COVID-19 subject UPHS-1231

2021-06-23

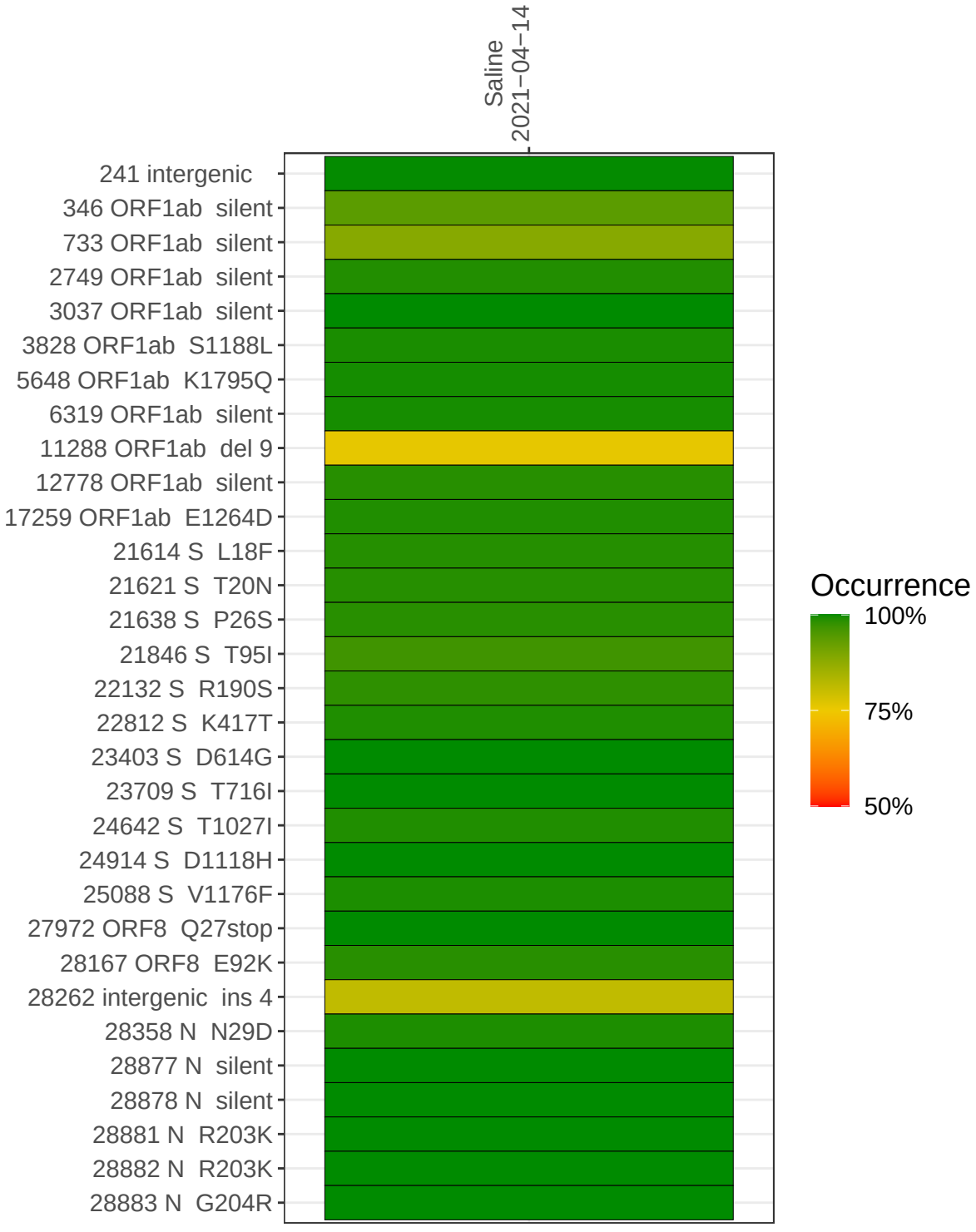
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

