COVID-19 subject UPHS-0056

2021-05-05

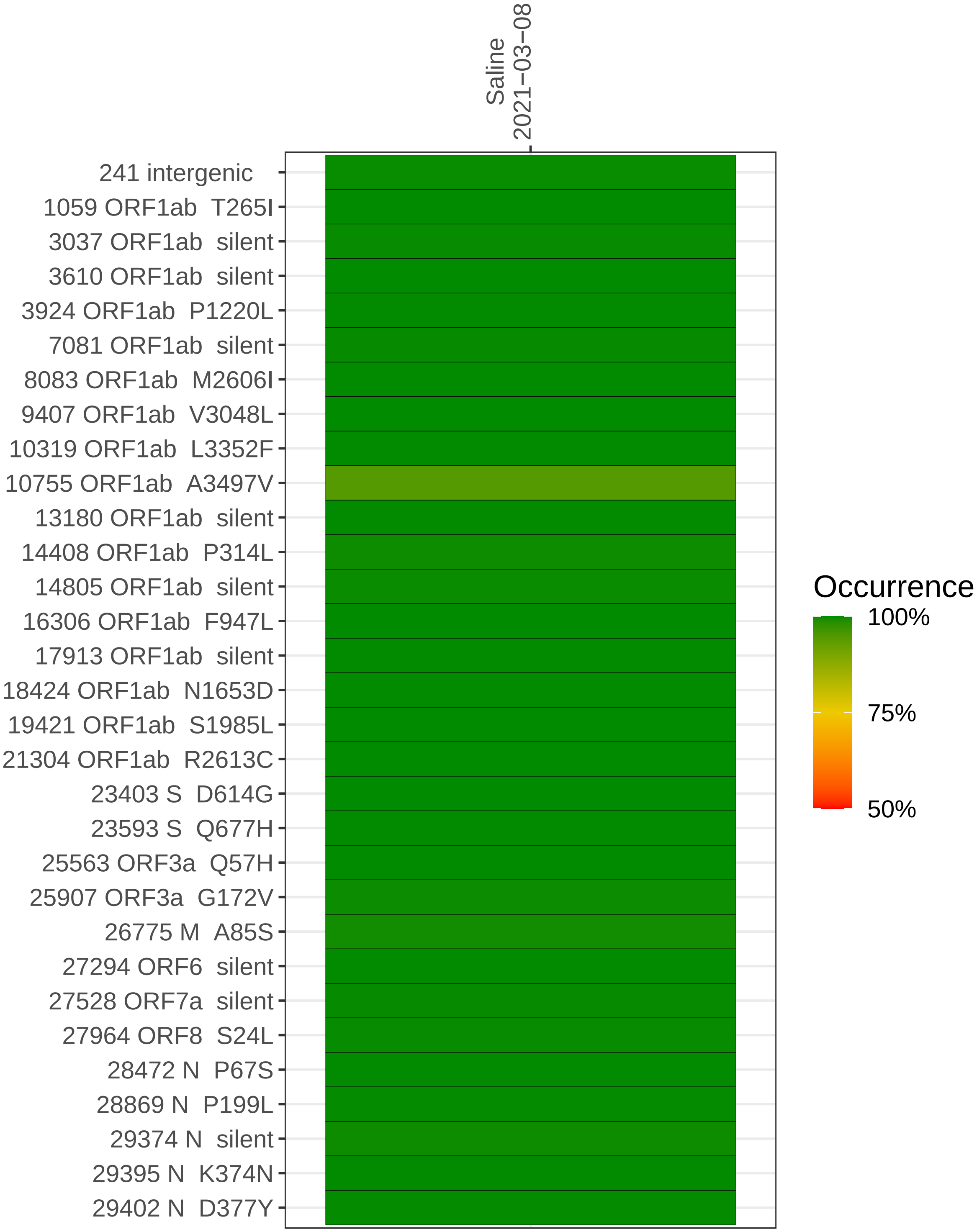
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

