COVID-19 subject HUP Q-0041

2021-04-01

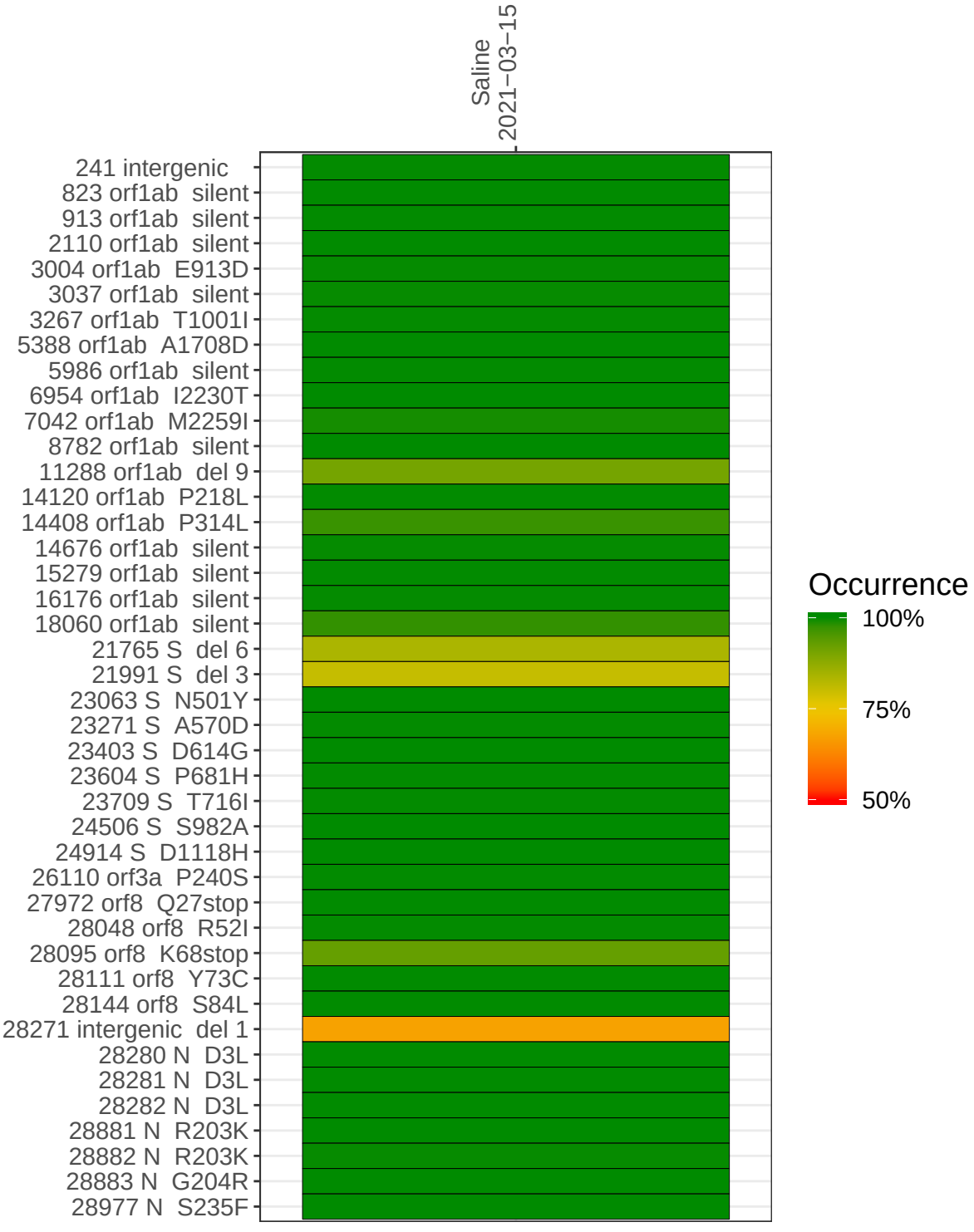
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

