COVID-19 subject UPHS-1641

2021-06-23

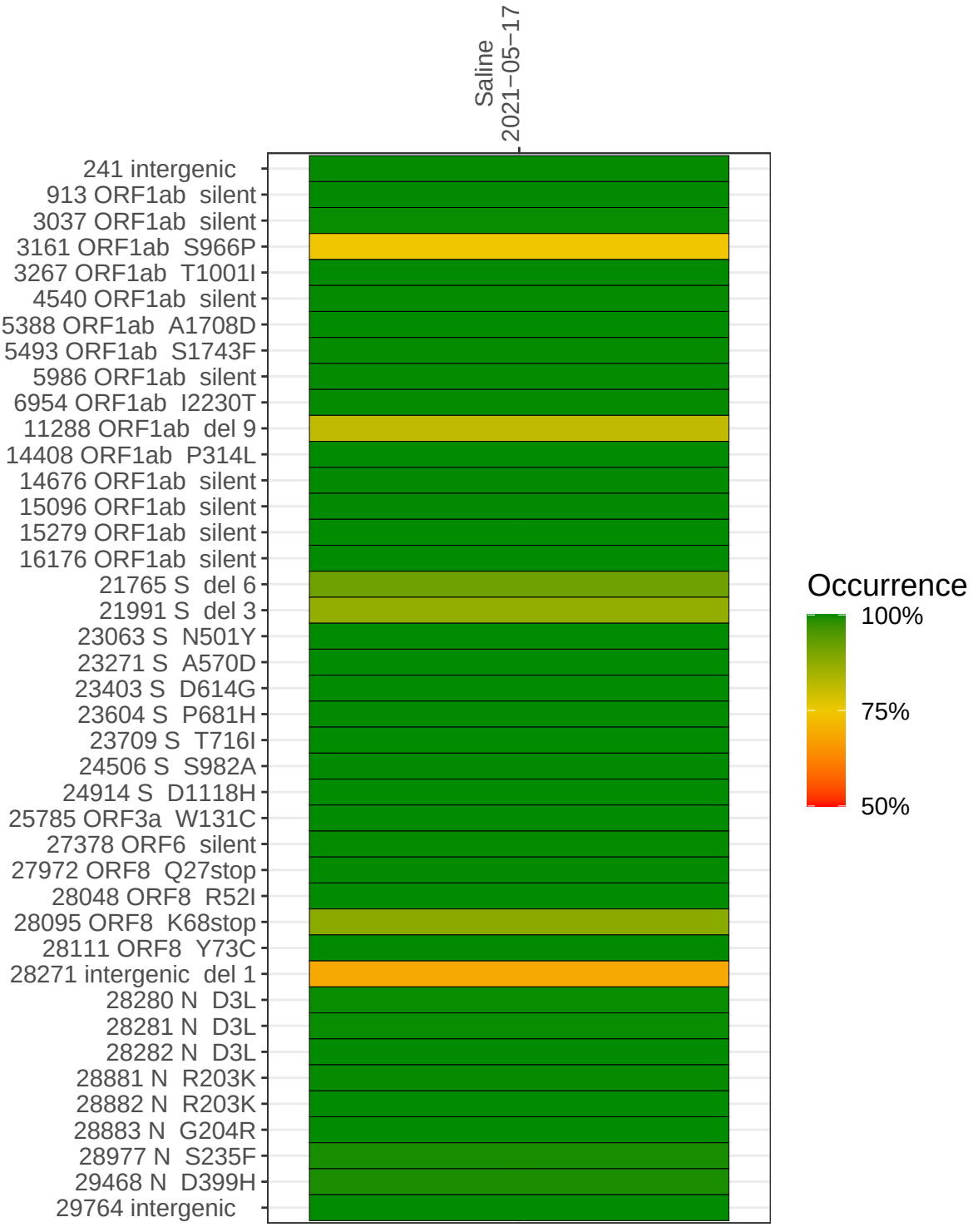
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

