COVID-19 subject UPHS-0036

2021-04-17

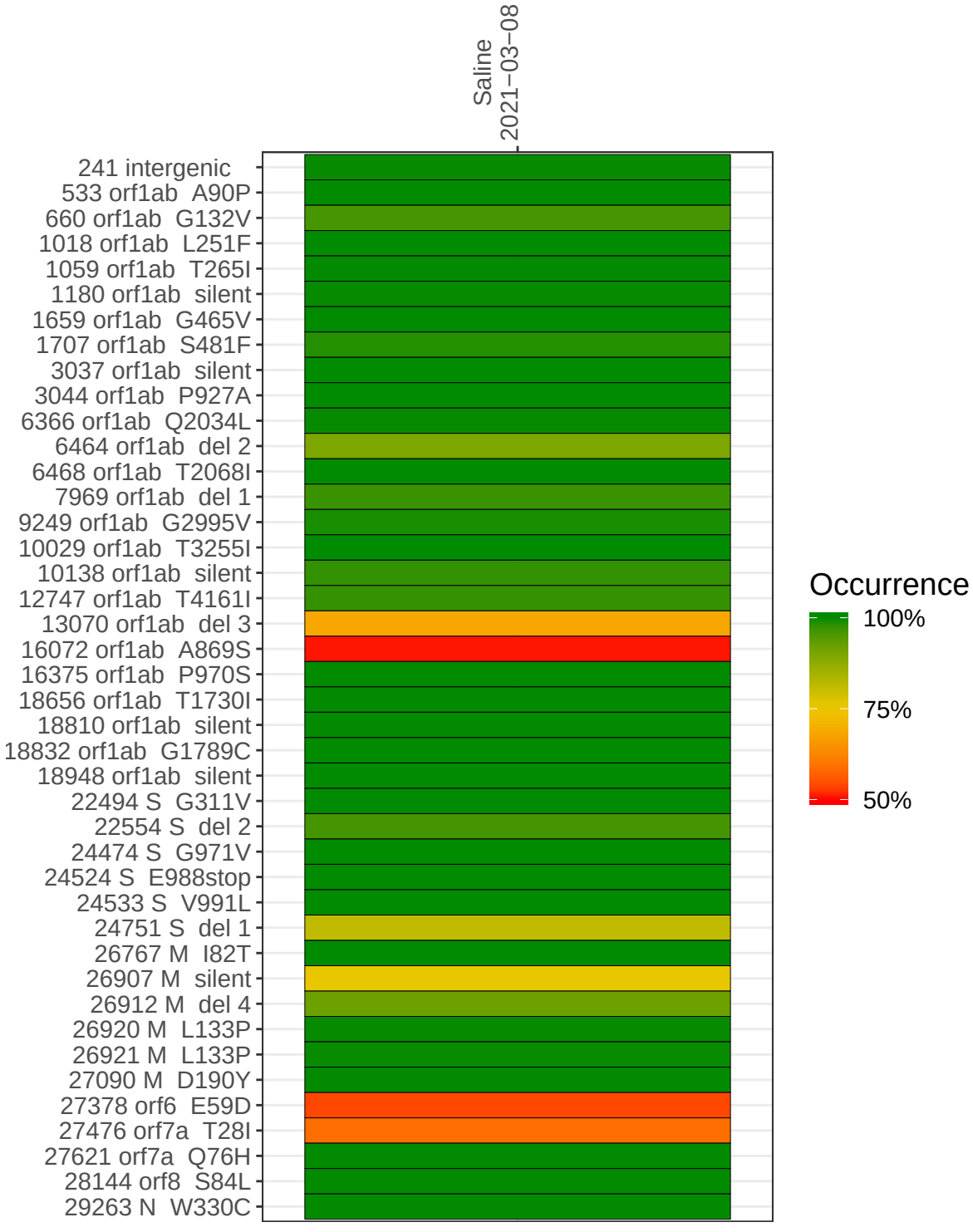
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

