COVID-19 subject UPHS-1603

2021-06-03

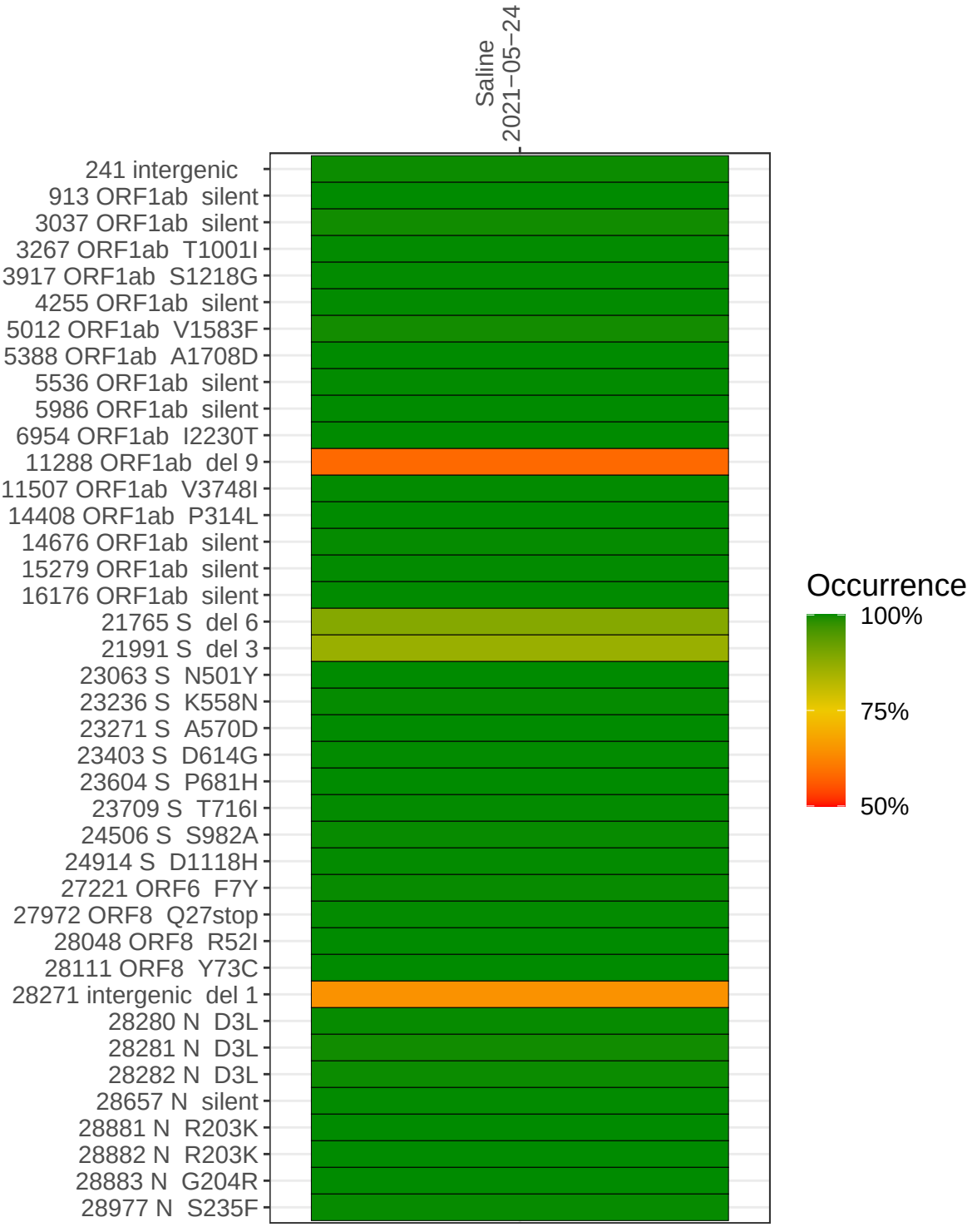
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

