COVID-19 subject UPHS-0091

2021-04-17

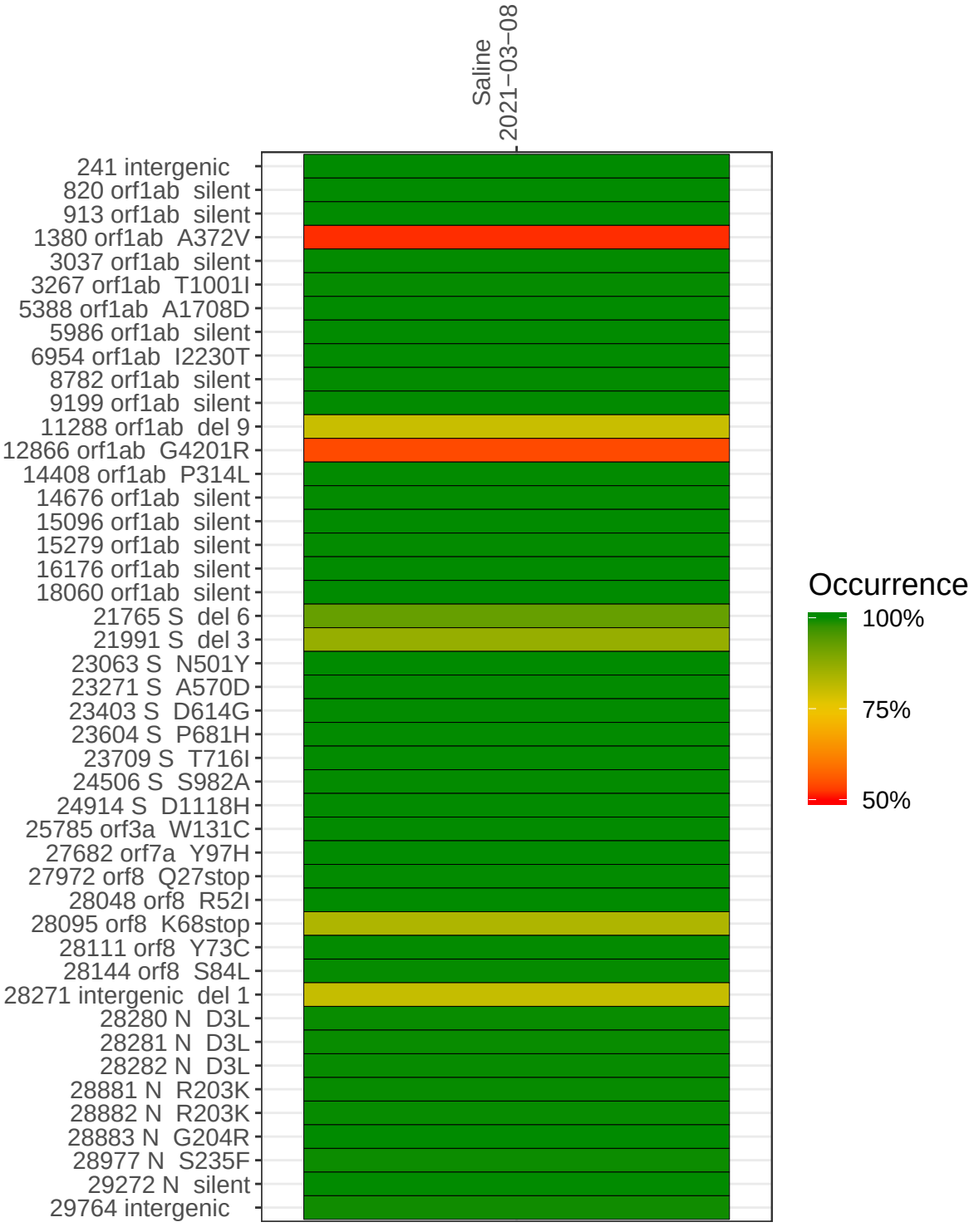
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

