COVID-19 subject SRR11783611

2020-09-29

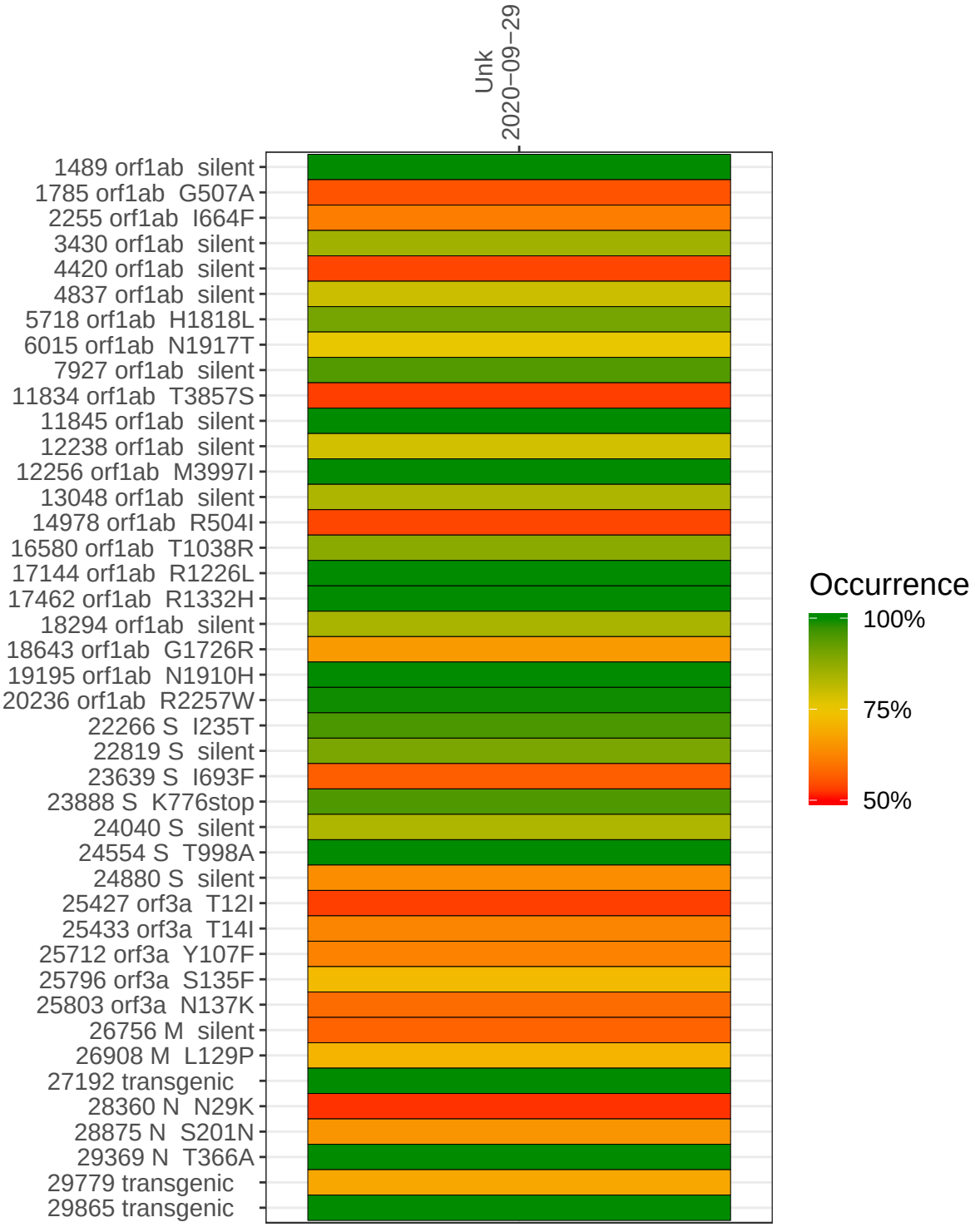
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

