COVID-19 subject SRR11783606

2020-09-29

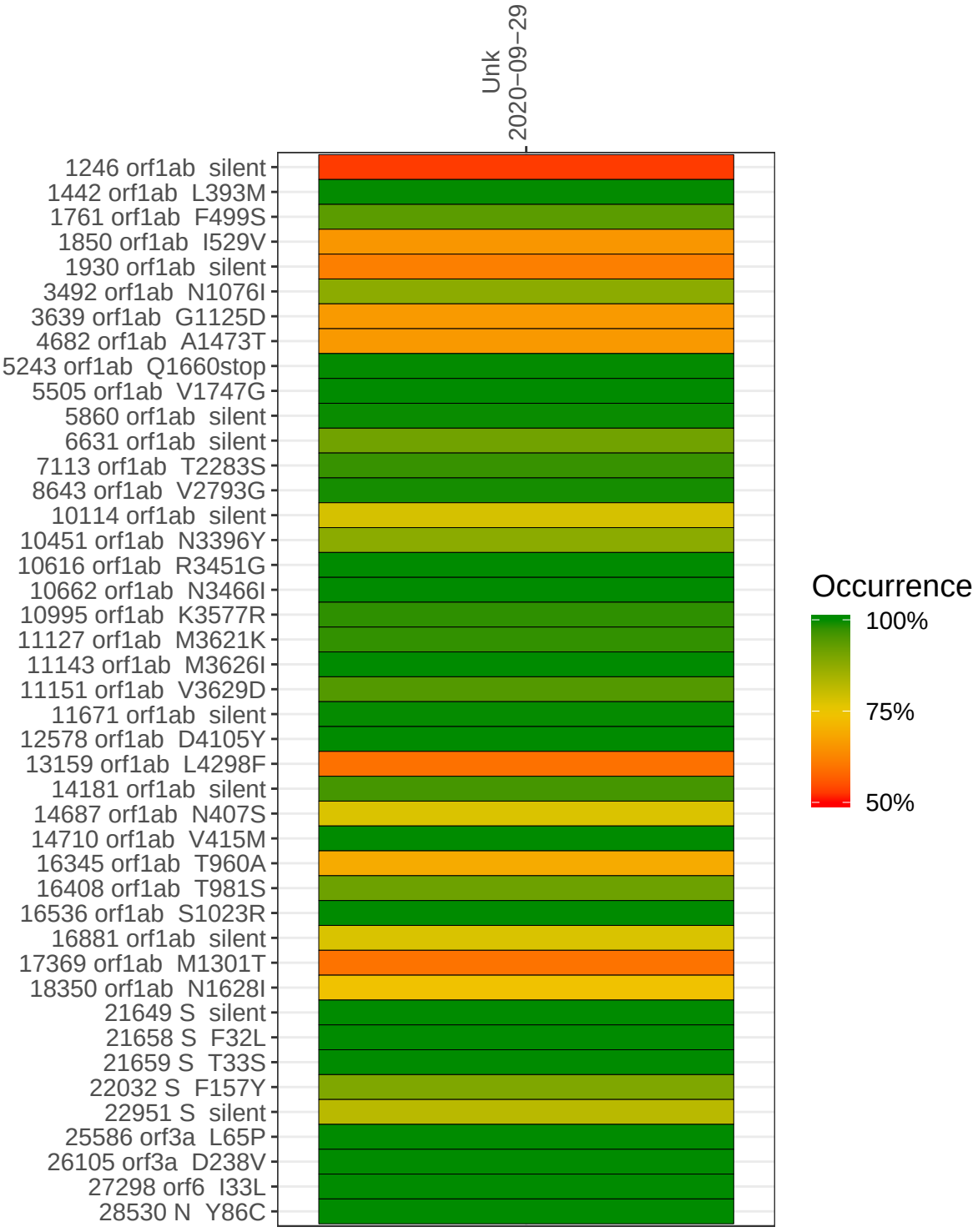
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

