COVID-19 subject UPHS-1048

2021-06-23

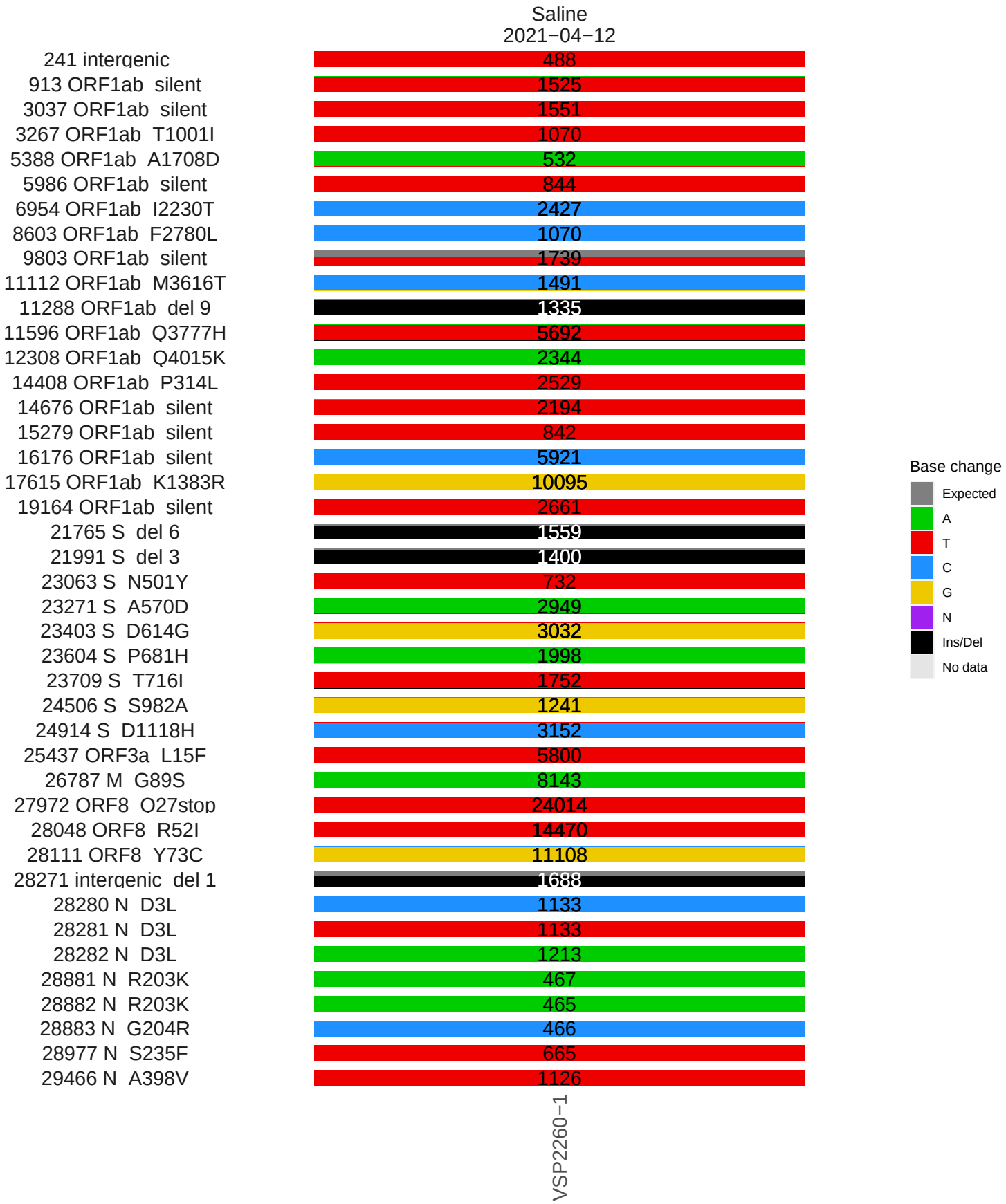
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2260-1	single experiment	NA	Saline	2021-04-12	25.98	B.1.1.7	98.4%	98.4%

