COVID-19 subject UPHS-1580

2021-06-23

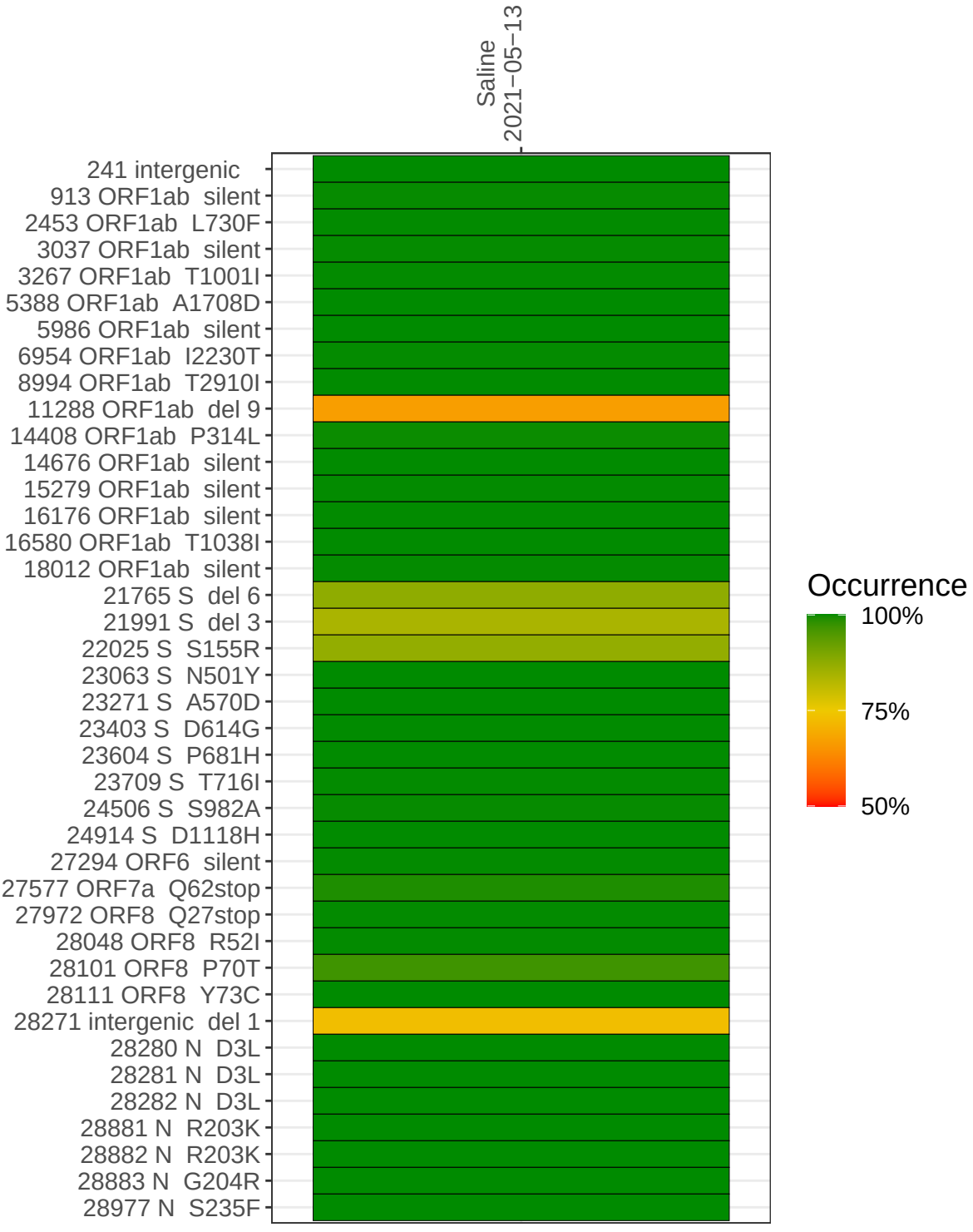
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

