COVID-19 subject UPHS-1605

2021-06-03

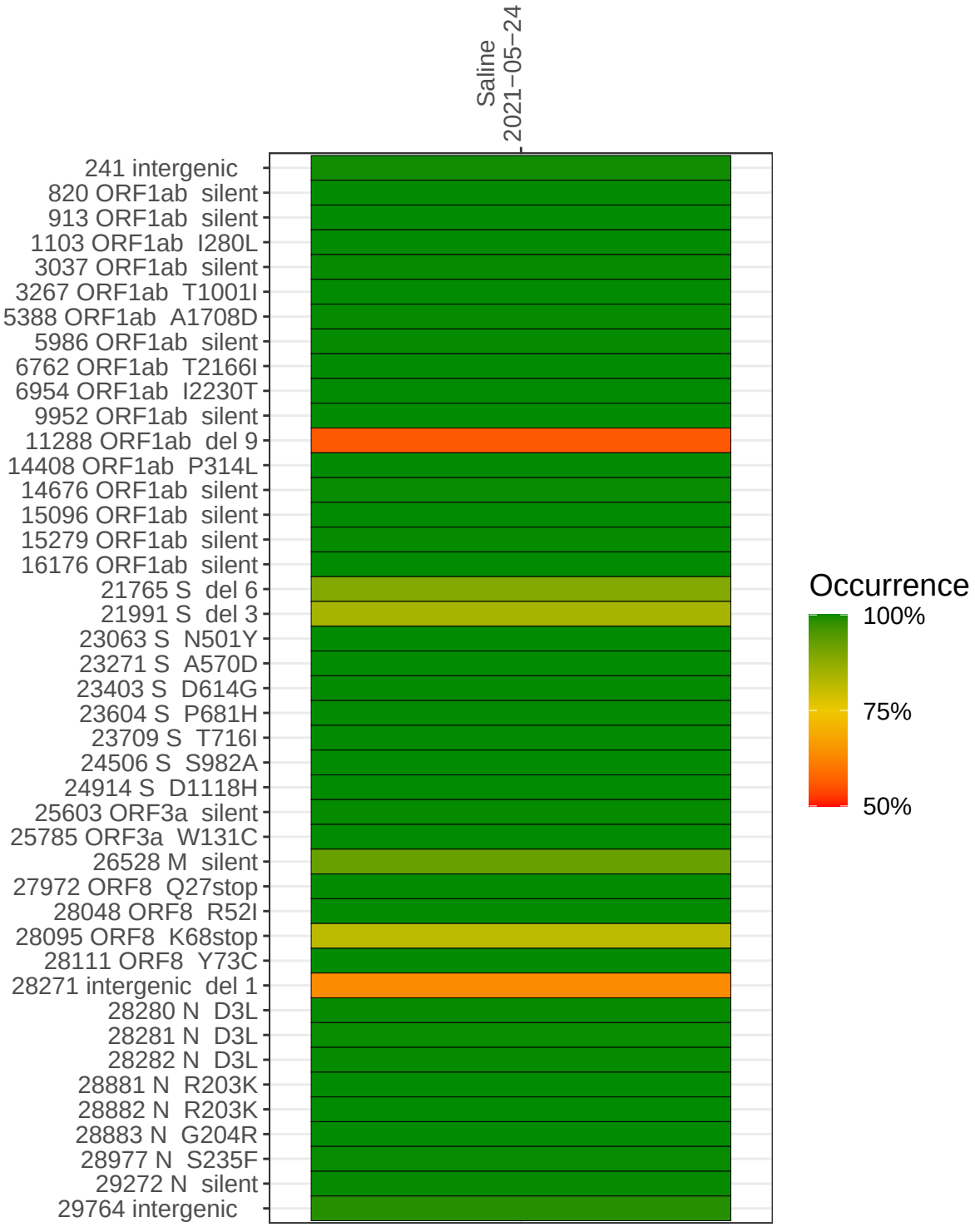
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