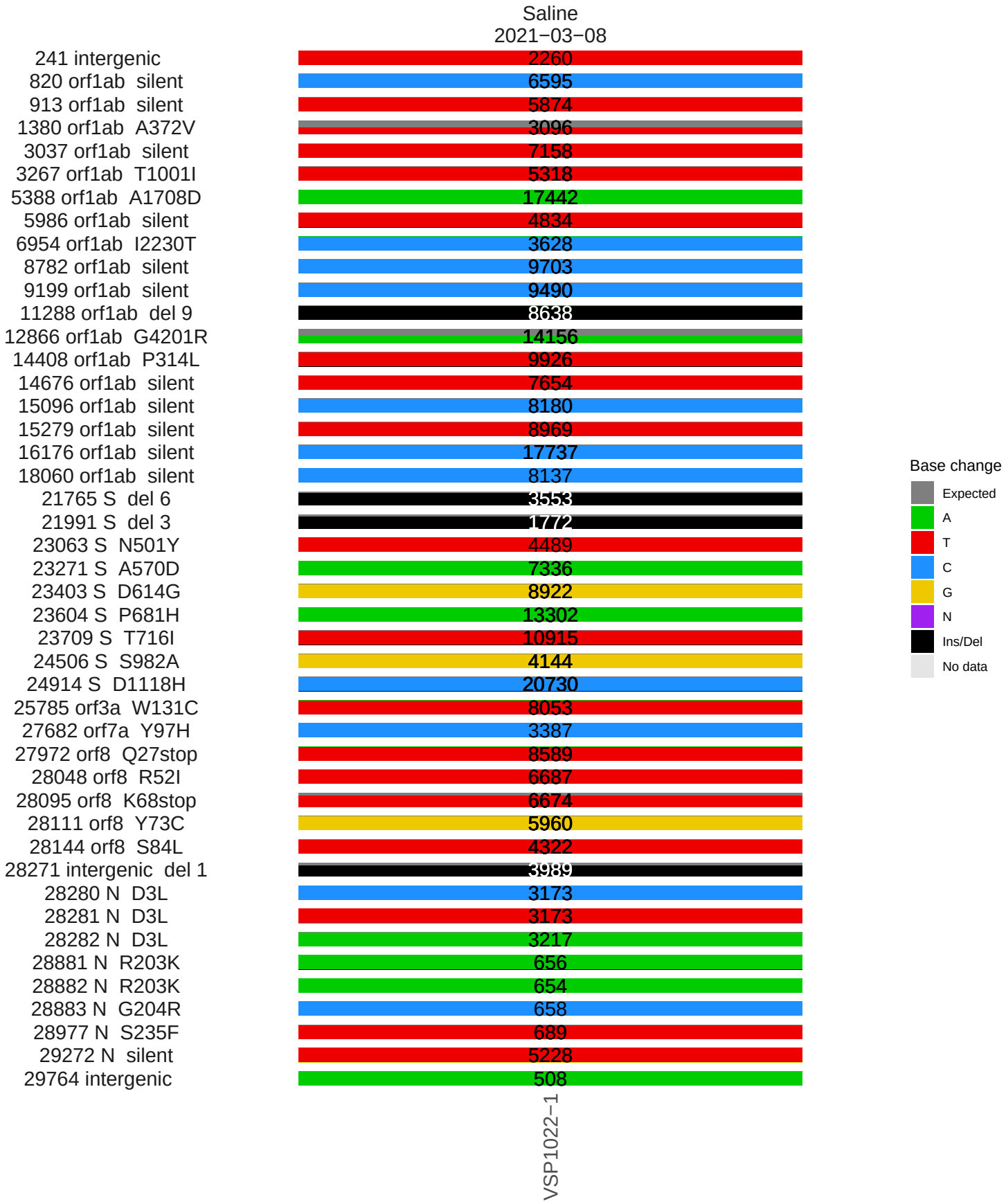
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1022-1	single experiment	NA	Saline	2021-03-08	29.85	B.1.1.7	99.9%	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.