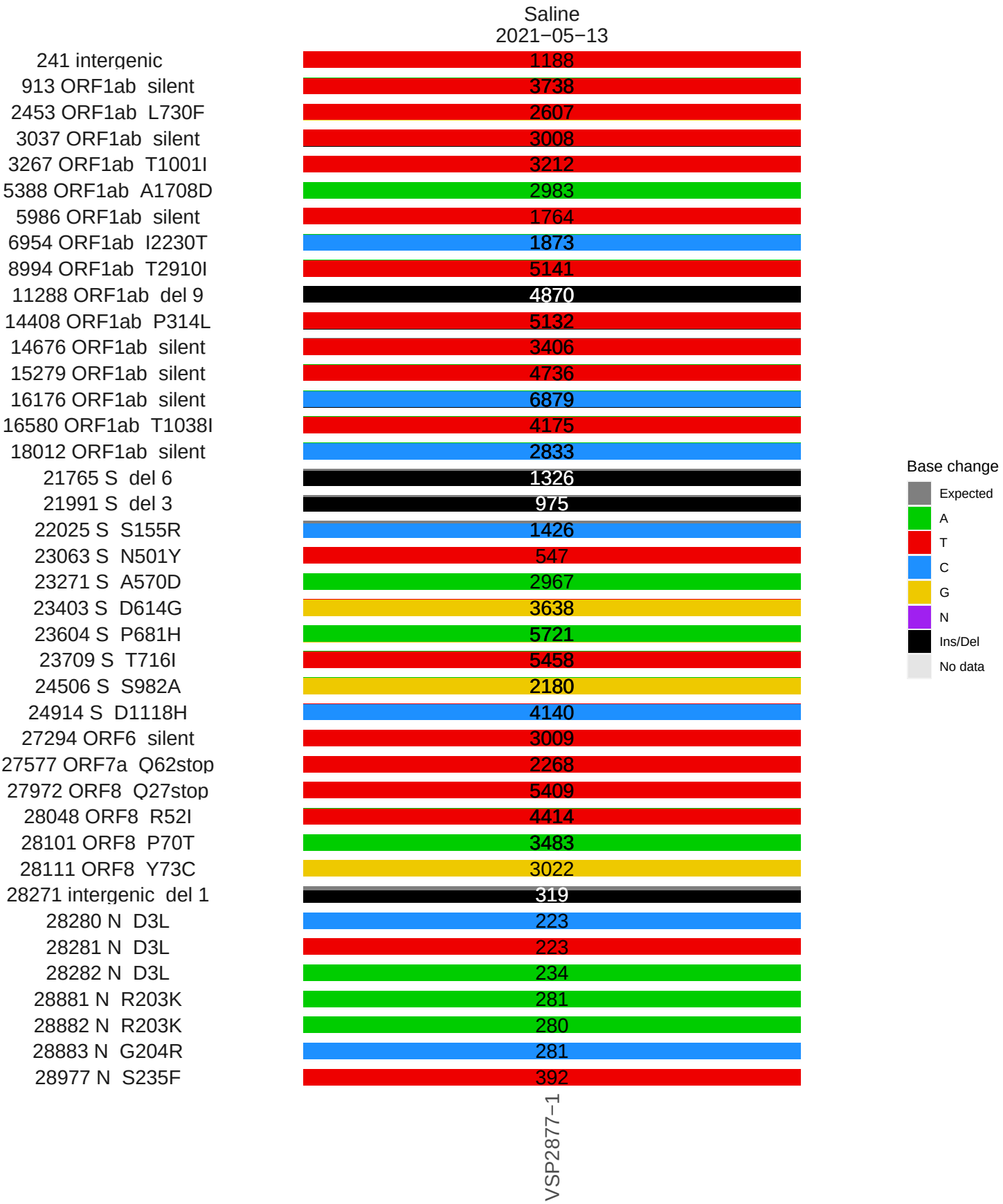
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2877-1	single experiment	NA	Saline	2021-05-13	29.87	B.1.1.7	100.0%	99.8%

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.

