COVID-19 subject SARS_CoV_303

2021-06-29

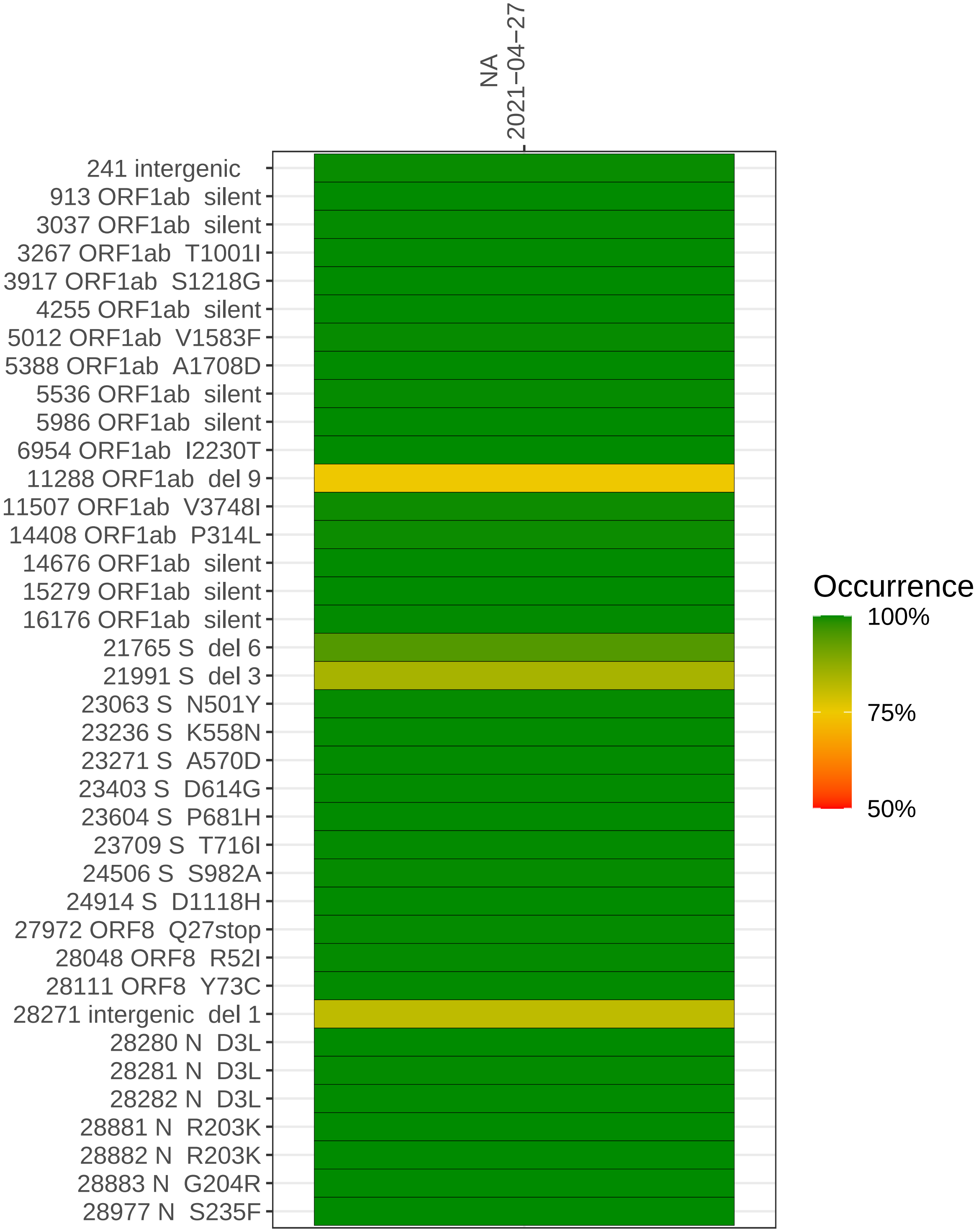
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

