COVID-19 subject UPHS-1517

2021-06-23

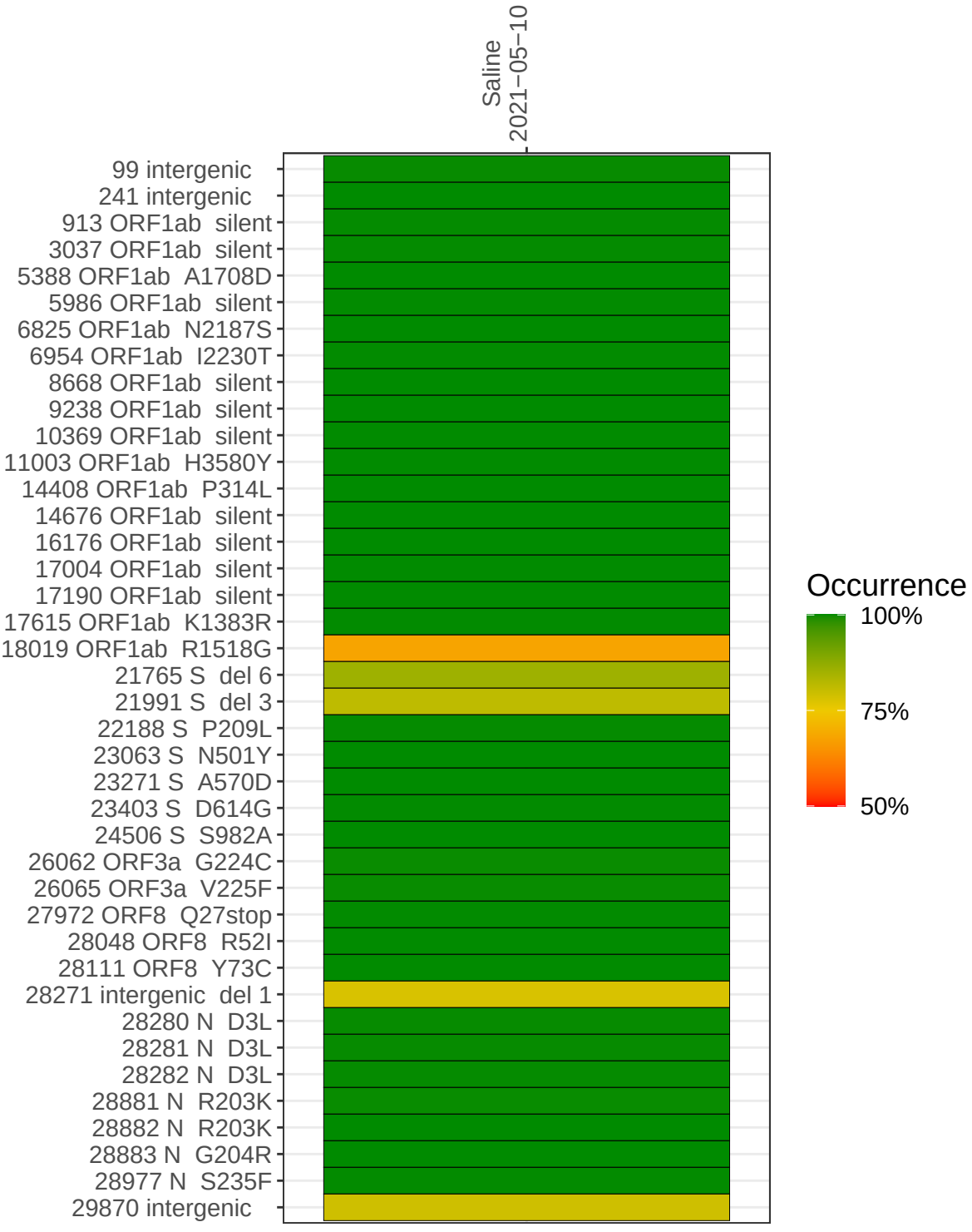
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

