COVID-19 subject UPHS-1606

2021-06-03

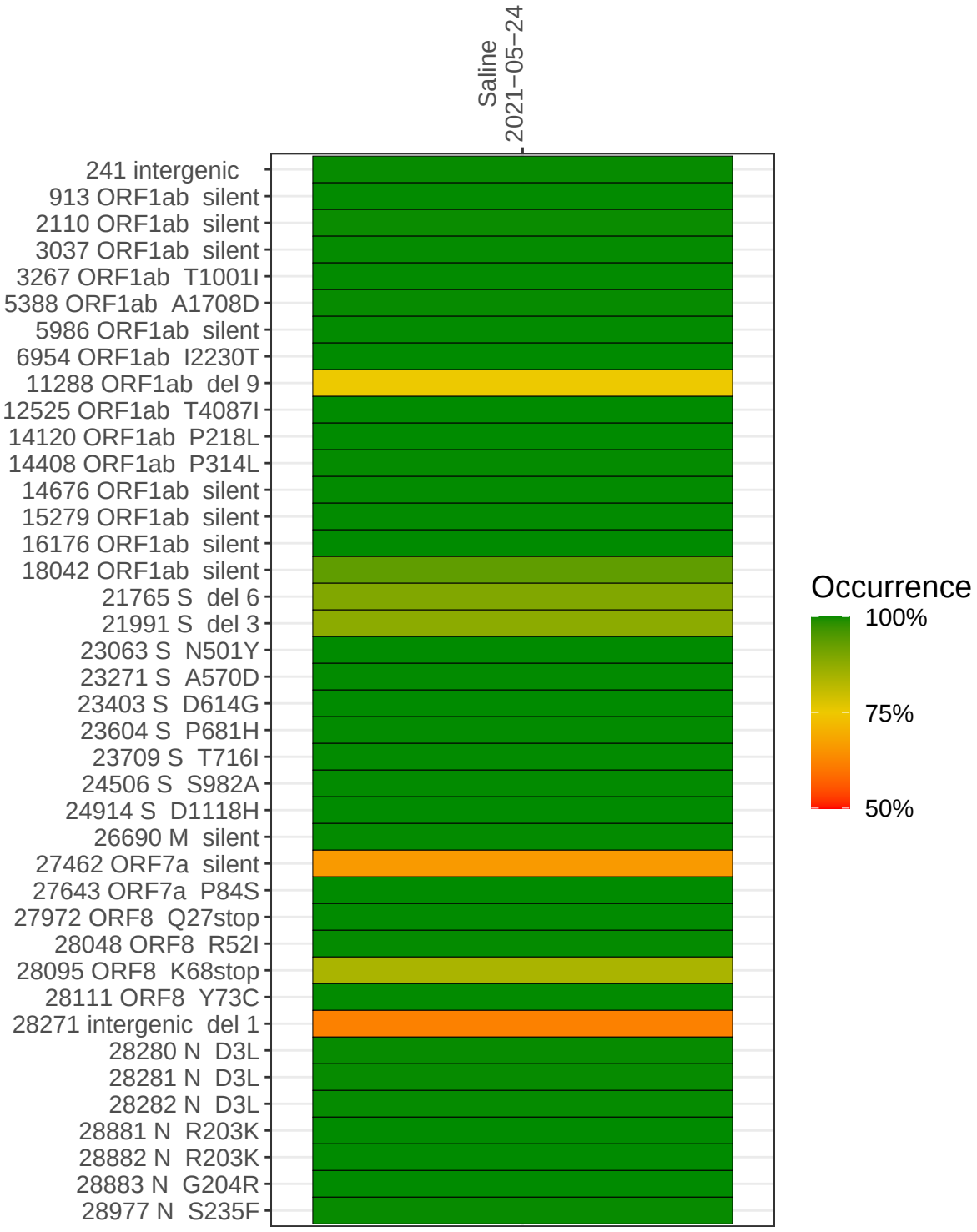
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