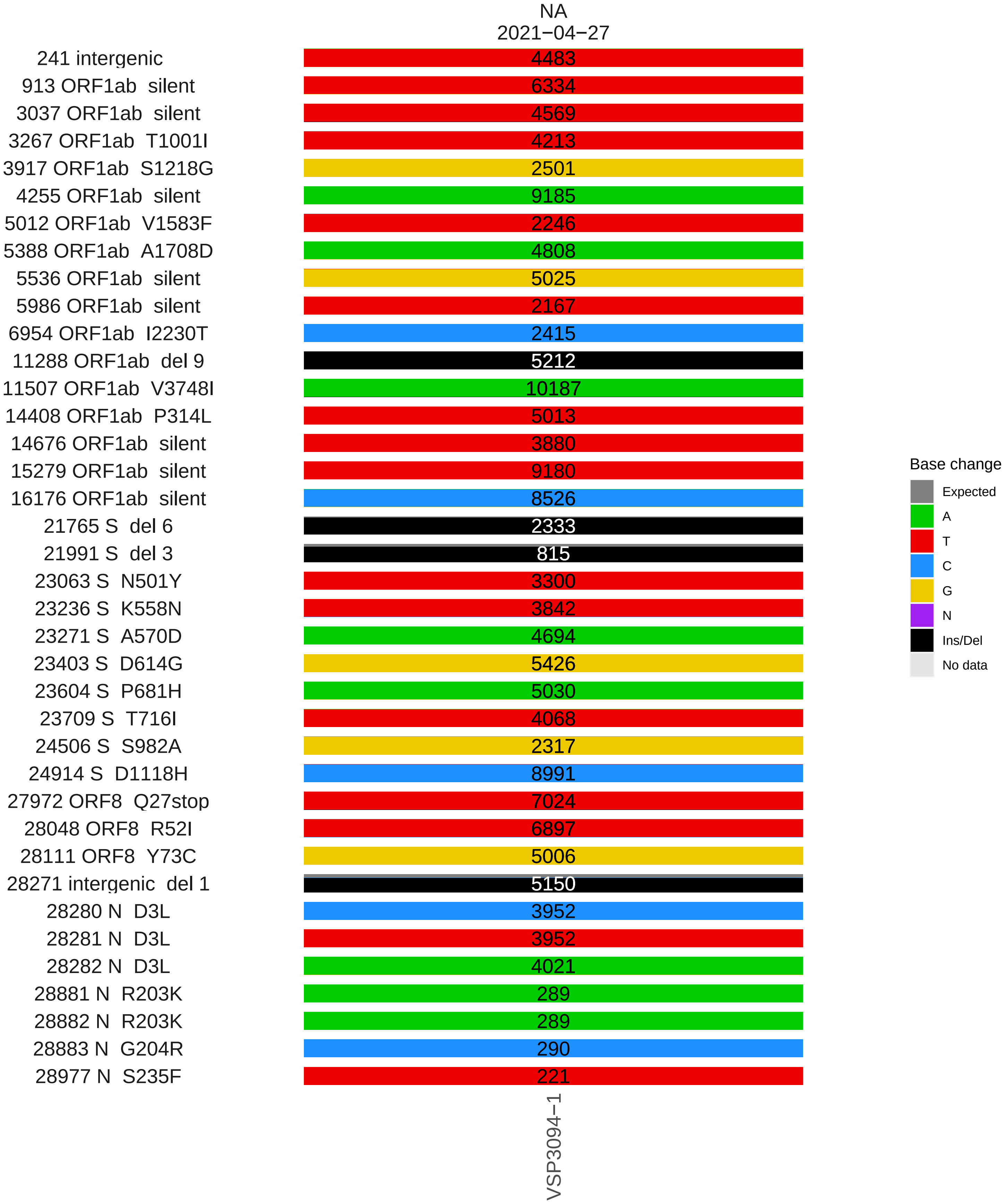
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP3094-1	single experiment	NA	NA	2021-04-27	29.89	B.1.1.7	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/NC_04551 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.

