COVID-19 subject HUP Q-0015

2021-05-05

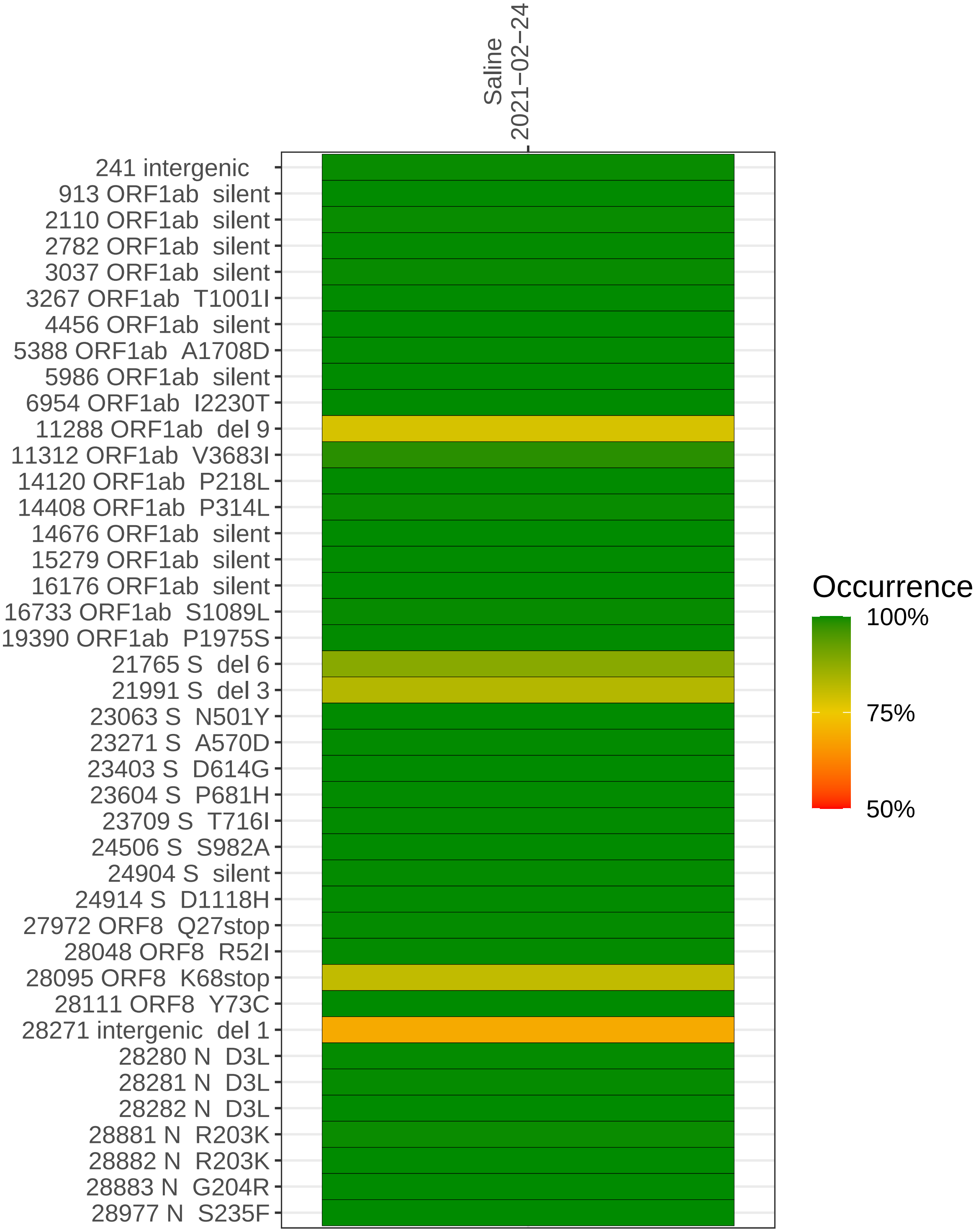
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