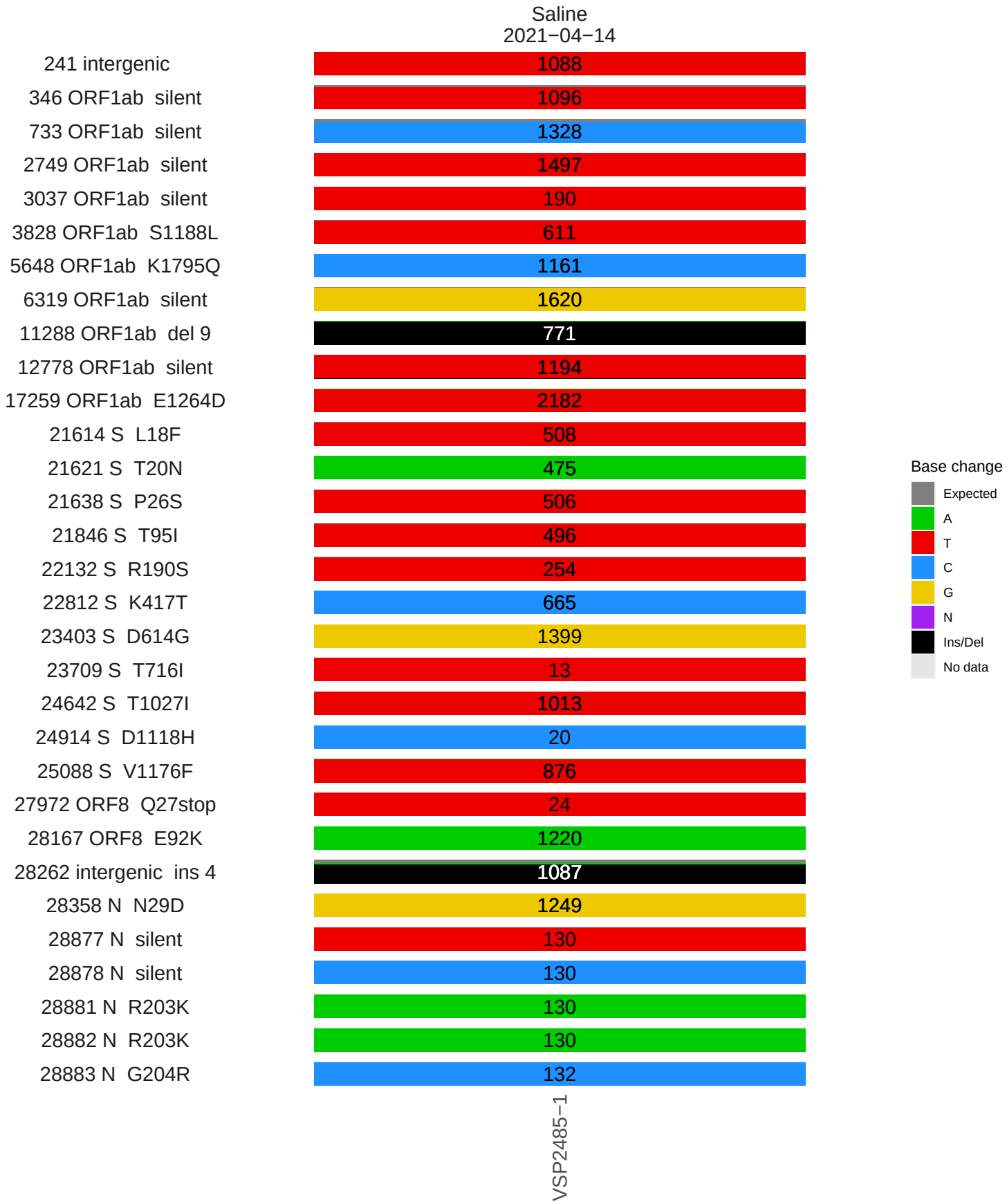
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2485-1	single experiment	NA	Saline	2021-04-14	12.35	P.1	99.2%	95.5%

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.

