COVID-19 subject HUP Q-0029

2021-04-17

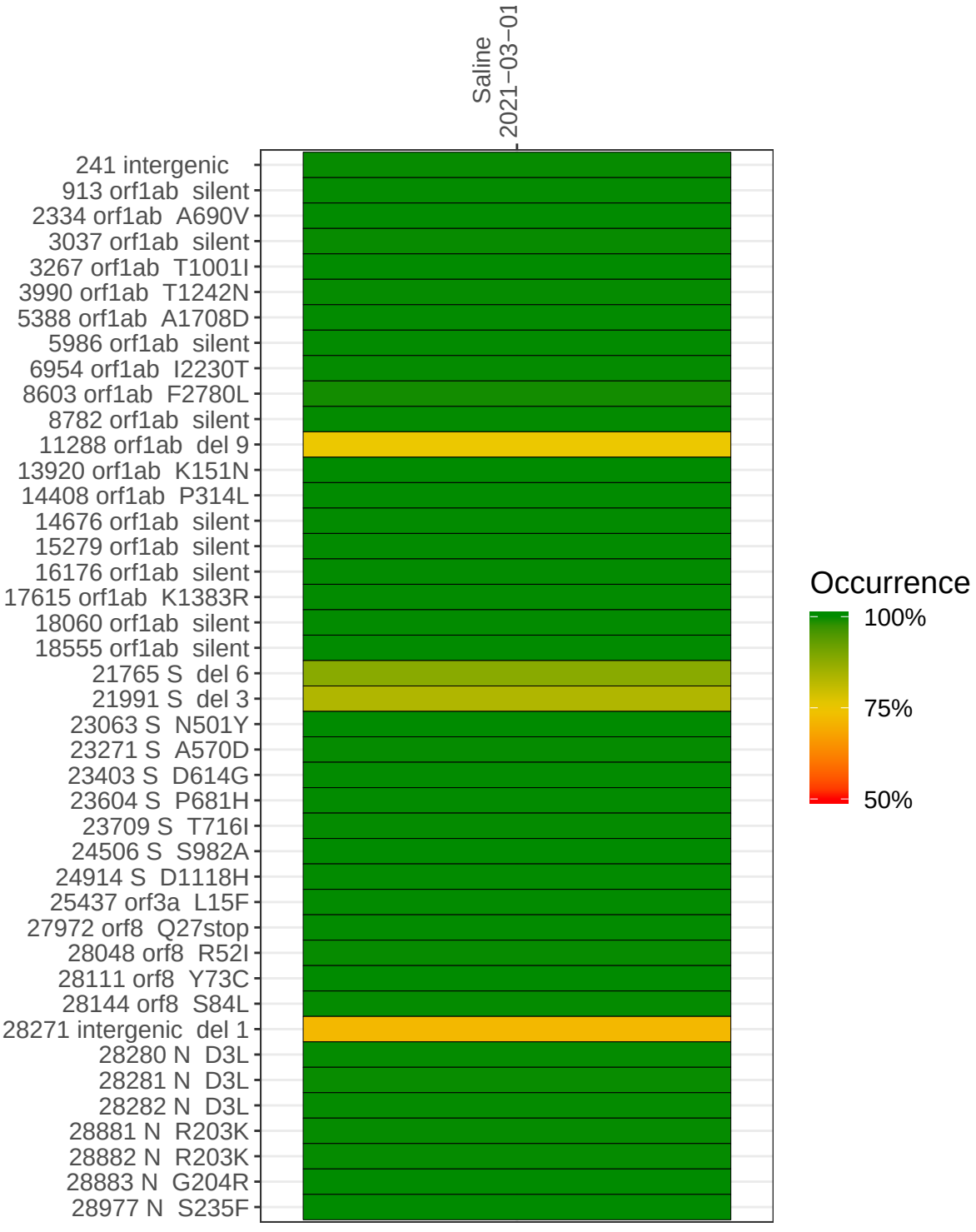
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