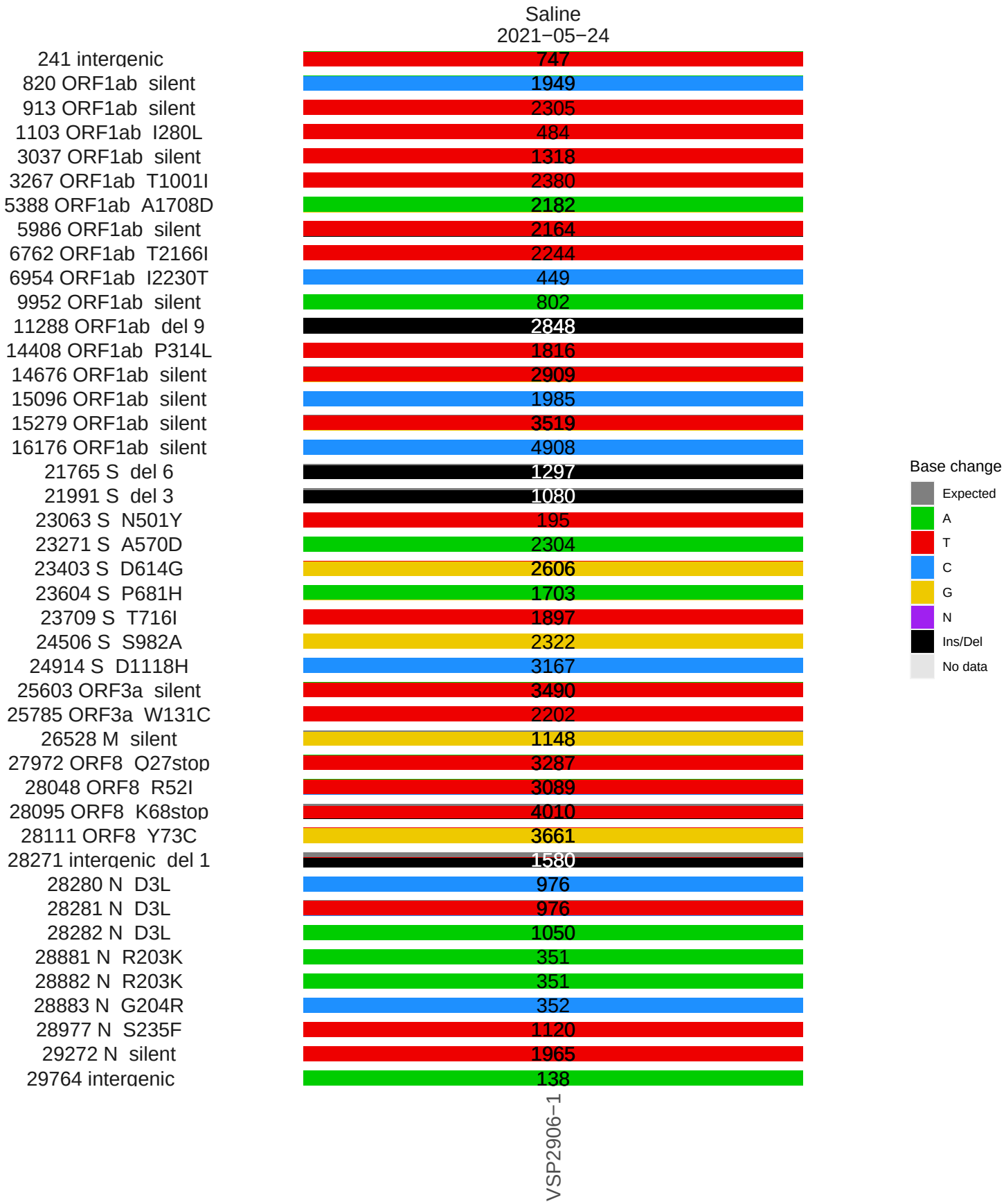
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2906-1	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.

