COVID-19 subject SRR11783603

2020-09-29

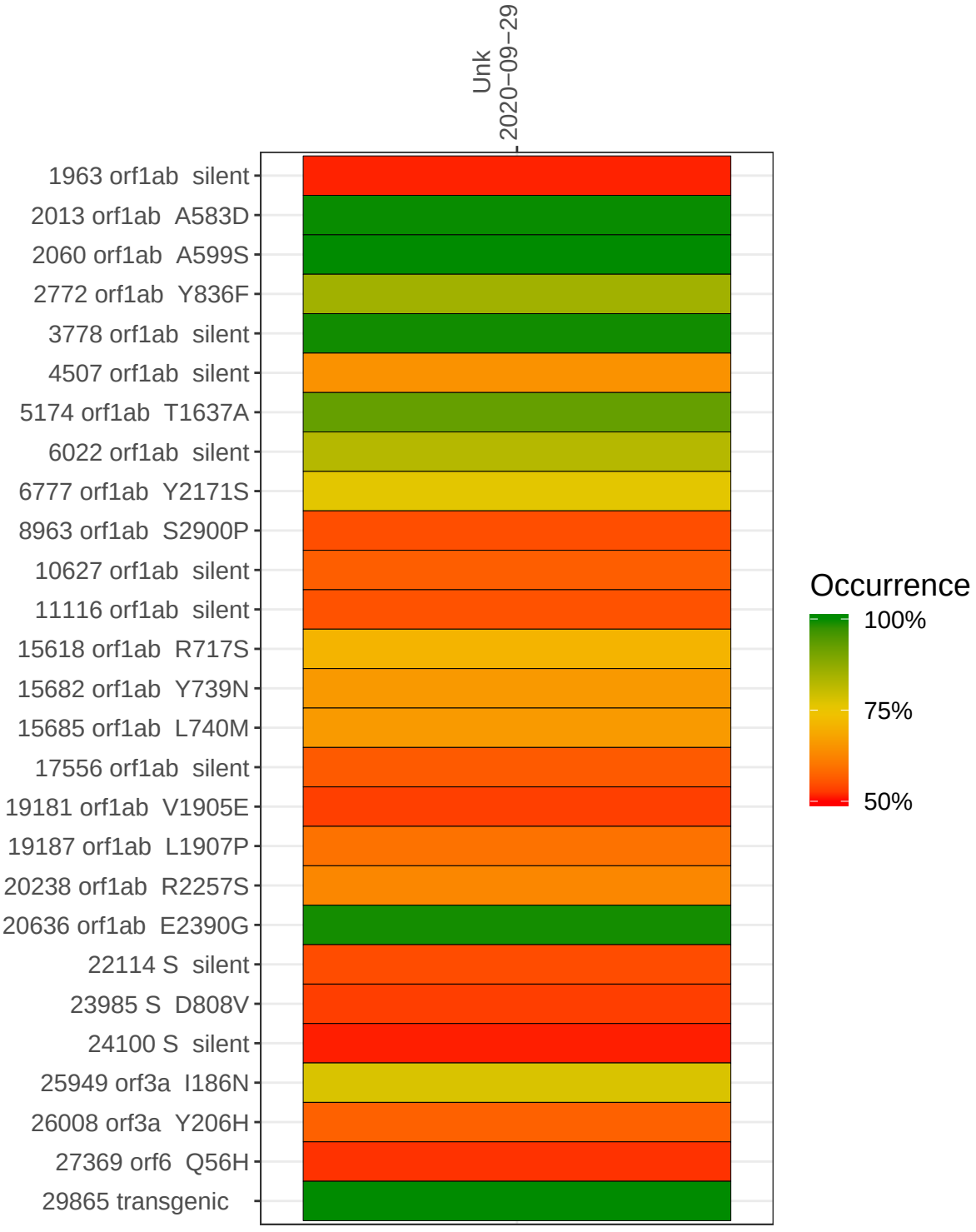
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

