COVID-19 subject UPHS-0305

2021-04-17

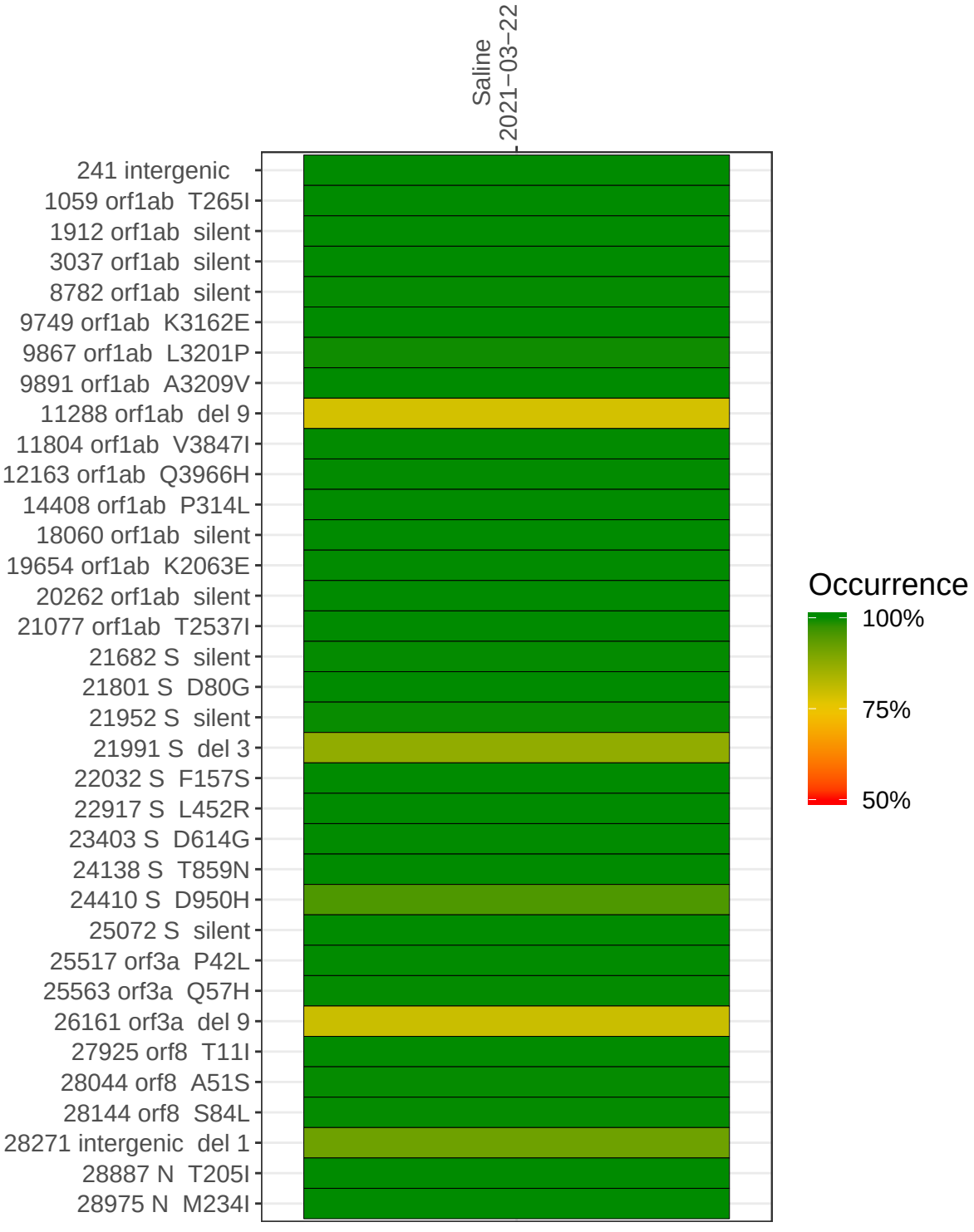
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

