COVID-19 subject HUP Q-0222

2021-05-21

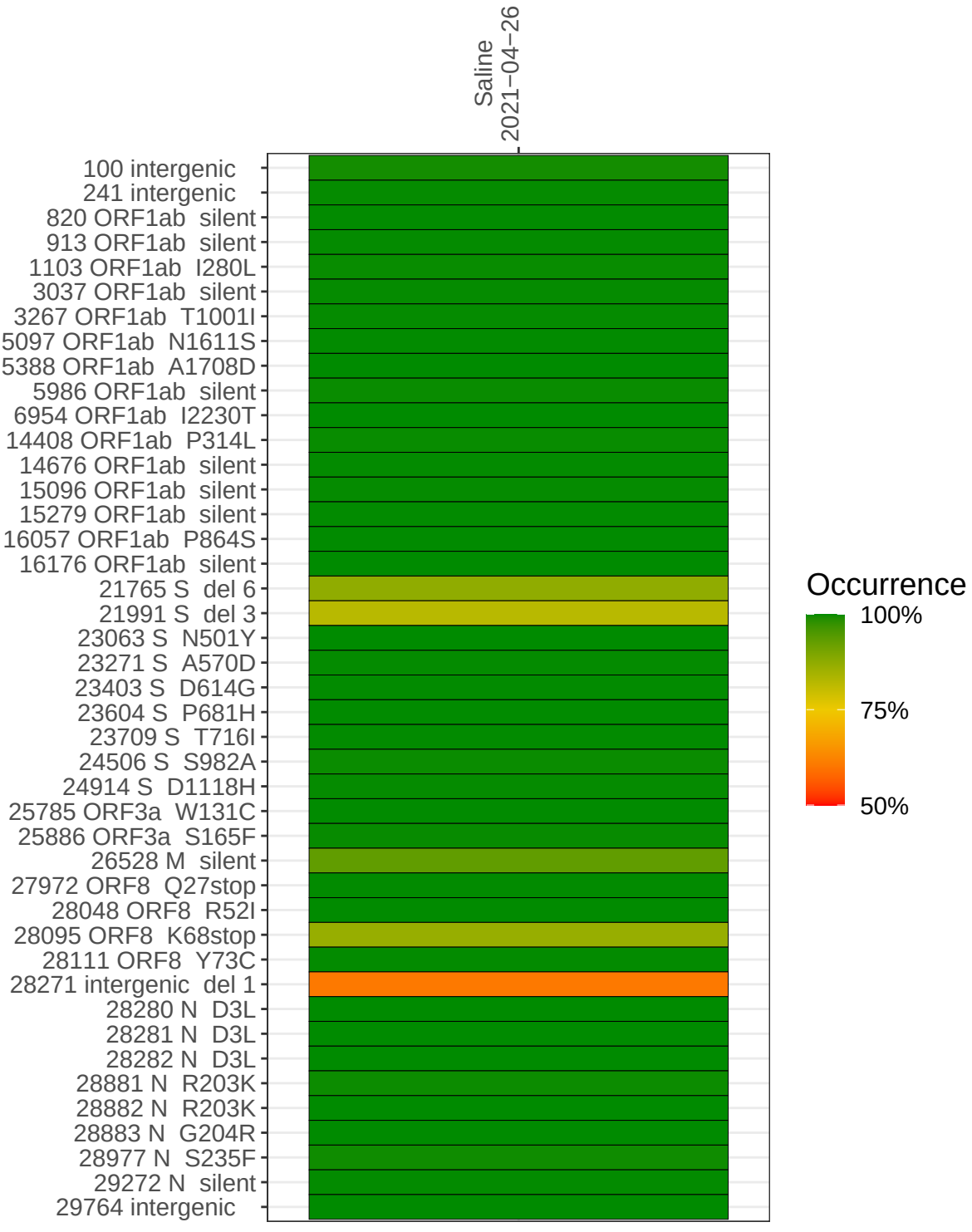
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