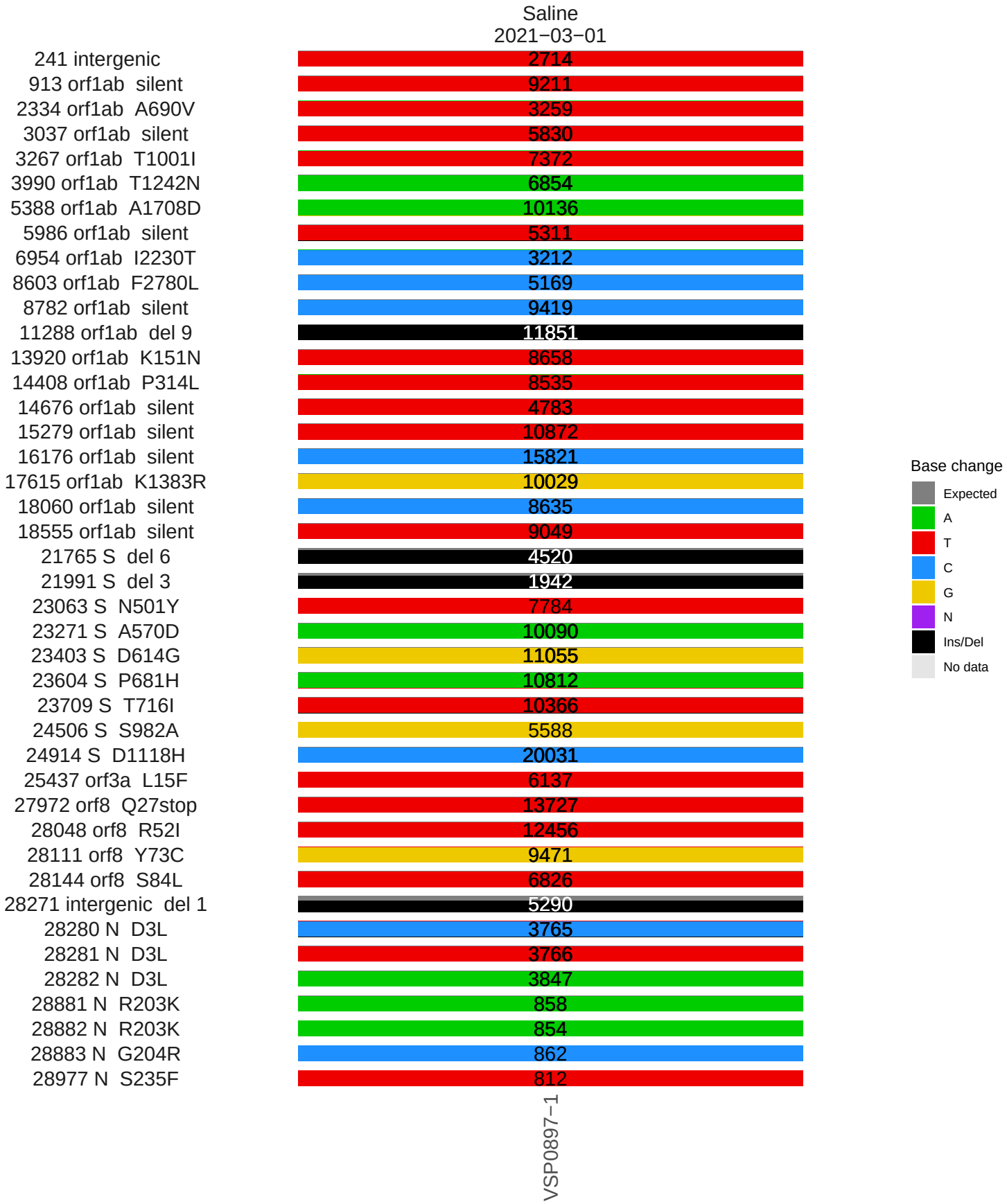
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0897-1	single experiment	NA	Saline	2021-03-01	29.84	B.1.1.7	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

