COVID-19 subject UPHS-1511

2021-06-23

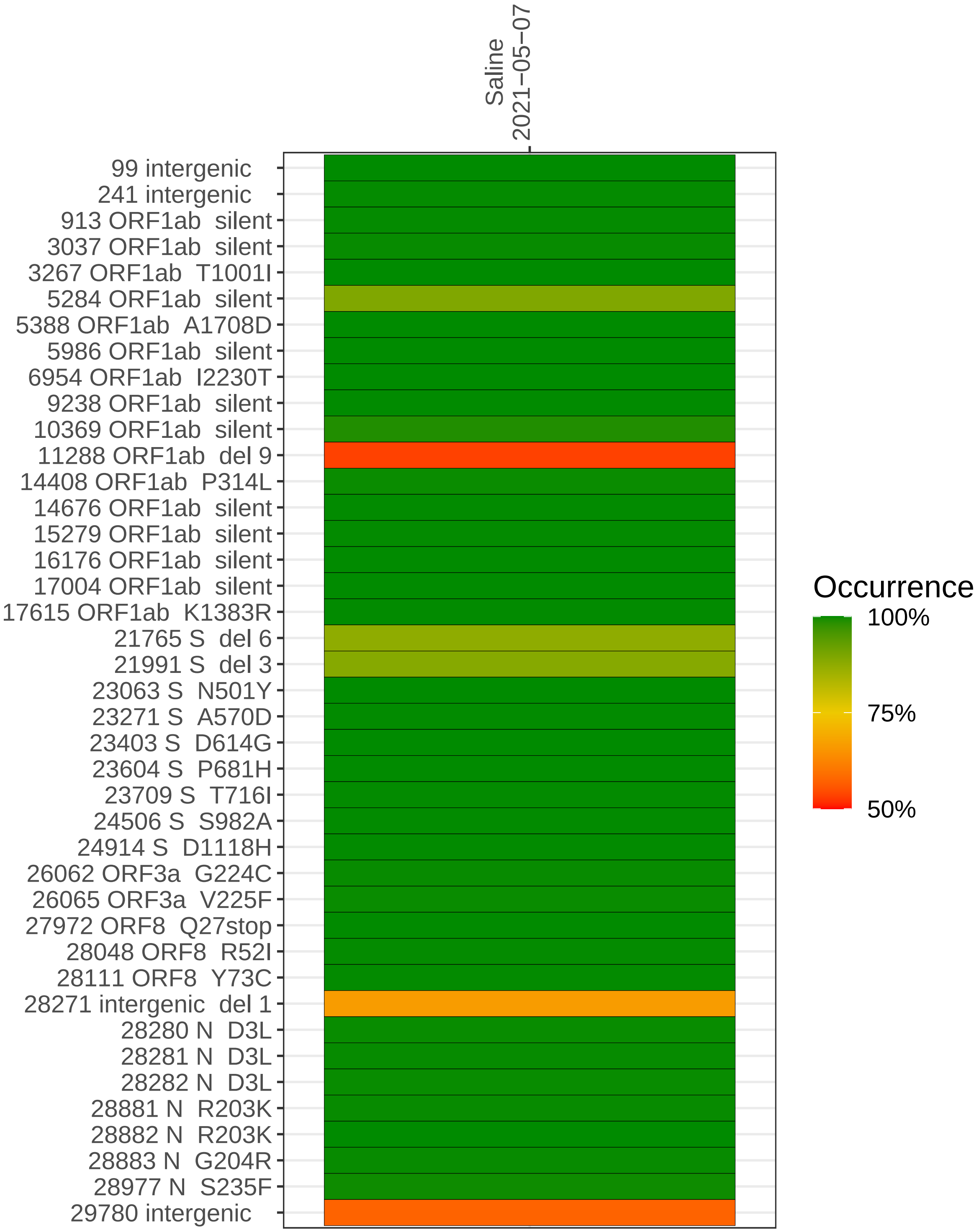
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