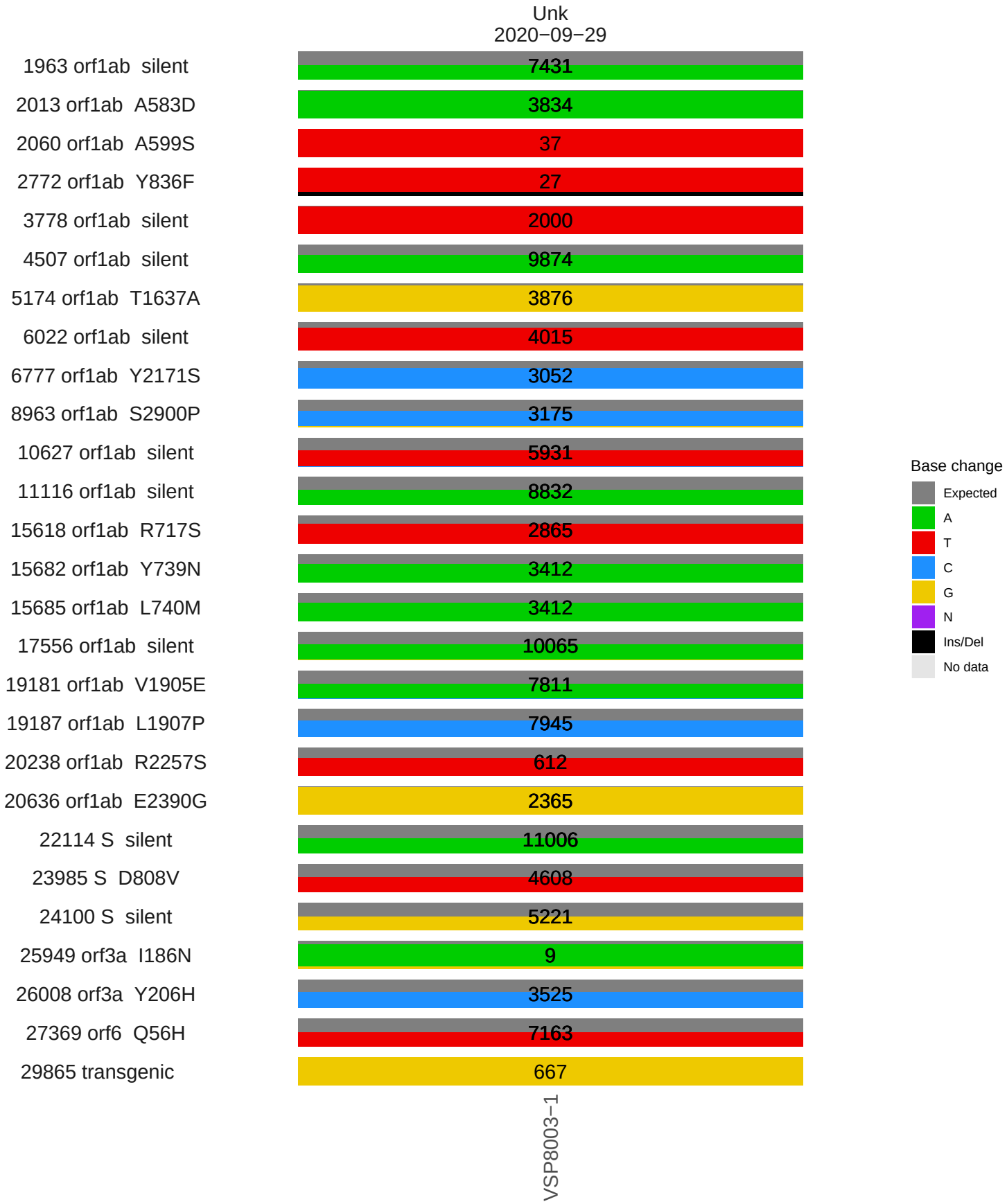
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8003-1	single experiment	NA	Unk	2020-09-29	8.63	99.3%	99.0%

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.