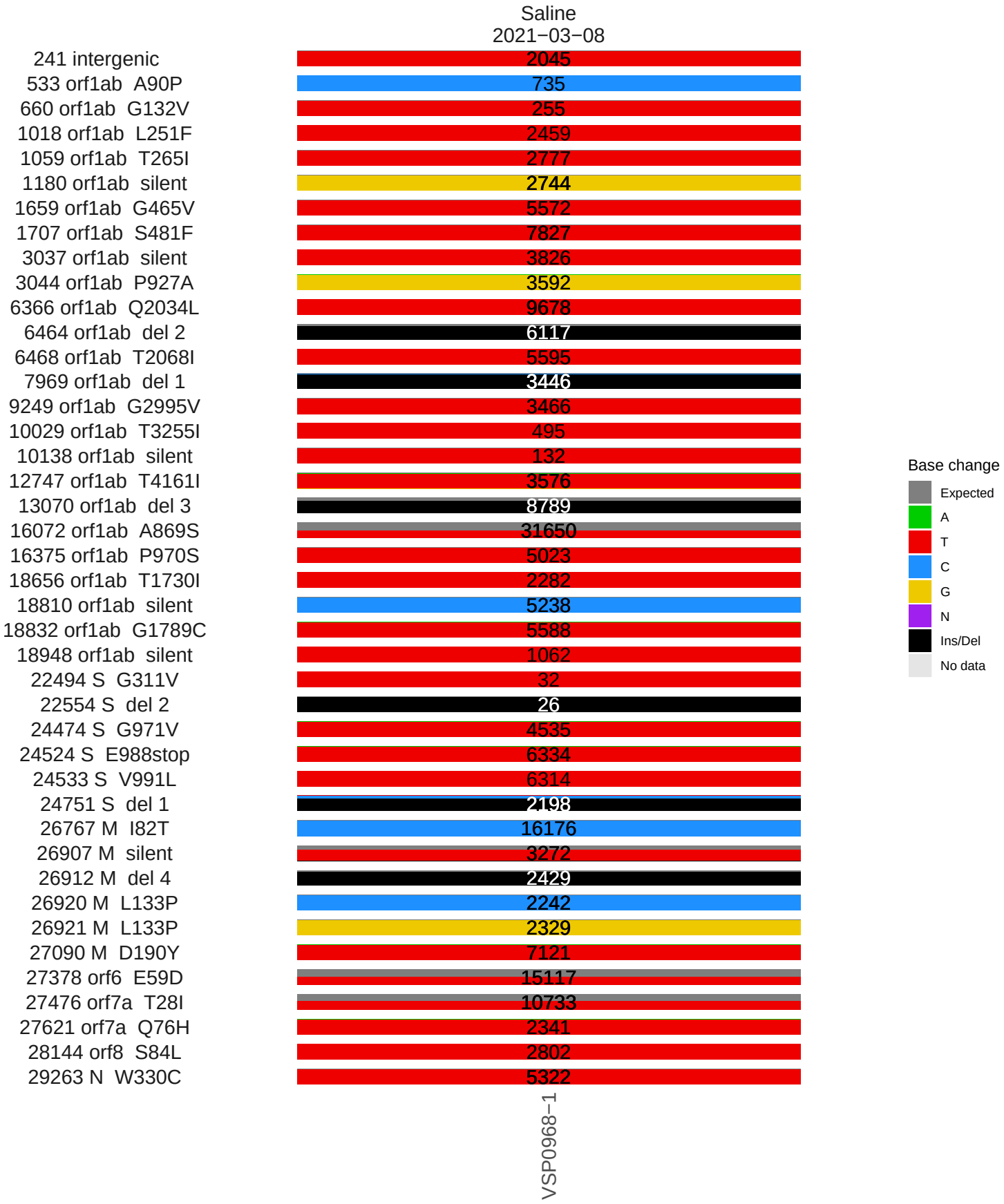
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0968-1	single experiment	NA	Saline	2021-03-08	1.67	NA	38.6%	37.7%

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.

