COVID-19 subject HUP-Q-0028

2021-05-05

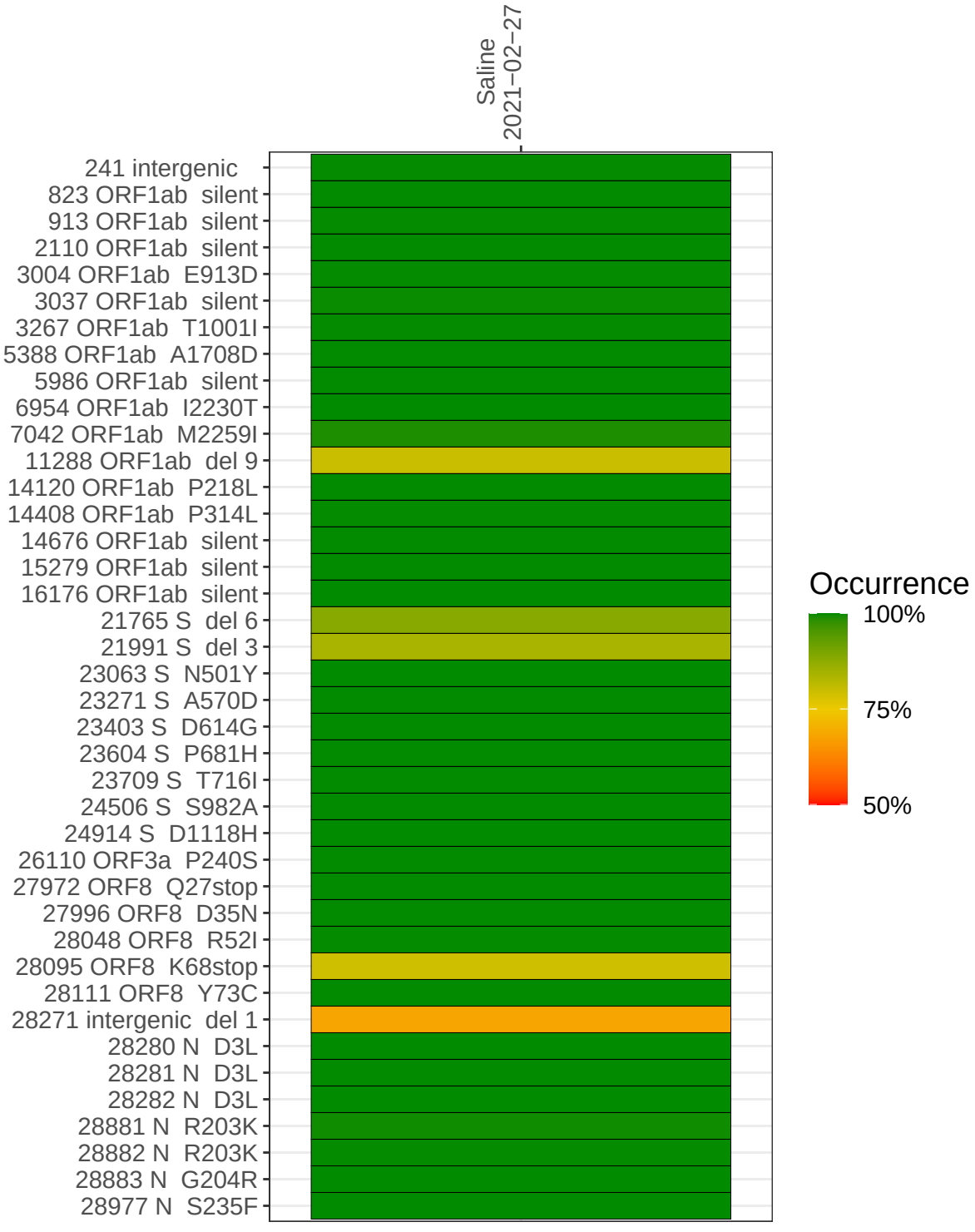
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

