COVID-19 subject 211

2020-11-30

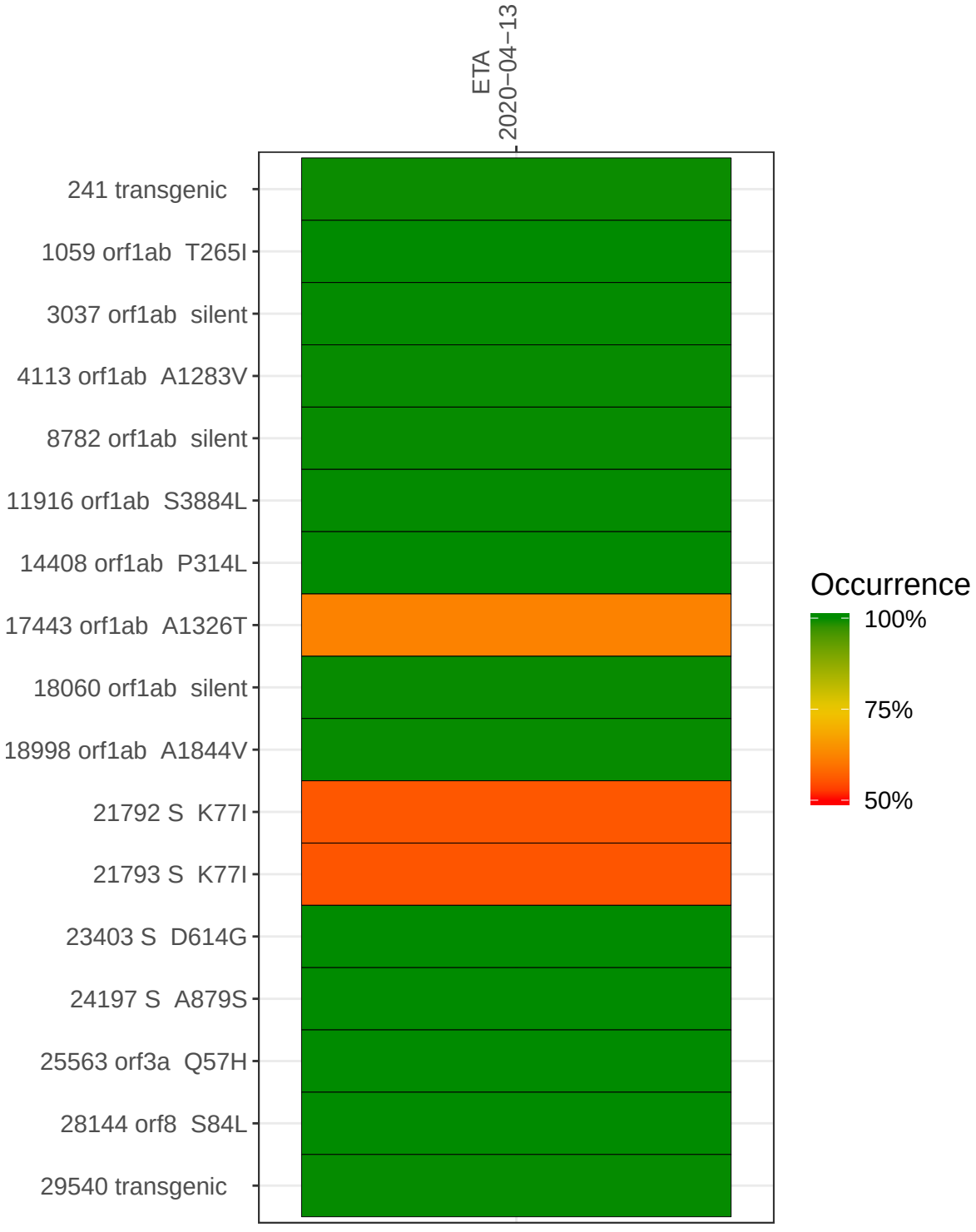
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

