COVID-19 subject UPHS-0292

2021-04-17

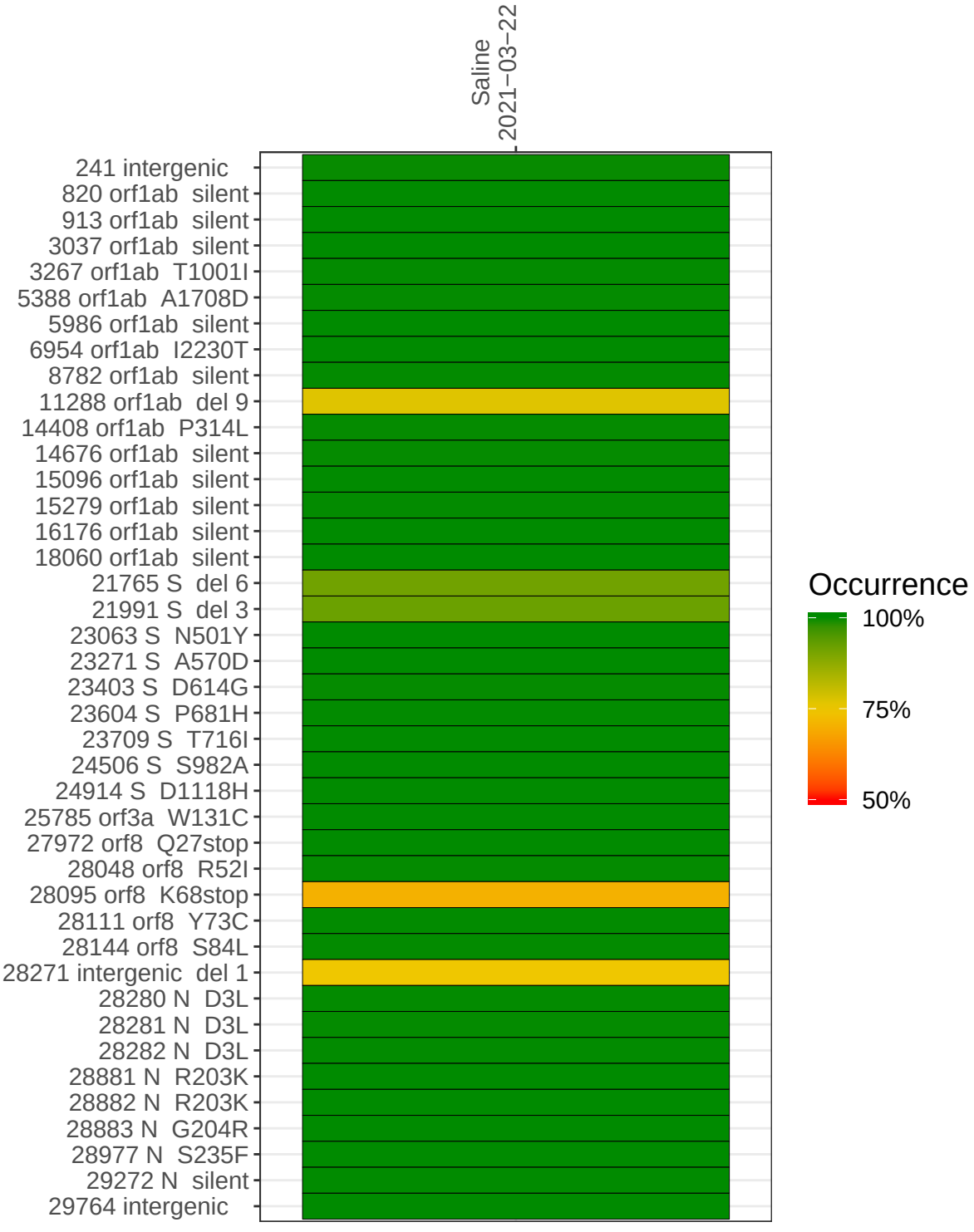
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