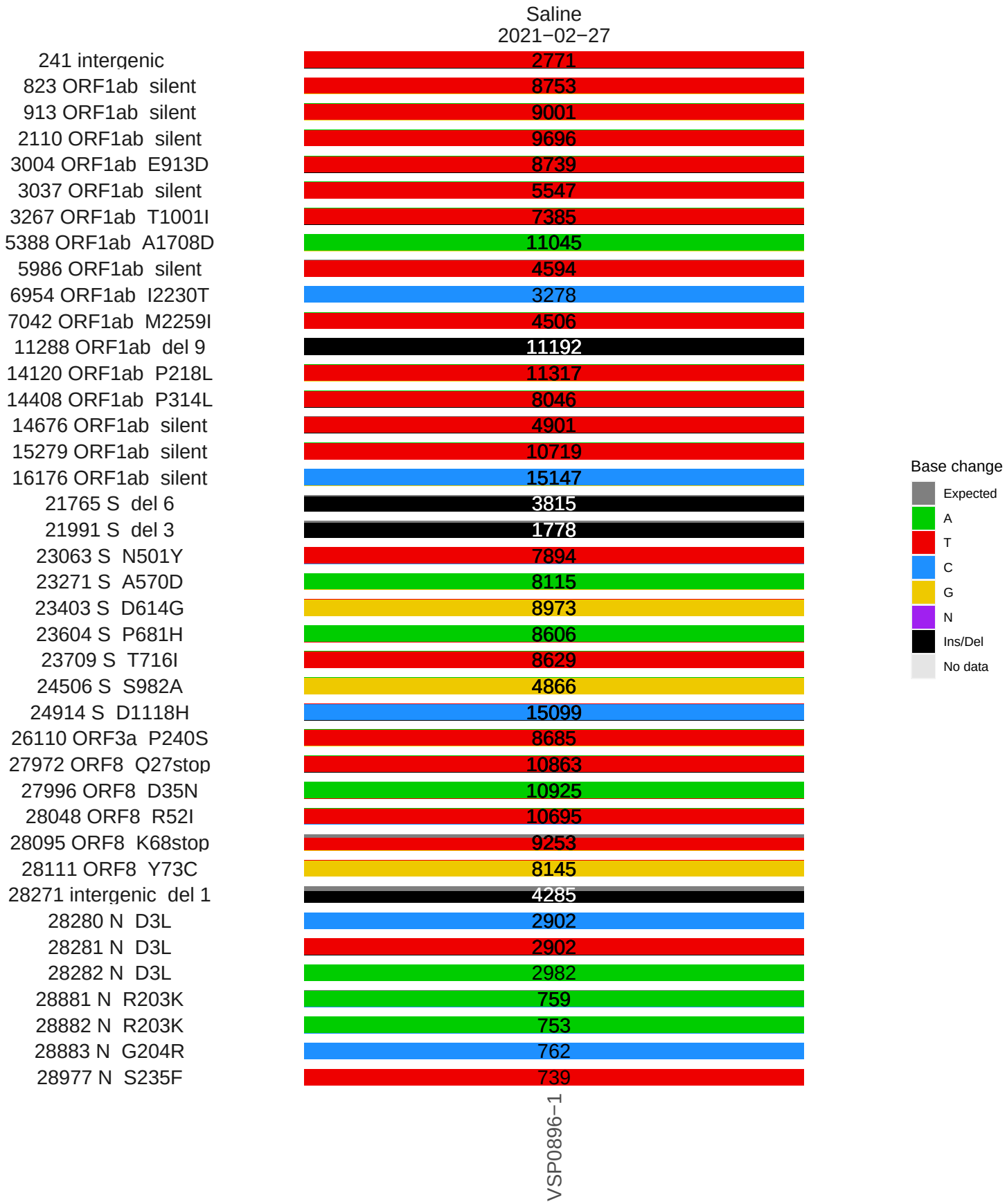
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0896-1	single experiment	NA	Saline	2021-02-27	29.87	B.1.1.7	99.9%	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.

