COVID-19 subject UPHS-1050

2021-05-10

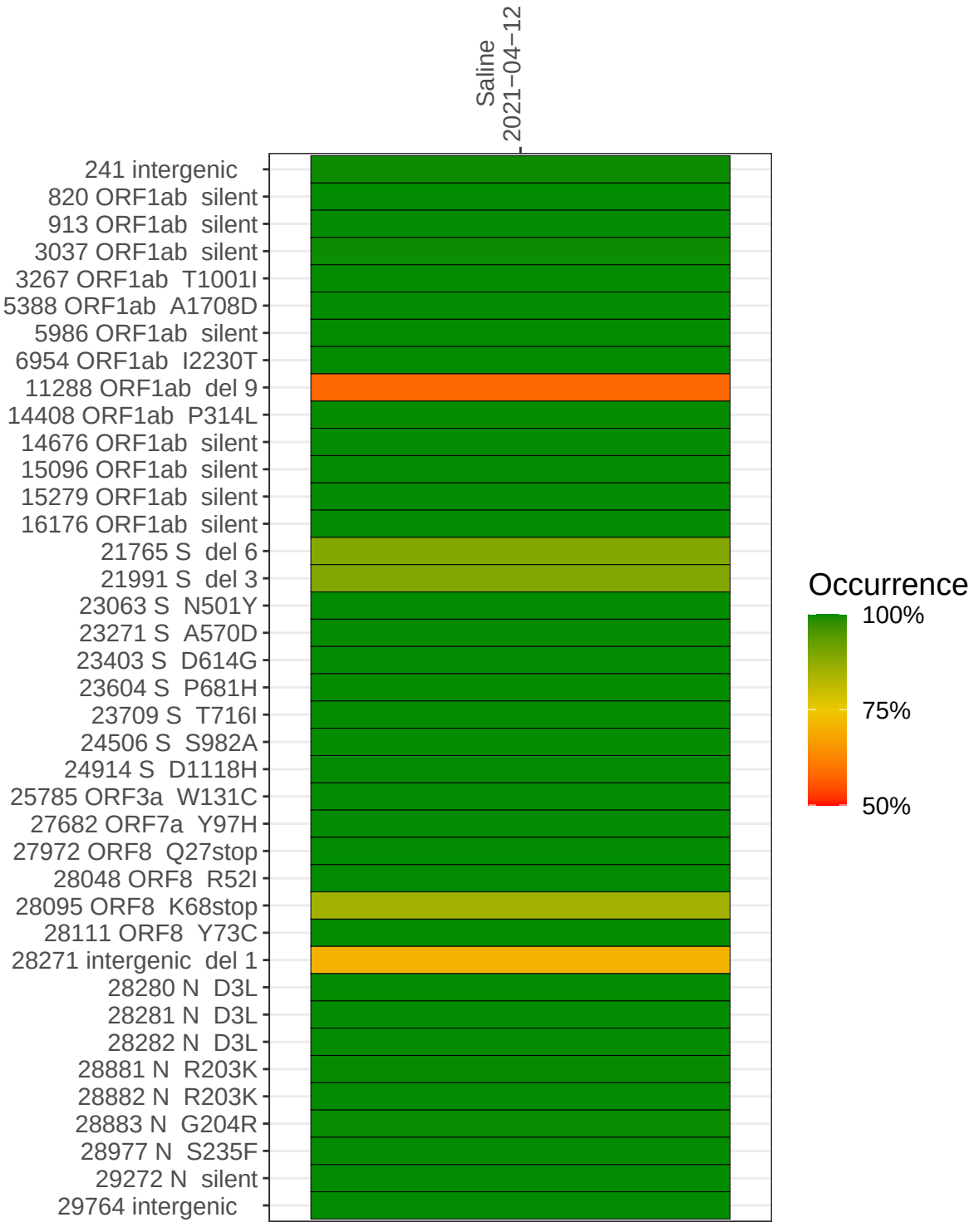
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