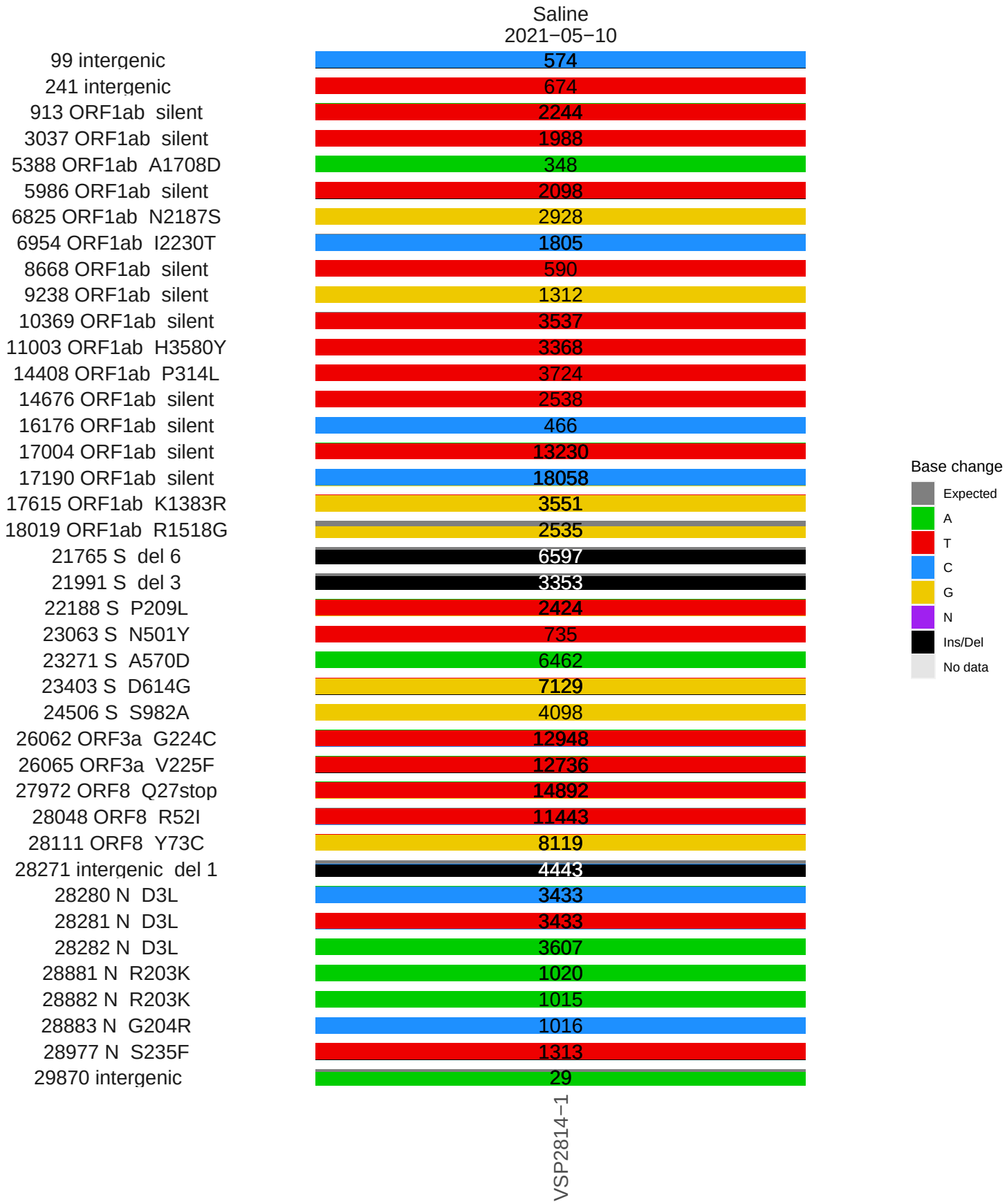
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2814-1	single experiment	NA	Saline	2021-05-10	3.22	NA	74.4%	74.1%

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.