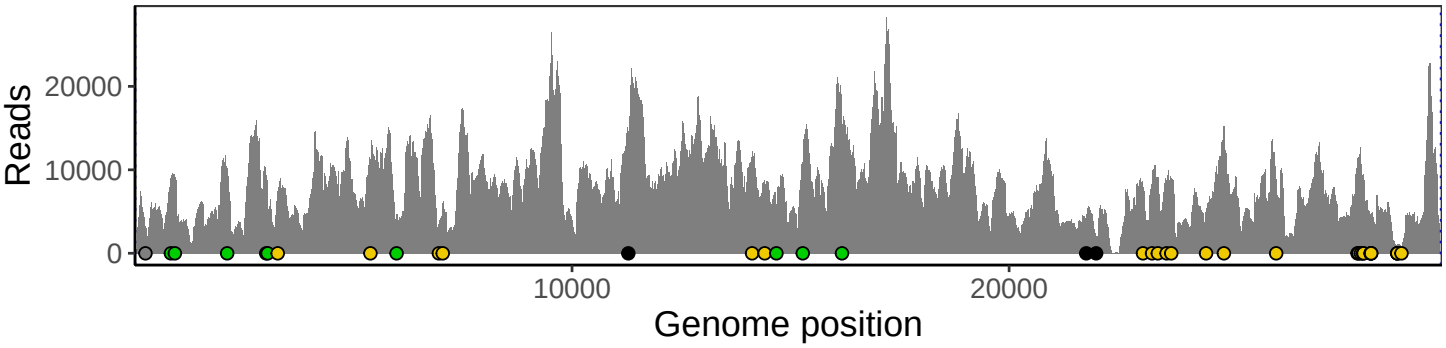



Saline
2021−02−27
241 intergenic 2771
823 ORF1ab silent 8753
913 ORF1ab silent 9001
2110 ORF1ab silent 9696
3004 ORF1ab E913D 8739
3037 ORF1ab silent 5547
3267 ORF1ab T1001I 7385
5388 ORF1ab A1708D 11045
5986 ORF1ab silent 4594
6954 ORF1ab I2230T 3278
7042 ORF1ab M2259I 4506
11288 ORF1ab del 9 11192
14120 ORF1ab P218L 11317
14408 ORF1ab P314L 8046
14676 ORF1ab silent 4901
15279 ORF1ab silent 10719
16176 ORF1ab silent 15147
21765 S del 6 3815
21991 S del 3 1778
23063 S N501Y 7894
23271 S A570D 8115
23403 S D614G 8973
23604 S P681H 8606
23709 S T716I 8629
24506 S S982A 4866
24914 S D1118H 15099
26110 ORF3a P240S 8685
27972 ORF8 Q27stop 10863
27996 ORF8 D35N 10925
28048 ORF8 R52I 10695
28095 ORF8 K68stop 9253
28111 ORF8 Y73C 8145
28271 intergenic del 1 4285
28280 N D3L 2902
28281 N D3L 2902
28282 N D3L 2982
28881 N R203K 759
28882 N R203K 753
28883 N G204R 762
28977 N S235F 739
VSP0896−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

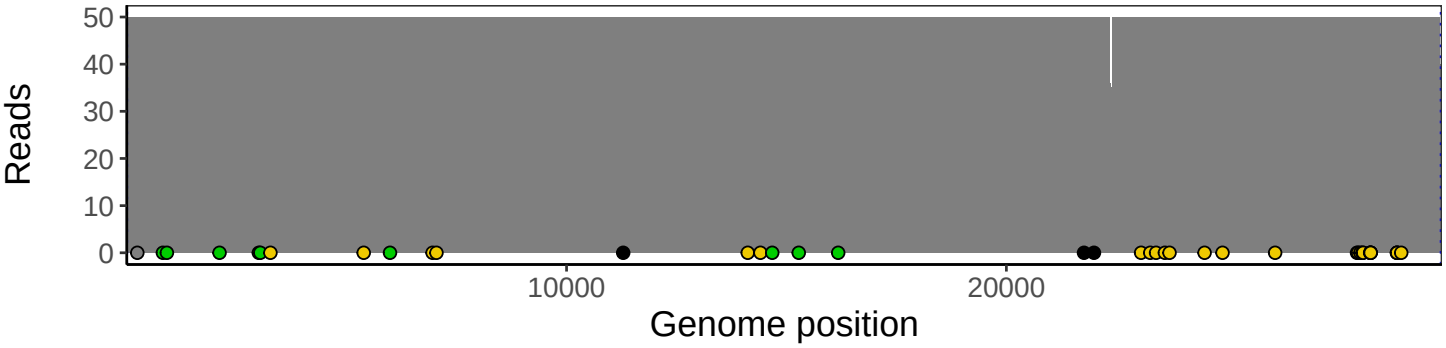
Analyses of individual experiments and composite results

VSP0896-1 | 2021-02-27 | Saline | HUP-Q-0028 | genomes | single experiment

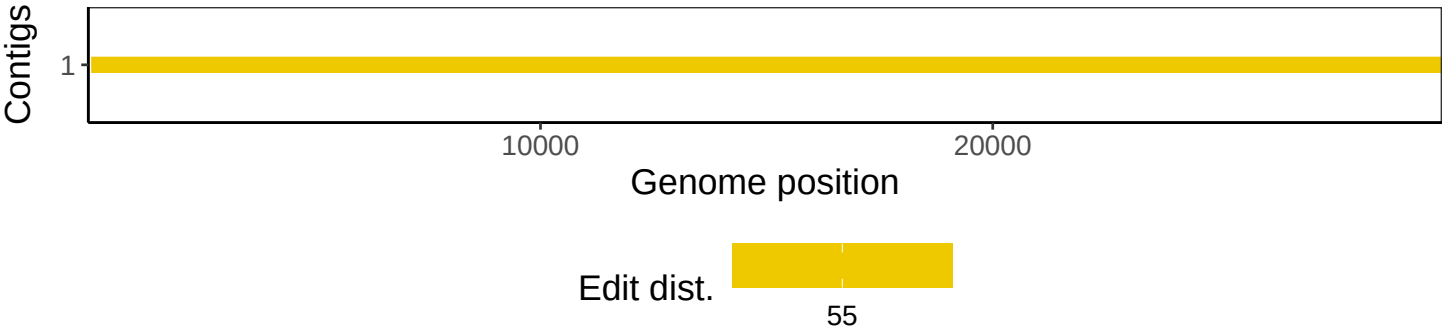
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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