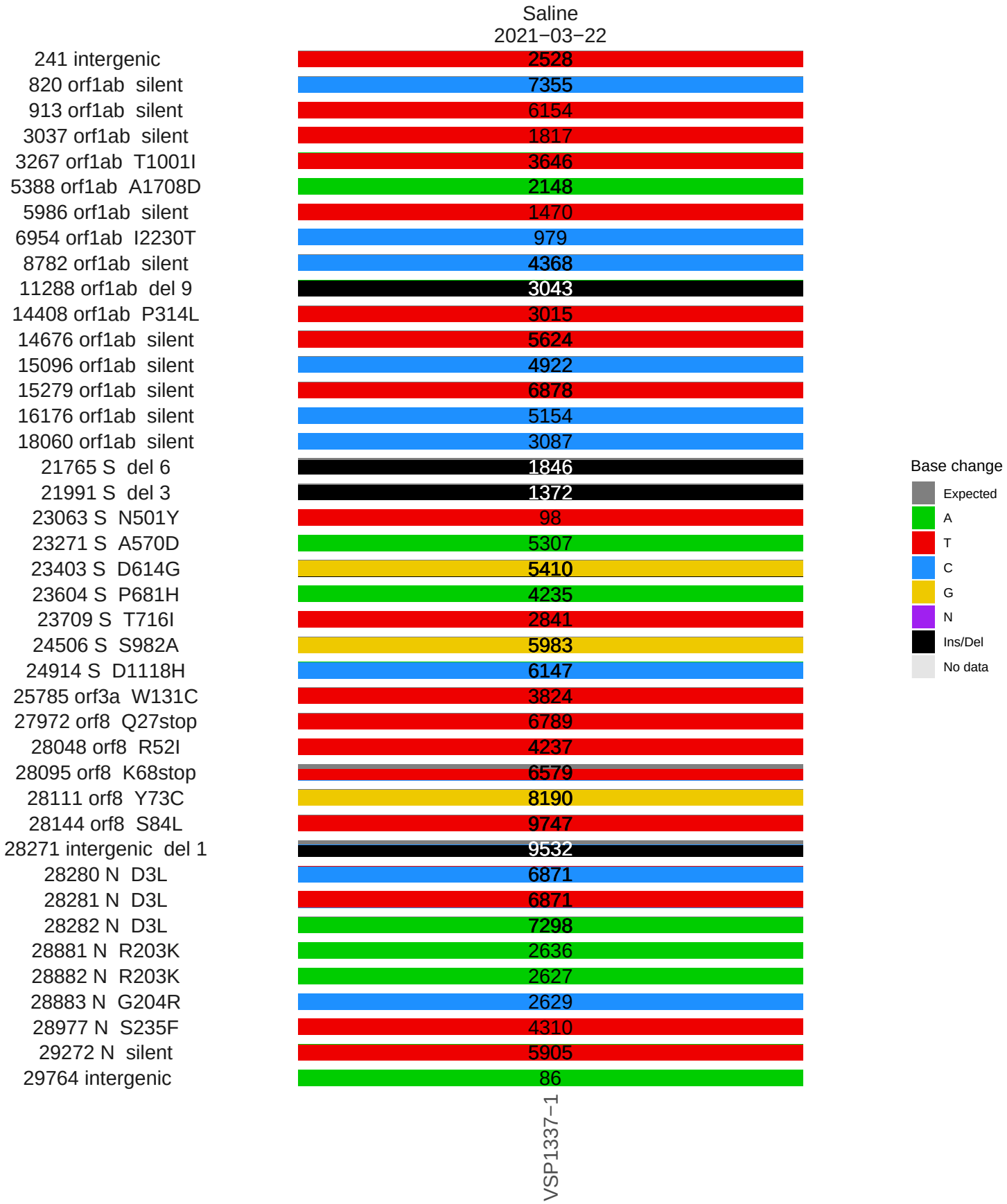
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1337-1	single experiment	NA	Saline	2021-03-22	29.81	B.1.1.7	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.