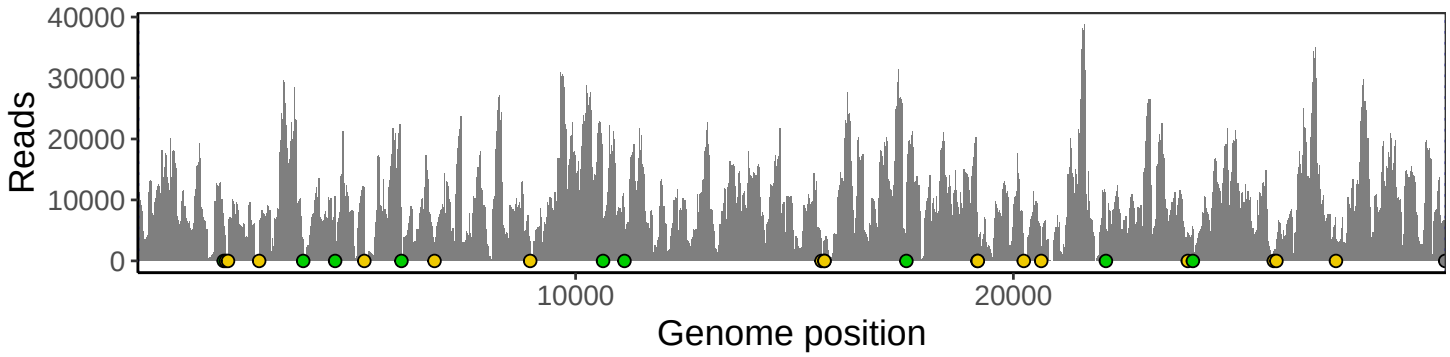



Unk
2020−09−29
1963 orf1ab silent
2013 orf1ab A583D
2060 orf1ab A599S
2772 orf1ab Y836F
3778 orf1ab silent
4507 orf1ab silent
5174 orf1ab T1637A
6022 orf1ab silent
6777 orf1ab Y2171S
8963 orf1ab S2900P
10627 orf1ab silent
11116 orf1ab silent
15618 orf1ab R717S
15682 orf1ab Y739N
15685 orf1ab L740M
17556 orf1ab silent
19181 orf1ab V1905E
19187 orf1ab L1907P
20238 orf1ab R2257S
20636 orf1ab E2390G
22114 S silent
23985 S D808V
24100 S silent
25949 orf3a I186N
26008 orf3a Y206H
27369 orf6 Q56H
29865 transgenic
7431
3834
37
27
2000
9874
3876
4015
3052
3175
5931
8832
2865
3412
3412
10065
7811
7945
612
2365
11006
4608
5221
9
3525
7163
667
VSP8003−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

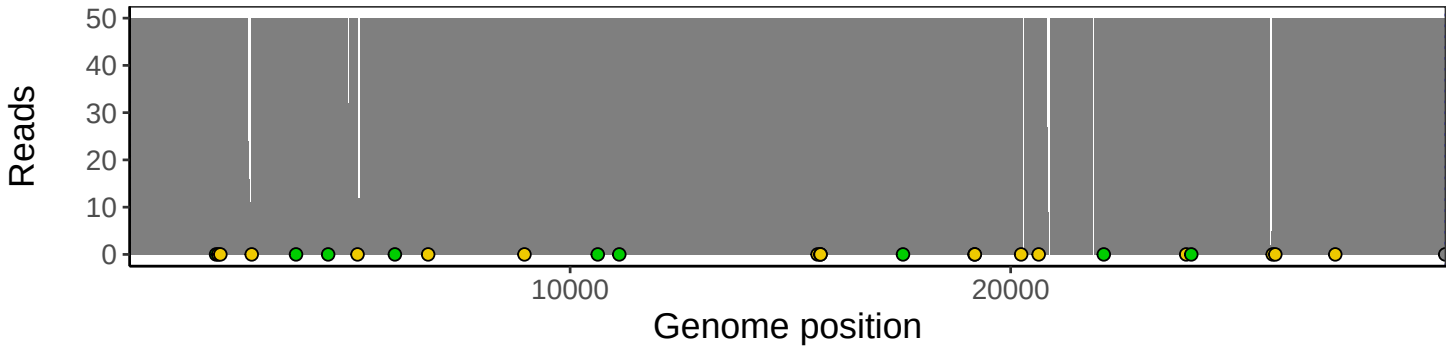
Analyses of individual experiments and composite results.

VSP8003-1 | 2020-09-29 | Unk | SRR11783603 | 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.