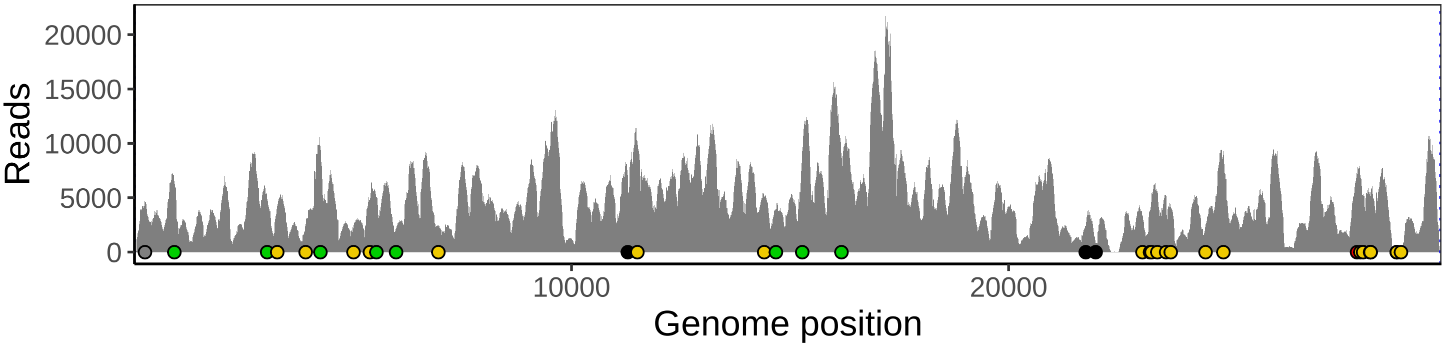



NA
2021−04−27
241 intergenic
4483
913 ORF1ab silent
6334
3037 ORF1ab silent
4569
3267 ORF1ab T1001I
4213
3917 ORF1ab S1218G
2501
4255 ORF1ab silent
9185
5012 ORF1ab V1583F
2246
5388 ORF1ab A1708D
4808
5536 ORF1ab silent
5025
5986 ORF1ab silent
2167
6954 ORF1ab I2230T
2415
11288 ORF1ab del 9
5212
11507 ORF1ab V3748I
10187
14408 ORF1ab P314L
5013
14676 ORF1ab silent
3880
15279 ORF1ab silent
9180
16176 ORF1ab silent
8526
21765 S del 6
2333
21991 S del 3
815
23063 S N501Y
3300
23236 S K558N
3842
23271 S A570D
4694
23403 S D614G
5426
23604 S P681H
5030
23709 S T716I
4068
24506 S S982A
2317
24914 S D1118H
8991
27972 ORF8 Q27stop
7024
28048 ORF8 R52I
6897
28111 ORF8 Y73C
5006
28271 intergenic del 1
5150
28280 N D3L
3952
28281 N D3L
3952
28282 N D3L
4021
28881 N R203K
289
28882 N R203K
289
28883 N G204R
290
28977 N S235F
221
VSP3094−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

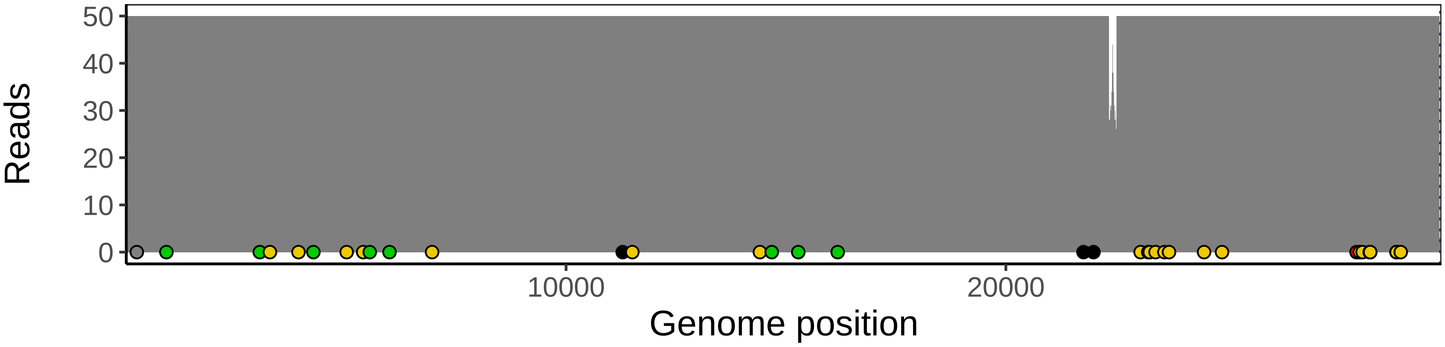
Analyses of individual experiments and composite results

VSP3094-1 | 2021-04-27 | NA | SARS_CoV_303 | genomes | single experiment

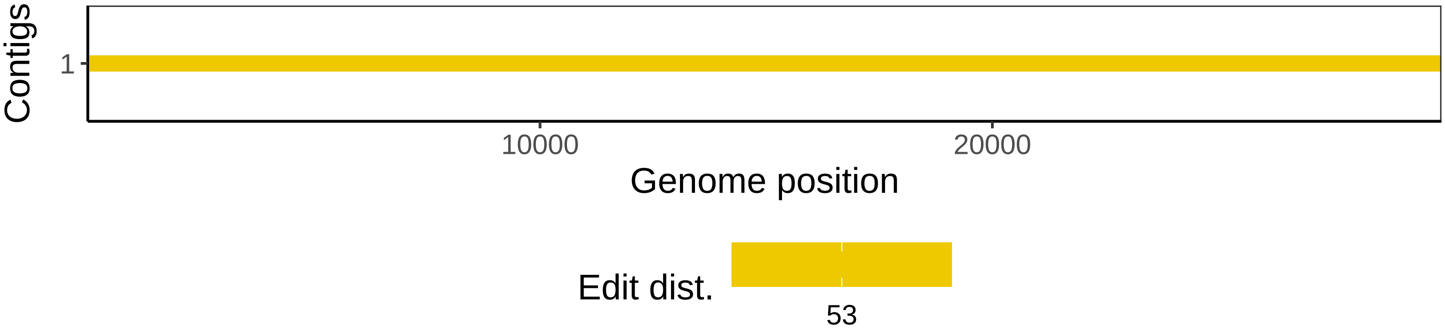
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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