COVID-19 subject UPHS-1520

2021-06-23

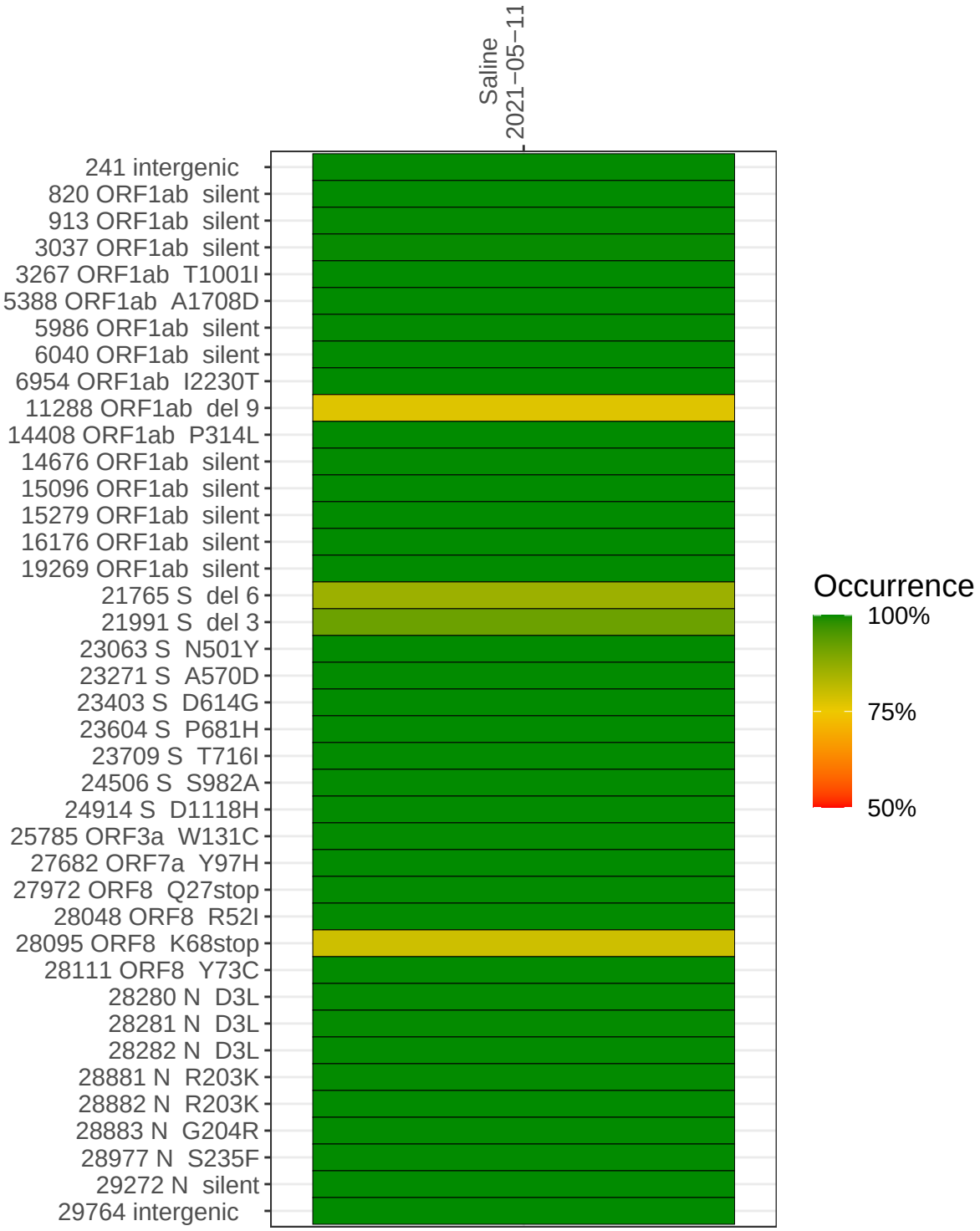
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