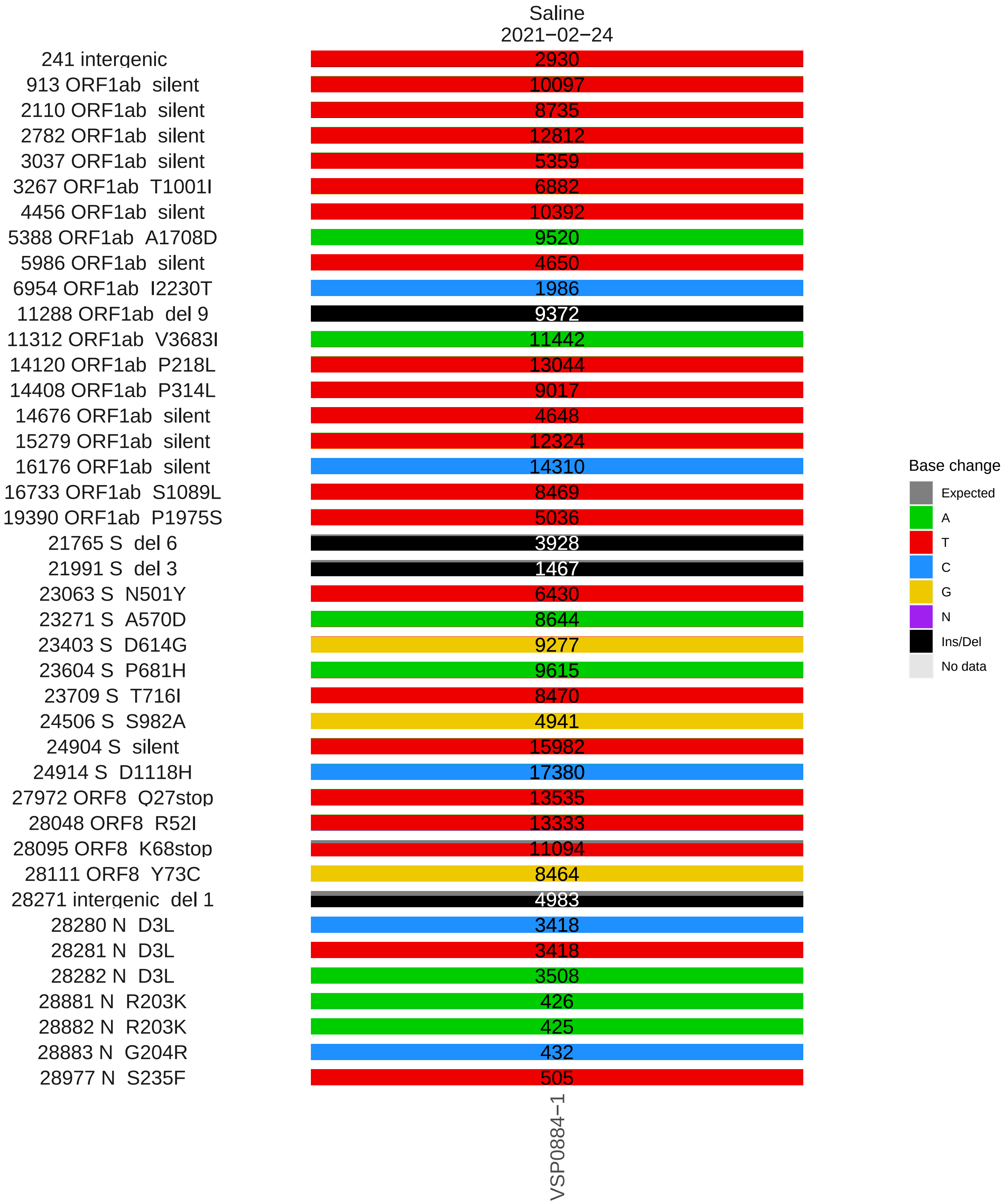
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0884-1	single experiment	NA	Saline	2021-02-24	29.86	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/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.

