COVID-19 subject SRR11783584

2020-09-29

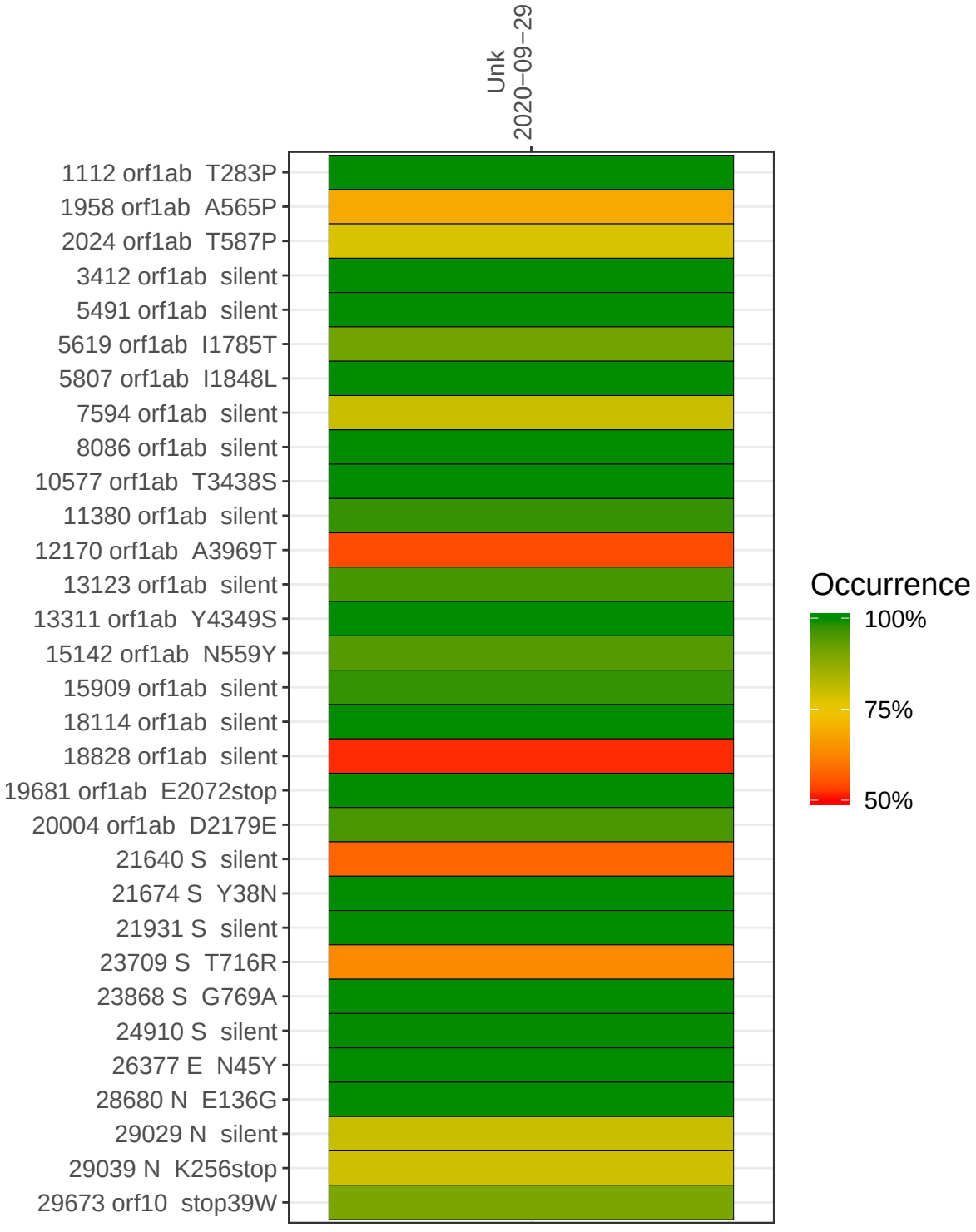
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

