COVID-19 subject UPHS-0180

2021-04-17

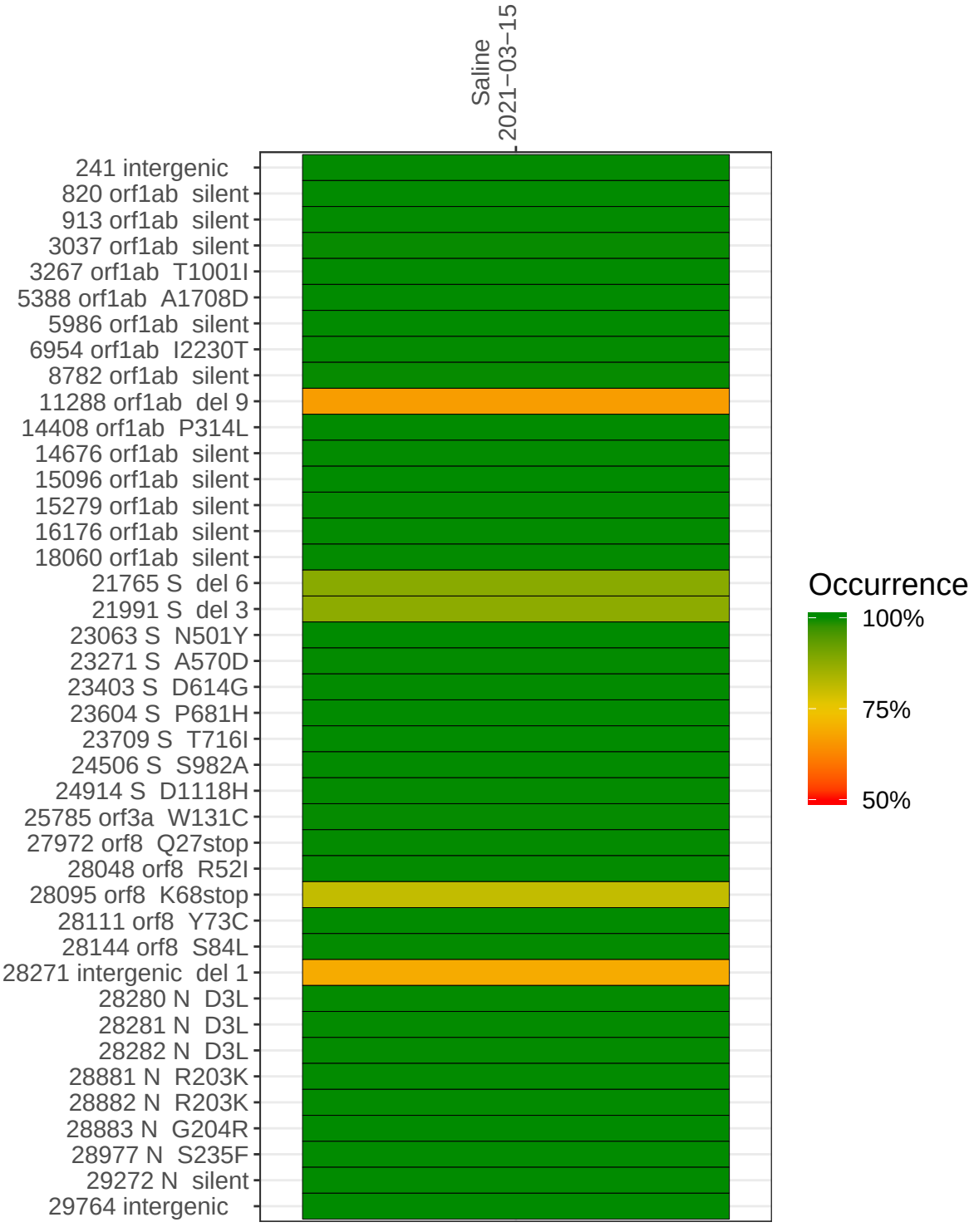
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