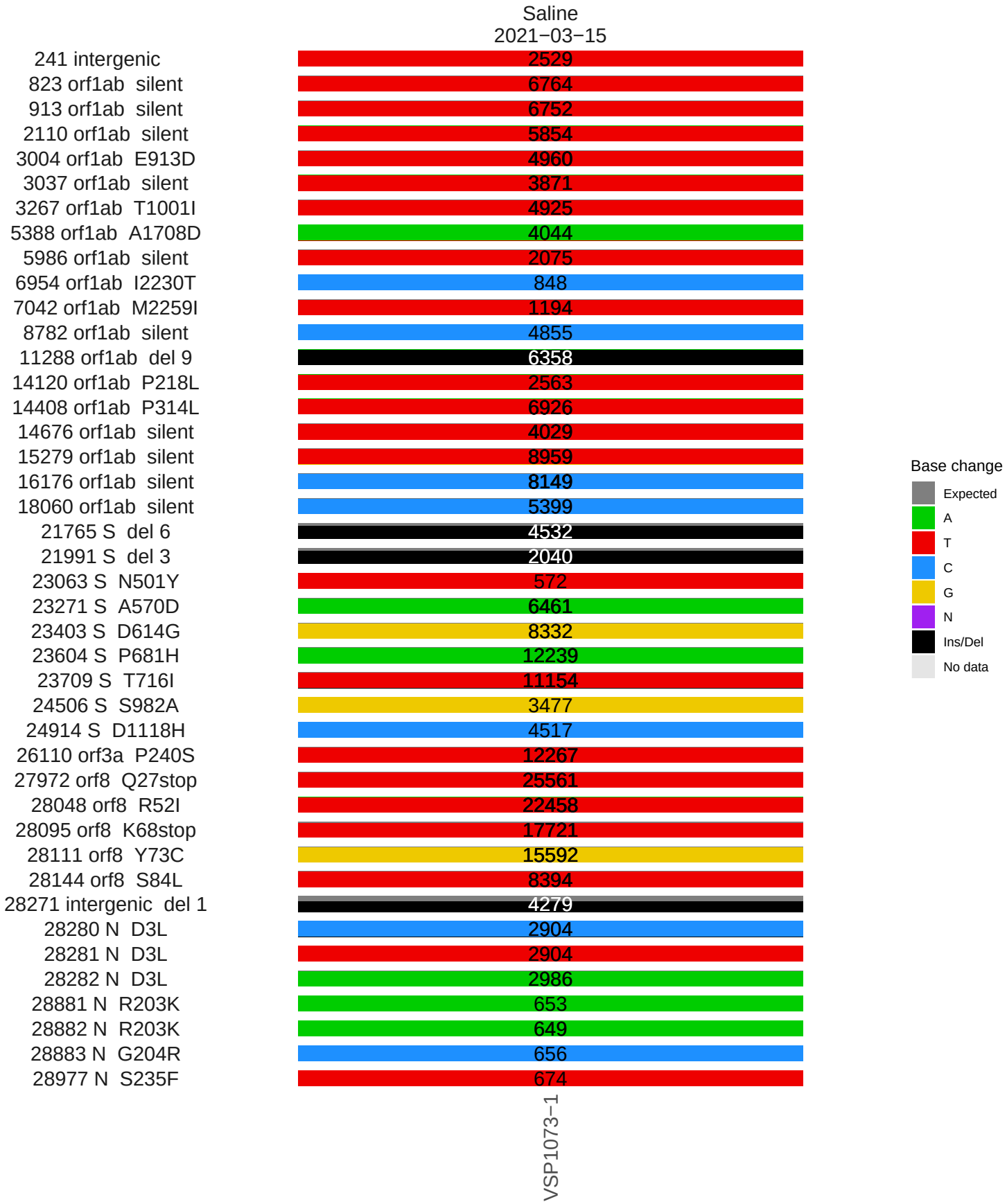
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1073-1	single experiment	NA	Saline	2021-03-15	29.63	B.1.1.7	99.3%	99.2%

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.