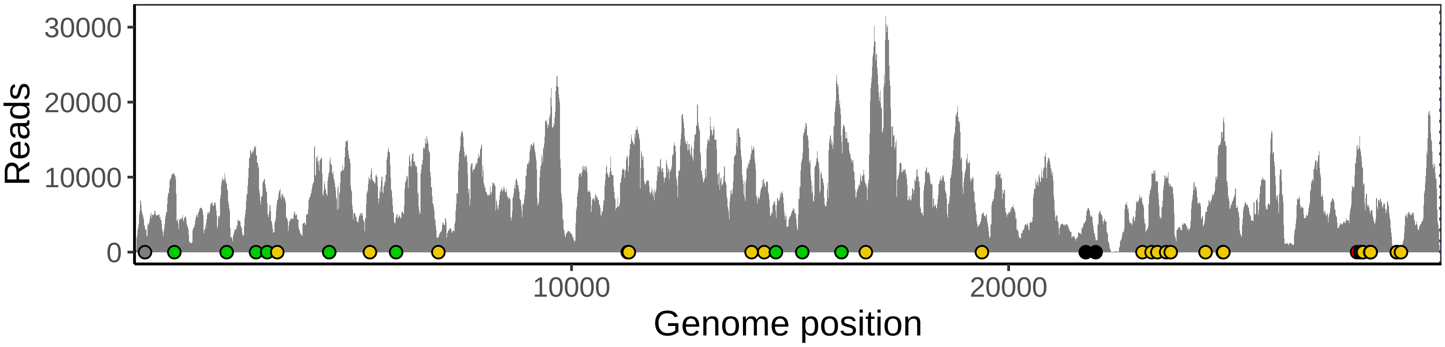



Saline
2021−02−24
241 intergenic 2930
913 ORF1ab silent 10097
2110 ORF1ab silent 8735
2782 ORF1ab silent 12812
3037 ORF1ab silent 5359
3267 ORF1ab T1001I 6882
4456 ORF1ab silent 10392
5388 ORF1ab A1708D 9520
5986 ORF1ab silent 4650
6954 ORF1ab I2230T 1986
11288 ORF1ab del 9 9372
11312 ORF1ab V3683I 11442
14120 ORF1ab P218L 13044
14408 ORF1ab P314L 9017
14676 ORF1ab silent 4648
15279 ORF1ab silent 12324
16176 ORF1ab silent 14310
16733 ORF1ab S1089L 8469
19390 ORF1ab P1975S 5036
21765 S del 6 3928
21991 S del 3 1467
23063 S N501Y 6430
23271 S A570D 8644
23403 S D614G 9277
23604 S P681H 9615
23709 S T716I 8470
24506 S S982A 4941
24904 S silent 15982
24914 S D1118H 17380
27972 ORF8 Q27stop 13535
28048 ORF8 R52I 13333
28095 ORF8 K68stop 11094
28111 ORF8 Y73C 8464
28271 intergenic del 1 4983
28280 N D3L 3418
28281 N D3L 3418
28282 N D3L 3508
28881 N R203K 426
28882 N R203K 425
28883 N G204R 432
28977 N S235F 505
VSP0884−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

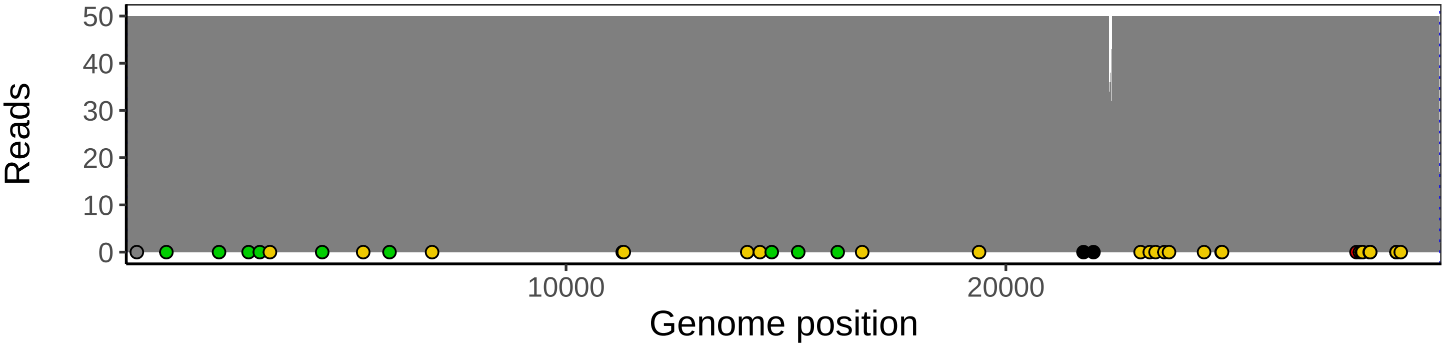
Analyses of individual experiments and composite results

VSP0884-1 | 2021-02-24 | Saline | HUP Q-0015 | genomes | single experiment

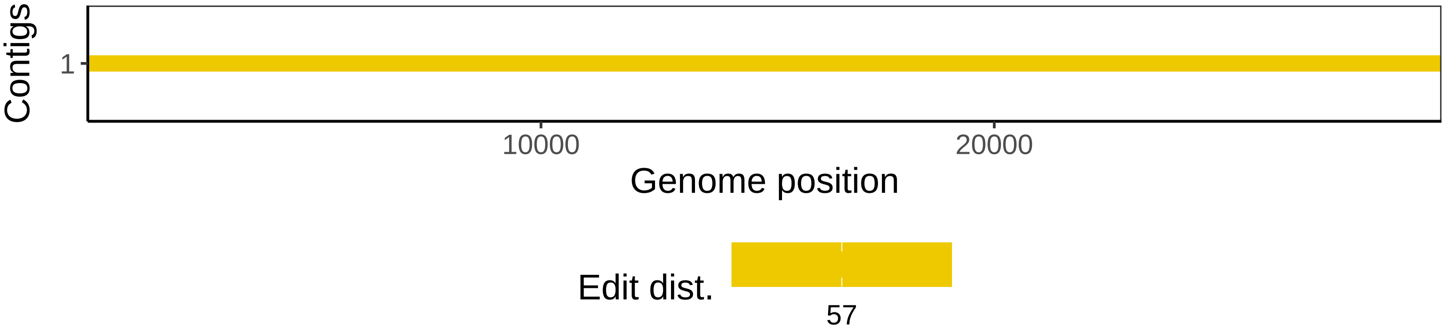
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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