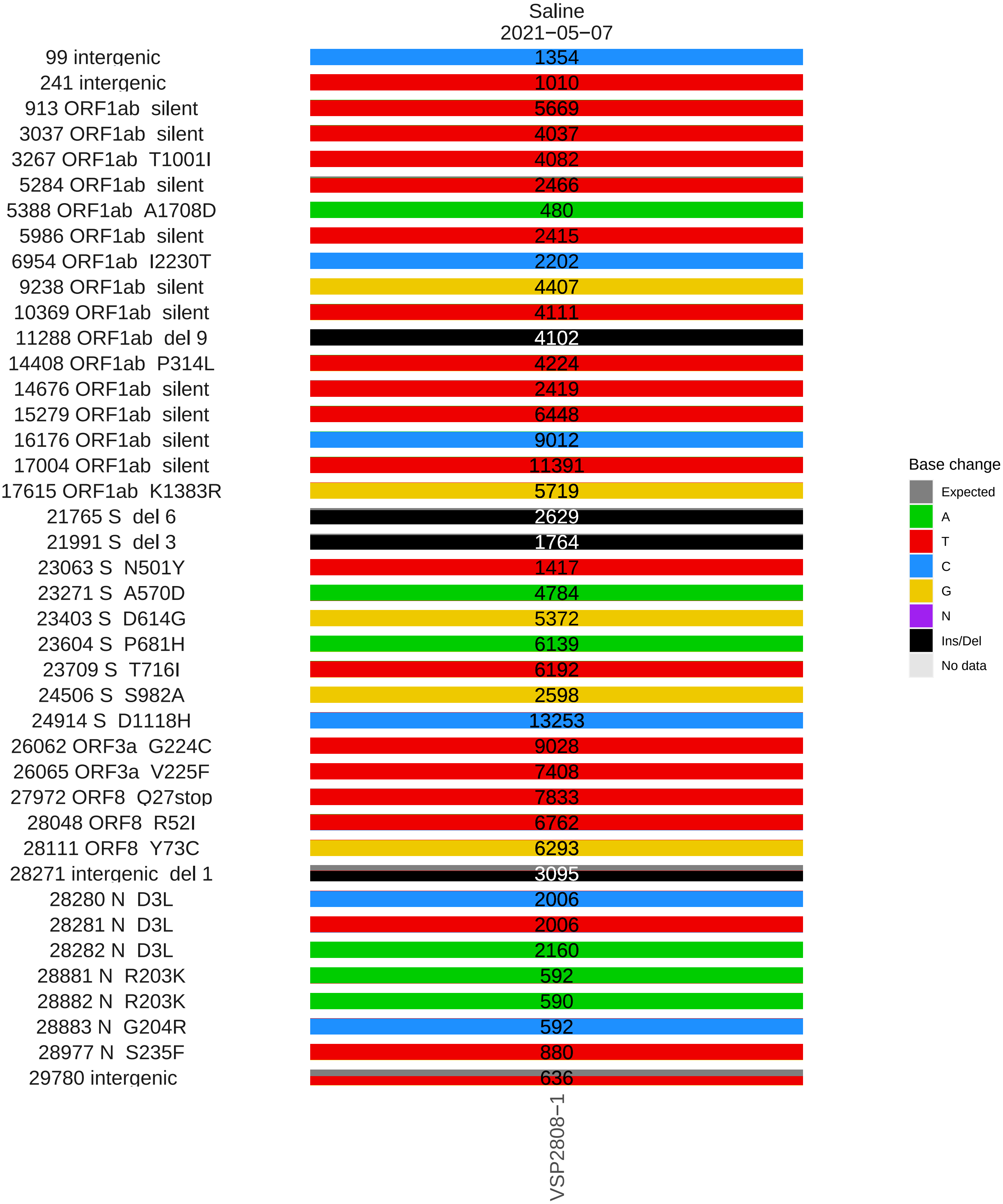
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2808-1	single experiment	NA	Saline	2021-05-07	29.91	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.