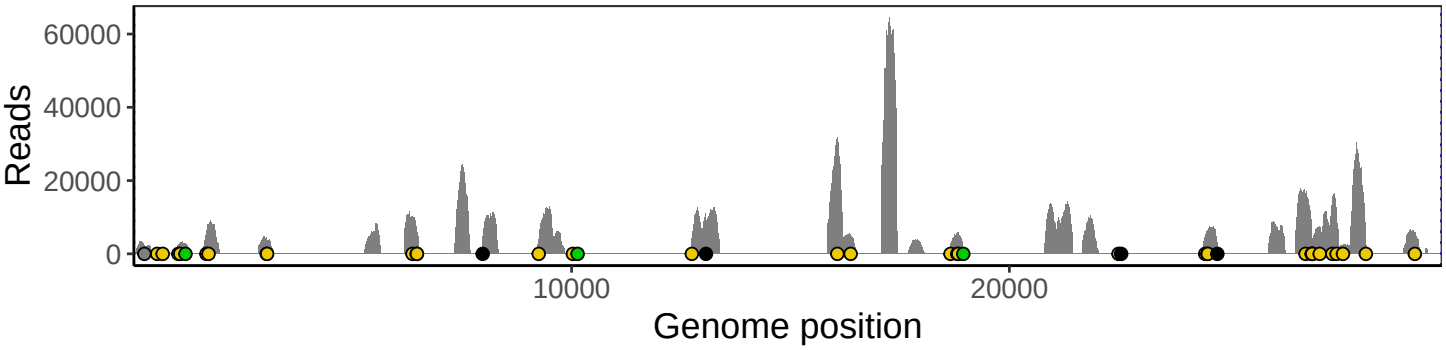



Saline
2021−03−08
241 intergenic
533 orf1ab A90P
660 orf1ab G132V
1018 orf1ab L251F
1059 orf1ab T265I
1180 orf1ab silent
1659 orf1ab G465V
1707 orf1ab S481F
3037 orf1ab silent
3044 orf1ab P927A
6366 orf1ab Q2034L
6464 orf1ab del 2
6468 orf1ab T2068I
7969 orf1ab del 1
9249 orf1ab G2995V
10029 orf1ab T3255I
10138 orf1ab silent
12747 orf1ab T4161I
13070 orf1ab del 3
16072 orf1ab A869S
16375 orf1ab P970S
18656 orf1ab T1730I
18810 orf1ab silent
18832 orf1ab G1789C
18948 orf1ab silent
22494 S G311V
22554 S del 2
24474 S G971V
24524 S E988stop
24533 S V991L
24751 S del 1
26767 M I82T
26907 M silent
26912 M del 4
26920 M L133P
26921 M L133P
27090 M D190Y
27378 orf6 E59D
27476 orf7a T28I
27621 orf7a Q76H
28144 orf8 S84L
29263 N W330C
2045
735
255
2459
2777
2744
5572
7827
3826
3592
9678
6117
5595
3446
3466
495
132
3576
8789
31650
5023
2282
5238
5588
1062
32
26
4535
6334
6314
2198
16176
3272
2429
2242
2329
7121
15117
10733
2341
2802
5322
VSP0968−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

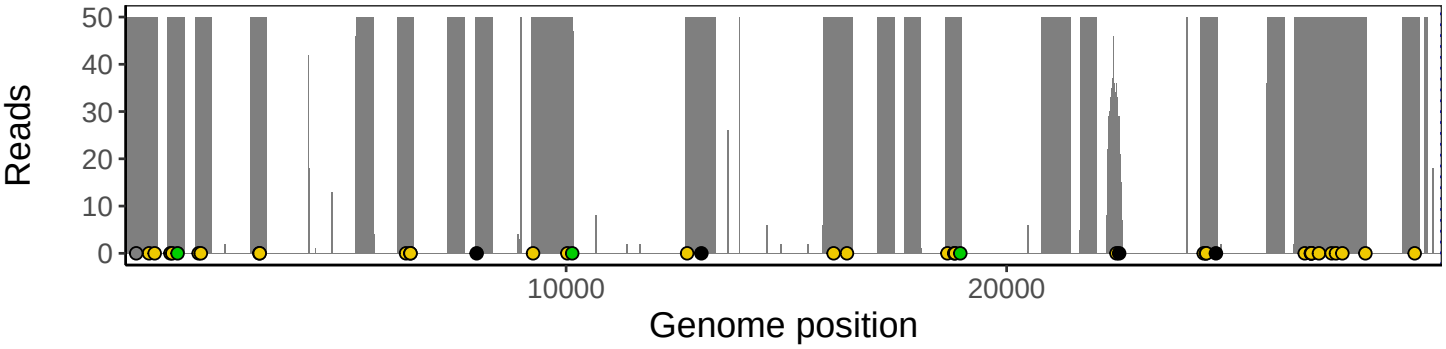
Analyses of individual experiments and composite results

VSP0968-1 | 2021-03-08 | Saline | UPHS-0036 | genomes | single experiment

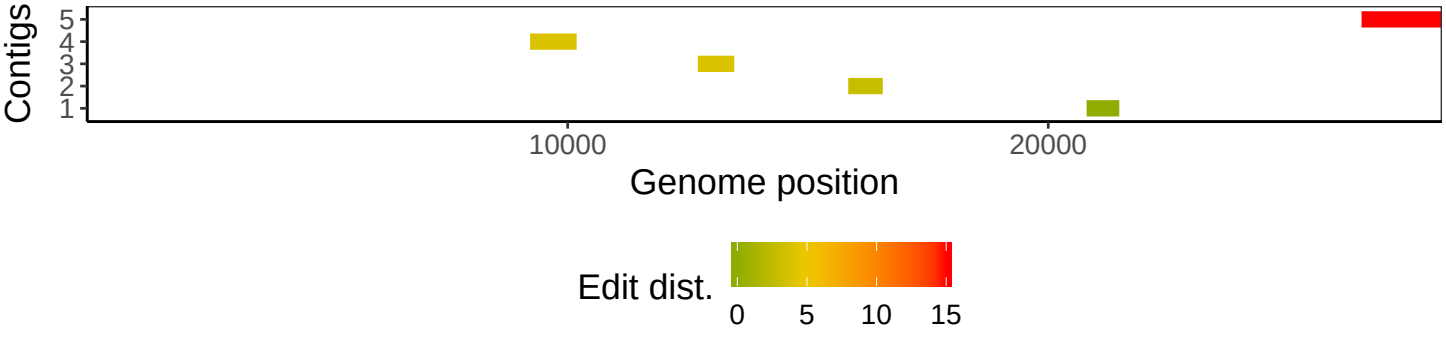
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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