COVID-19 subject UPHS-1413

2021-06-23

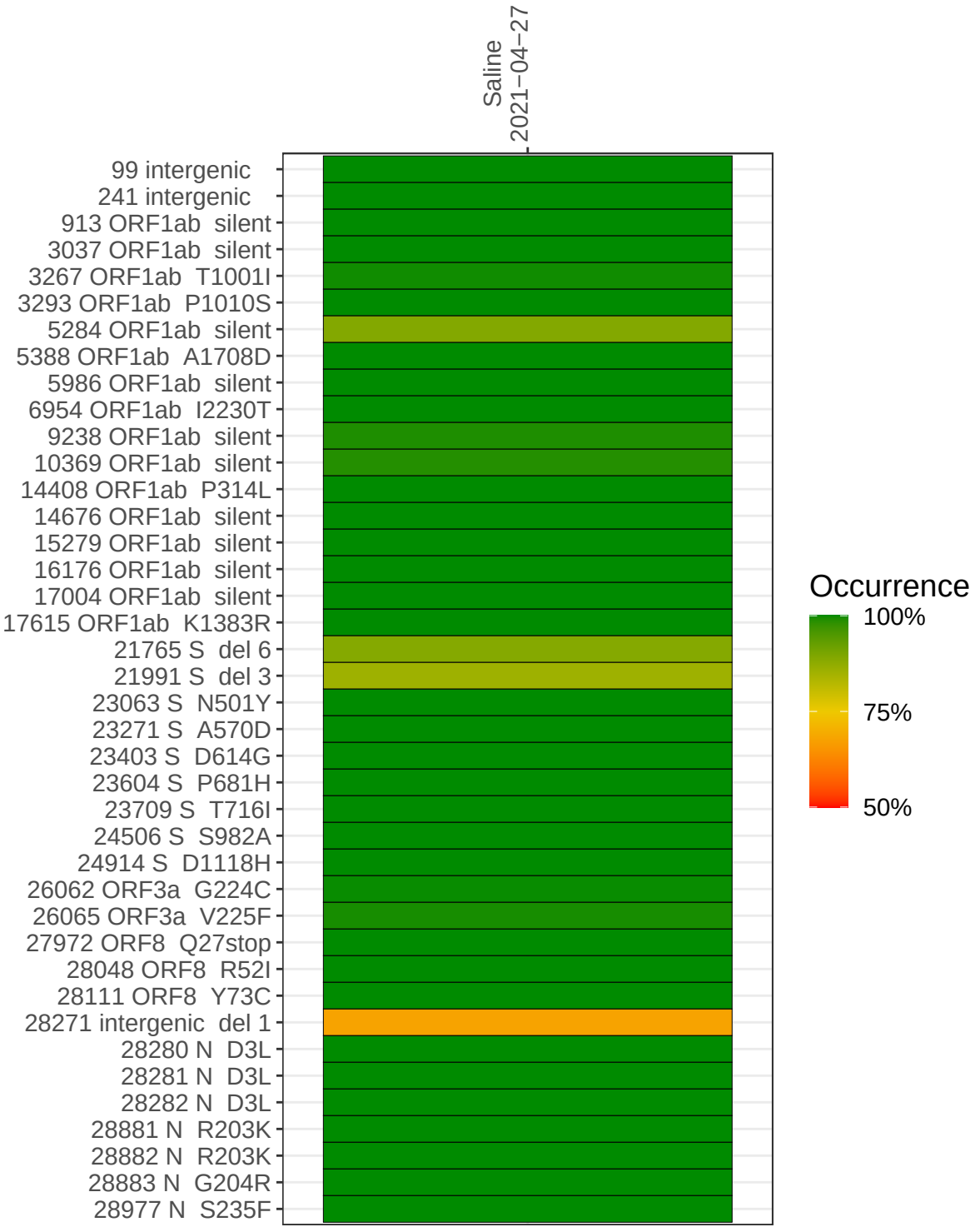
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

