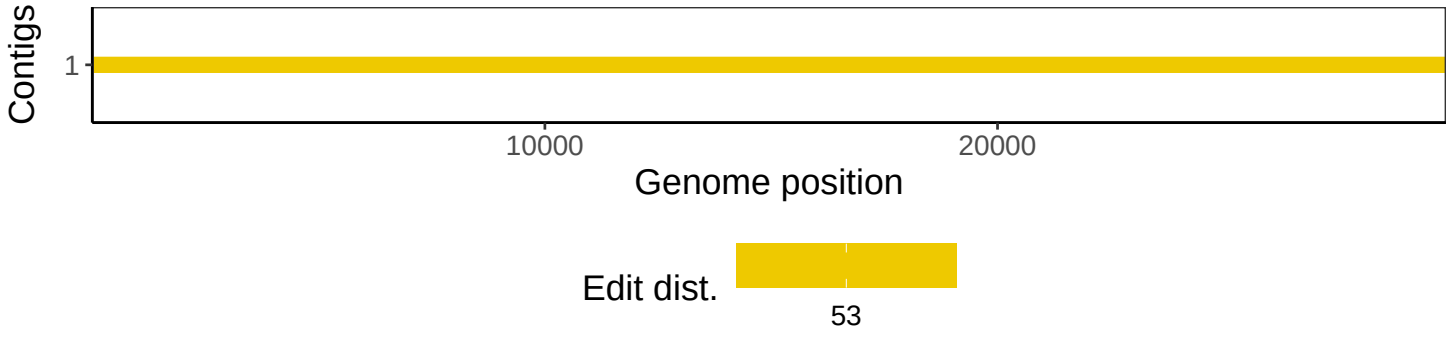
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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