COVID-19 subject HUP Q-0016

2021-03-29

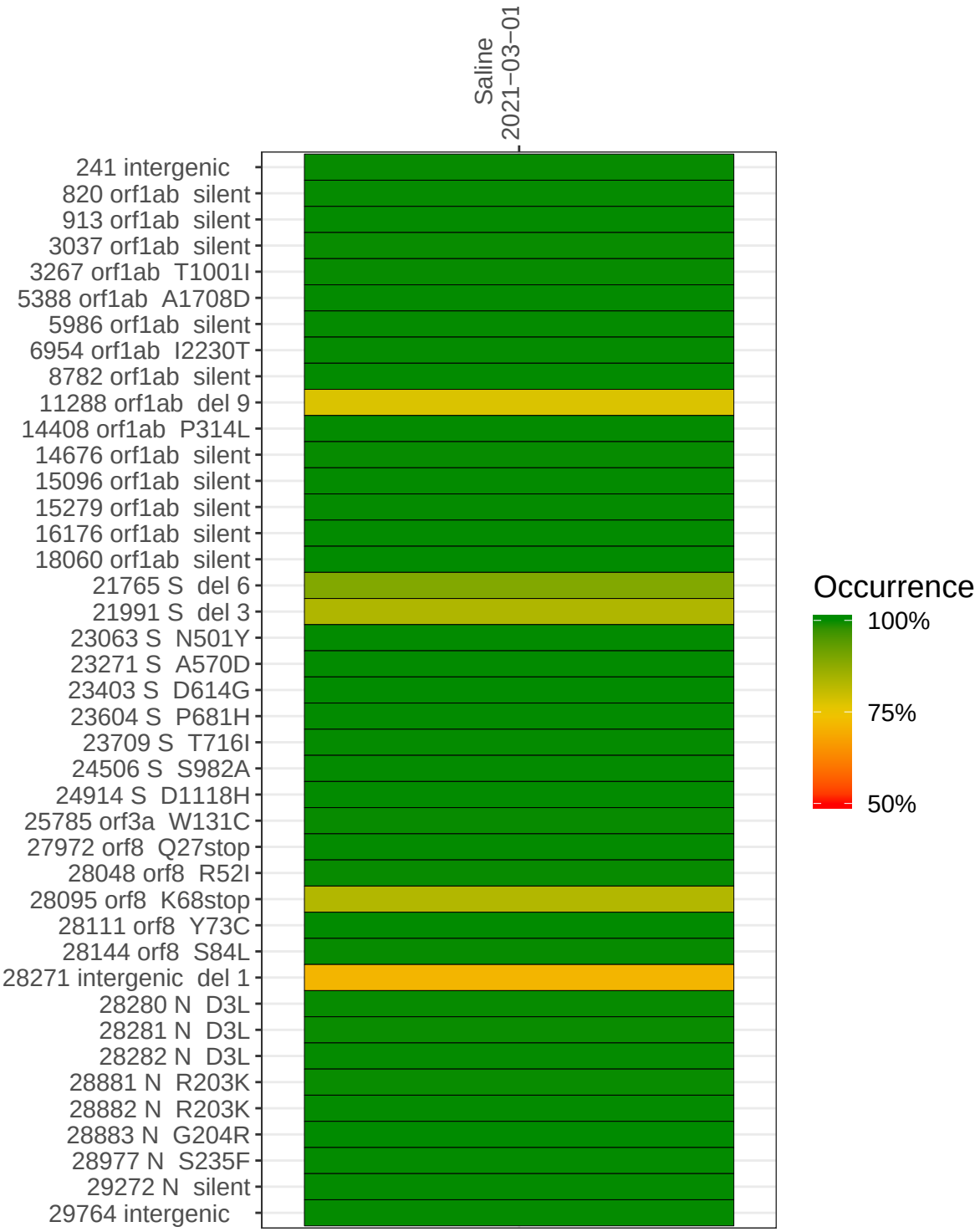
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