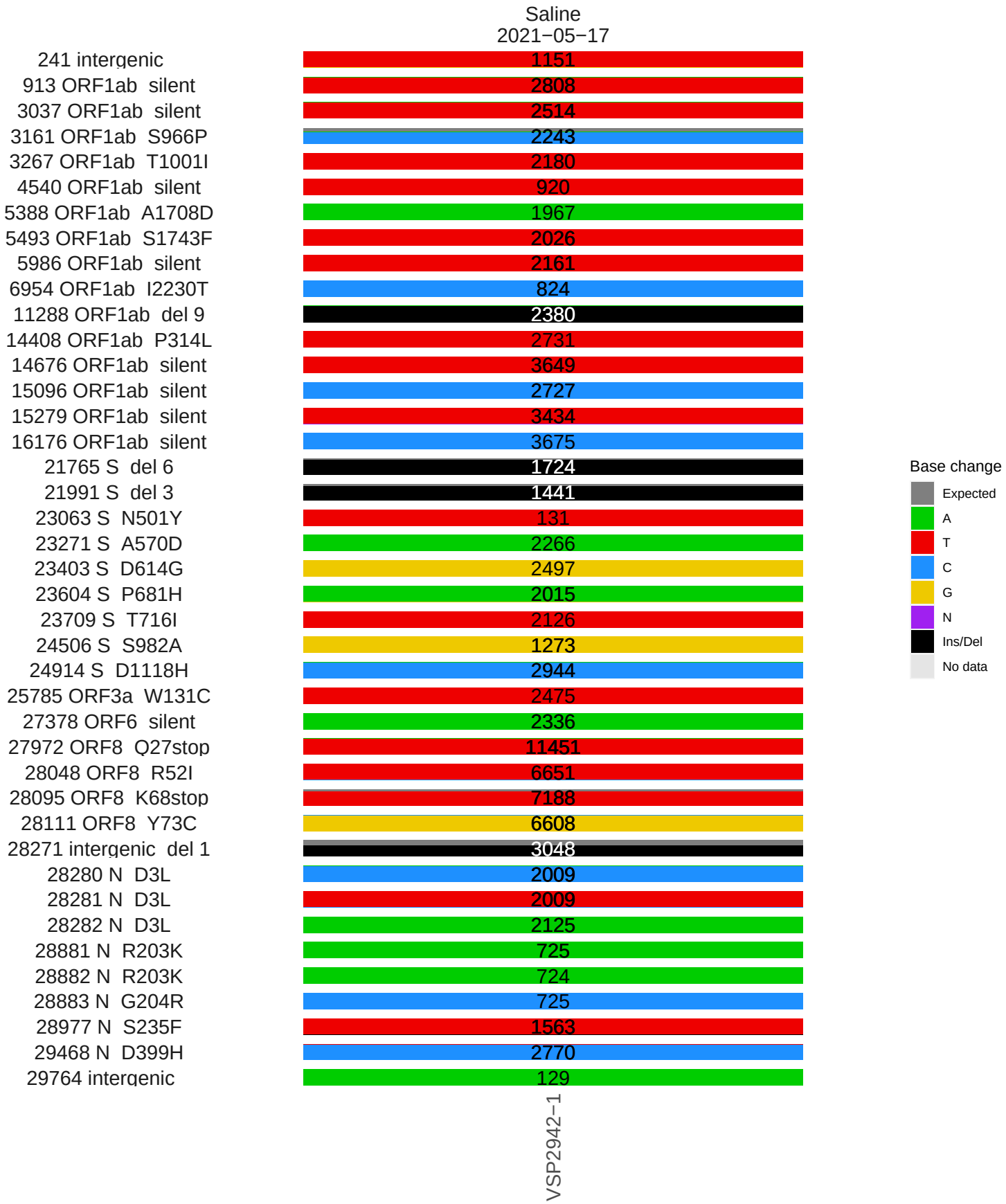
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2942-1	single experiment	NA	Saline	2021-05-17	29.81	B.1.1.7	99.9%	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.

