COVID-19 subject UPHS-0867

2021-05-21

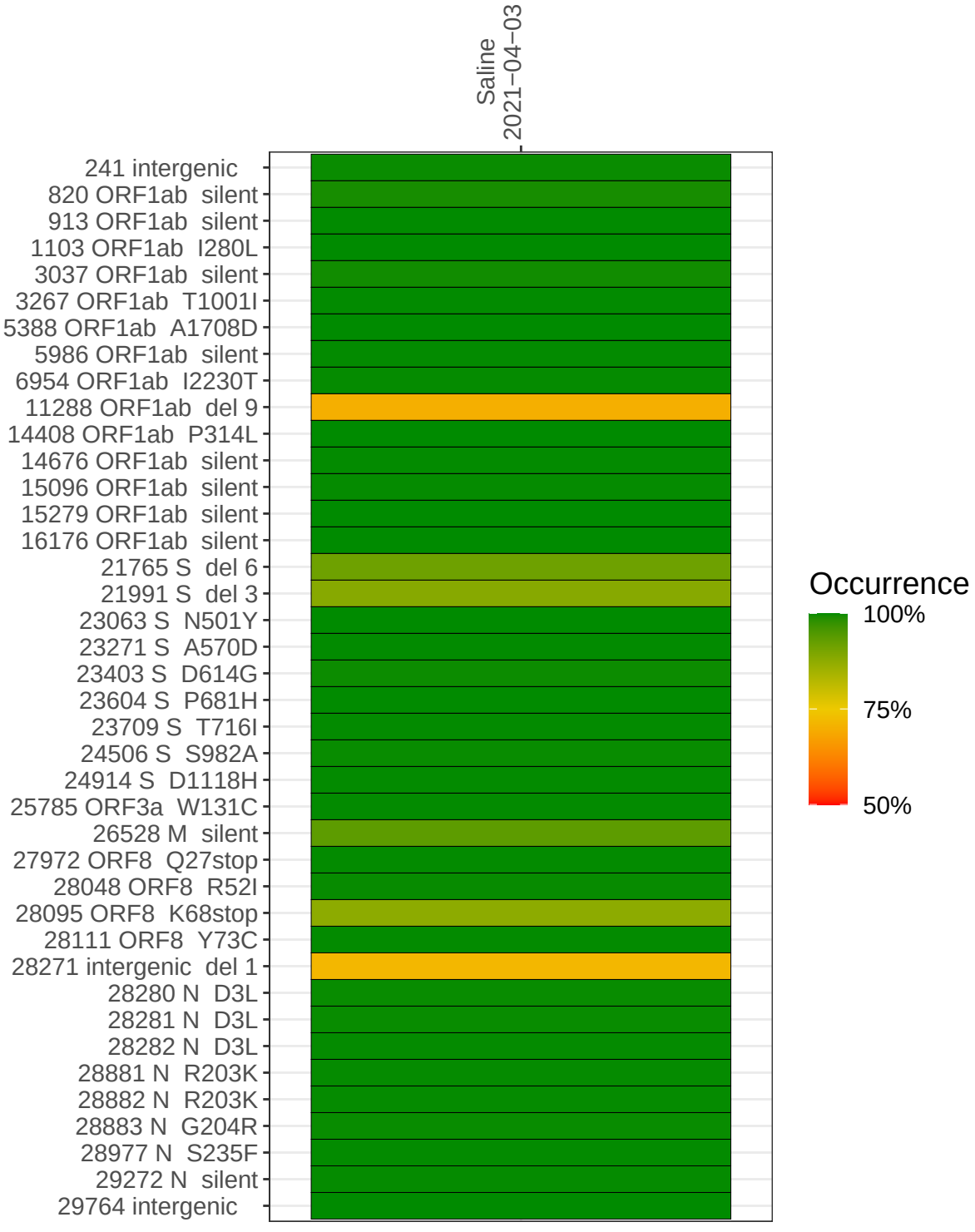
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