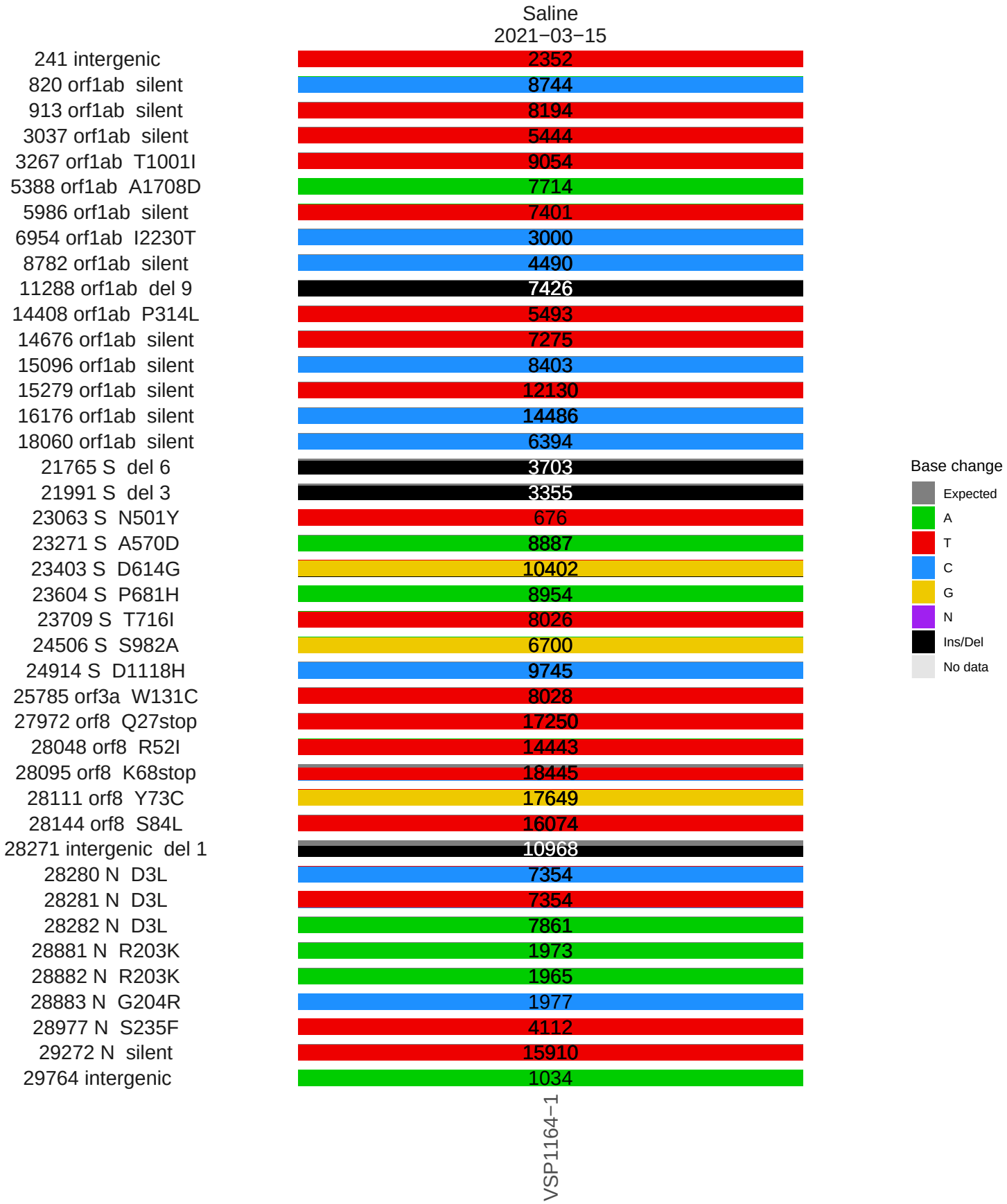
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1164-1	single experiment	NA	Saline	2021-03-15	29.85	B.1.1.7	99.9%	99.9%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