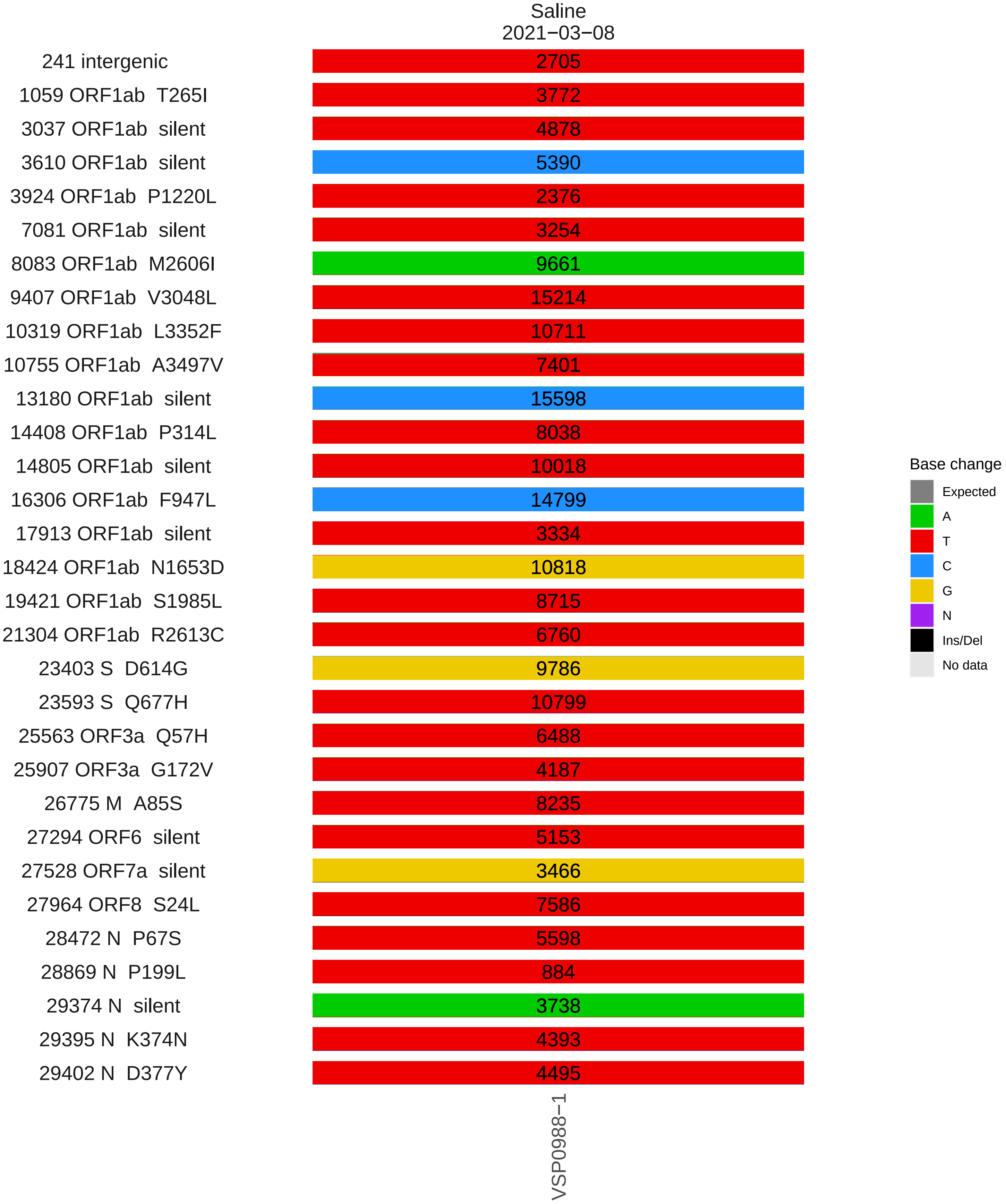
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0988-1	single experiment	NA	Saline	2021-03-08	27.53	B.1.2	99.9%	99.7%

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.