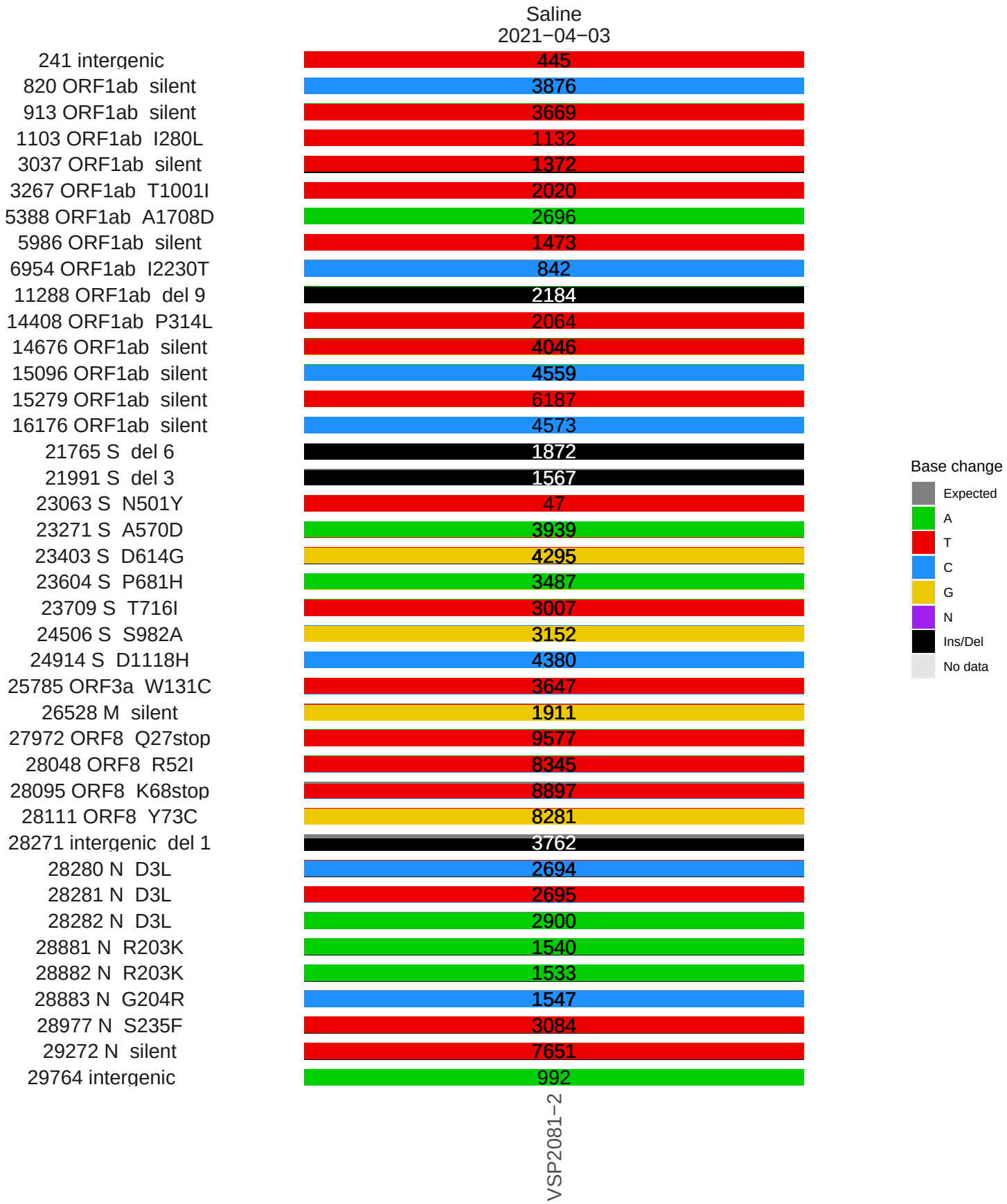
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2081-2	single experiment	NA	Saline	2021-04-03	29.81	B.1.1.7	99.9%	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.