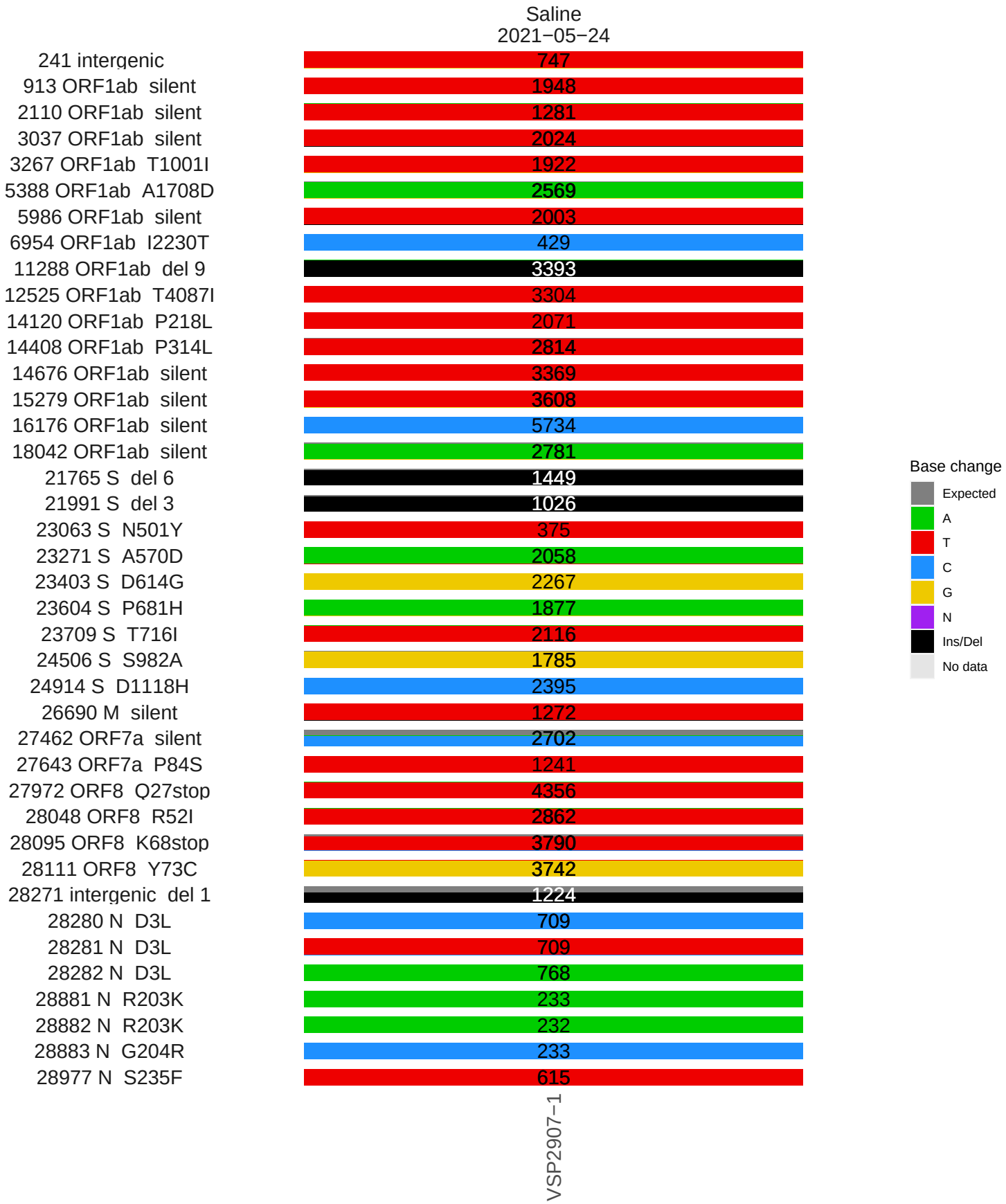
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2907-1	single experiment	NA	Saline	2021-05-24	29.86	B.1.1.7	99.8%	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.

