COVID-19 subject HUP Q-0007

2021-05-05

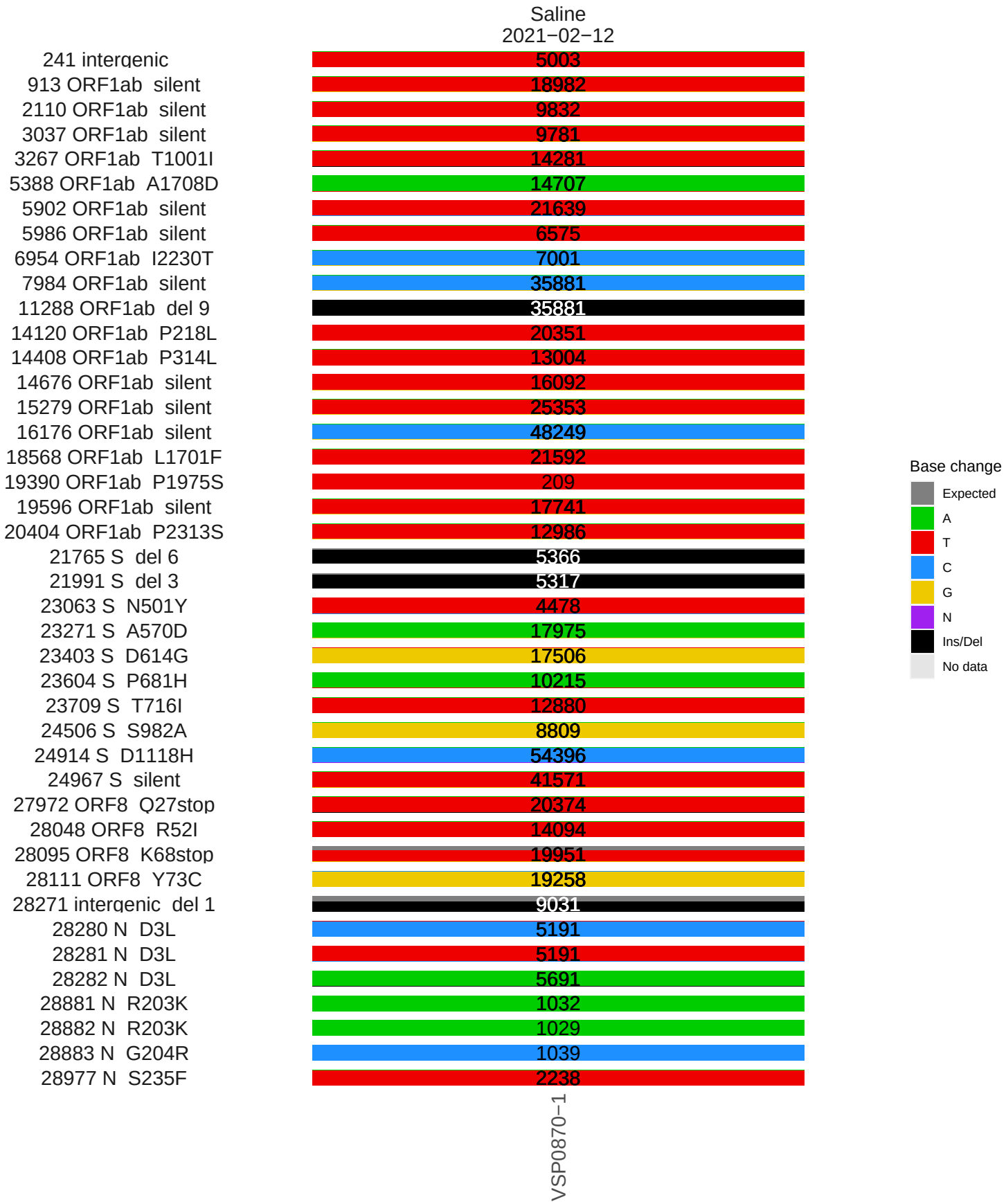
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0870-1	single experiment	NA	Saline	2021-02-12	29.86	B.1.1.7	99.8%	99.8%