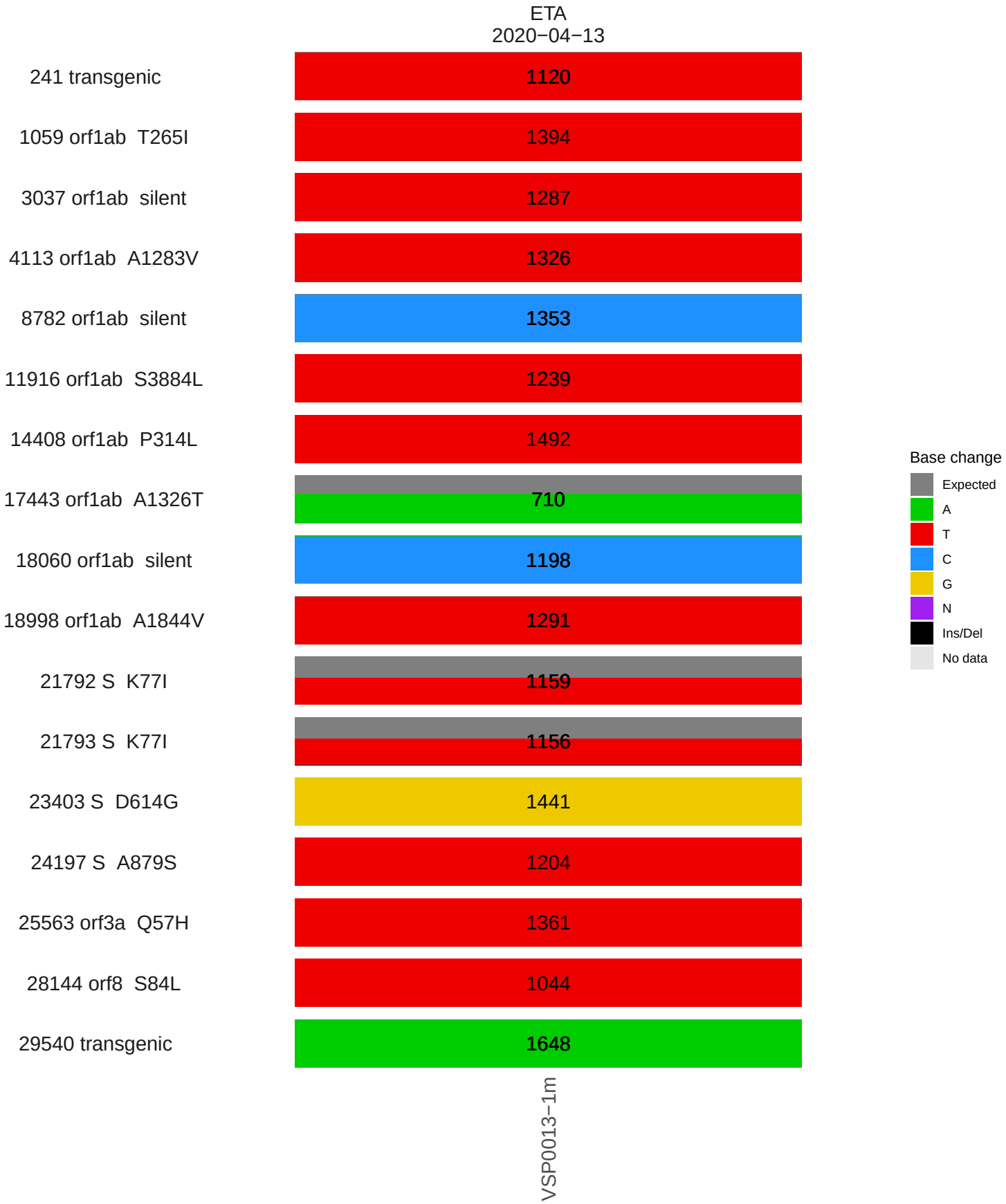
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0013-1m	single experiment	NA	ETA	2020-04-13	29.90	99.8%	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 for 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.