Variants shared across samples

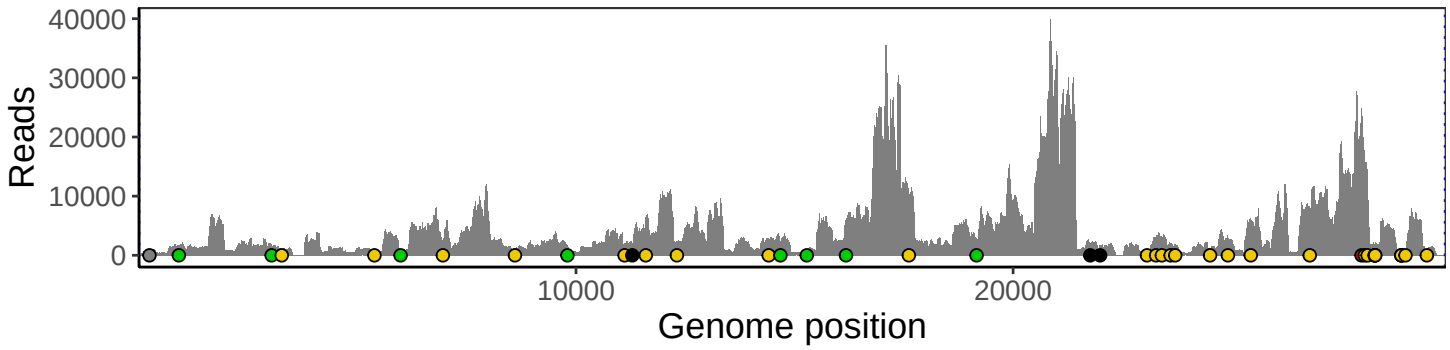
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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
2021−04−12
241 intergenic 488
913 ORF1ab silent 1525
3037 ORF1ab silent 1551
3267 ORF1ab T1001I 1070
5388 ORF1ab A1708D 532
5986 ORF1ab silent 844
6954 ORF1ab I2230T 2427
8603 ORF1ab F2780L 1070
9803 ORF1ab silent 1739
11112 ORF1ab M3616T 1491
11288 ORF1ab del 9 1335
11596 ORF1ab Q3777H 5692
12308 ORF1ab Q4015K 2344
14408 ORF1ab P314L 2529
14676 ORF1ab silent 2194
15279 ORF1ab silent 842
16176 ORF1ab silent 5921
17615 ORF1ab K1383R 10095
19164 ORF1ab silent 2661
21765 S del 6 1559
21991 S del 3 1400
23063 S N501Y 732
23271 S A570D 2949
23403 S D614G 3032
23604 S P681H 1998
23709 S T716I 1752
24506 S S982A 1241
24914 S D1118H 3152
25437 ORF3a L15F 5800
26787 M G89S 8143
27972 ORF8 Q27stop 24014
28048 ORF8 R52I 14470
28111 ORF8 Y73C 11108
28271 intergenic del 1 1688
28280 N D3L 1133
28281 N D3L 1133
28282 N D3L 1213
28881 N R203K 467
28882 N R203K 465
28883 N G204R 466
28977 N S235F 665
29466 N A398V 1126
VSP2260−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

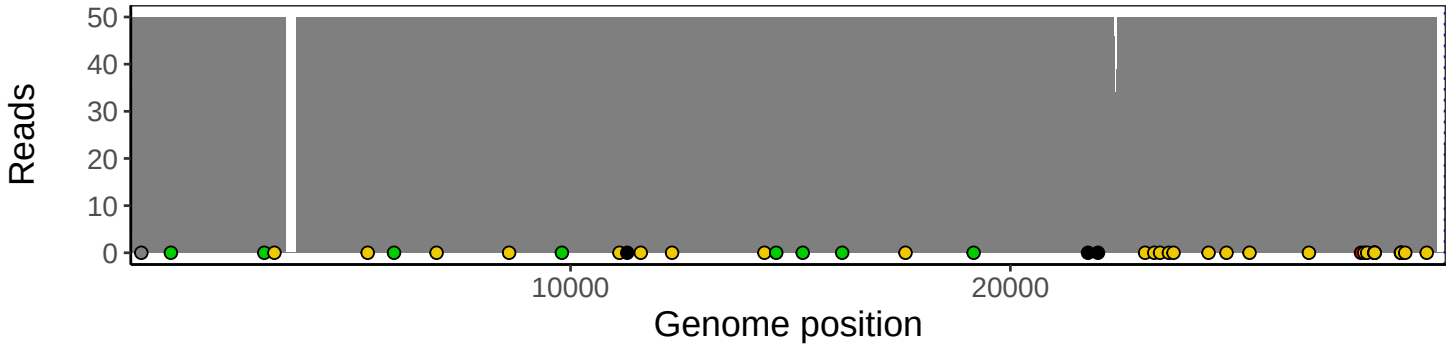
Analyses of individual experiments and composite results

VSP2260-1 | 2021-04-12 | Saline | UPHS-1048 | genomes | single experiment

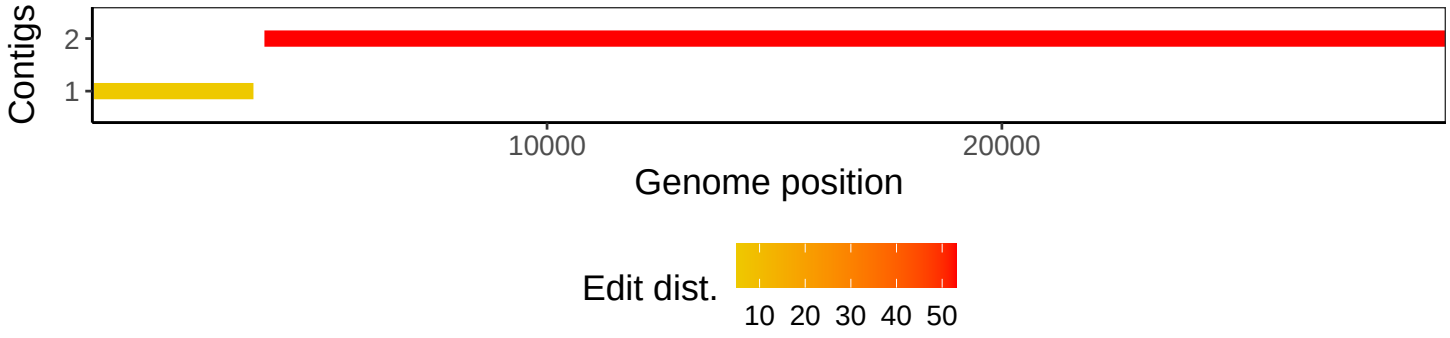
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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