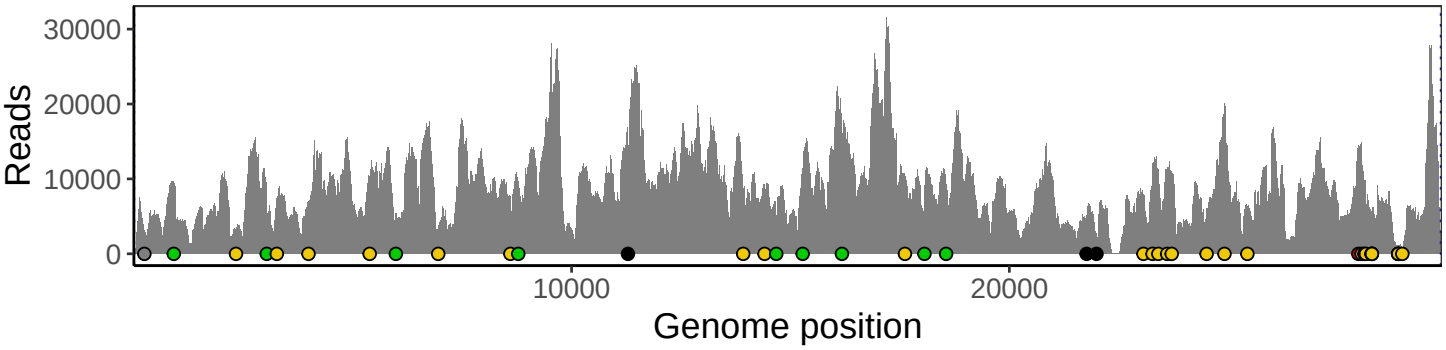



Saline
2021−03−01
241 intergenic 2714
913 orf1ab silent 9211
2334 orf1ab A690V 3259
3037 orf1ab silent 5830
3267 orf1ab T1001I 7372
3990 orf1ab T1242N 6854
5388 orf1ab A1708D 10136
5986 orf1ab silent 5311
6954 orf1ab I2230T 3212
8603 orf1ab F2780L 5169
8782 orf1ab silent 9419
11288 orf1ab del 9 11851
13920 orf1ab K151N 8658
14408 orf1ab P314L 8535
14676 orf1ab silent 4783
15279 orf1ab silent 10872
16176 orf1ab silent 15821
17615 orf1ab K1383R 10029
18060 orf1ab silent 8635
18555 orf1ab silent 9049
21765 S del 6 4520
21991 S del 3 1942
23063 S N501Y 7784
23271 S A570D 10090
23403 S D614G 11055
23604 S P681H 10812
23709 S T716I 10366
24506 S S982A 5588
24914 S D1118H 20031
25437 orf3a L15F 6137
27972 orf8 Q27stop 13727
28048 orf8 R52I 12456
28111 orf8 Y73C 9471
28144 orf8 S84L 6826
28271 intergenic del 1 5290
28280 N D3L 3765
28281 N D3L 3766
28282 N D3L 3847
28881 N R203K 858
28882 N R203K 854
28883 N G204R 862
28977 N S235F 812
VSP0897−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

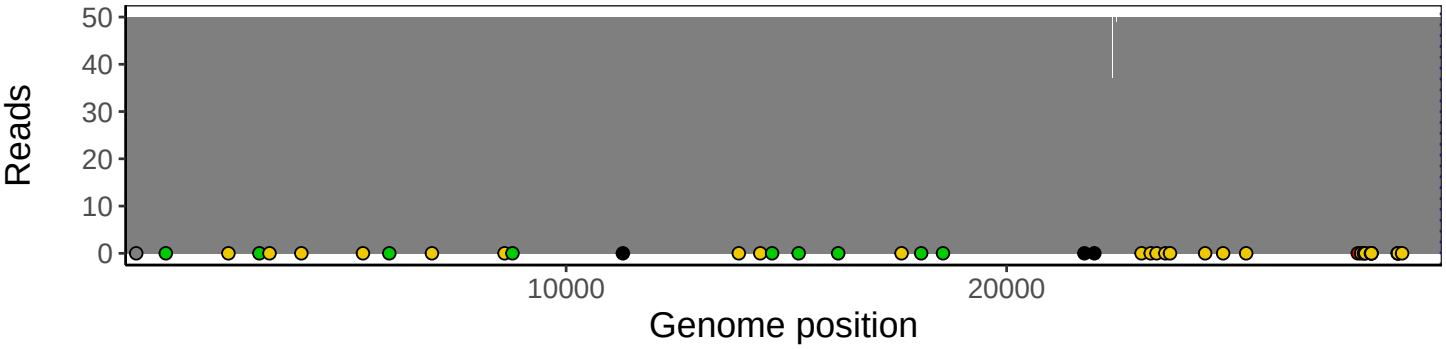
Analyses of individual experiments and composite results

VSP0897-1 | 2021-03-01 | Saline | HUP Q-0029 | genomes | single experiment

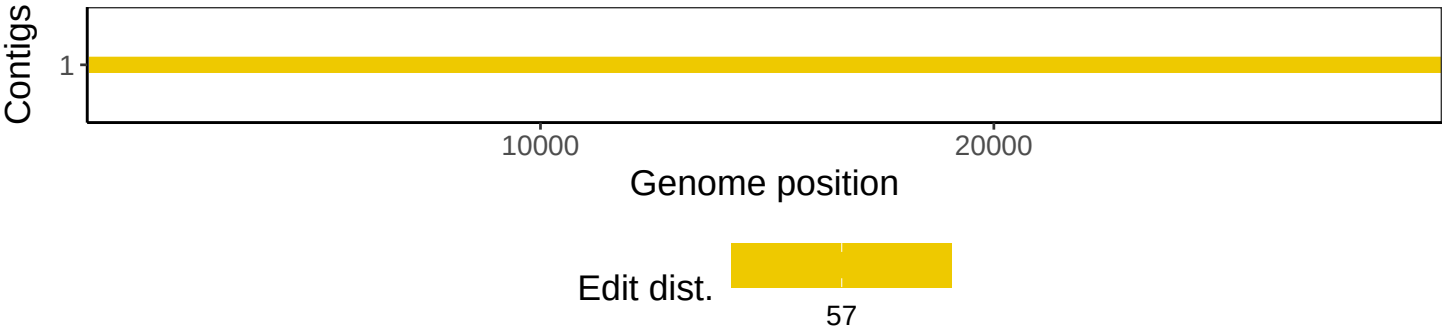
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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