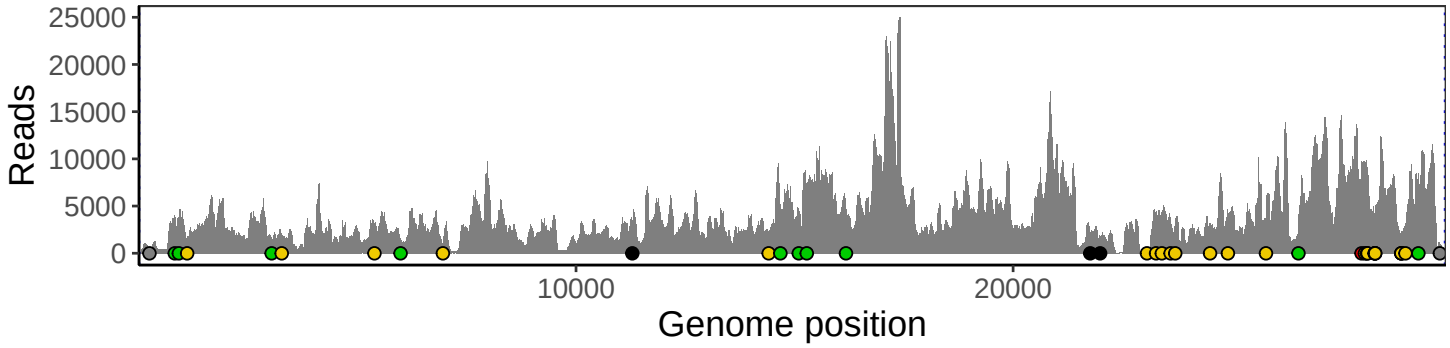



Saline
2021−04−03
241 intergenic 445
820 ORF1ab silent 3876
913 ORF1ab silent 3669
1103 ORF1ab I280L 1132
3037 ORF1ab silent 1372
3267 ORF1ab T1001I 2020
5388 ORF1ab A1708D 2696
5986 ORF1ab silent 1473
6954 ORF1ab I2230T 842
11288 ORF1ab del 9 2184
14408 ORF1ab P314L 2064
14676 ORF1ab silent 4046
15096 ORF1ab silent 4559
15279 ORF1ab silent 6187
16176 ORF1ab silent 4573
21765 S del 6 1872
21991 S del 3 1567
23063 S N501Y 47
23271 S A570D 3939
23403 S D614G 4295
23604 S P681H 3487
23709 S T716I 3007
24506 S S982A 3152
24914 S D1118H 4380
25785 ORF3a W131C 3647
26528 M silent 1911
27972 ORF8 Q27stop 9577
28048 ORF8 R52I 8345
28095 ORF8 K68stop 8897
28111 ORF8 Y73C 8281
28271 intergenic del 1 3762
28280 N D3L 2694
28281 N D3L 2695
28282 N D3L 2900
28881 N R203K 1540
28882 N R203K 1533
28883 N G204R 1547
28977 N S235F 3084
29272 N silent 7651
29764 intergenic 992
VSP2081−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

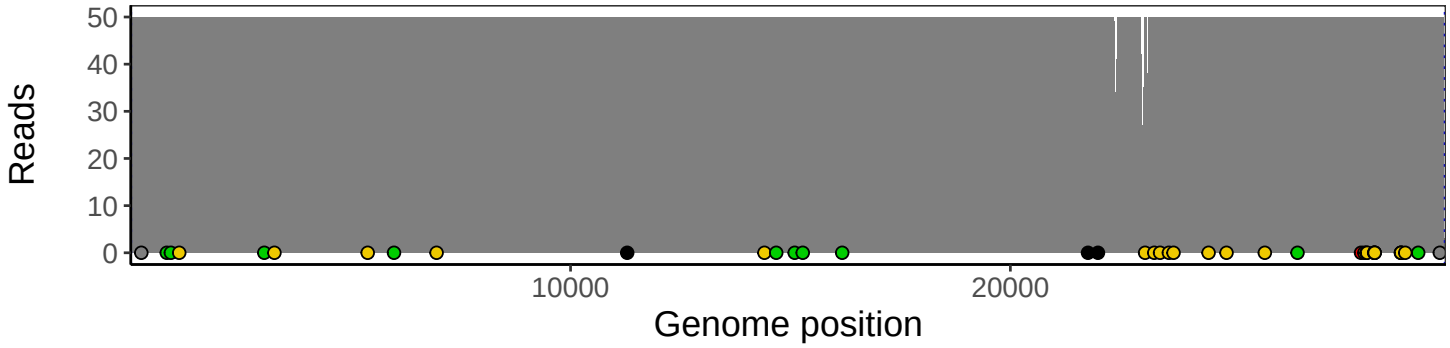
Analyses of individual experiments and composite results

VSP2081-2 | 2021-04-03 | Saline | UPHS-0867 | genomes | single experiment

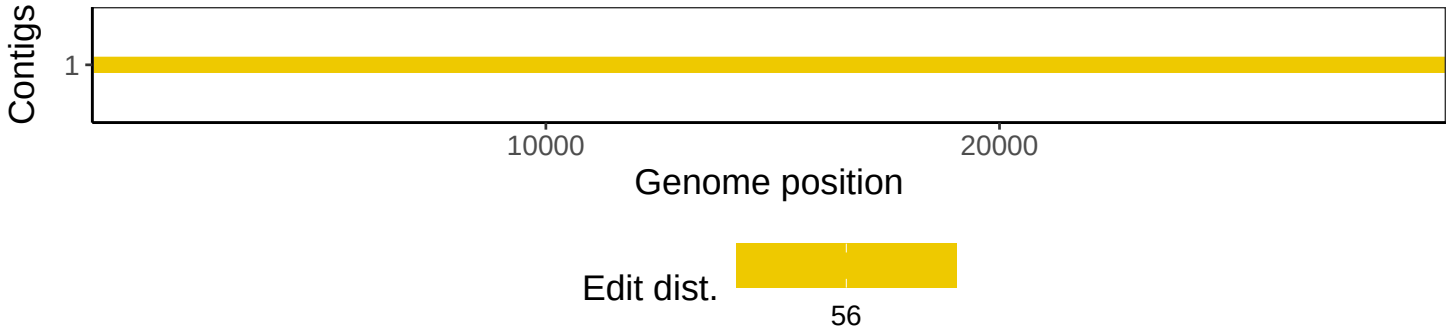
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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