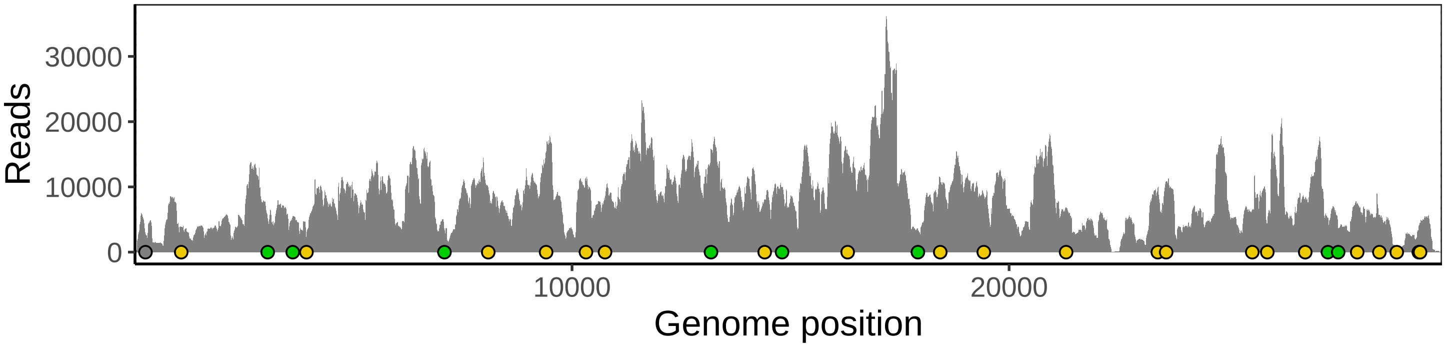



Saline
2021−03−08
241 intergenic
2705
1059 ORF1ab T265I
3772
3037 ORF1ab silent
4878
3610 ORF1ab silent
5390
3924 ORF1ab P1220L
2376
7081 ORF1ab silent
3254
8083 ORF1ab M2606I
9661
9407 ORF1ab V3048L
15214
10319 ORF1ab L3352F
10711
10755 ORF1ab A3497V
7401
13180 ORF1ab silent
15598
14408 ORF1ab P314L
8038
14805 ORF1ab silent
10018
16306 ORF1ab F947L
14799
17913 ORF1ab silent
3334
18424 ORF1ab N1653D
10818
19421 ORF1ab S1985L
8715
21304 ORF1ab R2613C
6760
23403 S D614G
9786
23593 S Q677H
10799
25563 ORF3a Q57H
6488
25907 ORF3a G172V
4187
26775 M A85S
8235
27294 ORF6 silent
5153
27528 ORF7a silent
3466
27964 ORF8 S24L
7586
28472 N P67S
5598
28869 N P199L
884
29374 N silent
3738
29395 N K374N
4393
29402 N D377Y
4495
VSP0988−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

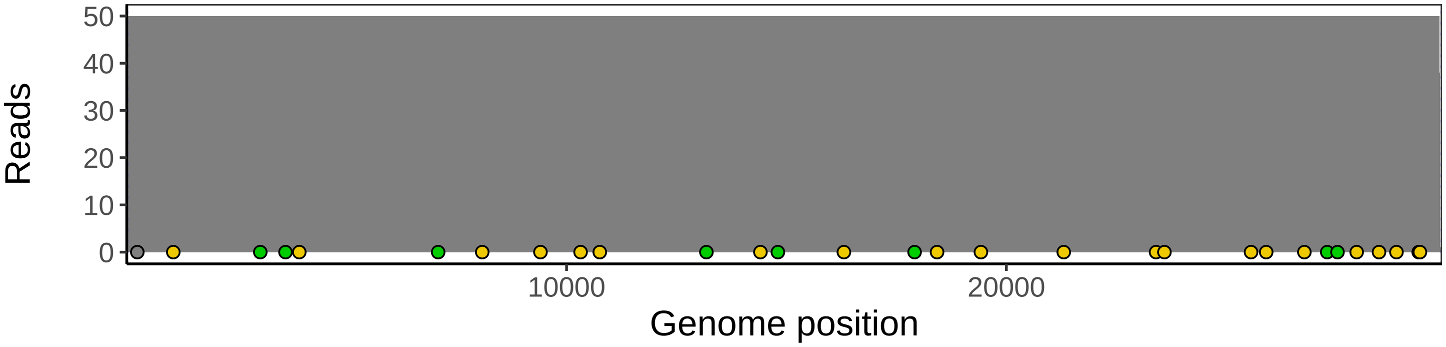
Analyses of individual experiments and composite results

VSP0988-1 | 2021-03-08 | Saline | UPHS-0056 | genomes | single experiment

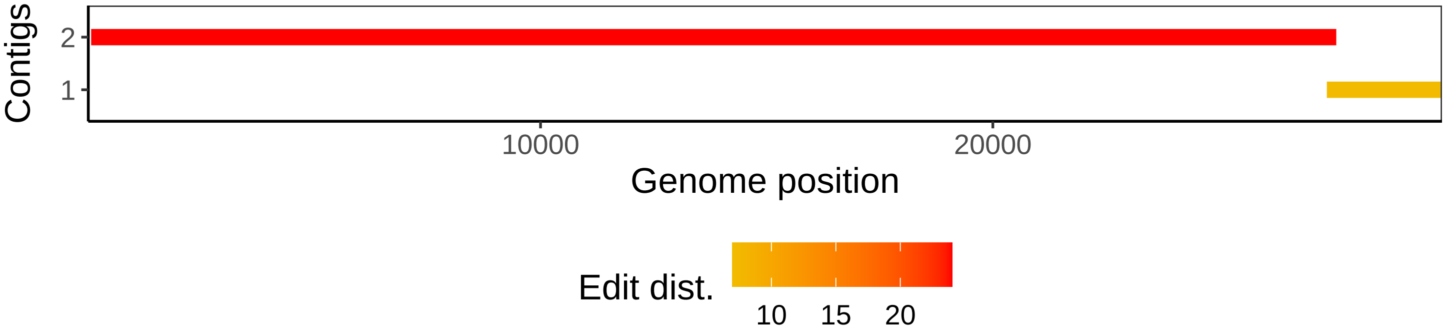
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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