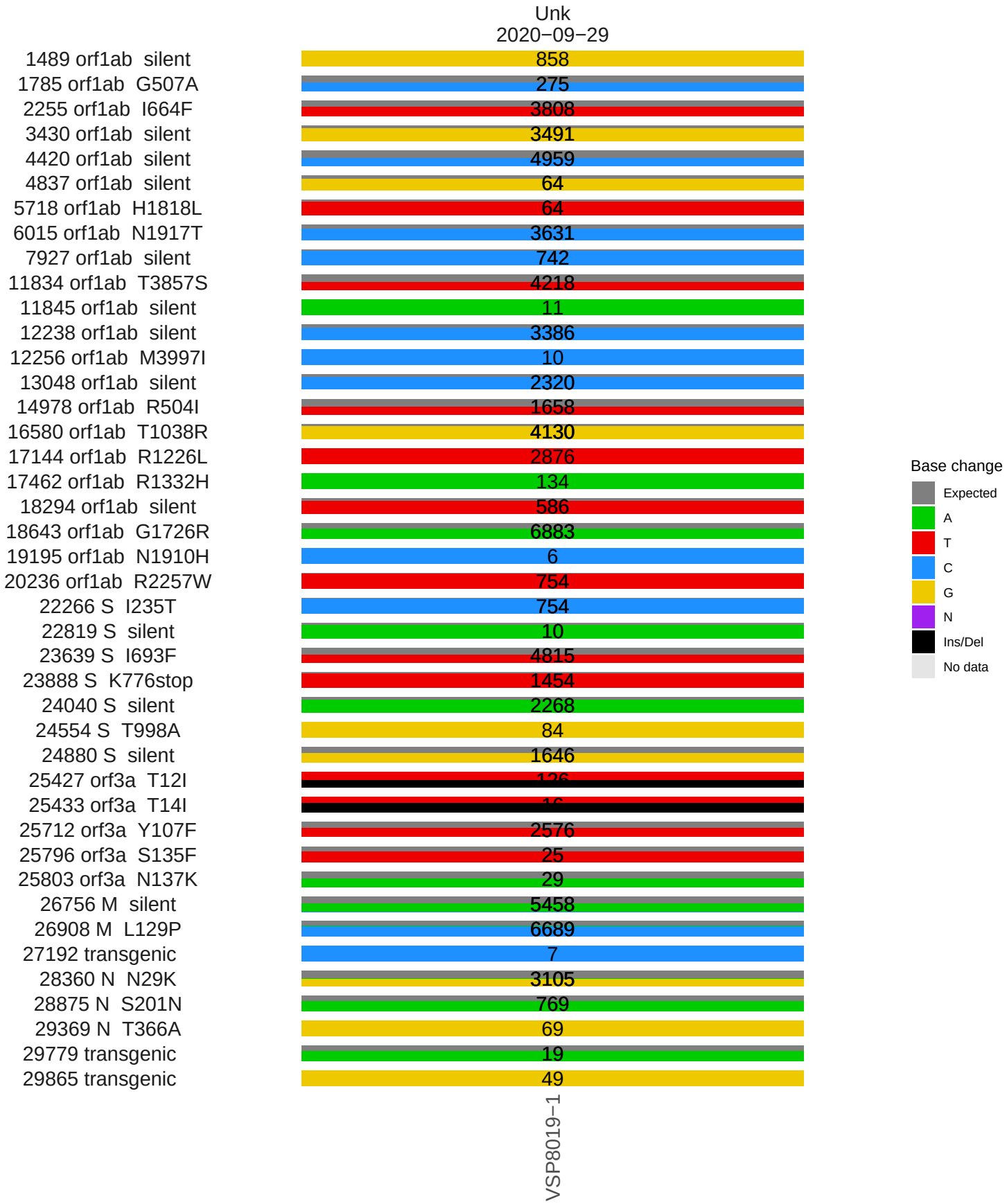
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8019-1	single experiment	NA	Unk	2020-09-29	1.65	94.5%	92.9%

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.