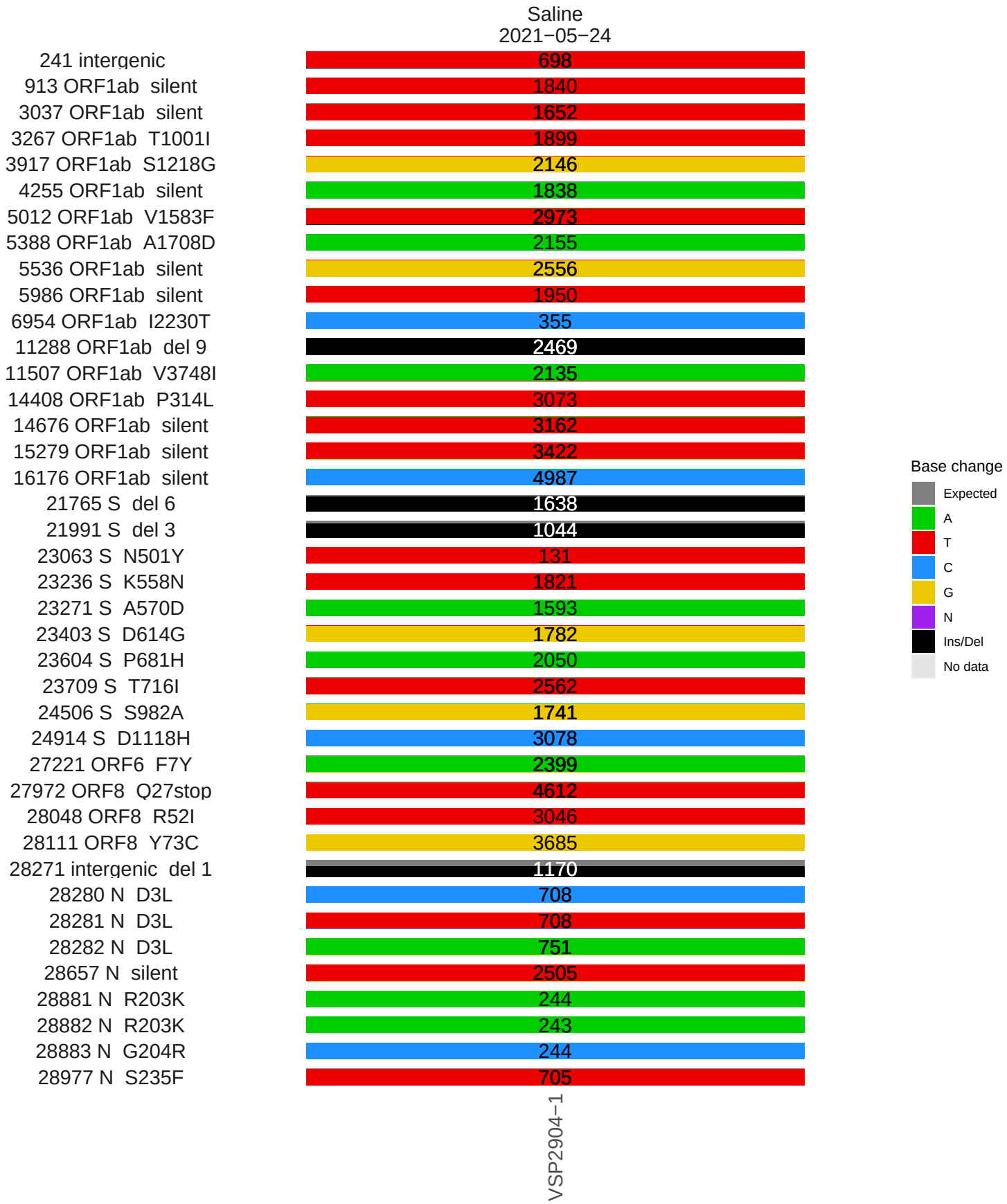
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2904-1	single experiment	NA	Saline	2021-05-24	29.85	B.1.1.7	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.

