COVID-19 subject SRR11783580

2020-09-29

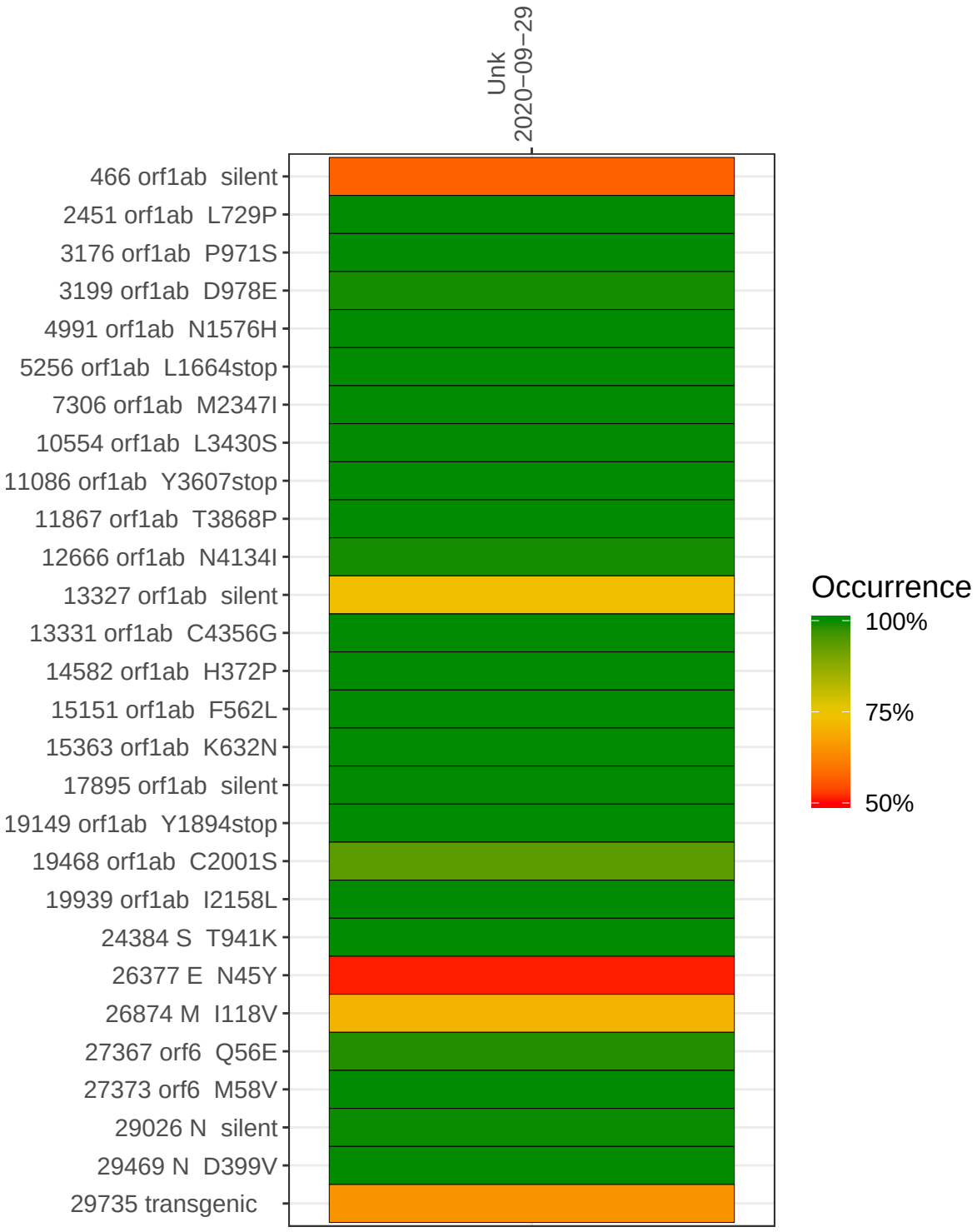
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