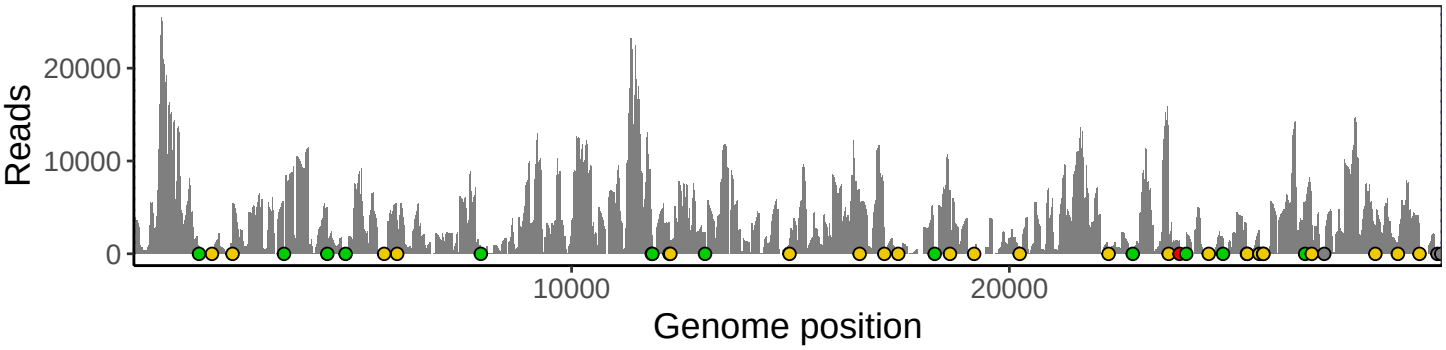



Unk
2020−09−29
1489 orf1ab silent
1785 orf1ab G507A
2255 orf1ab I664F
3430 orf1ab silent
4420 orf1ab silent
4837 orf1ab silent
5718 orf1ab H1818L
6015 orf1ab N1917T
7927 orf1ab silent
11834 orf1ab T3857S
11845 orf1ab silent
12238 orf1ab silent
12256 orf1ab M3997I
13048 orf1ab silent
14978 orf1ab R504I
16580 orf1ab T1038R
17144 orf1ab R1226L
17462 orf1ab R1332H
18294 orf1ab silent
18643 orf1ab G1726R
19195 orf1ab N1910H
20236 orf1ab R2257W
22266 S I235T
22819 S silent
23639 S I693F
23888 S K776stop
24040 S silent
24554 S T998A
24880 S silent
25427 orf3a T12I
25433 orf3a T14I
25712 orf3a Y107F
25796 orf3a S135F
25803 orf3a N137K
26756 M silent
26908 M L129P
27192 transgenic
28360 N N29K
28875 N S201N
29369 N T366A
29779 transgenic
29865 transgenic
858
275
3808
3491
4959
64
64
3631
742
4218
11
3386
10
2320
1658
4130
2876
134
586
6883
6
754
754
10
4815
1454
2268
84
1646
126
16
2576
25
29
5458
6689
7
3105
769
69
19
49
VSP8019−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

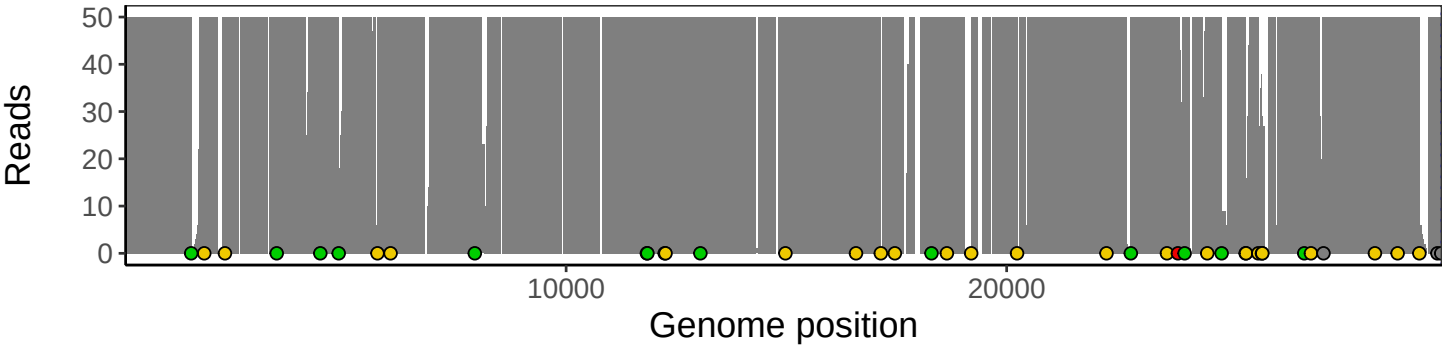
Analyses of individual experiments and composite results.

VSP8019-1 | 2020-09-29 | Unk | SRR11783611 | 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.