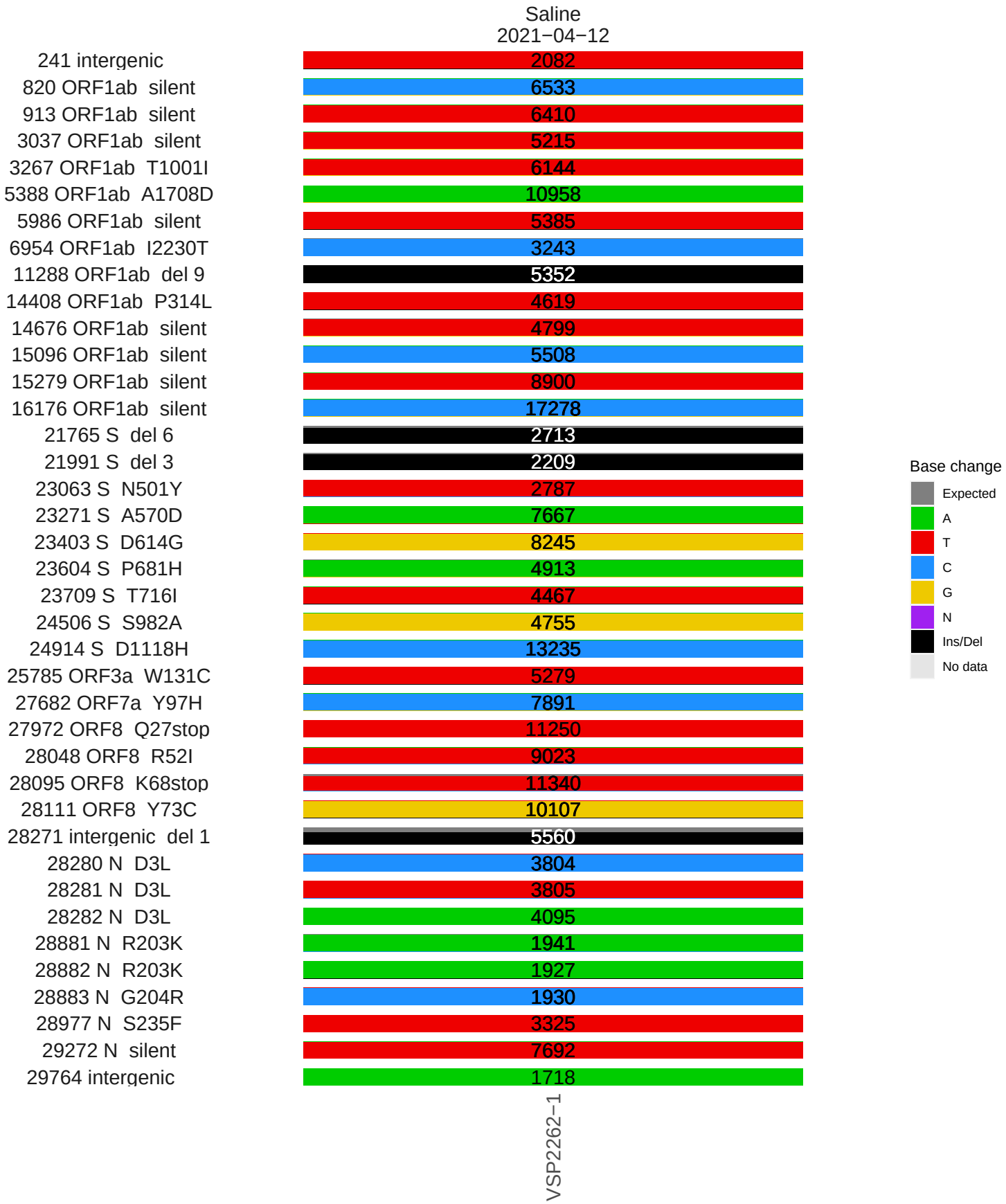
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2262-1	single experiment	NA	Saline	2021-04-12	29.87	B.1.1.7	99.8%	99.8%

