COVID-19 subject UPHS-0073

2021-04-17

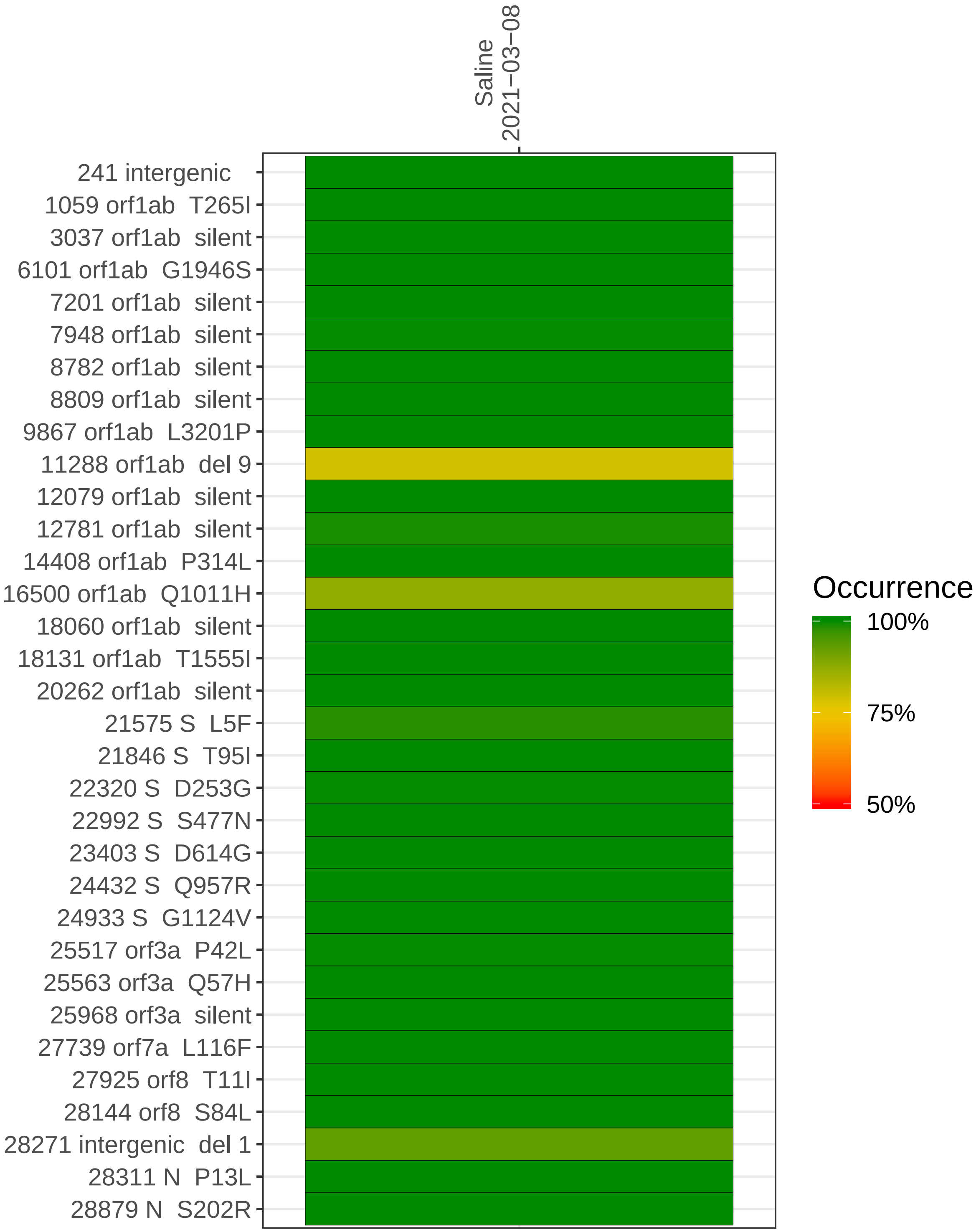
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