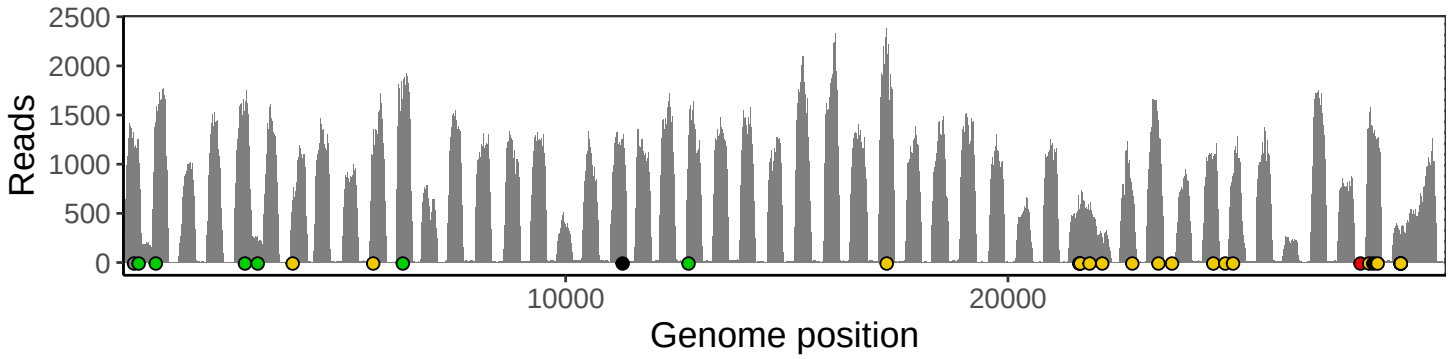



Saline
2021−04−14
241 intergenic
346 ORF1ab silent
733 ORF1ab silent
2749 ORF1ab silent
3037 ORF1ab silent
3828 ORF1ab S1188L
5648 ORF1ab K1795Q
6319 ORF1ab silent
11288 ORF1ab del 9
12778 ORF1ab silent
17259 ORF1ab E1264D
21614 S L18F
21621 S T20N
21638 S P26S
21846 S T95I
22132 S R190S
22812 S K417T
23403 S D614G
23709 S T716I
24642 S T1027I
24914 S D1118H
25088 S V1176F
27972 ORF8 Q27stop
28167 ORF8 E92K
28262 intergenic ins 4
28358 N N29D
28877 N silent
28878 N silent
28881 N R203K
28882 N R203K
28883 N G204R
1088
1096
1328
1497
190
611
1161
1620
771
1194
2182
508
475
506
496
254
665
1399
13
1013
20
876
24
1220
1087
1249
130
130
130
132
VSP2485−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

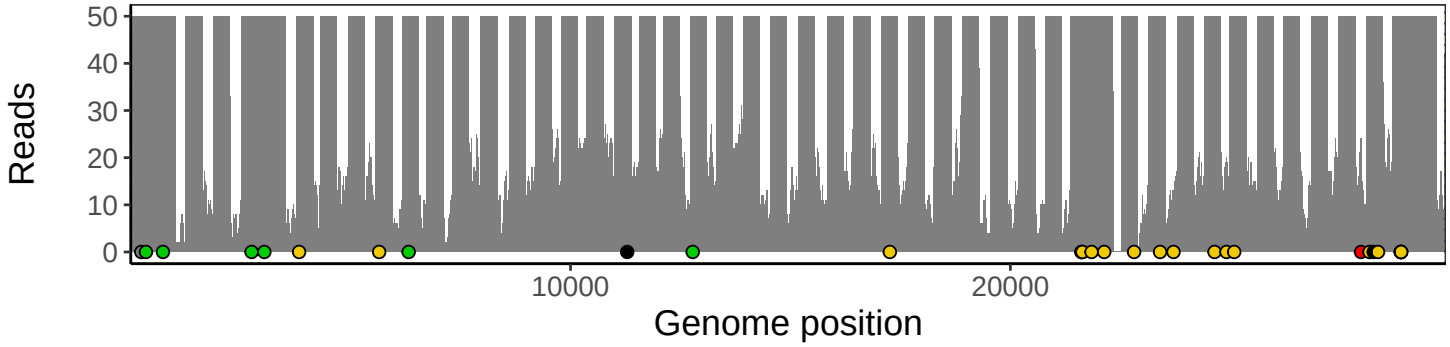
Analyses of individual experiments and composite results

VSP2485-1 | 2021-04-14 | Saline | UPHS-1231 | genomes | single experiment

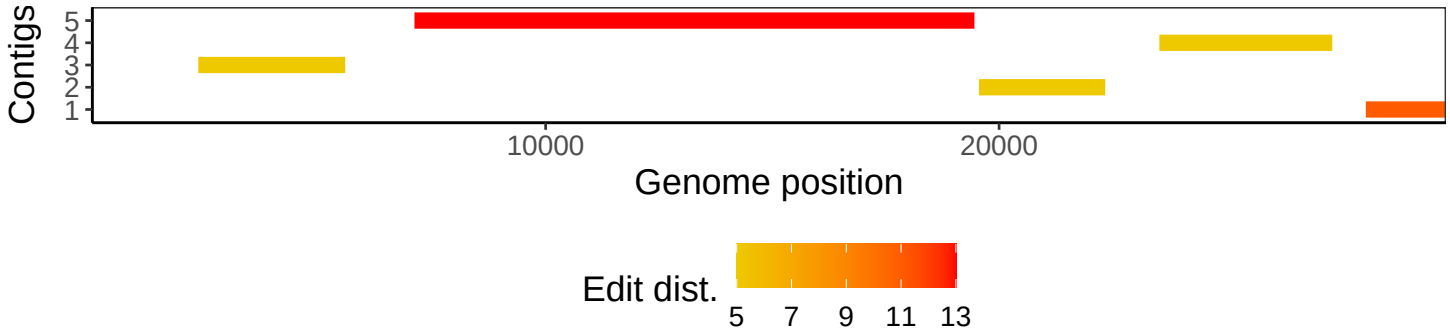
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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