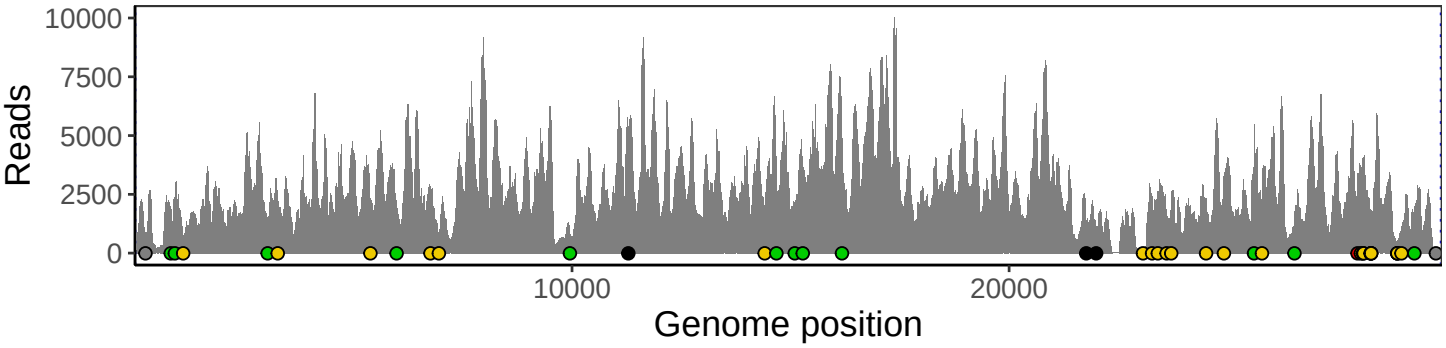



Saline
2021−05−24
241 intergenic 747
820 ORF1ab silent 1949
913 ORF1ab silent 2305
1103 ORF1ab I280L 484
3037 ORF1ab silent 1318
3267 ORF1ab T1001I 2380
5388 ORF1ab A1708D 2182
5986 ORF1ab silent 2164
6762 ORF1ab T2166I 2244
6954 ORF1ab I2230T 449
9952 ORF1ab silent 802
11288 ORF1ab del 9 2848
14408 ORF1ab P314L 1816
14676 ORF1ab silent 2909
15096 ORF1ab silent 1985
15279 ORF1ab silent 3519
16176 ORF1ab silent 4908
21765 S del 6 1297
21991 S del 3 1080
23063 S N501Y 195
23271 S A570D 2304
23403 S D614G 2606
23604 S P681H 1703
23709 S T716I 1897
24506 S S982A 2322
24914 S D1118H 3167
25603 ORF3a silent 3490
25785 ORF3a W131C 2202
26528 M silent 1148
27972 ORF8 Q27stop 3287
28048 ORF8 R52I 3089
28095 ORF8 K68stop 4010
28111 ORF8 Y73C 3661
28271 intergenic del 1 1580
28280 N D3L 976
28281 N D3L 976
28282 N D3L 1050
28881 N R203K 351
28882 N R203K 351
28883 N G204R 352
28977 N S235F 1120
29272 N silent 1965
29764 intergenic 138
VSP2906−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

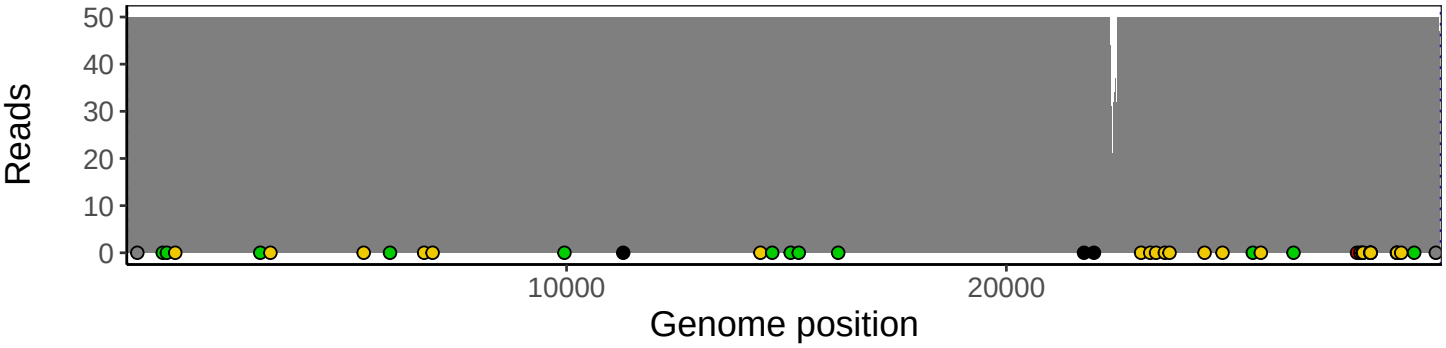
Analyses of individual experiments and composite results

VSP2906-1 | 2021-05-24 | Saline | UPHS-1605 | genomes | single experiment

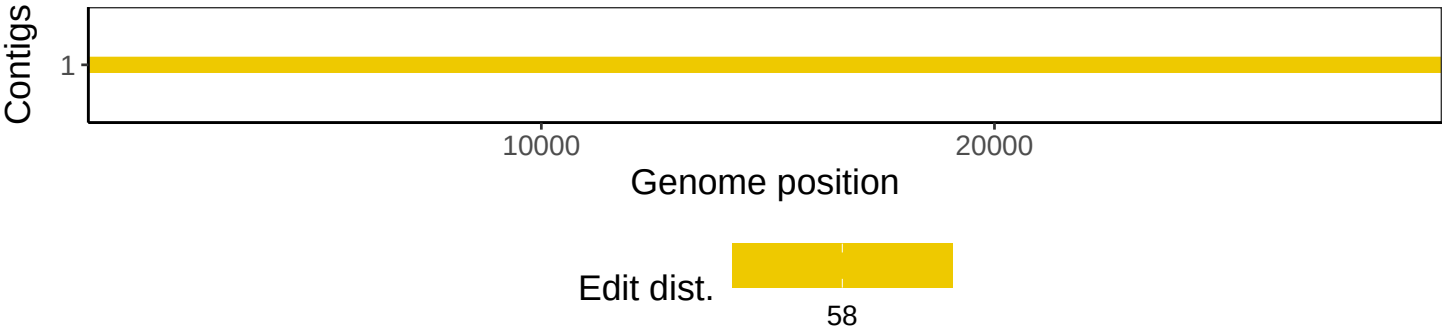
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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