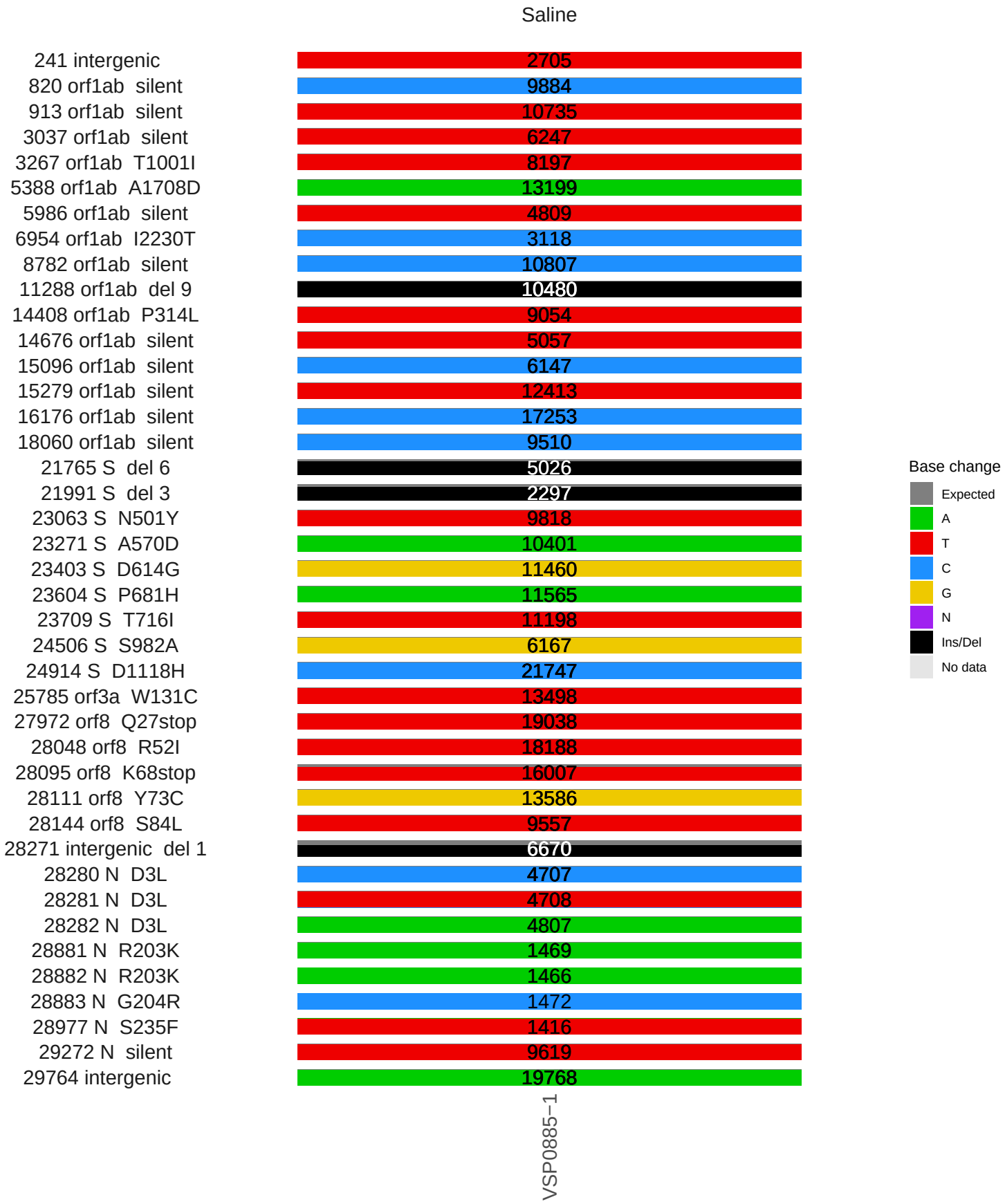
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0885-1	single experiment	NA	Saline	2021-03-01	29.88	B.1.1.7	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

