COVID-19 subject HUP Q-0005

2021-05-05

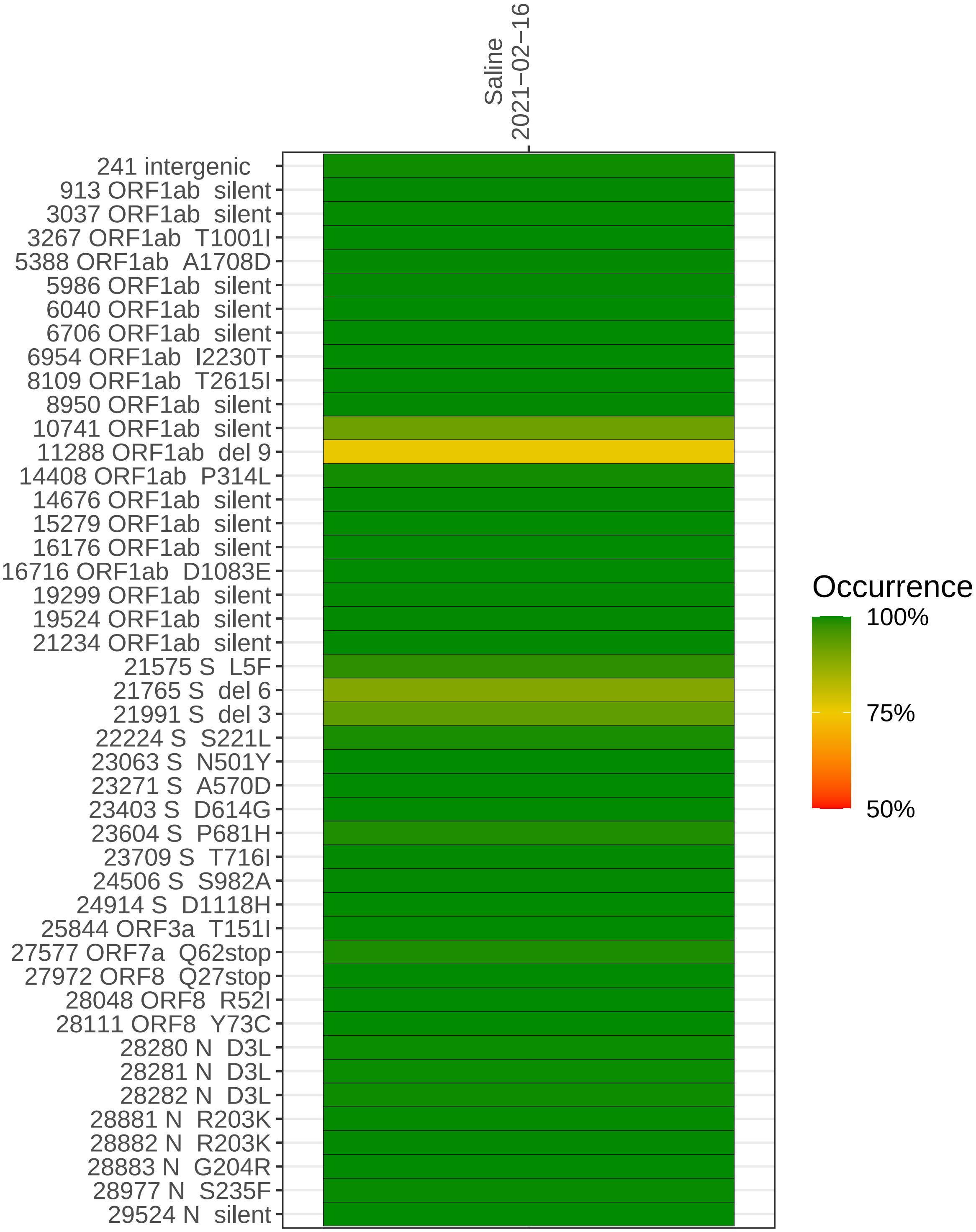
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