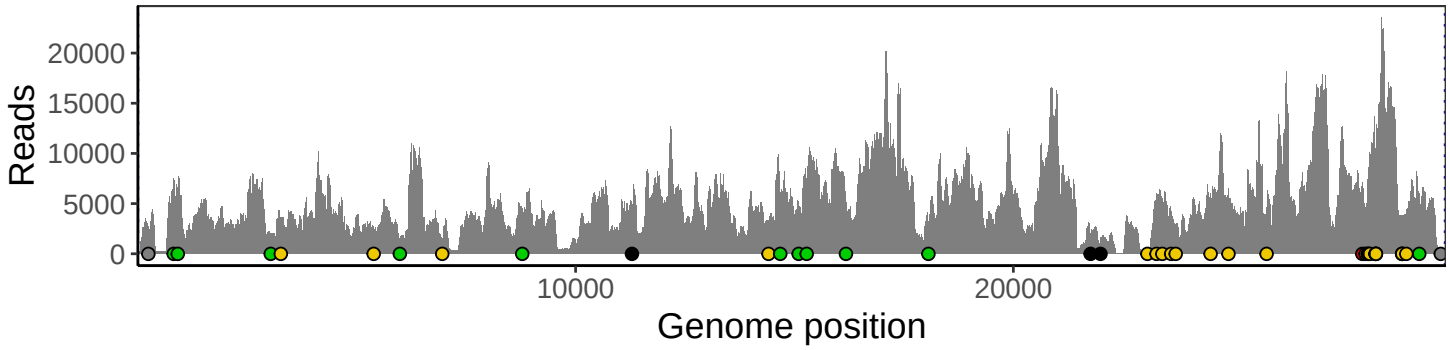



Saline
2021−03−22
241 intergenic 2528
820 orf1ab silent 7355
913 orf1ab silent 6154
3037 orf1ab silent 1817
3267 orf1ab T1001I 3646
5388 orf1ab A1708D 2148
5986 orf1ab silent 1470
6954 orf1ab I2230T 979
8782 orf1ab silent 4368
11288 orf1ab del 9 3043
14408 orf1ab P314L 3015
14676 orf1ab silent 5624
15096 orf1ab silent 4922
15279 orf1ab silent 6878
16176 orf1ab silent 5154
18060 orf1ab silent 3087
21765 S del 6 1846
21991 S del 3 1372
23063 S N501Y 98
23271 S A570D 5307
23403 S D614G 5410
23604 S P681H 4235
23709 S T716I 2841
24506 S S982A 5983
24914 S D1118H 6147
25785 orf3a W131C 3824
27972 orf8 Q27stop 6789
28048 orf8 R52I 4237
28095 orf8 K68stop 6579
28111 orf8 Y73C 8190
28144 orf8 S84L 9747
28271 intergenic del 1 9532
28280 N D3L 6871
28281 N D3L 6871
28282 N D3L 7298
28881 N R203K 2636
28882 N R203K 2627
28883 N G204R 2629
28977 N S235F 4310
29272 N silent 5905
29764 intergenic 86
VSP1337−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

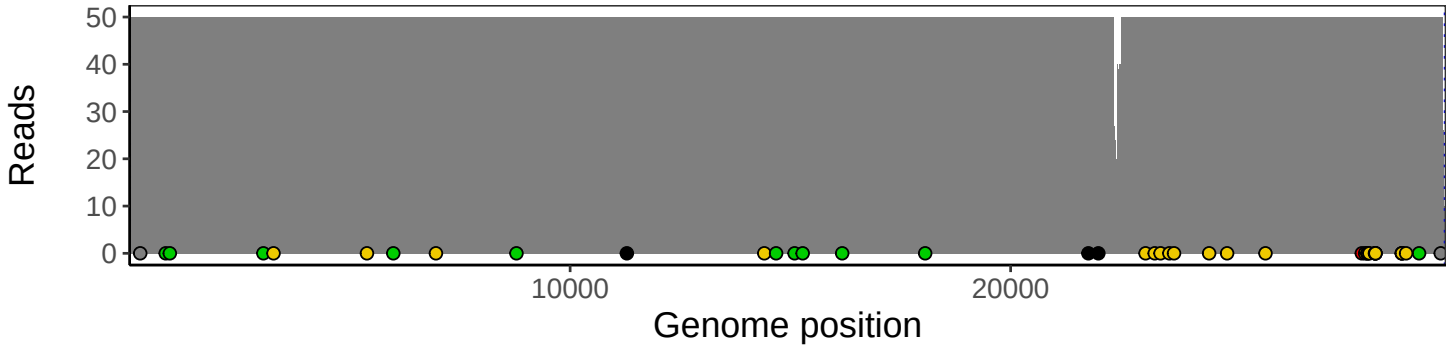
Analyses of individual experiments and composite results

VSP1337-1 | 2021-03-22 | Saline | UPHS-0292 | genomes | single experiment

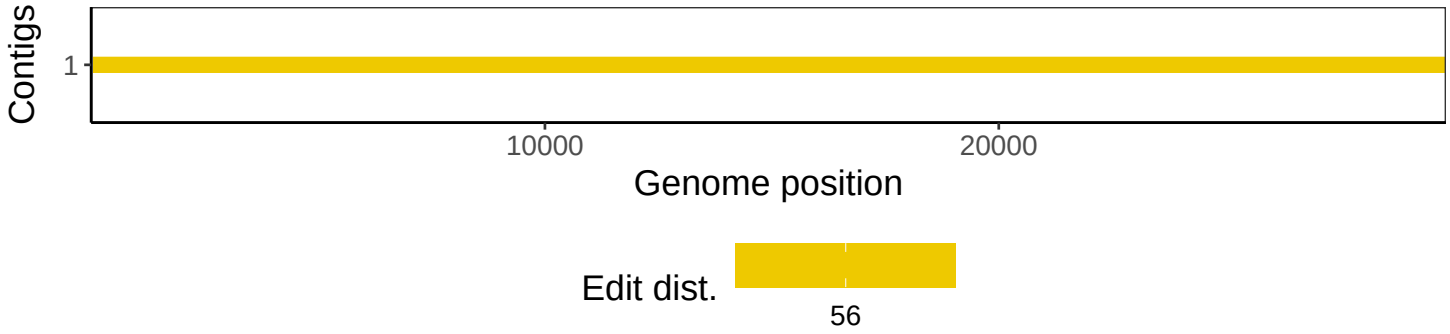
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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