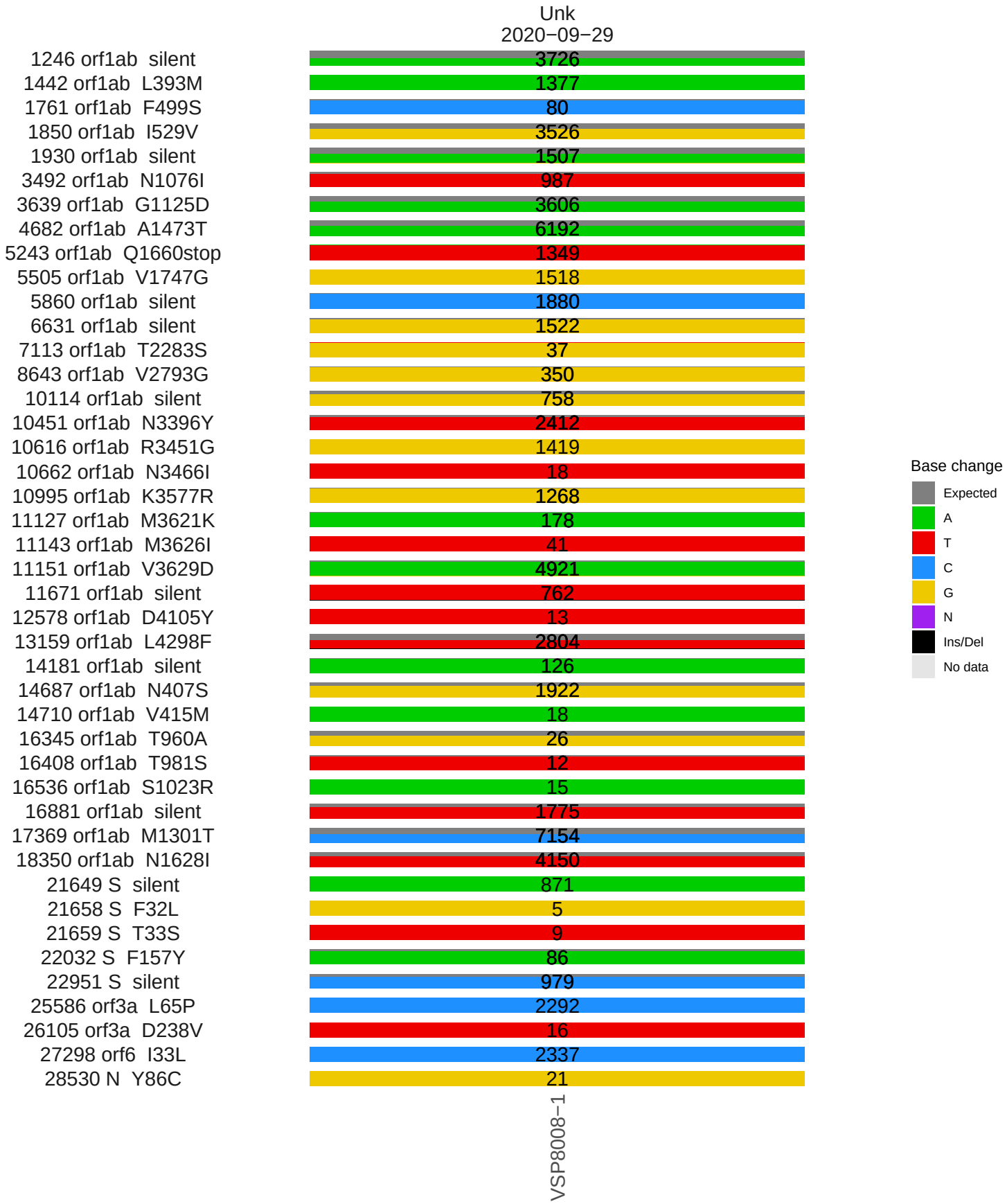
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8008-1	single experiment	NA	Unk	2020-09-29	1.12	79.0%	77.1%

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.