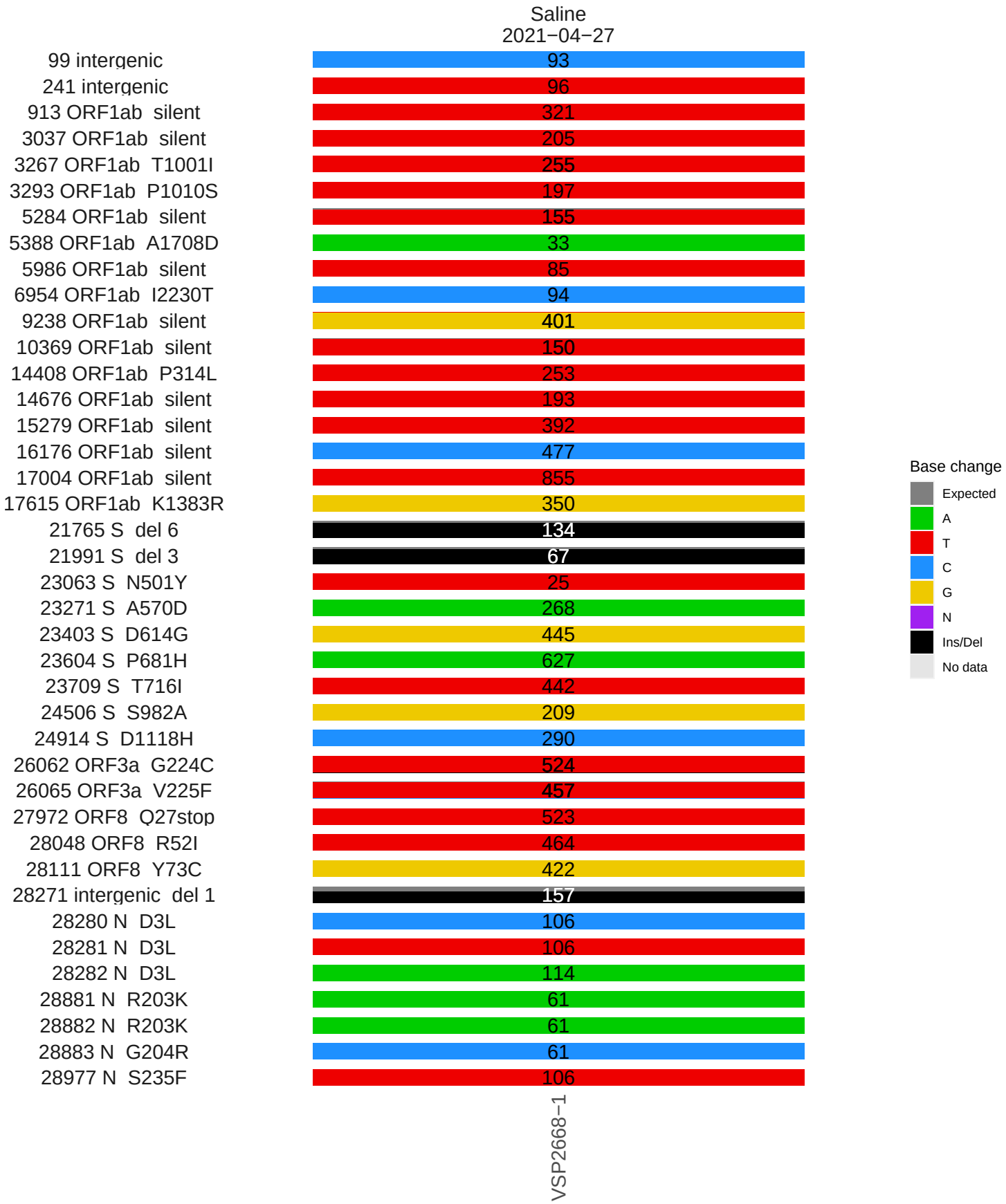
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2668-1	single experiment	NA	Saline	2021-04-27	29.79	B.1.1.7	99.7%	99.6%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