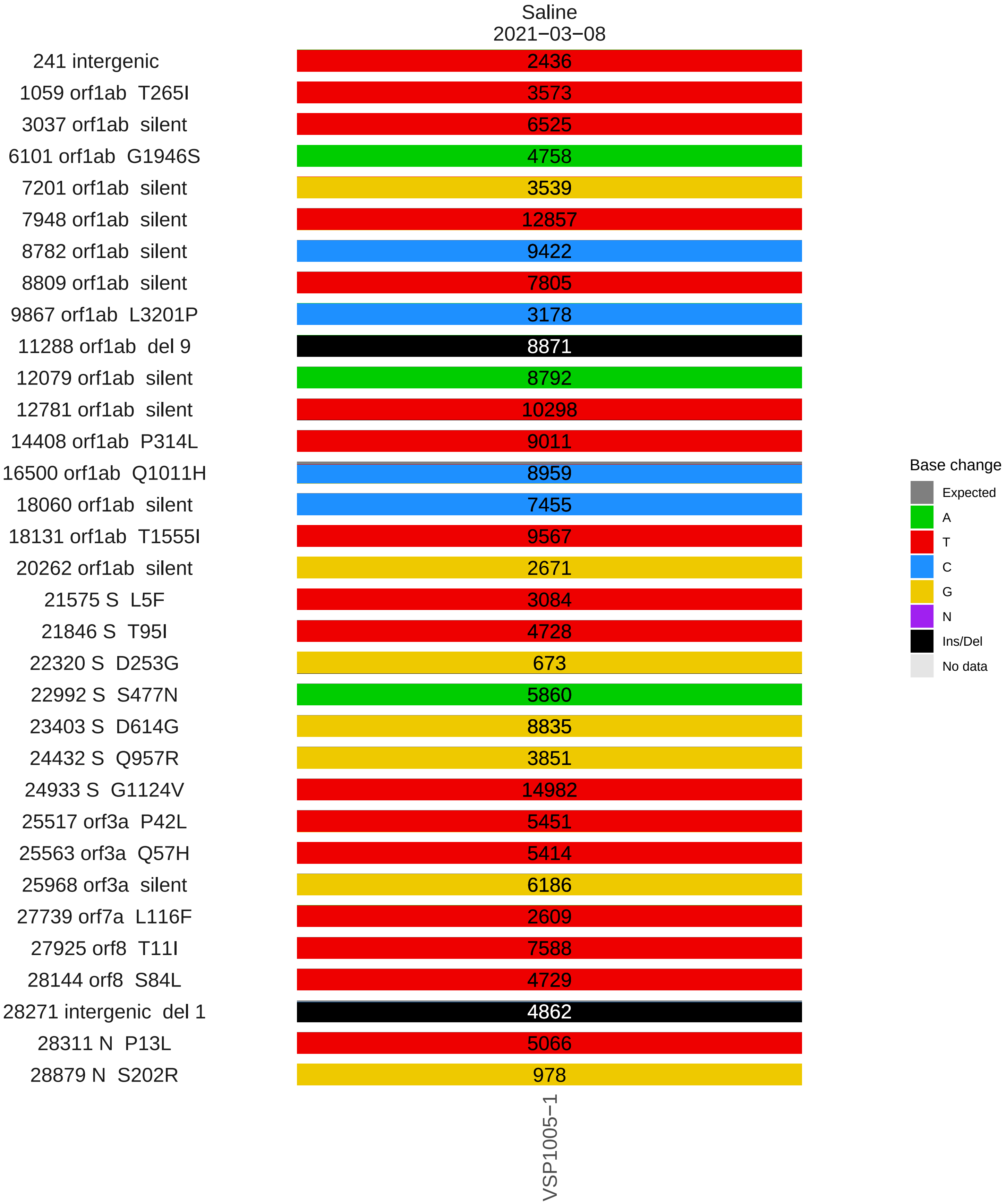
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1005-1	single experiment	NA	Saline	2021-03-08	29.92	B.1.526.2	99.8%	99.8%

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.