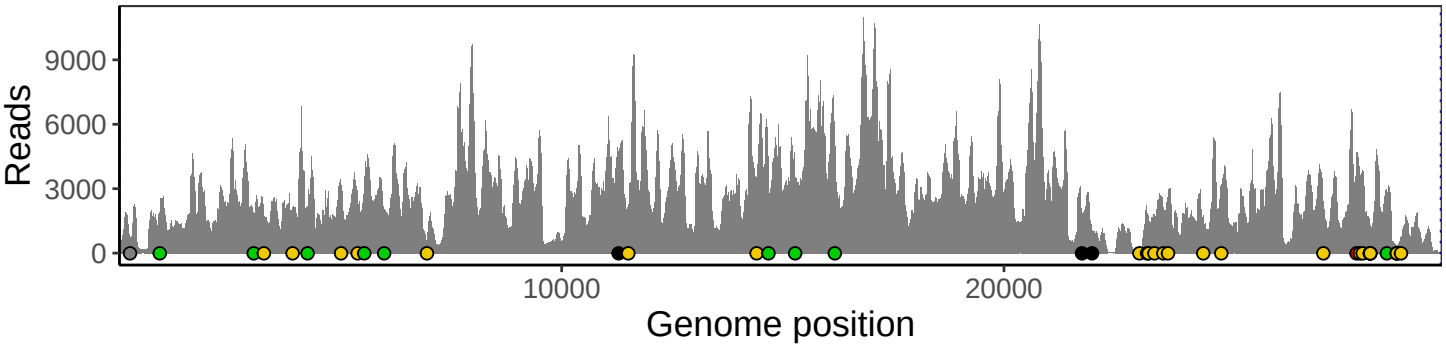



Saline
2021−05−24
241 intergenic 698
913 ORF1ab silent 1840
3037 ORF1ab silent 1652
3267 ORF1ab T1001I 1899
3917 ORF1ab S1218G 2146
4255 ORF1ab silent 1838
5012 ORF1ab V1583F 2973
5388 ORF1ab A1708D 2155
5536 ORF1ab silent 2556
5986 ORF1ab silent 1950
6954 ORF1ab I2230T 355
11288 ORF1ab del 9 2469
11507 ORF1ab V3748I 2135
14408 ORF1ab P314L 3073
14676 ORF1ab silent 3162
15279 ORF1ab silent 3422
16176 ORF1ab silent 4987
21765 S del 6 1638
21991 S del 3 1044
23063 S N501Y 131
23236 S K558N 1821
23271 S A570D 1593
23403 S D614G 1782
23604 S P681H 2050
23709 S T716I 2562
24506 S S982A 1741
24914 S D1118H 3078
27221 ORF6 F7Y 2399
27972 ORF8 Q27stop 4612
28048 ORF8 R52I 3046
28111 ORF8 Y73C 3685
28271 intergenic del 1 1170
28280 N D3L 708
28281 N D3L 708
28282 N D3L 751
28657 N silent 2505
28881 N R203K 244
28882 N R203K 243
28883 N G204R 244
28977 N S235F 705
VSP2904−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

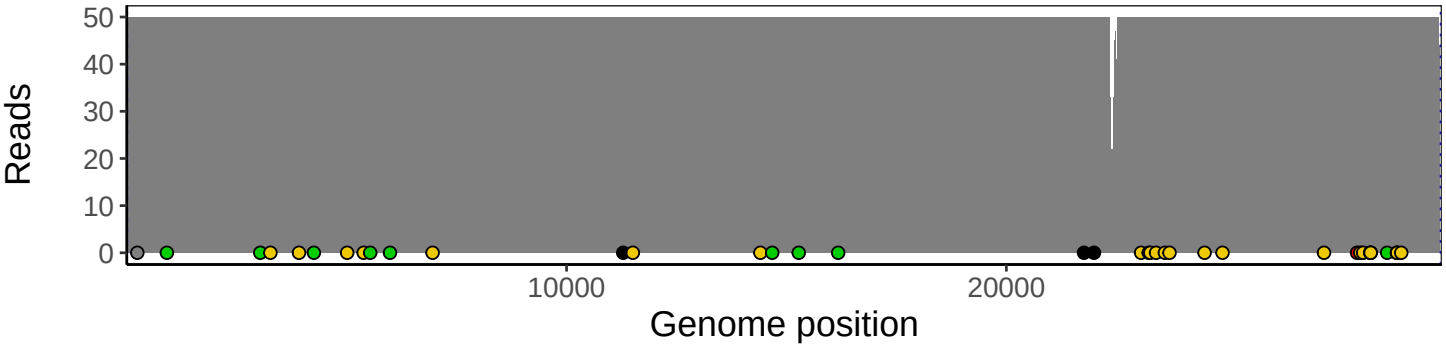
Analyses of individual experiments and composite results

VSP2904-1 | 2021-05-24 | Saline | UPHS-1603 | genomes | single experiment

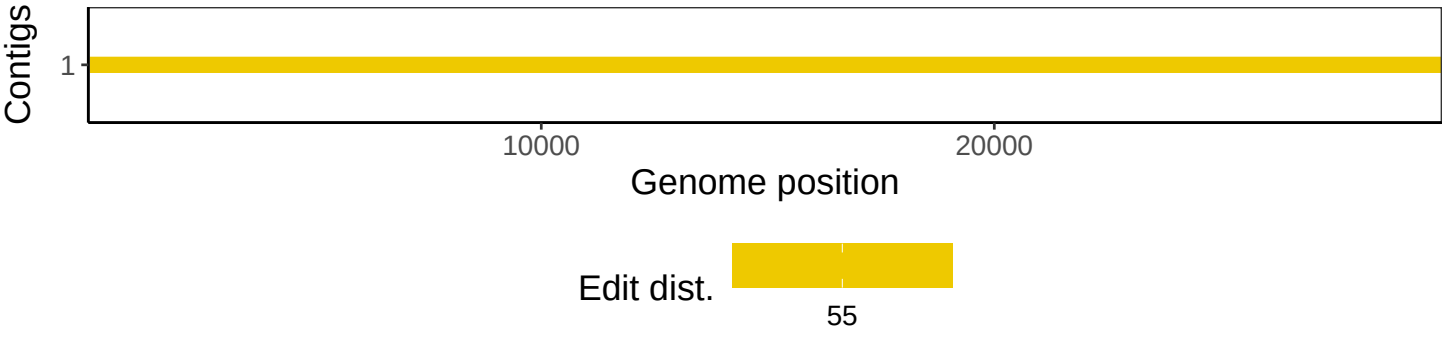
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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