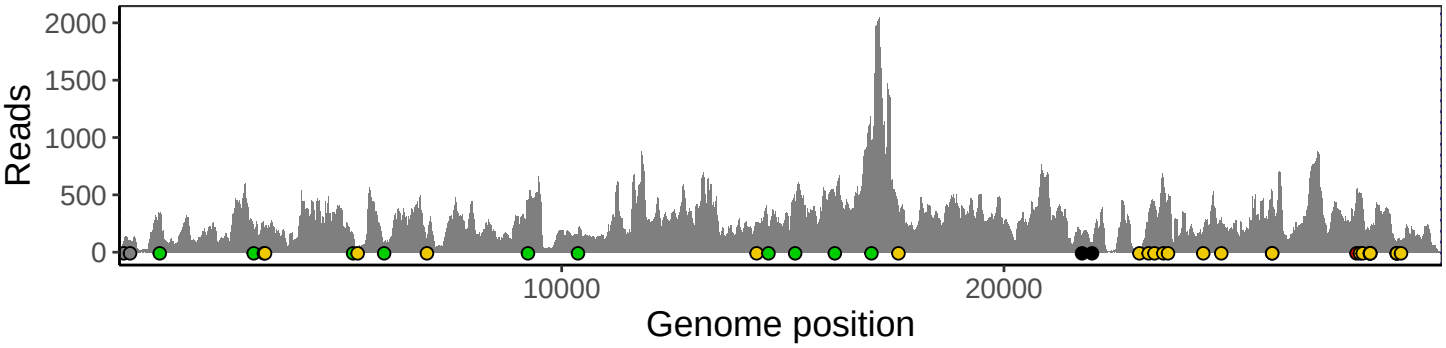



Saline
2021−04−27
99 intergenic 93
241 intergenic 96
913 ORF1ab silent 321
3037 ORF1ab silent 205
3267 ORF1ab T1001I 255
3293 ORF1ab P1010S 197
5284 ORF1ab silent 155
5388 ORF1ab A1708D 33
5986 ORF1ab silent 85
6954 ORF1ab I2230T 94
9238 ORF1ab silent 401
10369 ORF1ab silent 150
14408 ORF1ab P314L 253
14676 ORF1ab silent 193
15279 ORF1ab silent 392
16176 ORF1ab silent 477
17004 ORF1ab silent 855
17615 ORF1ab K1383R 350
21765 S del 6 134
21991 S del 3 67
23063 S N501Y 25
23271 S A570D 268
23403 S D614G 445
23604 S P681H 627
23709 S T716I 442
24506 S S982A 209
24914 S D1118H 290
26062 ORF3a G224C 524
26065 ORF3a V225F 457
27972 ORF8 Q27stop 523
28048 ORF8 R52I 464
28111 ORF8 Y73C 422
28271 intergenic del 1 157
28280 N D3L 106
28281 N D3L 106
28282 N D3L 114
28881 N R203K 61
28882 N R203K 61
28883 N G204R 61
28977 N S235F 106
VSP2668−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

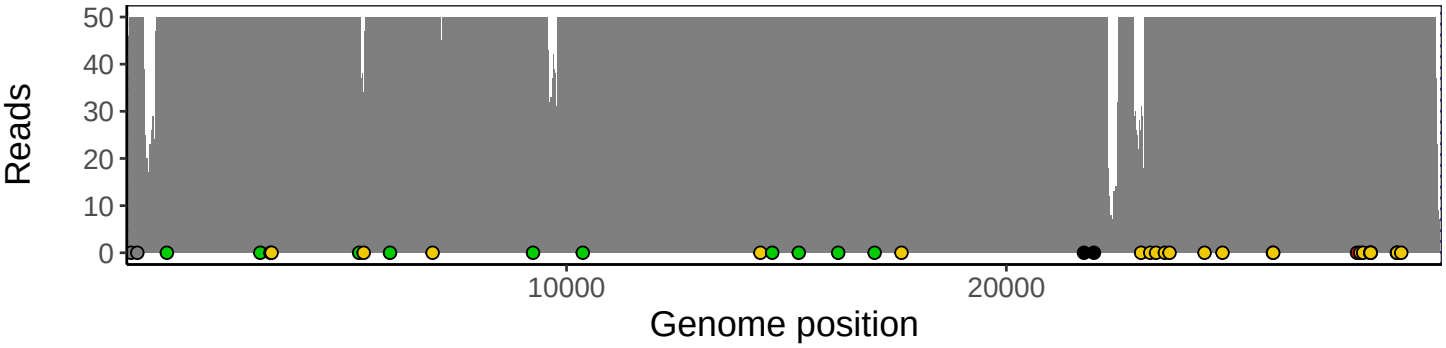
Analyses of individual experiments and composite results

VSP2668-1 | 2021-04-27 | Saline | UPHS-1413 | genomes | single experiment

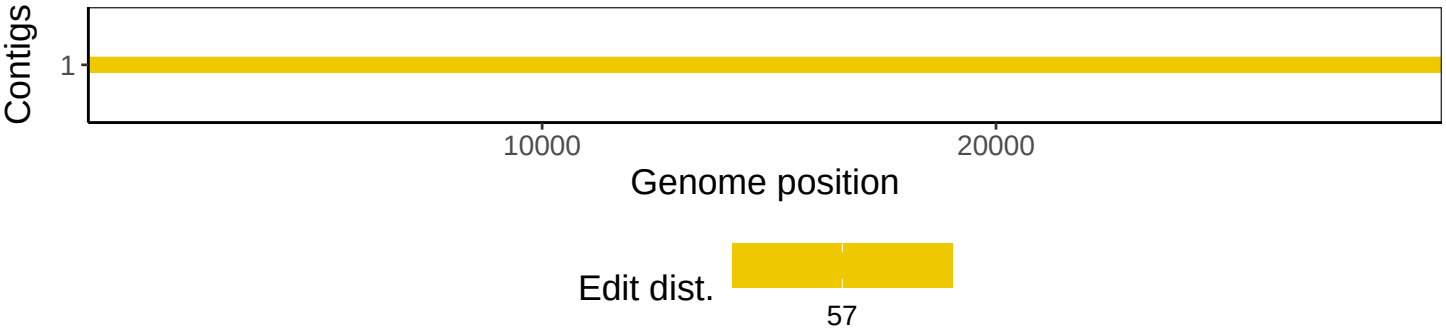
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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