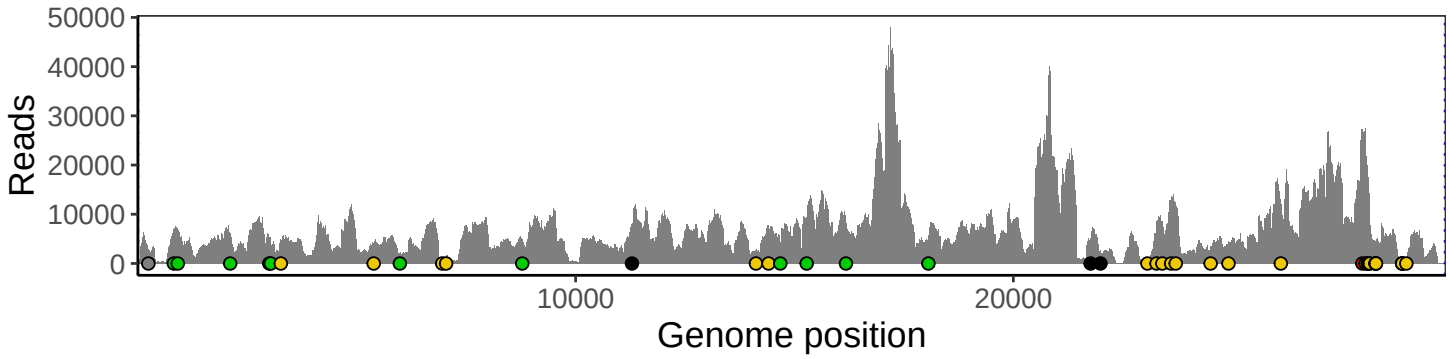



Saline
2021−03−15
241 intergenic 2529
823 orf1ab silent 6764
913 orf1ab silent 6752
2110 orf1ab silent 5854
3004 orf1ab E913D 4960
3037 orf1ab silent 3871
3267 orf1ab T1001I 4925
5388 orf1ab A1708D 4044
5986 orf1ab silent 2075
6954 orf1ab I2230T 848
7042 orf1ab M2259I 1194
8782 orf1ab silent 4855
11288 orf1ab del 9 6358
14120 orf1ab P218L 2563
14408 orf1ab P314L 6926
14676 orf1ab silent 4029
15279 orf1ab silent 8959
16176 orf1ab silent 8149
18060 orf1ab silent 5399
21765 S del 6 4532
21991 S del 3 2040
23063 S N501Y 572
23271 S A570D 6461
23403 S D614G 8332
23604 S P681H 12239
23709 S T716I 11154
24506 S S982A 3477
24914 S D1118H 4517
26110 orf3a P240S 12267
27972 orf8 Q27stop 25561
28048 orf8 R52I 22458
28095 orf8 K68stop 17721
28111 orf8 Y73C 15592
28144 orf8 S84L 8394
28271 intergenic del 1 4279
28280 N D3L 2904
28281 N D3L 2904
28282 N D3L 2986
28881 N R203K 653
28882 N R203K 649
28883 N G204R 656
28977 N S235F 674
VSP1073−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

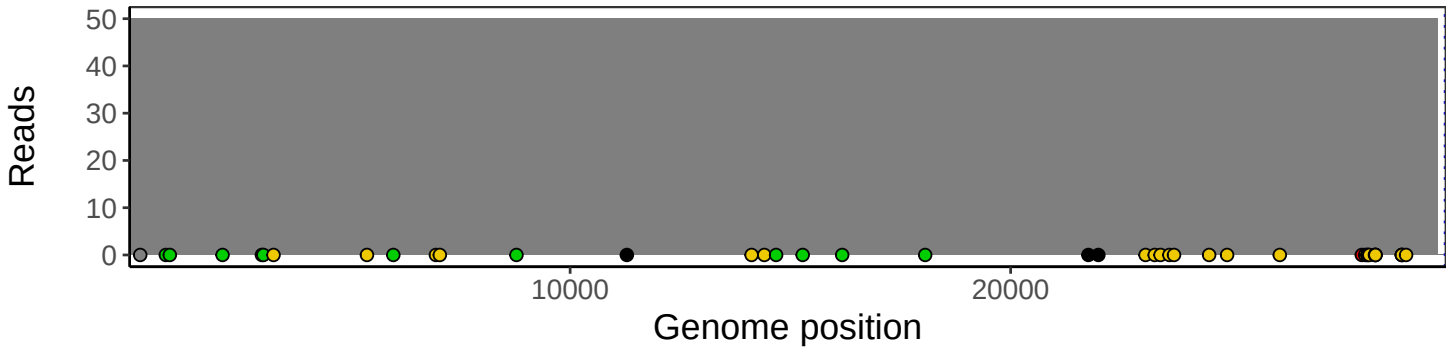
Analyses of individual experiments and composite results

VSP1073-1 | 2021-03-15 | Saline | HUP Q-0041 | genomes | single experiment

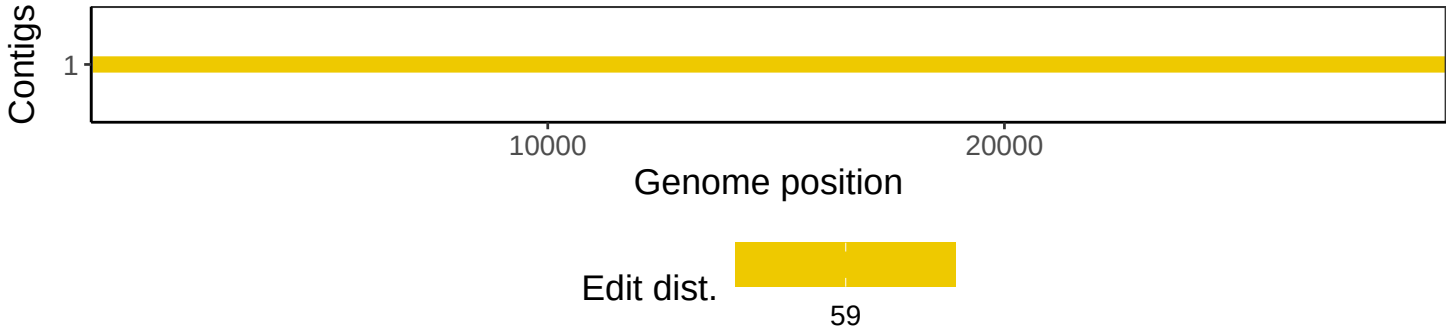
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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