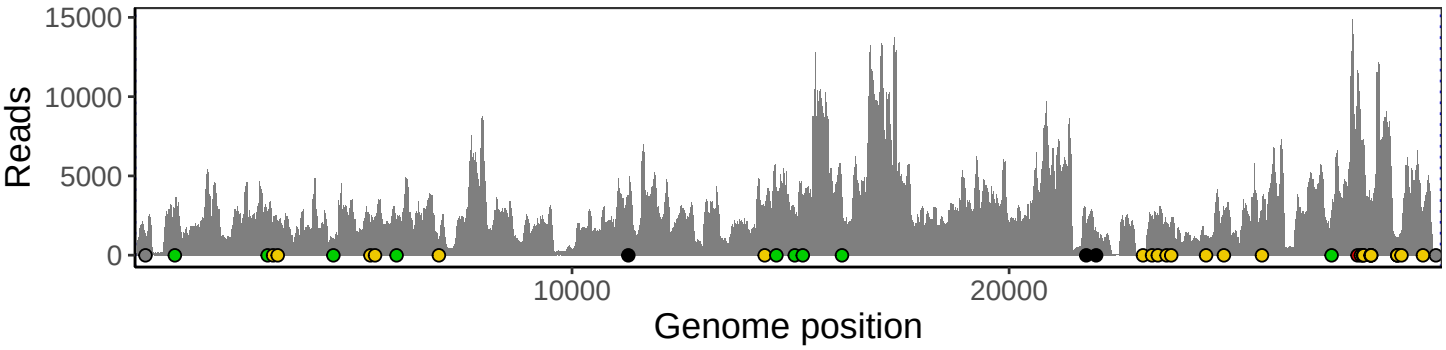



Saline
2021−05−17
241 intergenic 1151
913 ORF1ab silent 2808
3037 ORF1ab silent 2514
3161 ORF1ab S966P 2243
3267 ORF1ab T1001I 2180
4540 ORF1ab silent 920
5388 ORF1ab A1708D 1967
5493 ORF1ab S1743F 2026
5986 ORF1ab silent 2161
6954 ORF1ab I2230T 824
11288 ORF1ab del 9 2380
14408 ORF1ab P314L 2731
14676 ORF1ab silent 3649
15096 ORF1ab silent 2727
15279 ORF1ab silent 3434
16176 ORF1ab silent 3675
21765 S del 6 1724
21991 S del 3 1441
23063 S N501Y 131
23271 S A570D 2266
23403 S D614G 2497
23604 S P681H 2015
23709 S T716I 2126
24506 S S982A 1273
24914 S D1118H 2944
25785 ORF3a W131C 2475
27378 ORF6 silent 2336
27972 ORF8 Q27stop 11451
28048 ORF8 R52I 6651
28095 ORF8 K68stop 7188
28111 ORF8 Y73C 6608
28271 intergenic del 1 3048
28280 N D3L 2009
28281 N D3L 2009
28282 N D3L 2125
28881 N R203K 725
28882 N R203K 724
28883 N G204R 725
28977 N S235F 1563
29468 N D399H 2770
29764 intergenic 129
VSP2942−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

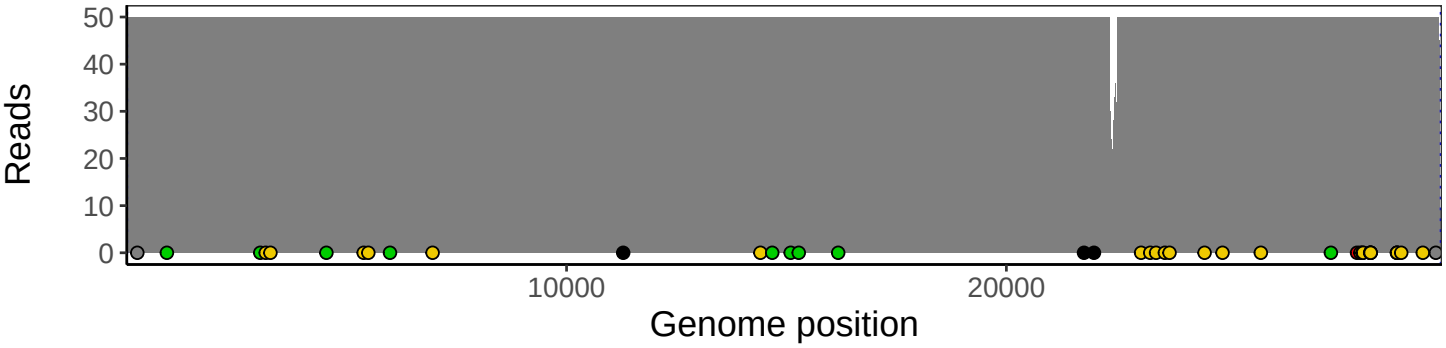
Analyses of individual experiments and composite results

VSP2942-1 | 2021-05-17 | Saline | UPHS-1641 | genomes | single experiment

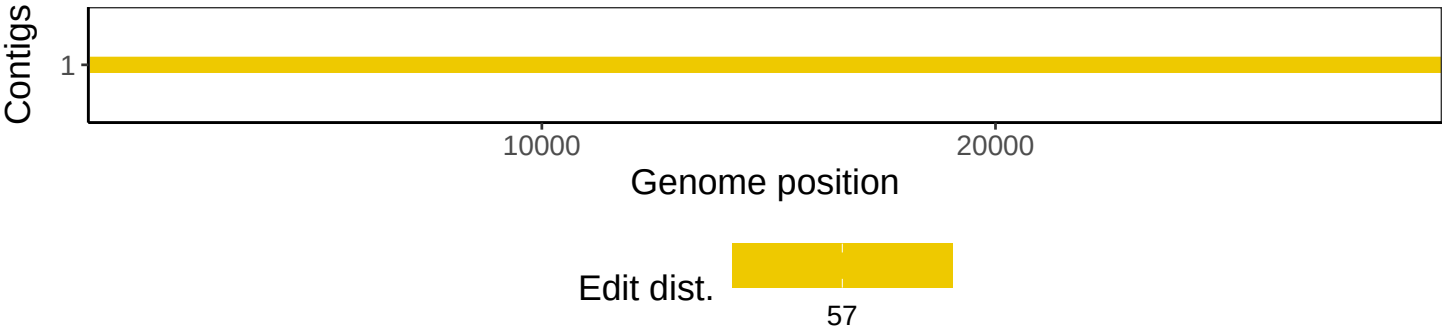
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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