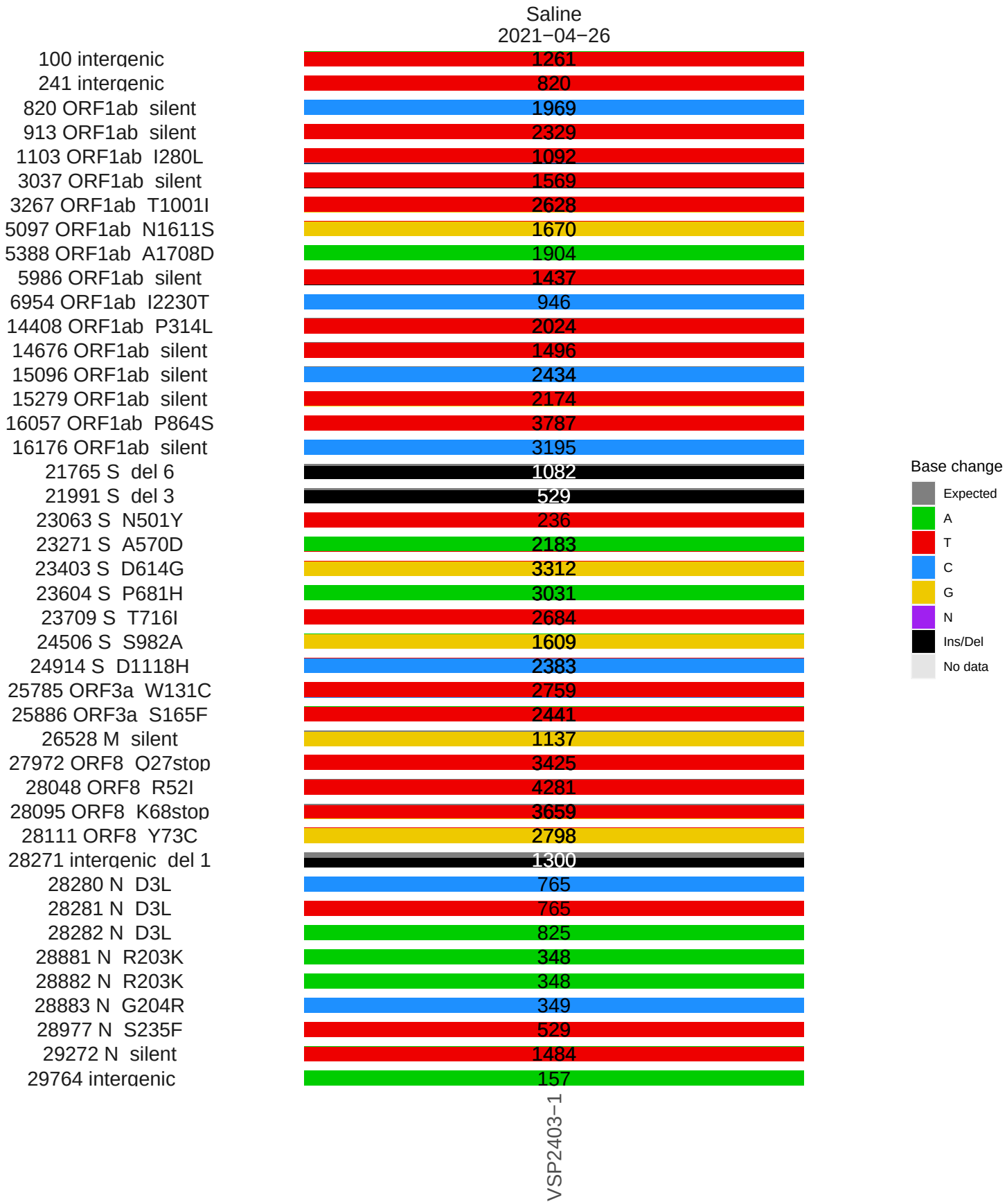
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2403-1	single experiment	NA	Saline	2021-04-26	29.81	B.1.1.7	99.8%	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.