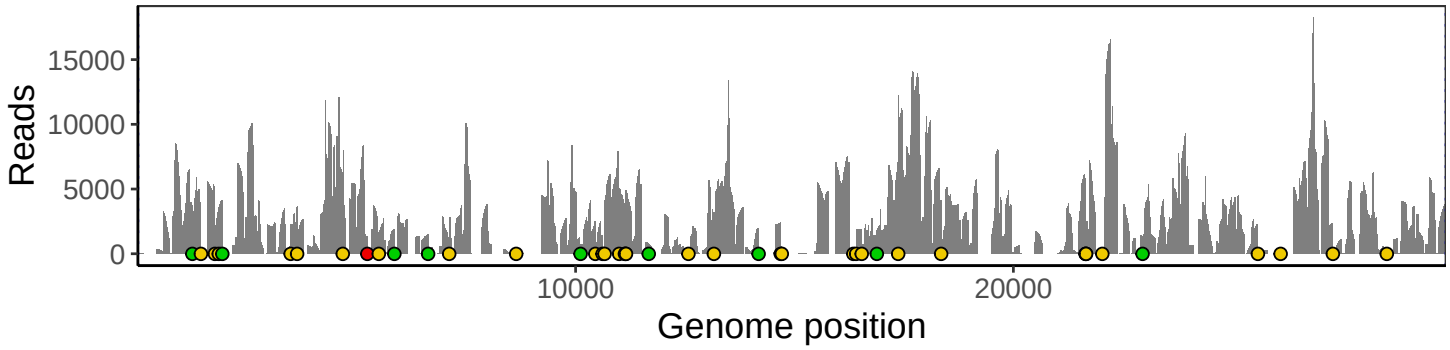



Unk
2020−09−29
1246 orf1ab silent
1442 orf1ab L393M
1761 orf1ab F499S
1850 orf1ab I529V
1930 orf1ab silent
3492 orf1ab N1076I
3639 orf1ab G1125D
4682 orf1ab A1473T
5243 orf1ab Q1660stop
5505 orf1ab V1747G
5860 orf1ab silent
6631 orf1ab silent
7113 orf1ab T2283S
8643 orf1ab V2793G
10114 orf1ab silent
10451 orf1ab N3396Y
10616 orf1ab R3451G
10662 orf1ab N3466I
10995 orf1ab K3577R
11127 orf1ab M3621K
11143 orf1ab M3626I
11151 orf1ab V3629D
11671 orf1ab silent
12578 orf1ab D4105Y
13159 orf1ab L4298F
14181 orf1ab silent
14687 orf1ab N407S
14710 orf1ab V415M
16345 orf1ab T960A
16408 orf1ab T981S
16536 orf1ab S1023R
16881 orf1ab silent
17369 orf1ab M1301T
18350 orf1ab N1628I
21649 S silent
21658 S F32L
21659 S T33S
22032 S F157Y
22951 S silent
25586 orf3a L65P
26105 orf3a D238V
27298 orf6 I33L
28530 N Y86C
3726
1377
80
3526
1507
987
3606
6192
1349
1518
1880
1522
37
350
758
2412
1419
18
1268
178
41
4921
762
13
2804
126
1922
18
26
12
15
1775
7154
4150
871
5
9
86
979
2292
16
2337
21
VSP8008−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

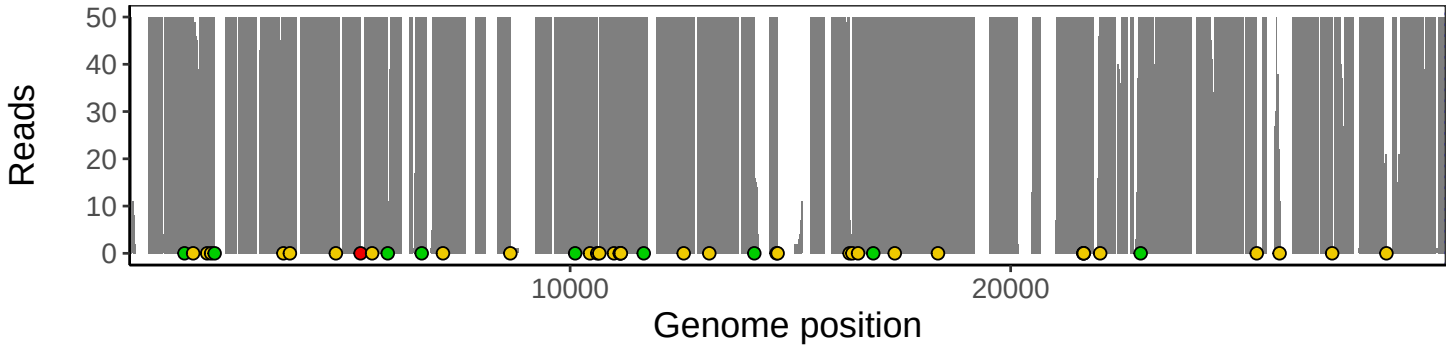
Analyses of individual experiments and composite results.

VSP8008-1 | 2020-09-29 | Unk | SRR11783606 | 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.