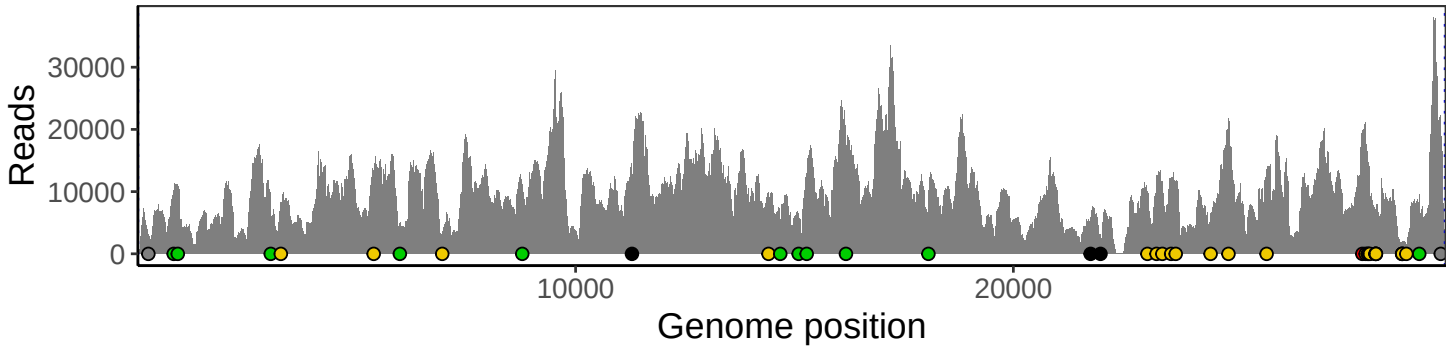



Saline
241 intergenic 2705
820 orf1ab silent 9884
913 orf1ab silent 10735
3037 orf1ab silent 6247
3267 orf1ab T1001I 8197
5388 orf1ab A1708D 13199
5986 orf1ab silent 4809
6954 orf1ab I2230T 3118
8782 orf1ab silent 10807
11288 orf1ab del 9 10480
14408 orf1ab P314L 9054
14676 orf1ab silent 5057
15096 orf1ab silent 6147
15279 orf1ab silent 12413
16176 orf1ab silent 17253
18060 orf1ab silent 9510
21765 S del 6 5026
21991 S del 3 2297
23063 S N501Y 9818
23271 S A570D 10401
23403 S D614G 11460
23604 S P681H 11565
23709 S T716I 11198
24506 S S982A 6167
24914 S D1118H 21747
25785 orf3a W131C 13498
27972 orf8 Q27stop 19038
28048 orf8 R52I 18188
28095 orf8 K68stop 16007
28111 orf8 Y73C 13586
28144 orf8 S84L 9557
28271 intergenic del 1 6670
28280 N D3L 4707
28281 N D3L 4708
28282 N D3L 4807
28881 N R203K 1469
28882 N R203K 1466
28883 N G204R 1472
28977 N S235F 1416
29272 N silent 9619
29764 intergenic 19768
VSP0885−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

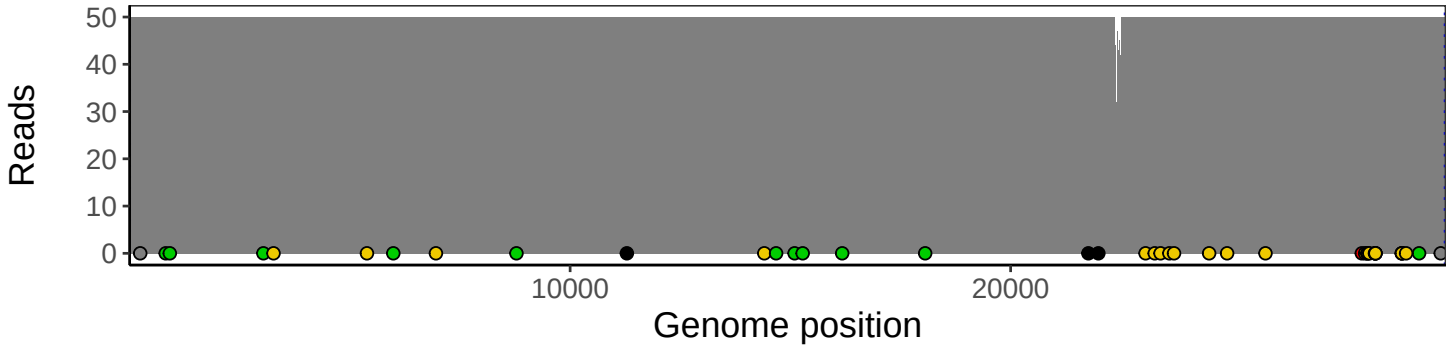
Analyses of individual experiments and composite results

VSP0885-1 | 2021-03-01 | Saline | HUP Q-0016 | genomes | single experiment

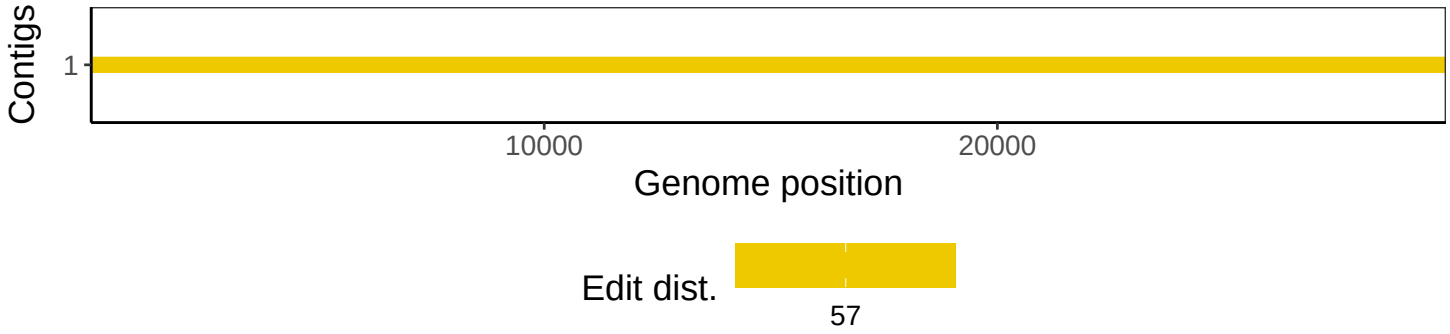
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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