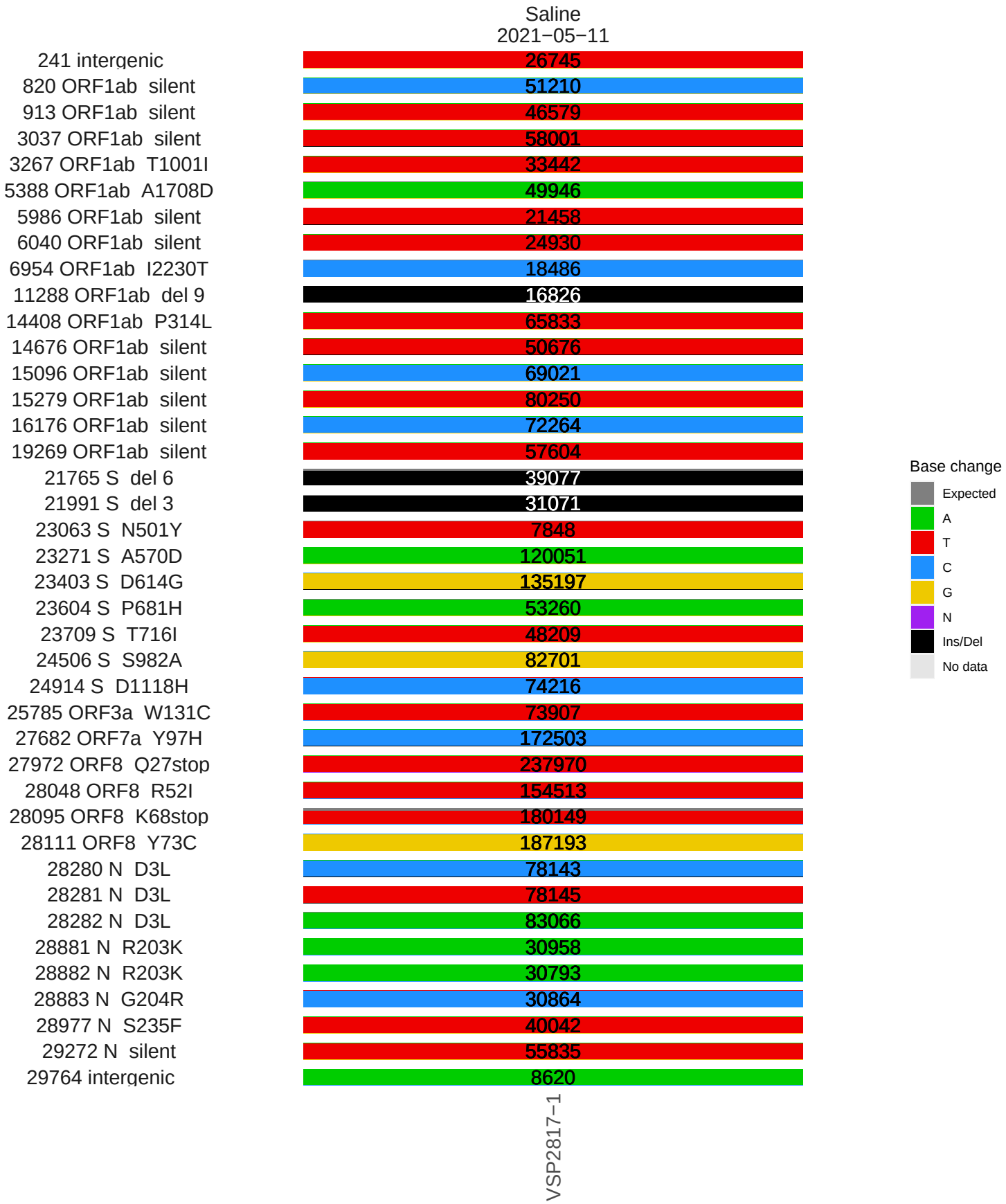
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2817-1	single experiment	NA	Saline	2021-05-11	19.18	B.1.1.7	99.2%	99.1%

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.