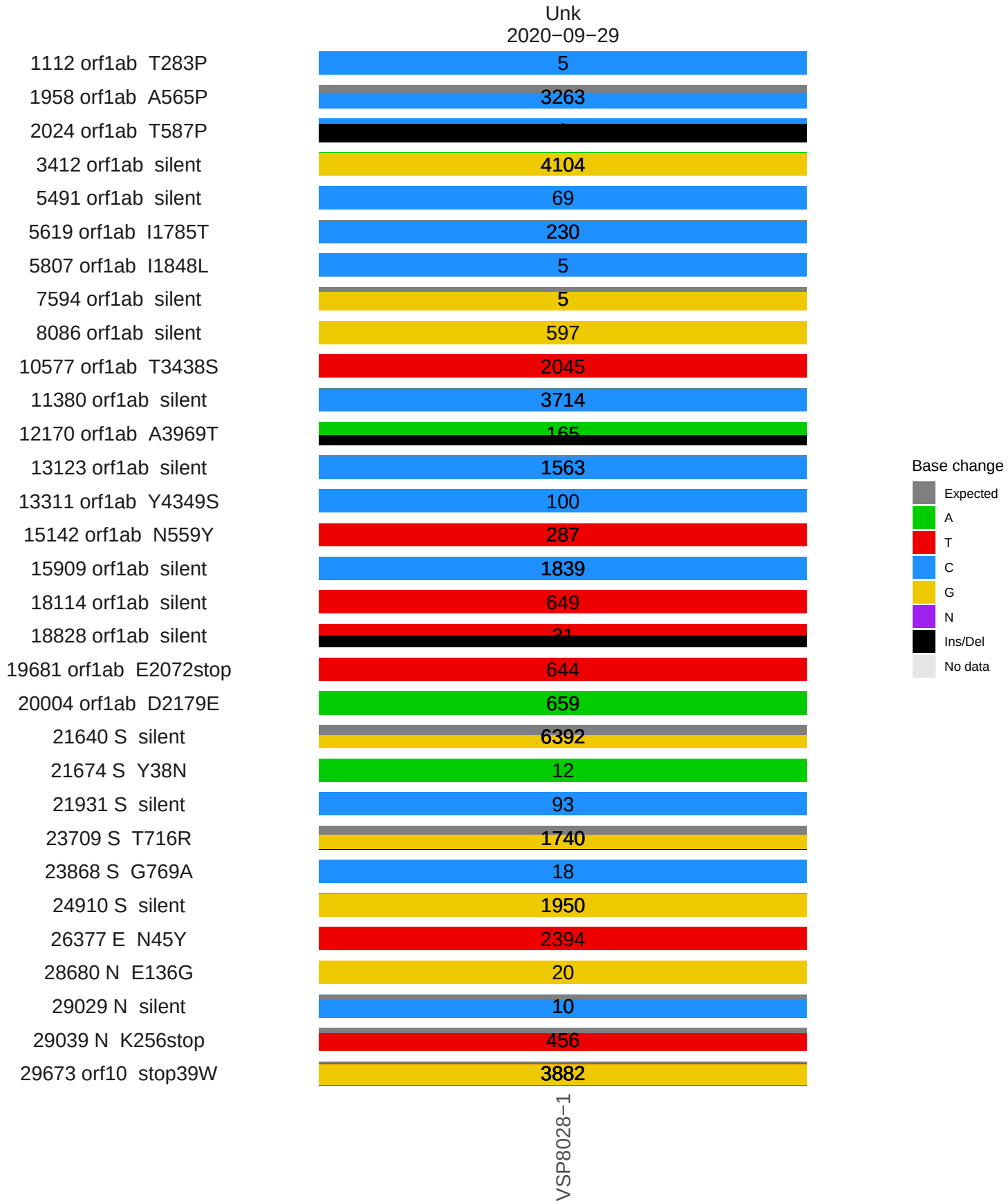
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8028-1	single experiment	NA	Unk	2020-09-29	0.59	62.4%	59.4%

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.