Variants shared across samples

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

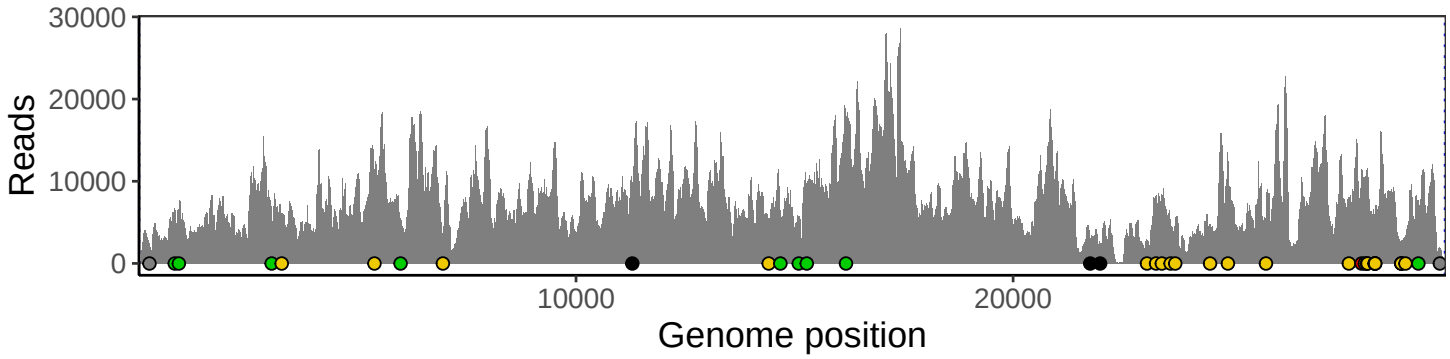



Saline
2021−04−12
241 intergenic 2082
820 ORF1ab silent 6533
913 ORF1ab silent 6410
3037 ORF1ab silent 5215
3267 ORF1ab T1001I 6144
5388 ORF1ab A1708D 10958
5986 ORF1ab silent 5385
6954 ORF1ab I2230T 3243
11288 ORF1ab del 9 5352
14408 ORF1ab P314L 4619
14676 ORF1ab silent 4799
15096 ORF1ab silent 5508
15279 ORF1ab silent 8900
16176 ORF1ab silent 17278
21765 S del 6 2713
21991 S del 3 2209
23063 S N501Y 2787
23271 S A570D 7667
23403 S D614G 8245
23604 S P681H 4913
23709 S T716I 4467
24506 S S982A 4755
24914 S D1118H 13235
25785 ORF3a W131C 5279
27682 ORF7a Y97H 7891
27972 ORF8 Q27stop 11250
28048 ORF8 R52I 9023
28095 ORF8 K68stop 11340
28111 ORF8 Y73C 10107
28271 intergenic del 1 5560
28280 N D3L 3804
28281 N D3L 3805
28282 N D3L 4095
28881 N R203K 1941
28882 N R203K 1927
28883 N G204R 1930
28977 N S235F 3325
29272 N silent 7692
29764 intergenic 1718
VSP2262−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

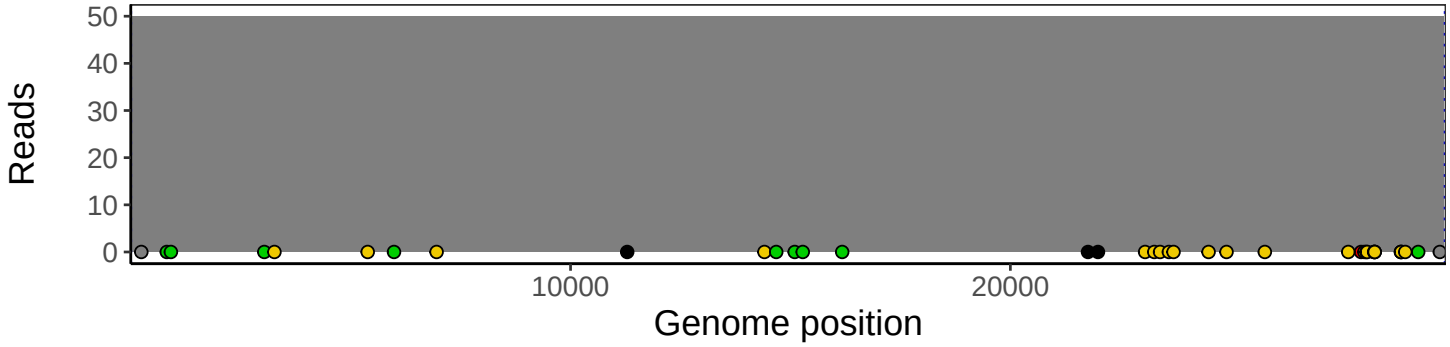
Analyses of individual experiments and composite results

VSP2262-1 | 2021-04-12 | Saline | UPHS-1050 | genomes | single experiment

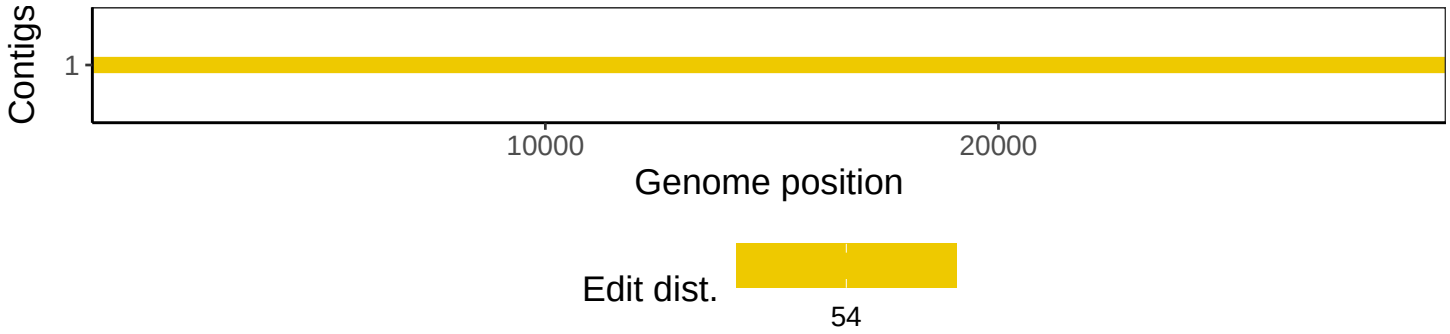
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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