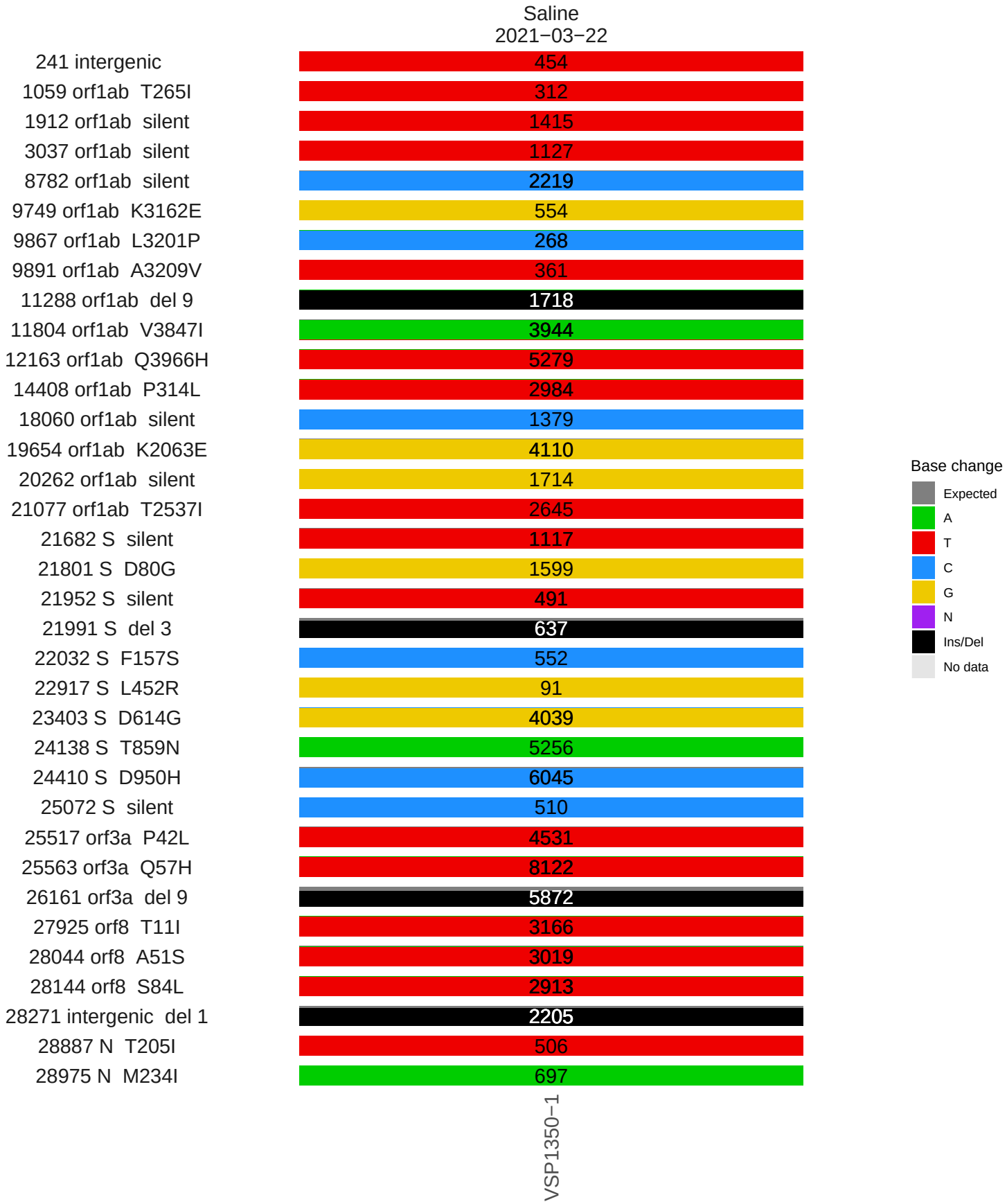
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1350-1	single experiment	NA	Saline	2021-03-22	28.29	B.1.526.1	99.2%	98.9%

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.