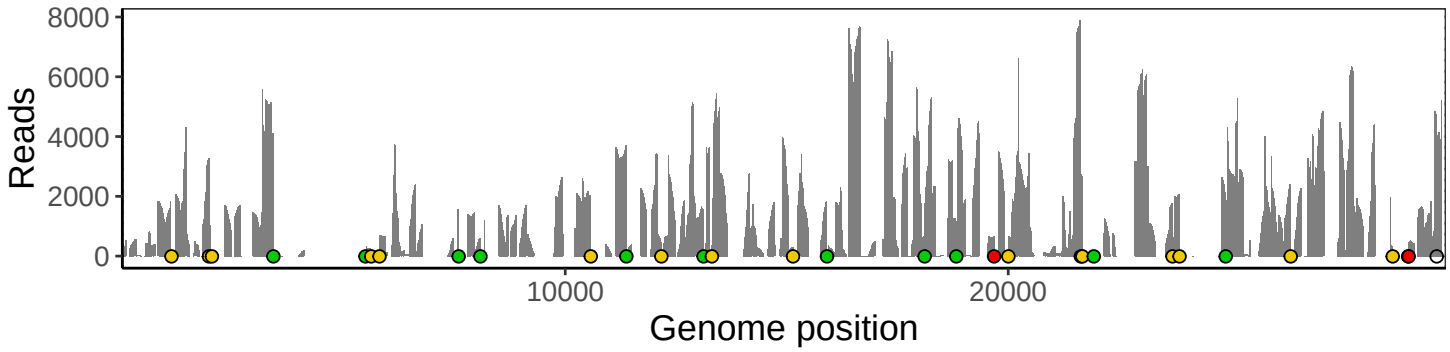



Unk
2020−09−29
1112 orf1ab T283P
1958 orf1ab A565P
2024 orf1ab T587P
3412 orf1ab silent
5491 orf1ab silent
5619 orf1ab I1785T
5807 orf1ab I1848L
7594 orf1ab silent
8086 orf1ab silent
10577 orf1ab T3438S
11380 orf1ab silent
12170 orf1ab A3969T
13123 orf1ab silent
13311 orf1ab Y4349S
15142 orf1ab N559Y
15909 orf1ab silent
18114 orf1ab silent
18828 orf1ab silent
19681 orf1ab E2072stop
20004 orf1ab D2179E
21640 S silent
21674 S Y38N
21931 S silent
23709 S T716R
23868 S G769A
24910 S silent
26377 E N45Y
28680 N E136G
29029 N silent
29039 N K256stop
29673 orf10 stop39W
5
3263
4104
69
230
5
5
597
2045
3714
1563
100
287
1839
649
644
659
6392
12
93
1740
18
1950
2394
20
10
456
3882
VSP8028−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

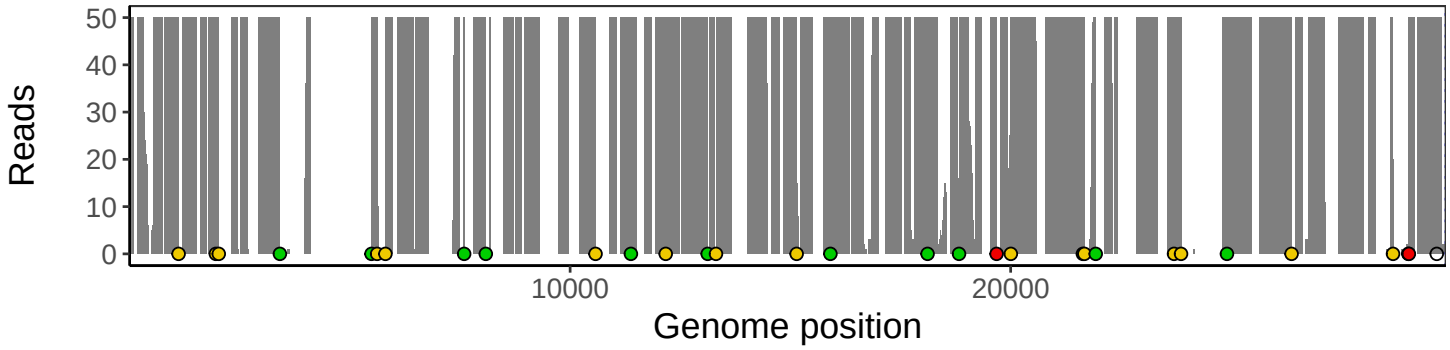
Analyses of individual experiments and composite results.

VSP8028-1 | 2020-09-29 | Unk | SRR11783584 | 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.