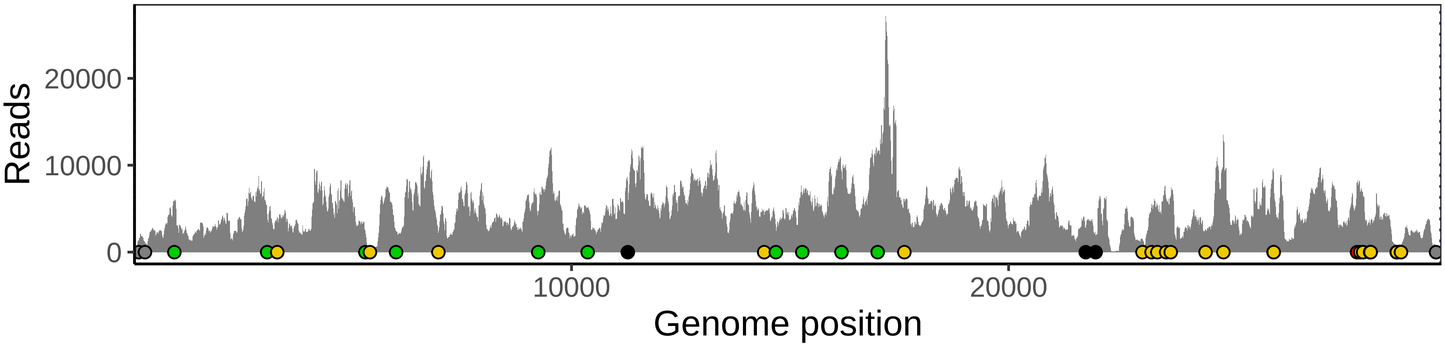



Saline
2021−05−07
99 intergenic 1354
241 intergenic 1010
913 ORF1ab silent 5669
3037 ORF1ab silent 4037
3267 ORF1ab T1001I 4082
5284 ORF1ab silent 2466
5388 ORF1ab A1708D 480
5986 ORF1ab silent 2415
6954 ORF1ab I2230T 2202
9238 ORF1ab silent 4407
10369 ORF1ab silent 4111
11288 ORF1ab del 9 4102
14408 ORF1ab P314L 4224
14676 ORF1ab silent 2419
15279 ORF1ab silent 6448
16176 ORF1ab silent 9012
17004 ORF1ab silent 11391
17615 ORF1ab K1383R 5719
21765 S del 6 2629
21991 S del 3 1764
23063 S N501Y 1417
23271 S A570D 4784
23403 S D614G 5372
23604 S P681H 6139
23709 S T716I 6192
24506 S S982A 2598
24914 S D1118H 13253
26062 ORF3a G224C 9028
26065 ORF3a V225F 7408
27972 ORF8 Q27stop 7833
28048 ORF8 R52I 6762
28111 ORF8 Y73C 6293
28271 intergenic del 1 3095
28280 N D3L 2006
28281 N D3L 2006
28282 N D3L 2160
28881 N R203K 592
28882 N R203K 590
28883 N G204R 592
28977 N S235F 880
29780 intergenic 636
VSP2808−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

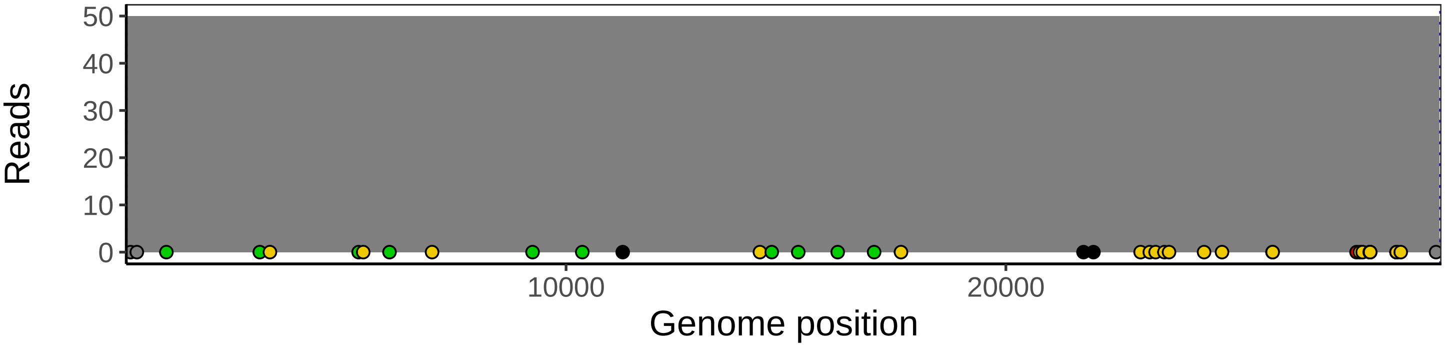
Analyses of individual experiments and composite results

VSP2808-1 | 2021-05-07 | Saline | UPHS-1511 | genomes | single experiment

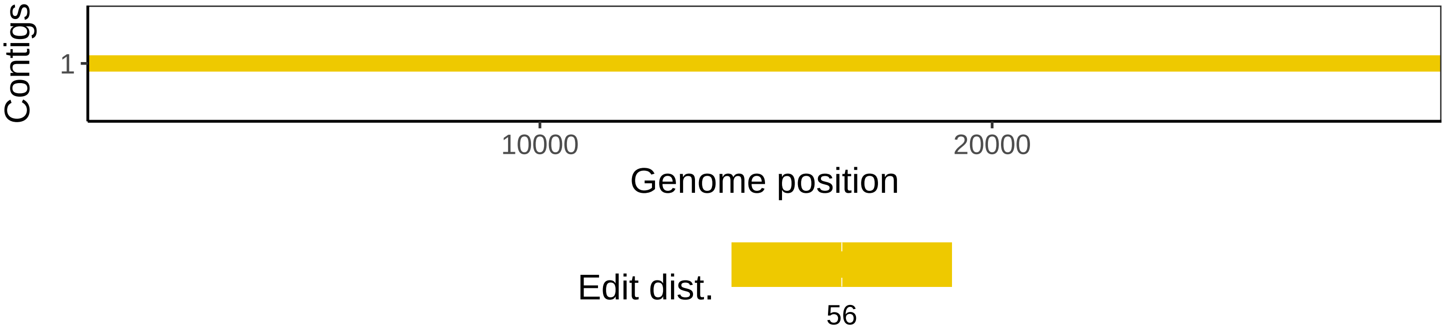
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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