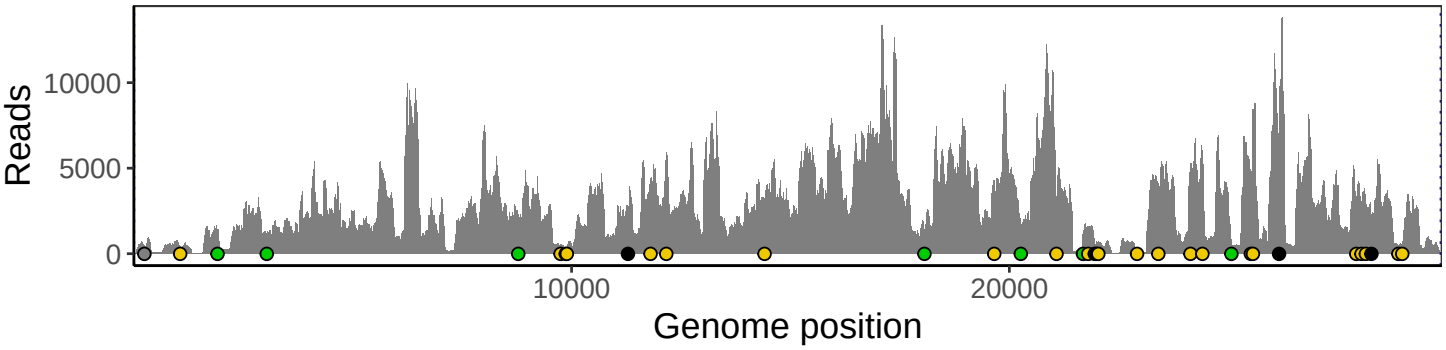



Saline
2021−03−22
241 intergenic 454
1059 orf1ab T265I 312
1912 orf1ab silent 1415
3037 orf1ab silent 1127
8782 orf1ab silent 2219
9749 orf1ab K3162E 554
9867 orf1ab L3201P 268
9891 orf1ab A3209V 361
11288 orf1ab del 9 1718
11804 orf1ab V3847I 3944
12163 orf1ab Q3966H 5279
14408 orf1ab P314L 2984
18060 orf1ab silent 1379
19654 orf1ab K2063E 4110
20262 orf1ab silent 1714
21077 orf1ab T2537I 2645
21682 S silent 1117
21801 S D80G 1599
21952 S silent 491
21991 S del 3 637
22032 S F157S 552
22917 S L452R 91
23403 S D614G 4039
24138 S T859N 5256
24410 S D950H 6045
25072 S silent 510
25517 orf3a P42L 4531
25563 orf3a Q57H 8122
26161 orf3a del 9 5872
27925 orf8 T11I 3166
28044 orf8 A51S 3019
28144 orf8 S84L 2913
28271 intergenic del 1 2205
28887 N T205I 506
28975 N M234I 697
VSP1350−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

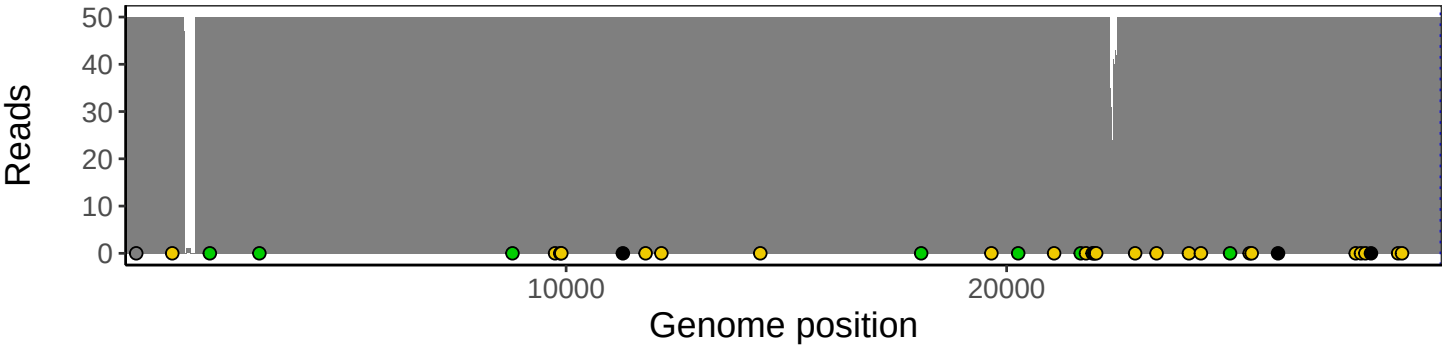
Analyses of individual experiments and composite results

VSP1350-1 | 2021-03-22 | Saline | UPHS-0305 | genomes | single experiment

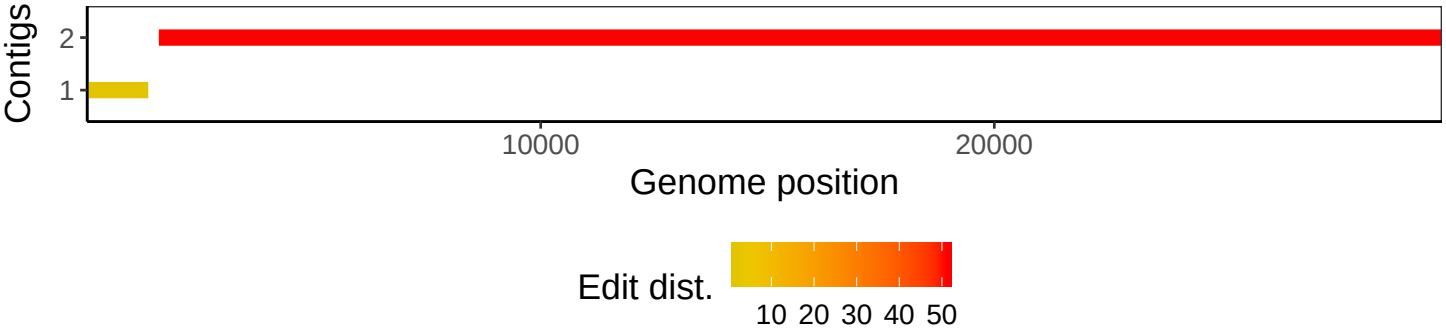
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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