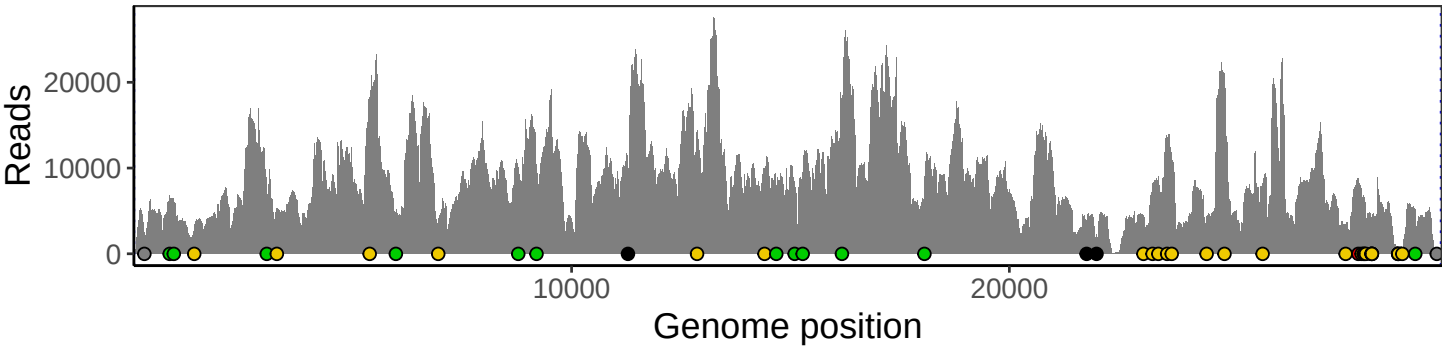



Saline
2021−03−08
241 intergenic 2260
820 orf1ab silent 6595
913 orf1ab silent 5874
1380 orf1ab A372V 3096
3037 orf1ab silent 7158
3267 orf1ab T1001I 5318
5388 orf1ab A1708D 17442
5986 orf1ab silent 4834
6954 orf1ab I2230T 3628
8782 orf1ab silent 9703
9199 orf1ab silent 9490
11288 orf1ab del 9 8638
12866 orf1ab G4201R 14156
14408 orf1ab P314L 9926
14676 orf1ab silent 7654
15096 orf1ab silent 8180
15279 orf1ab silent 8969
16176 orf1ab silent 17737
18060 orf1ab silent 8137
21765 S del 6 3553
21991 S del 3 1772
23063 S N501Y 4489
23271 S A570D 7336
23403 S D614G 8922
23604 S P681H 13302
23709 S T716I 10915
24506 S S982A 4144
24914 S D1118H 20730
25785 orf3a W131C 8053
27682 orf7a Y97H 3387
27972 orf8 Q27stop 8589
28048 orf8 R52I 6687
28095 orf8 K68stop 6674
28111 orf8 Y73C 5960
28144 orf8 S84L 4322
28271 intergenic del 1 3989
28280 N D3L 3173
28281 N D3L 3173
28282 N D3L 3217
28881 N R203K 656
28882 N R203K 654
28883 N G204R 658
28977 N S235F 689
29272 N silent 5228
29764 intergenic 508
VSP1022−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

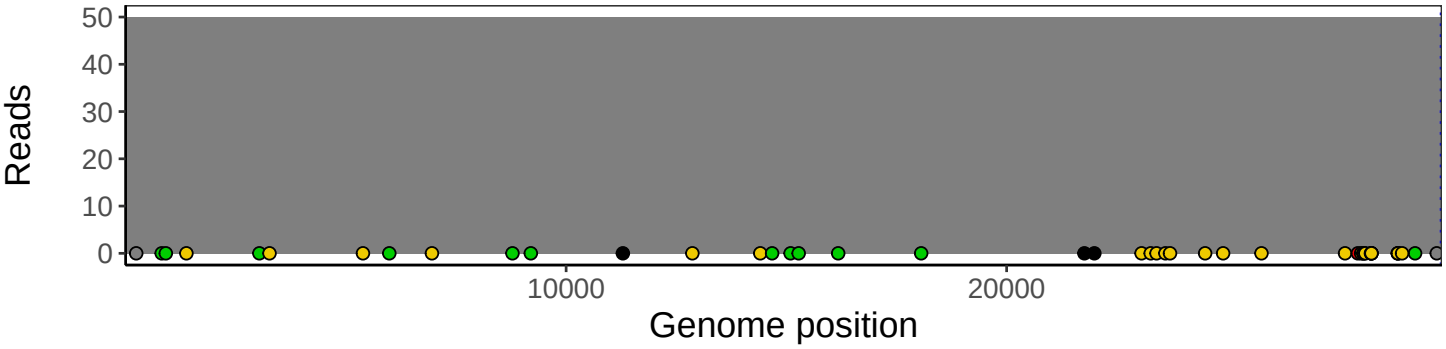
Analyses of individual experiments and composite results

VSP1022-1 | 2021-03-08 | Saline | UPHS-0091 | genomes | single experiment

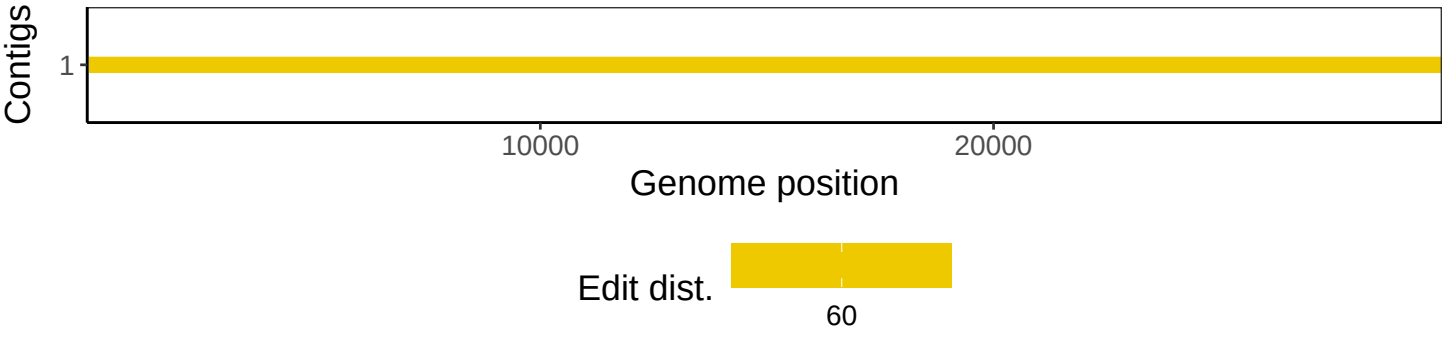
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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