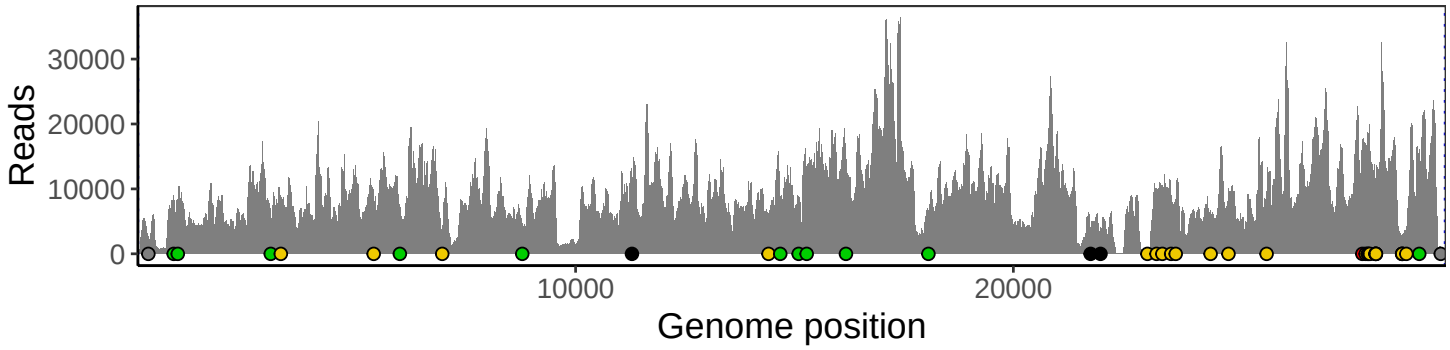



Saline
2021−03−15
241 intergenic 2352
820 orf1ab silent 8744
913 orf1ab silent 8194
3037 orf1ab silent 5444
3267 orf1ab T1001I 9054
5388 orf1ab A1708D 7714
5986 orf1ab silent 7401
6954 orf1ab I2230T 3000
8782 orf1ab silent 4490
11288 orf1ab del 9 7426
14408 orf1ab P314L 5493
14676 orf1ab silent 7275
15096 orf1ab silent 8403
15279 orf1ab silent 12130
16176 orf1ab silent 14486
18060 orf1ab silent 6394
21765 S del 6 3703
21991 S del 3 3355
23063 S N501Y 676
23271 S A570D 8887
23403 S D614G 10402
23604 S P681H 8954
23709 S T716I 8026
24506 S S982A 6700
24914 S D1118H 9745
25785 orf3a W131C 8028
27972 orf8 Q27stop 17250
28048 orf8 R52I 14443
28095 orf8 K68stop 18445
28111 orf8 Y73C 17649
28144 orf8 S84L 16074
28271 intergenic del 1 10968
28280 N D3L 7354
28281 N D3L 7354
28282 N D3L 7861
28881 N R203K 1973
28882 N R203K 1965
28883 N G204R 1977
28977 N S235F 4112
29272 N silent 15910
29764 intergenic 1034
VSP1164−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

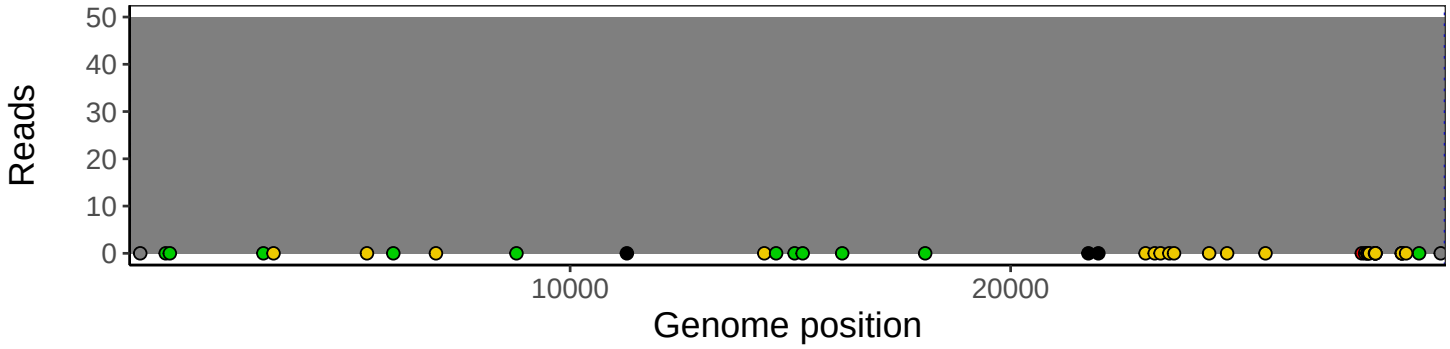
Analyses of individual experiments and composite results

VSP1164-1 | 2021-03-15 | Saline | UPHS-0180 | genomes | single experiment

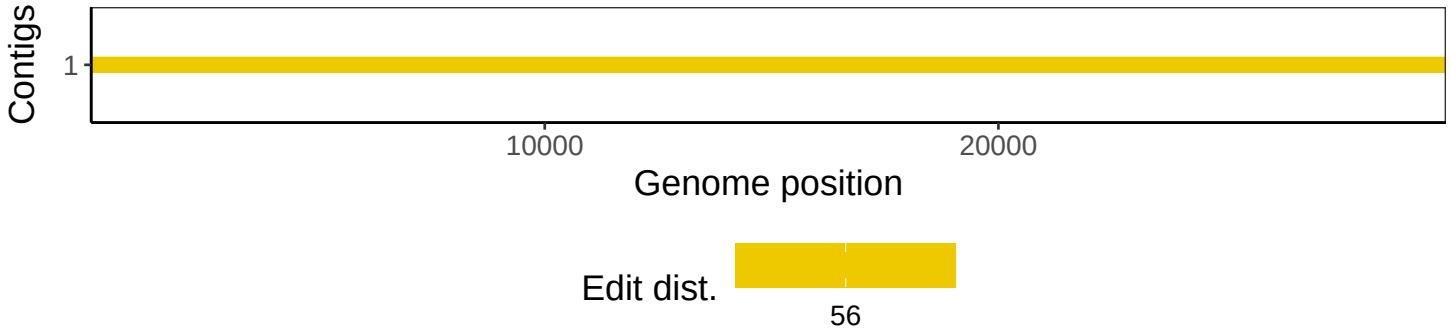
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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