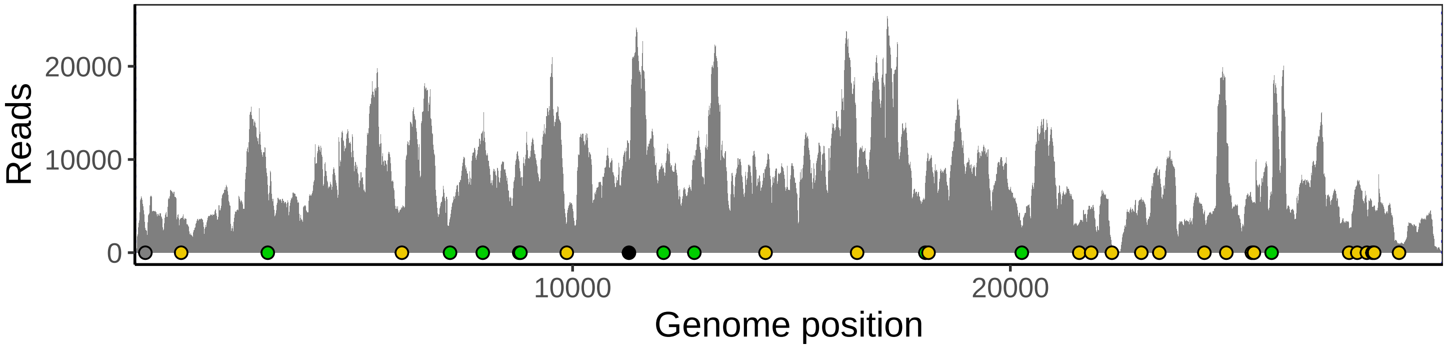



Saline
2021−03−08
241 intergenic
2436
1059 orf1ab T265I
3573
3037 orf1ab silent
6525
6101 orf1ab G1946S
4758
7201 orf1ab silent
3539
7948 orf1ab silent
12857
8782 orf1ab silent
9422
8809 orf1ab silent
7805
9867 orf1ab L3201P
3178
11288 orf1ab del 9
8871
12079 orf1ab silent
8792
12781 orf1ab silent
10298
14408 orf1ab P314L
9011
16500 orf1ab Q1011H
8959
18060 orf1ab silent
7455
18131 orf1ab T1555I
9567
20262 orf1ab silent
2671
21575 S L5F
3084
21846 S T95I
4728
22320 S D253G
673
22992 S S477N
5860
23403 S D614G
8835
24432 S Q957R
3851
24933 S G1124V
14982
25517 orf3a P42L
5451
25563 orf3a Q57H
5414
25968 orf3a silent
6186
27739 orf7a L116F
2609
27925 orf8 T11I
7588
28144 orf8 S84L
4729
28271 intergenic del 1
4862
28311 N P13L
5066
28879 N S202R
978
VSP1005−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

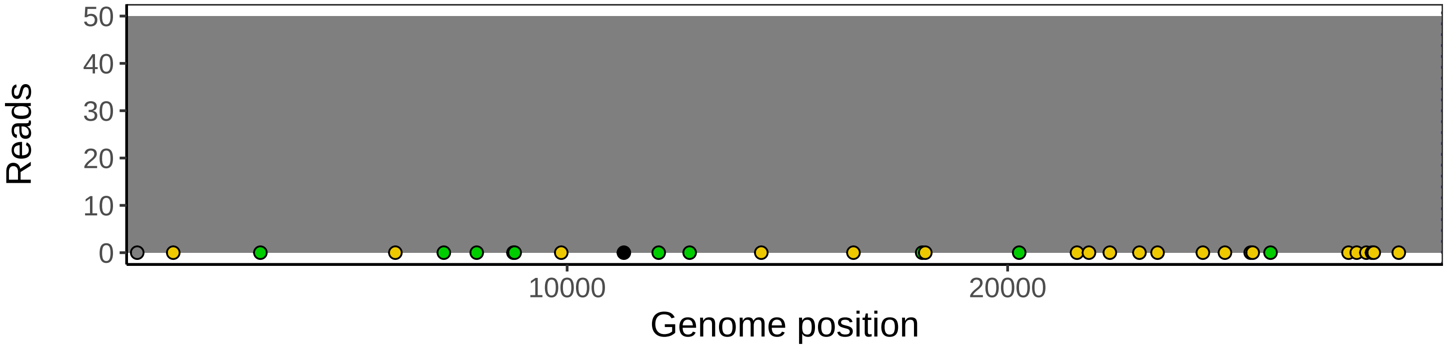
Analyses of individual experiments and composite results

VSP1005-1 | 2021-03-08 | Saline | UPHS-0073 | genomes | single experiment

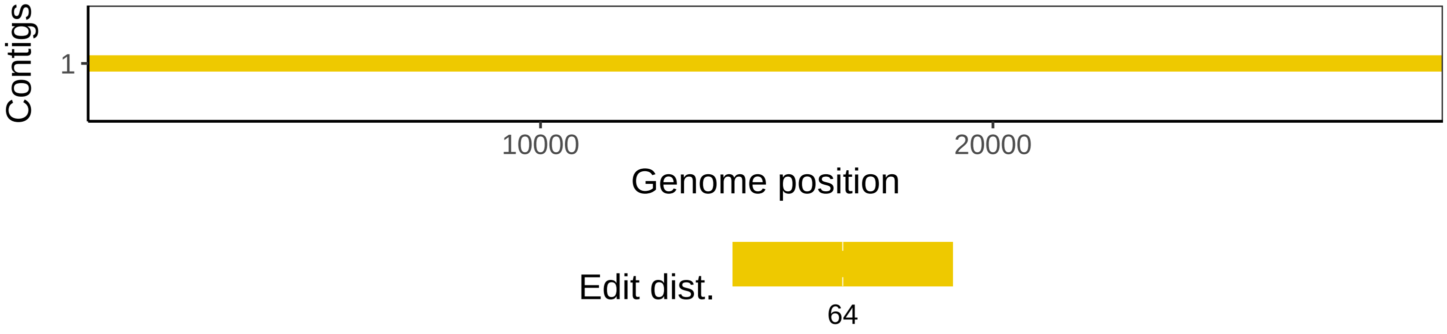
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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