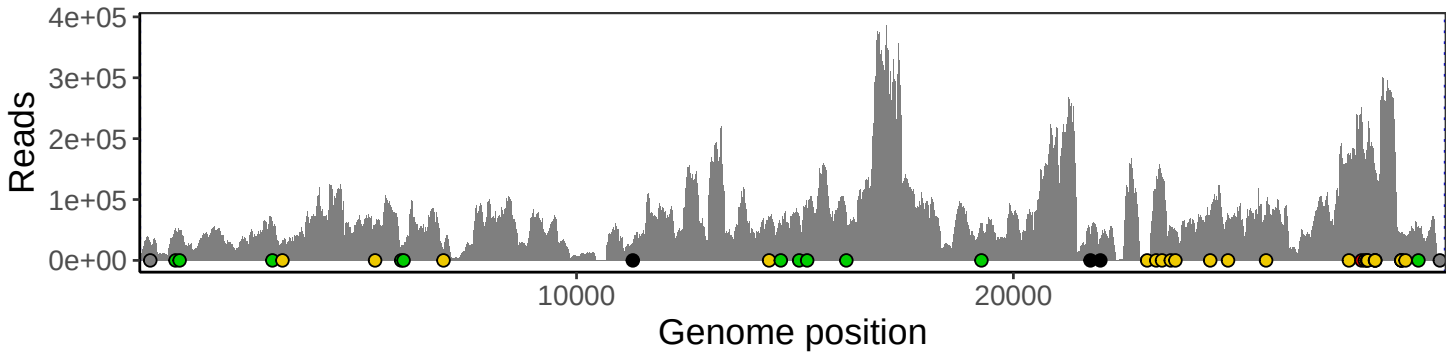



Saline
2021−05−11
241 intergenic 26745
820 ORF1ab silent 51210
913 ORF1ab silent 46579
3037 ORF1ab silent 58001
3267 ORF1ab T1001I 33442
5388 ORF1ab A1708D 49946
5986 ORF1ab silent 21458
6040 ORF1ab silent 24930
6954 ORF1ab I2230T 18486
11288 ORF1ab del 9 16826
14408 ORF1ab P314L 65833
14676 ORF1ab silent 50676
15096 ORF1ab silent 69021
15279 ORF1ab silent 80250
16176 ORF1ab silent 72264
19269 ORF1ab silent 57604
21765 S del 6 39077
21991 S del 3 31071
23063 S N501Y 7848
23271 S A570D 120051
23403 S D614G 135197
23604 S P681H 53260
23709 S T716I 48209
24506 S S982A 82701
24914 S D1118H 74216
25785 ORF3a W131C 73907
27682 ORF7a Y97H 172503
27972 ORF8 Q27stop 237970
28048 ORF8 R52I 154513
28095 ORF8 K68stop 180149
28111 ORF8 Y73C 187193
28280 N D3L 78143
28281 N D3L 78145
28282 N D3L 83066
28881 N R203K 30958
28882 N R203K 30793
28883 N G204R 30864
28977 N S235F 40042
29272 N silent 55835
29764 intergenic 8620
VSP2817−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

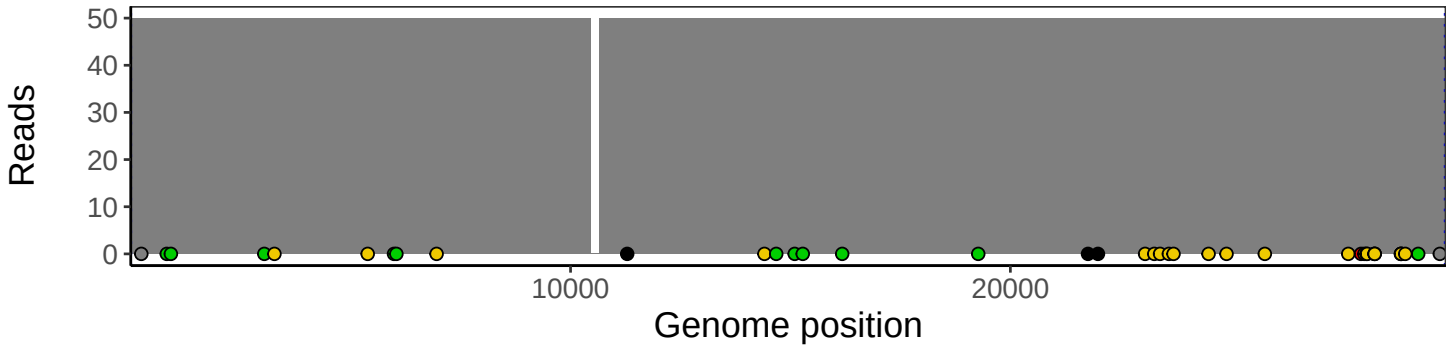
Analyses of individual experiments and composite results

VSP2817-1 | 2021-05-11 | Saline | UPHS-1520 | genomes | single experiment

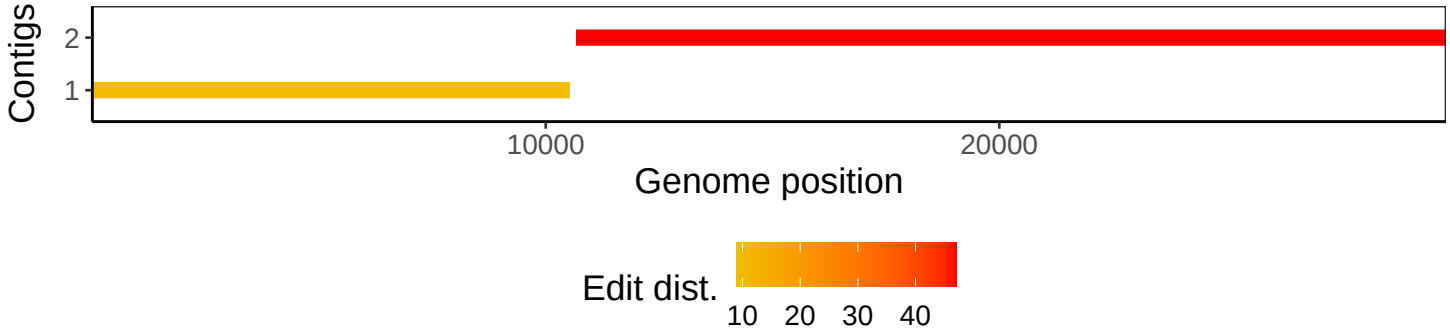
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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