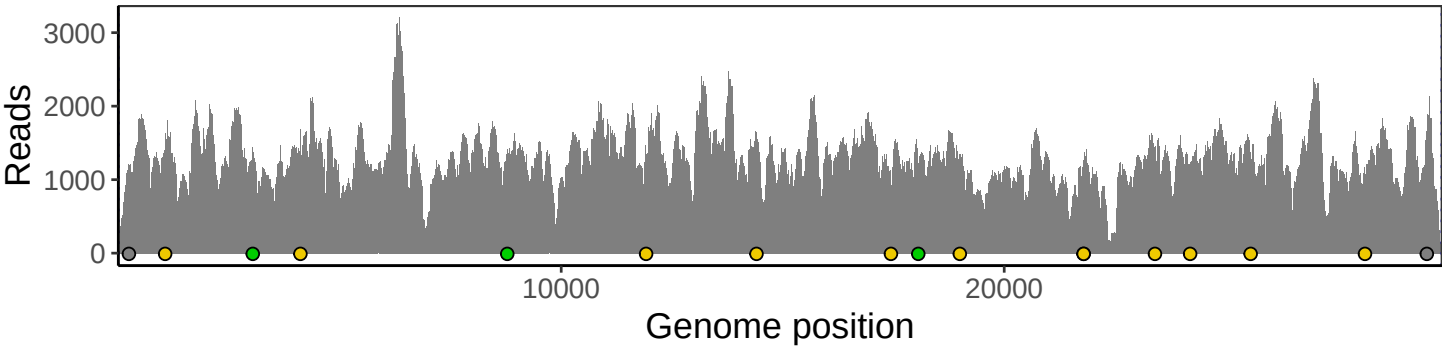



ETA
2020−04−13
241 transgenic
1120
1059 orf1ab T265I
1394
3037 orf1ab silent
1287
4113 orf1ab A1283V
1326
8782 orf1ab silent
1353
11916 orf1ab S3884L
1239
14408 orf1ab P314L
1492
17443 orf1ab A1326T
710
18060 orf1ab silent
1198
18998 orf1ab A1844V
1291
21792 S K77I
1159
21793 S K77I
1156
23403 S D614G
1441
24197 S A879S
1204
25563 orf3a Q57H
1361
28144 orf8 S84L
1044
29540 transgenic
1648
VSP0013−1m
Base change
Expected
A
T
C
G
N
Ins/Del
No data

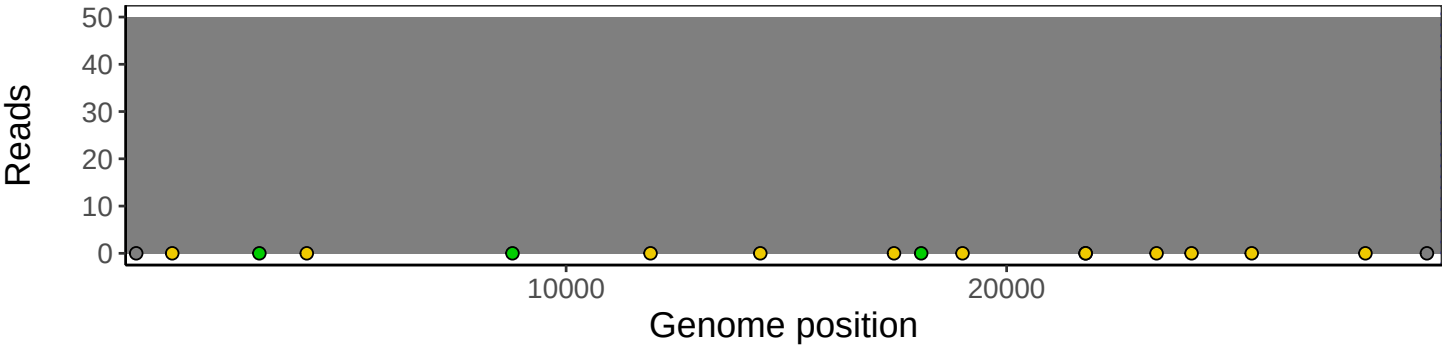
Analyses of individual experiments and composite results.

VSP0013-1m | 2020-04-13 | ETA | 211-tri | 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.