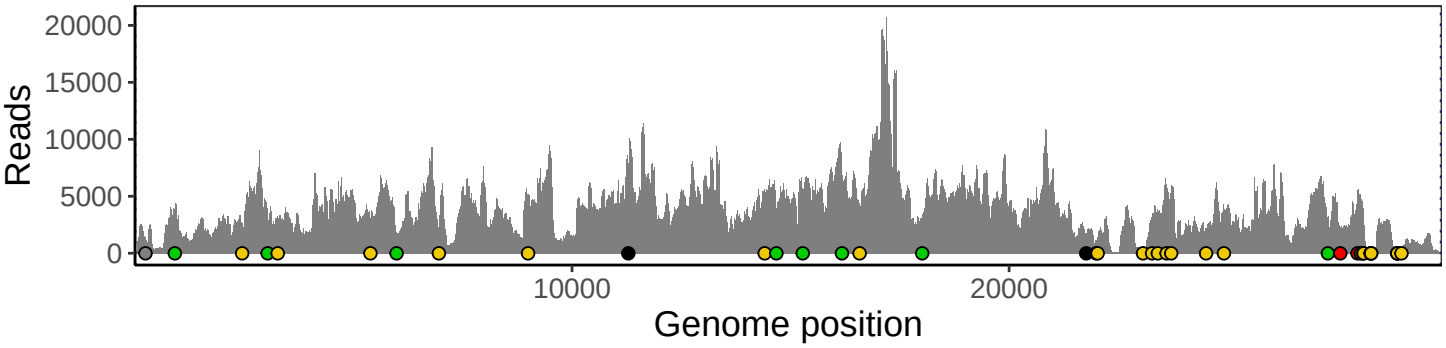



Saline
2021−05−13
241 intergenic 1188
913 ORF1ab silent 3738
2453 ORF1ab L730F 2607
3037 ORF1ab silent 3008
3267 ORF1ab T1001I 3212
5388 ORF1ab A1708D 2983
5986 ORF1ab silent 1764
6954 ORF1ab I2230T 1873
8994 ORF1ab T2910I 5141
11288 ORF1ab del 9 4870
14408 ORF1ab P314L 5132
14676 ORF1ab silent 3406
15279 ORF1ab silent 4736
16176 ORF1ab silent 6879
16580 ORF1ab T1038I 4175
18012 ORF1ab silent 2833
21765 S del 6 1326
21991 S del 3 975
22025 S S155R 1426
23063 S N501Y 547
23271 S A570D 2967
23403 S D614G 3638
23604 S P681H 5721
23709 S T716I 5458
24506 S S982A 2180
24914 S D1118H 4140
27294 ORF6 silent 3009
27577 ORF7a Q62stop 2268
27972 ORF8 Q27stop 5409
28048 ORF8 R52I 4414
28101 ORF8 P70T 3483
28111 ORF8 Y73C 3022
28271 intergenic del 1 319
28280 N D3L 223
28281 N D3L 223
28282 N D3L 234
28881 N R203K 281
28882 N R203K 280
28883 N G204R 281
28977 N S235F 392
VSP2877−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

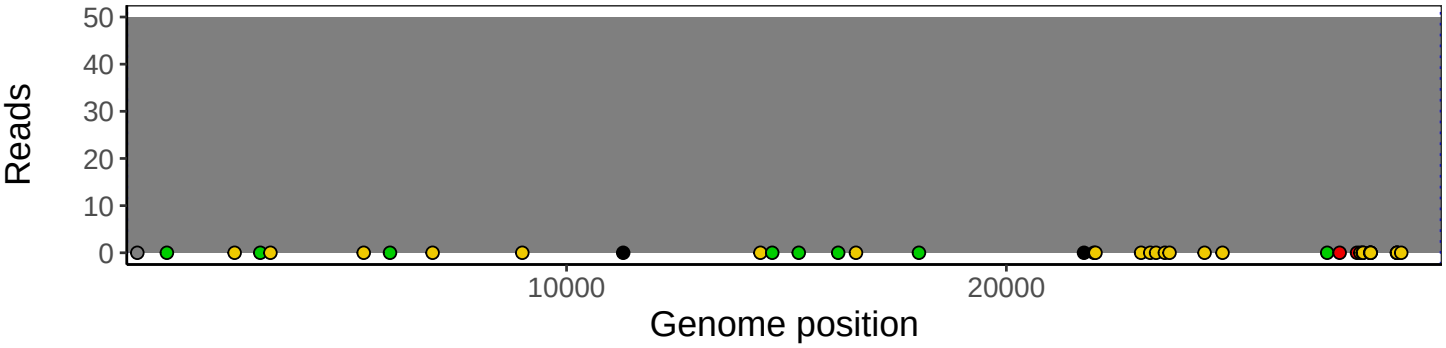
Analyses of individual experiments and composite results

VSP2877-1 | 2021-05-13 | Saline | UPHS-1580 | genomes | single experiment

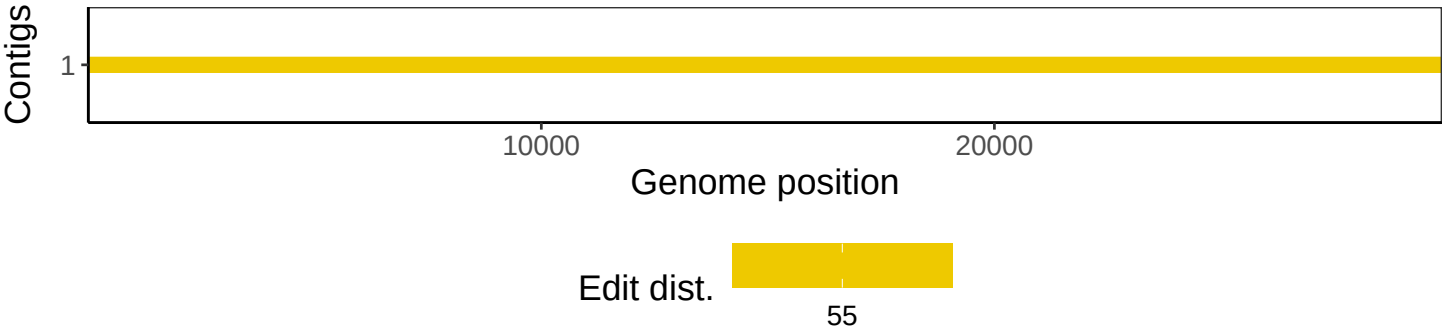
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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