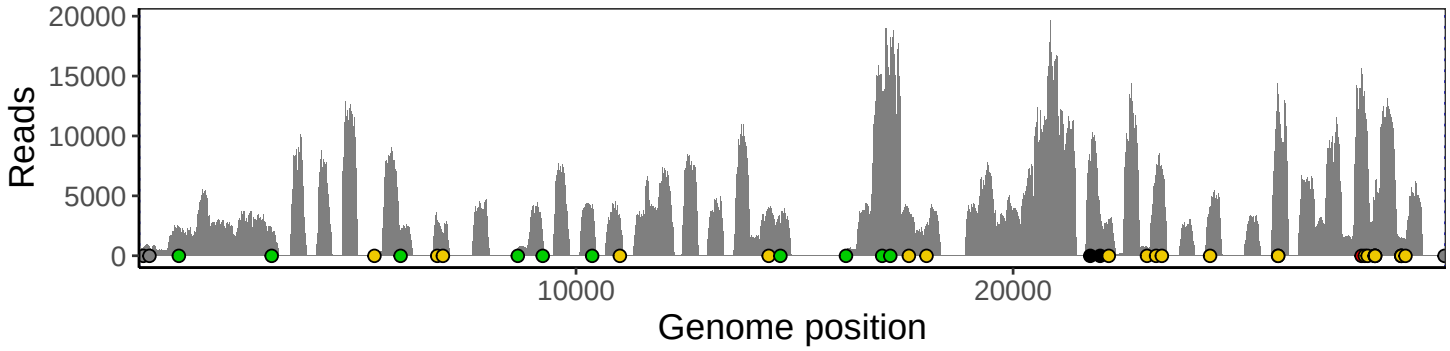



Saline
2021−05−10
99 intergenic
241 intergenic
913 ORF1ab silent
3037 ORF1ab silent
5388 ORF1ab A1708D
5986 ORF1ab silent
6825 ORF1ab N2187S
6954 ORF1ab I2230T
8668 ORF1ab silent
9238 ORF1ab silent
10369 ORF1ab silent
11003 ORF1ab H3580Y
14408 ORF1ab P314L
14676 ORF1ab silent
16176 ORF1ab silent
17004 ORF1ab silent
17190 ORF1ab silent
17615 ORF1ab K1383R
18019 ORF1ab R1518G
21765 S del 6
21991 S del 3
22188 S P209L
23063 S N501Y
23271 S A570D
23403 S D614G
24506 S S982A
26062 ORF3a G224C
26065 ORF3a V225F
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29870 intergenic
574
674
2244
1988
348
2098
2928
1805
590
1312
3537
3368
3724
2538
466
13230
18058
3551
2535
6597
3353
2424
735
6462
7129
4098
12948
12736
14892
11443
8119
4443
3433
3433
3607
1020
1015
1016
1313
29
VSP2814−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

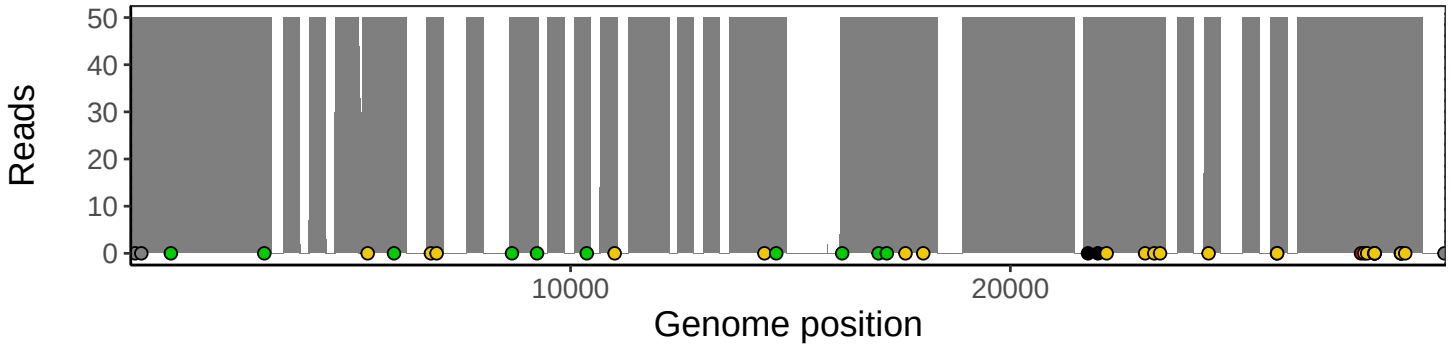
Analyses of individual experiments and composite results

VSP2814-1 | 2021-05-10 | Saline | UPHS-1517 | genomes | single experiment

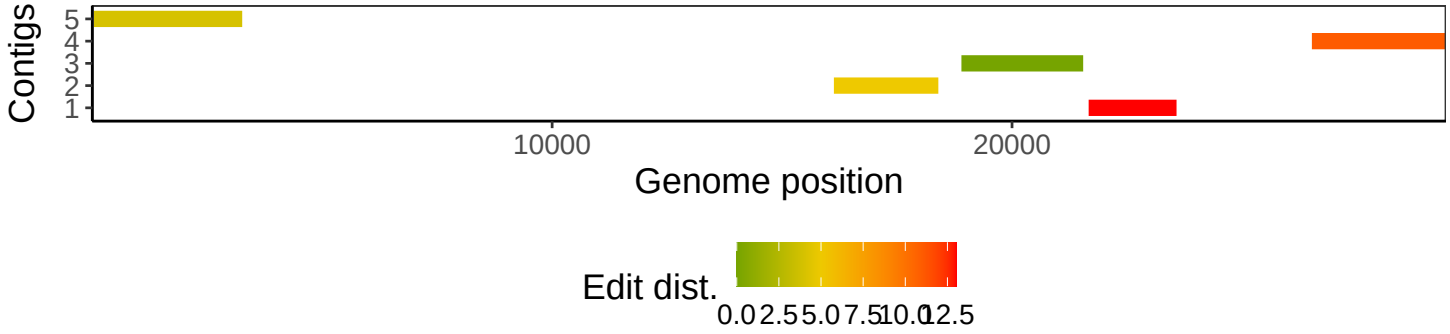
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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