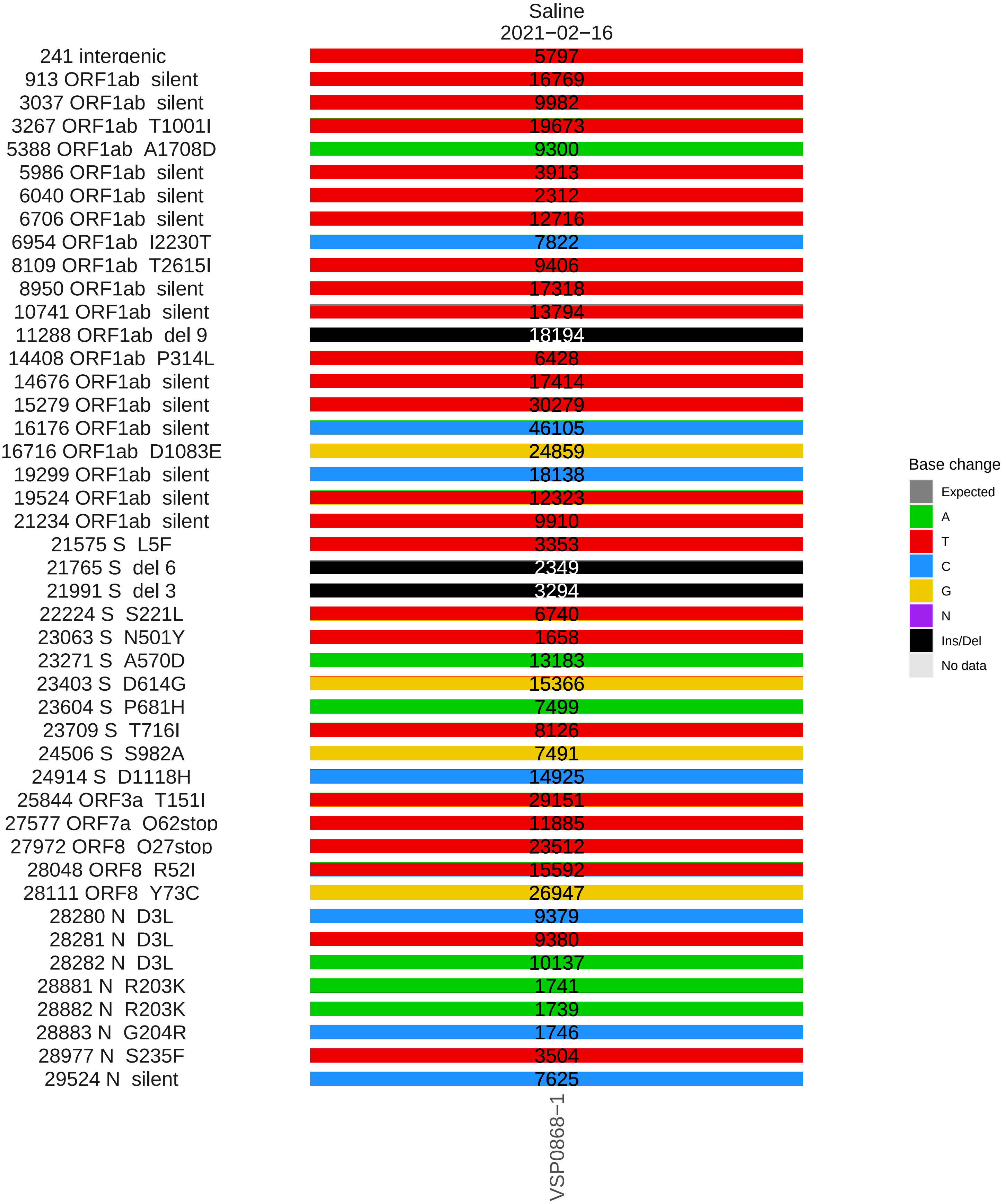
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0868-1	single experiment	NA	Saline	2021-02-16	29.82	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