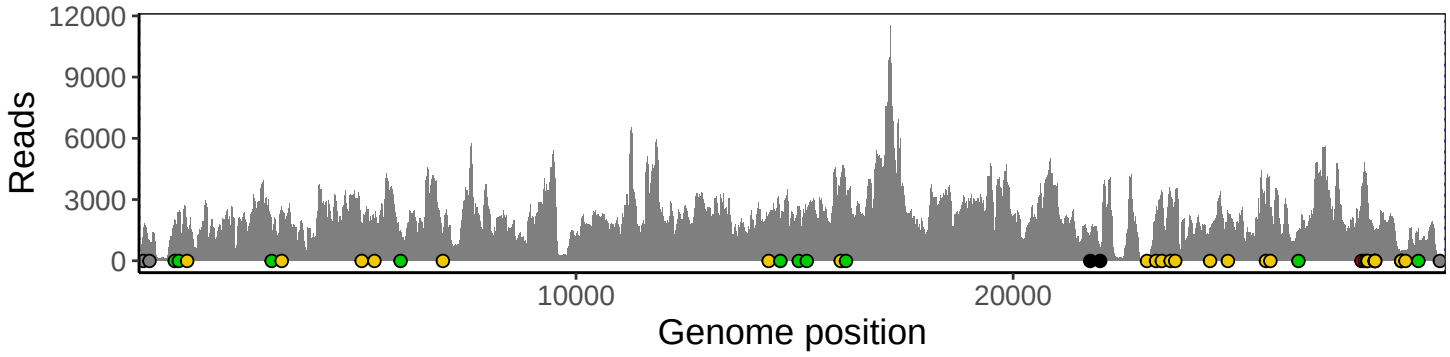



Saline
2021−04−26
100 intergenic 1261
241 intergenic 820
820 ORF1ab silent 1969
913 ORF1ab silent 2329
1103 ORF1ab I280L 1092
3037 ORF1ab silent 1569
3267 ORF1ab T1001I 2628
5097 ORF1ab N1611S 1670
5388 ORF1ab A1708D 1904
5986 ORF1ab silent 1437
6954 ORF1ab I2230T 946
14408 ORF1ab P314L 2024
14676 ORF1ab silent 1496
15096 ORF1ab silent 2434
15279 ORF1ab silent 2174
16057 ORF1ab P864S 3787
16176 ORF1ab silent 3195
21765 S del 6 1082
21991 S del 3 529
23063 S N501Y 236
23271 S A570D 2183
23403 S D614G 3312
23604 S P681H 3031
23709 S T716I 2684
24506 S S982A 1609
24914 S D1118H 2383
25785 ORF3a W131C 2759
25886 ORF3a S165F 2441
26528 M silent 1137
27972 ORF8 Q27stop 3425
28048 ORF8 R52I 4281
28095 ORF8 K68stop 3659
28111 ORF8 Y73C 2798
28271 intergenic del 1 1300
28280 N D3L 765
28281 N D3L 765
28282 N D3L 825
28881 N R203K 348
28882 N R203K 348
28883 N G204R 349
28977 N S235F 529
29272 N silent 1484
29764 intergenic 157
VSP2403−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

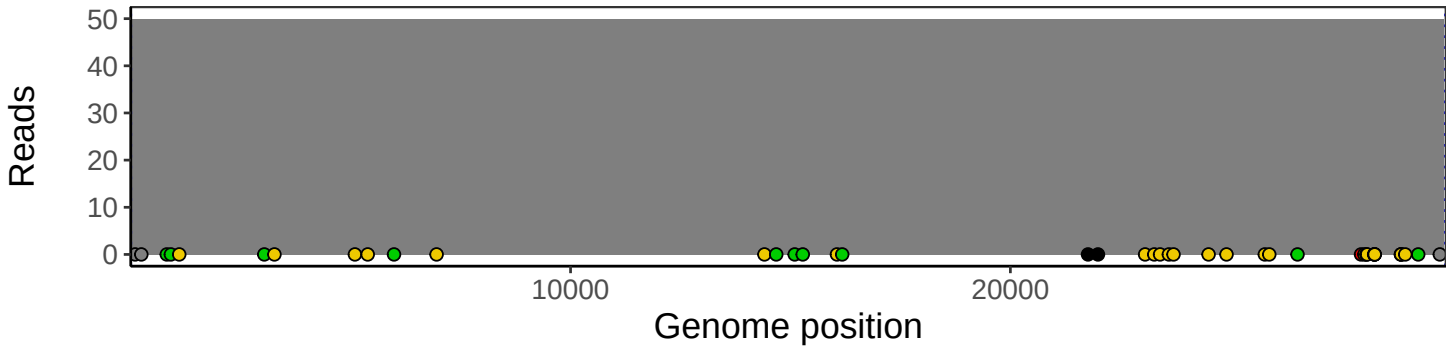
Analyses of individual experiments and composite results

VSP2403-1 | 2021-04-26 | Saline | HUP Q-0222 | genomes | single experiment

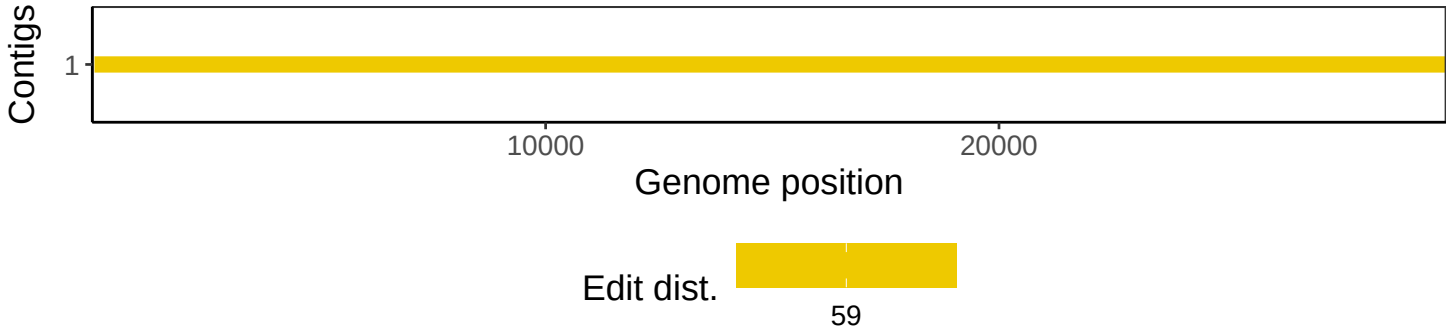
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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