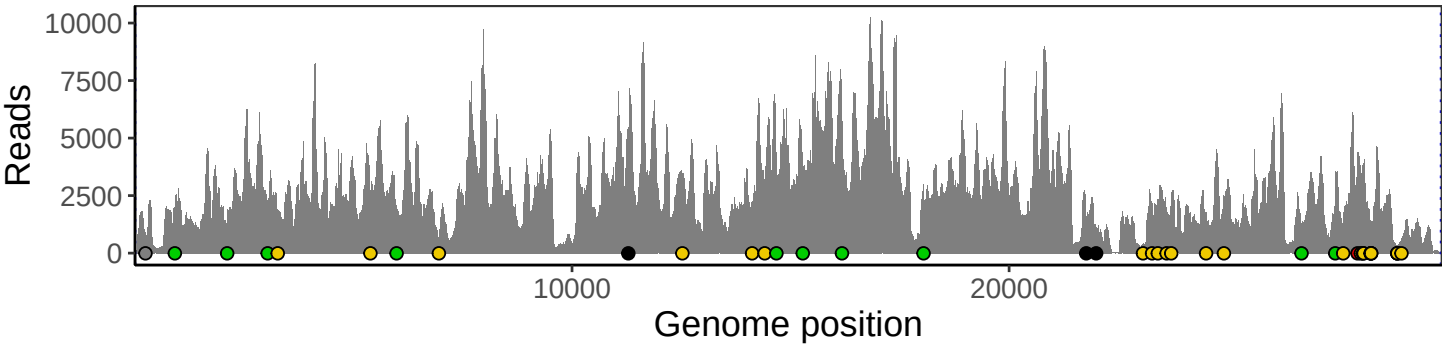



Saline
2021−05−24
241 intergenic 747
913 ORF1ab silent 1948
2110 ORF1ab silent 1281
3037 ORF1ab silent 2024
3267 ORF1ab T1001I 1922
5388 ORF1ab A1708D 2569
5986 ORF1ab silent 2003
6954 ORF1ab I2230T 429
11288 ORF1ab del 9 3393
12525 ORF1ab T4087I 3304
14120 ORF1ab P218L 2071
14408 ORF1ab P314L 2814
14676 ORF1ab silent 3369
15279 ORF1ab silent 3608
16176 ORF1ab silent 5734
18042 ORF1ab silent 2781
21765 S del 6 1449
21991 S del 3 1026
23063 S N501Y 375
23271 S A570D 2058
23403 S D614G 2267
23604 S P681H 1877
23709 S T716I 2116
24506 S S982A 1785
24914 S D1118H 2395
26690 M silent 1272
27462 ORF7a silent 2702
27643 ORF7a P84S 1241
27972 ORF8 Q27stop 4356
28048 ORF8 R52I 2862
28095 ORF8 K68stop 3790
28111 ORF8 Y73C 3742
28271 intergenic del 1 1224
28280 N D3L 709
28281 N D3L 709
28282 N D3L 768
28881 N R203K 233
28882 N R203K 232
28883 N G204R 233
28977 N S235F 615
VSP2907−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

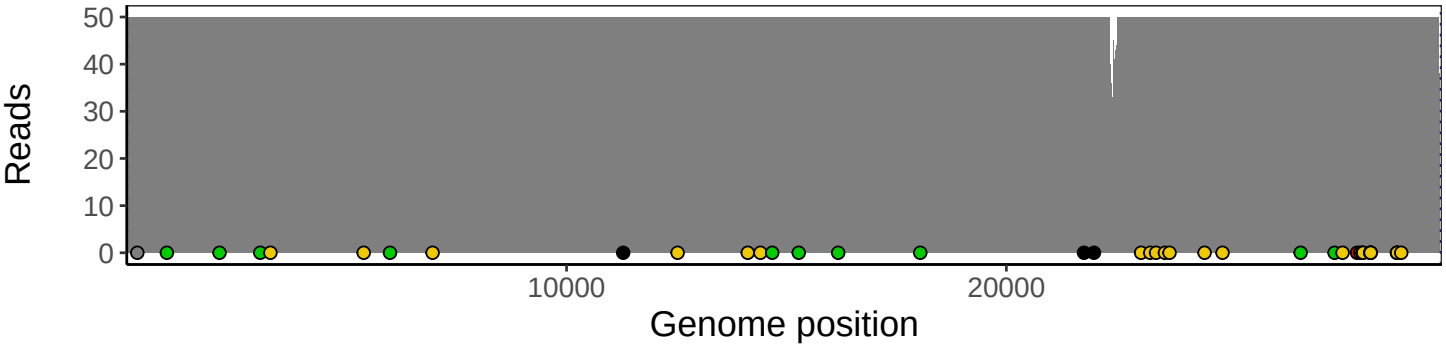
Analyses of individual experiments and composite results

VSP2907-1 | 2021-05-24 | Saline | UPHS-1606 | genomes | single experiment

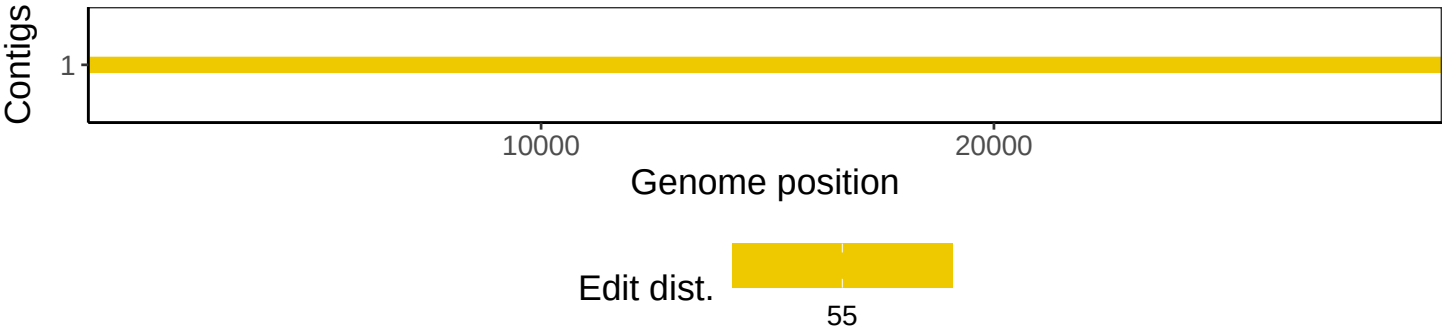
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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