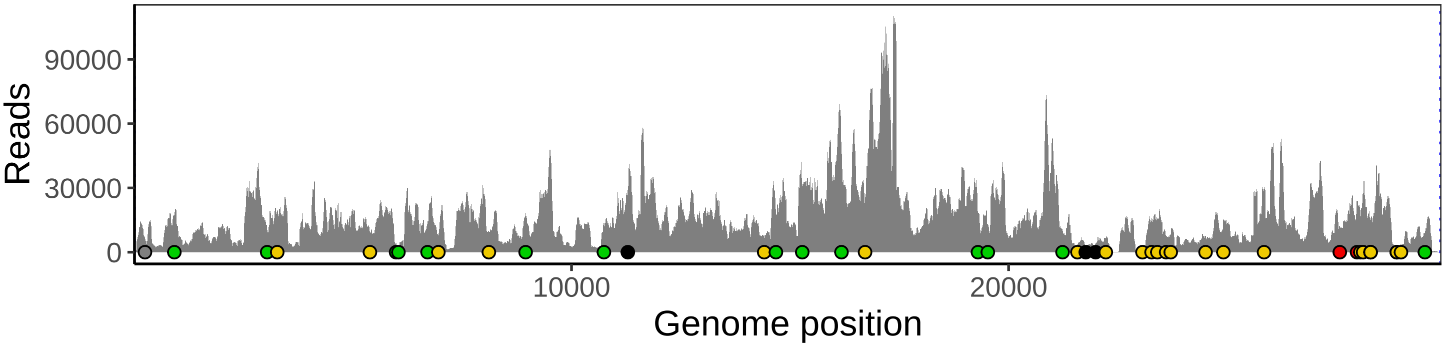



Saline
2021−02−16
241 intergenic
5797
913 ORF1ab silent
16769
3037 ORF1ab silent
9982
3267 ORF1ab T1001I
19673
5388 ORF1ab A1708D
9300
5986 ORF1ab silent
3913
6040 ORF1ab silent
2312
6706 ORF1ab silent
12716
6954 ORF1ab I2230T
7822
8109 ORF1ab T2615I
9406
8950 ORF1ab silent
17318
10741 ORF1ab silent
13794
11288 ORF1ab del 9
18194
14408 ORF1ab P314L
6428
14676 ORF1ab silent
17414
15279 ORF1ab silent
30279
16176 ORF1ab silent
46105
16716 ORF1ab D1083E
24859
19299 ORF1ab silent
18138
19524 ORF1ab silent
12323
21234 ORF1ab silent
9910
21575 S L5F
3353
21765 S del 6
2349
21991 S del 3
3294
22224 S S221L
6740
23063 S N501Y
1658
23271 S A570D
13183
23403 S D614G
15366
23604 S P681H
7499
23709 S T716I
8126
24506 S S982A
7491
24914 S D1118H
14925
25844 ORF3a T151I
29151
27577 ORF7a Q62stop
11885
27972 ORF8 Q27stop
23512
28048 ORF8 R52I
15592
28111 ORF8 Y73C
26947
28280 N D3L
9379
28281 N D3L
9380
28282 N D3L
10137
28881 N R203K
1741
28882 N R203K
1739
28883 N G204R
1746
28977 N S235F
3504
29524 N silent
7625
VSP0868−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

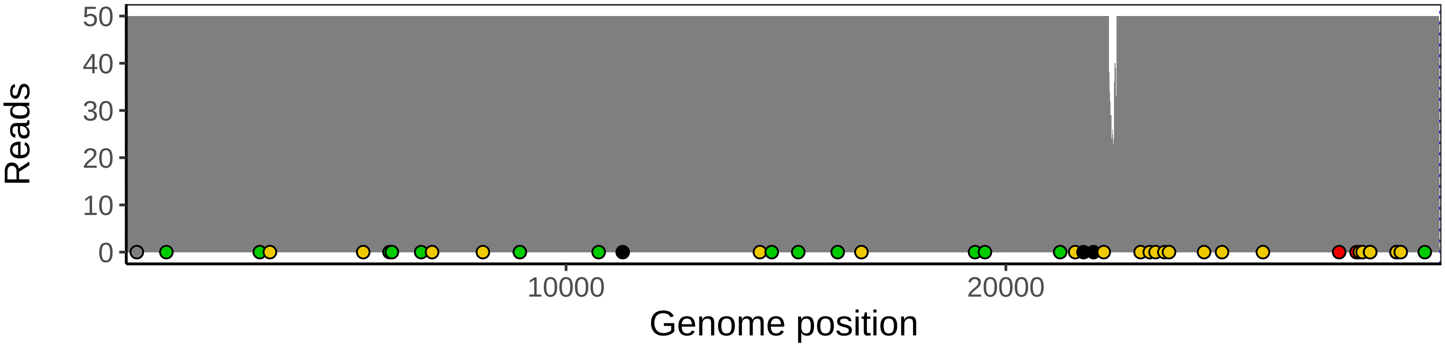
Analyses of individual experiments and composite results

VSP0868-1 | 2021-02-16 | Saline | HUP-Q-0005 | genomes | single experiment

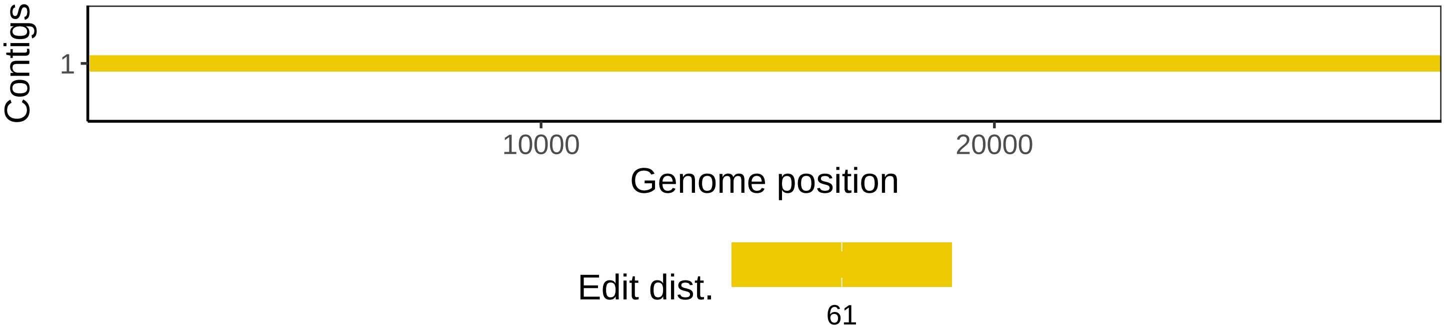
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.0.0
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