Variants shared across samples

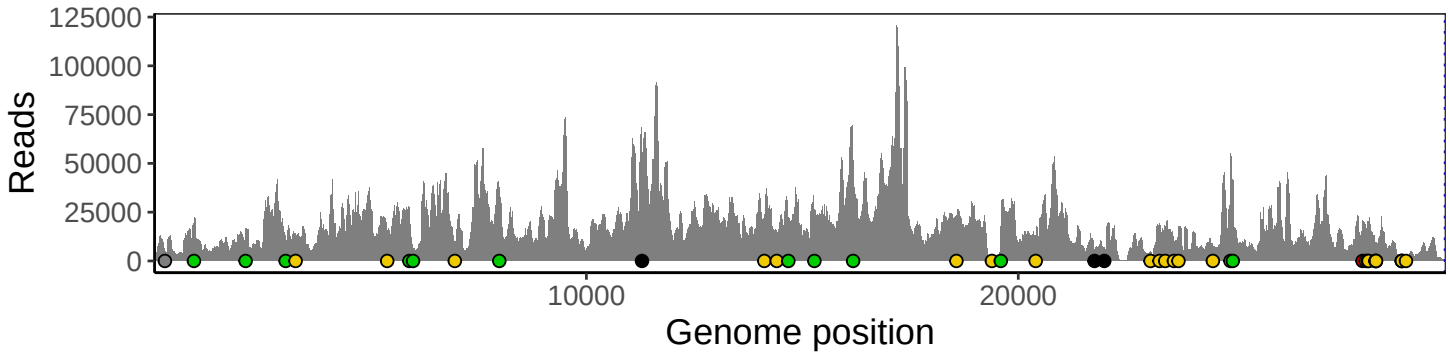
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of 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
2021−02−12
241 intergenic 5003
913 ORF1ab silent 18982
2110 ORF1ab silent 9832
3037 ORF1ab silent 9781
3267 ORF1ab T1001I 14281
5388 ORF1ab A1708D 14707
5902 ORF1ab silent 21639
5986 ORF1ab silent 6575
6954 ORF1ab I2230T 7001
7984 ORF1ab silent 35881
11288 ORF1ab del 9 35881
14120 ORF1ab P218L 20351
14408 ORF1ab P314L 13004
14676 ORF1ab silent 16092
15279 ORF1ab silent 25353
16176 ORF1ab silent 48249
18568 ORF1ab L1701F 21592
19390 ORF1ab P1975S 209
19596 ORF1ab silent 17741
20404 ORF1ab P2313S 12986
21765 S del 6 5366
21991 S del 3 5317
23063 S N501Y 4478
23271 S A570D 17975
23403 S D614G 17506
23604 S P681H 10215
23709 S T716I 12880
24506 S S982A 8809
24914 S D1118H 54396
24967 S silent 41571
27972 ORF8 Q27stop 20374
28048 ORF8 R52I 14094
28095 ORF8 K68stop 19951
28111 ORF8 Y73C 19258
28271 intergenic del 1 9031
28280 N D3L 5191
28281 N D3L 5191
28282 N D3L 5691
28881 N R203K 1032
28882 N R203K 1029
28883 N G204R 1039
28977 N S235F 2238
VSP0870−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

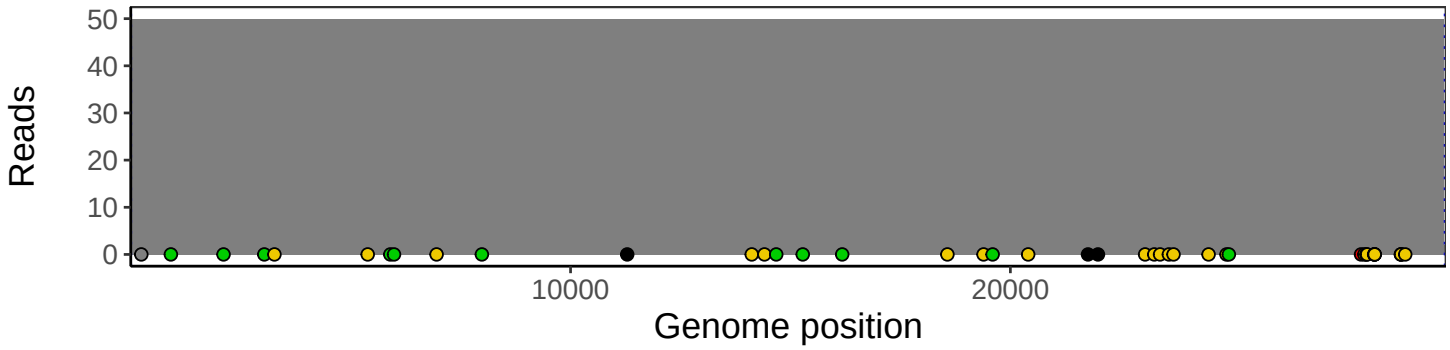
Analyses of individual experiments and composite results

VSP0870-1 | 2021-02-12 | Saline | HUP-Q-0007 | genomes | single experiment

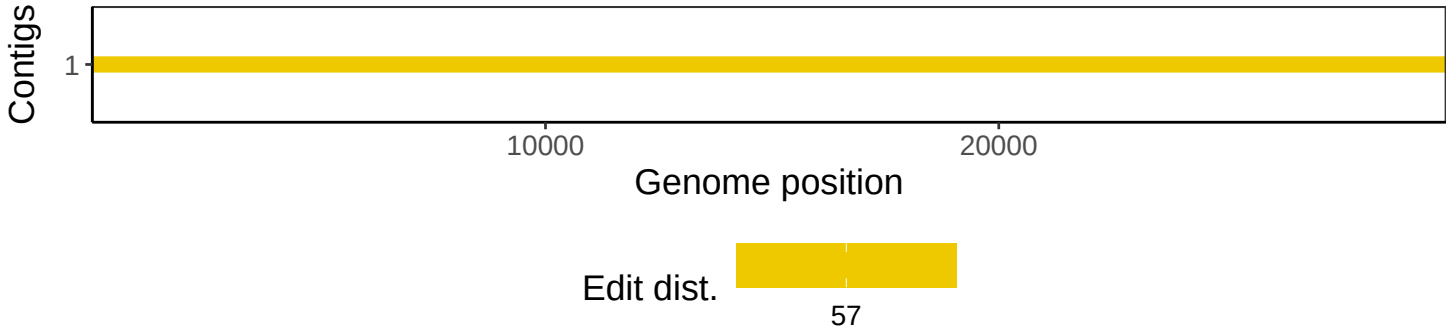
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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