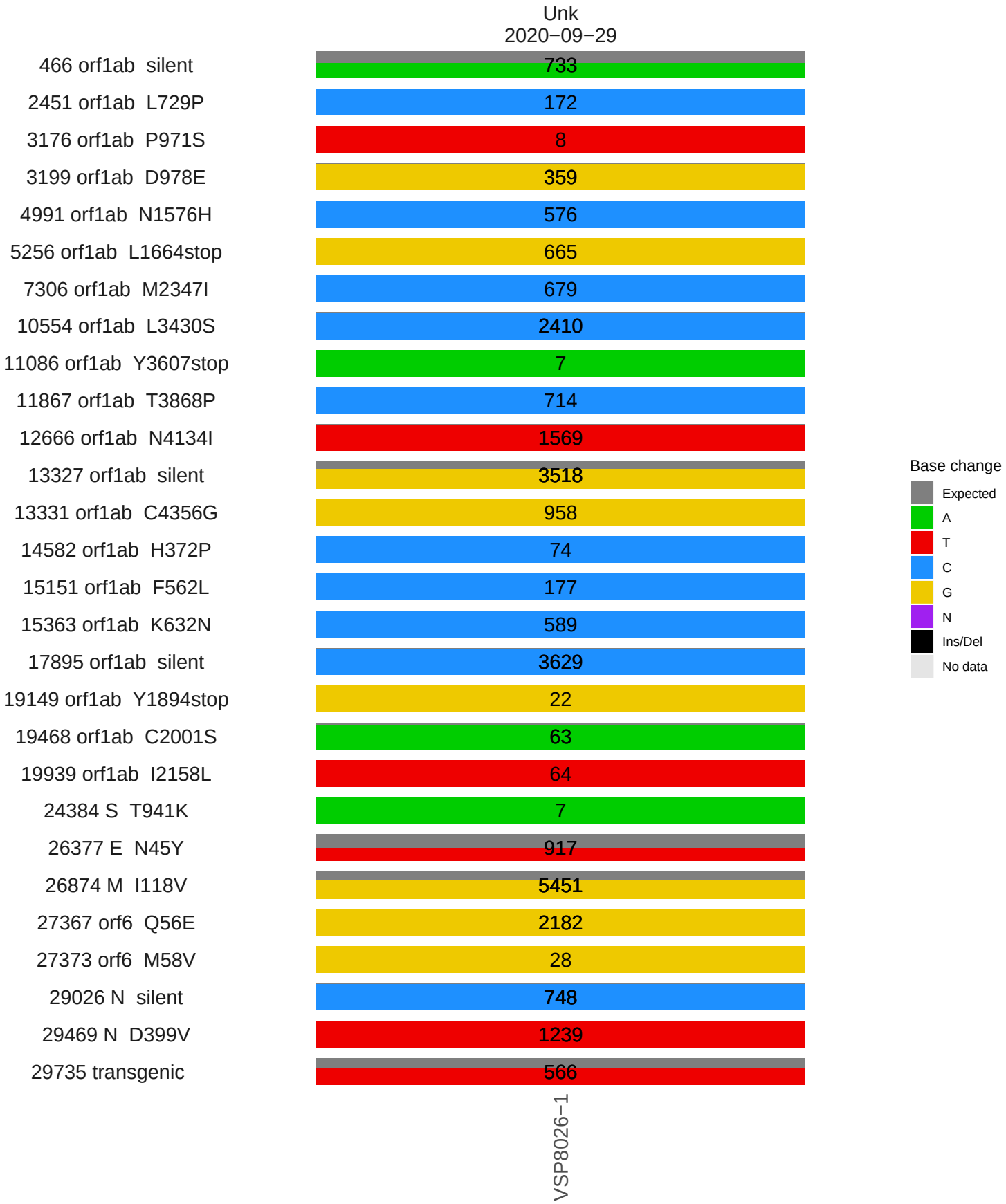
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8026-1	single experiment	NA	Unk	2020-09-29	0.62	35.5%	34.2%

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.

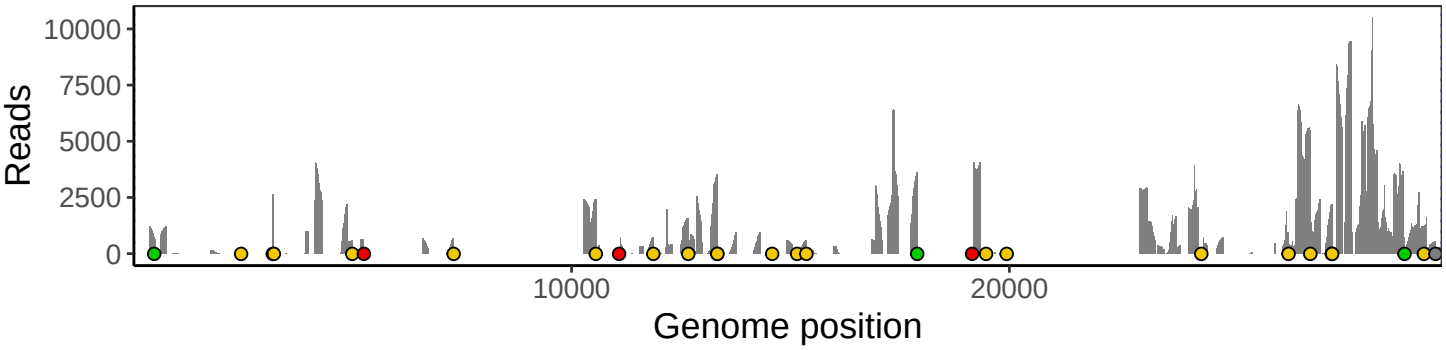



Unk
2020−09−29
466 orf1ab silent
733
2451 orf1ab L729P
172
3176 orf1ab P971S
8
3199 orf1ab D978E
359
4991 orf1ab N1576H
576
5256 orf1ab L1664stop
665
7306 orf1ab M2347I
679
10554 orf1ab L3430S
2410
11086 orf1ab Y3607stop
7
11867 orf1ab T3868P
714
12666 orf1ab N4134I
1569
13327 orf1ab silent
3518
13331 orf1ab C4356G
958
14582 orf1ab H372P
74
15151 orf1ab F562L
177
15363 orf1ab K632N
589
17895 orf1ab silent
3629
19149 orf1ab Y1894stop
22
19468 orf1ab C2001S
63
19939 orf1ab I2158L
64
24384 S T941K
7
26377 E N45Y
917
26874 M I118V
5451
27367 orf6 Q56E
2182
27373 orf6 M58V
28
29026 N silent
748
29469 N D399V
1239
29735 transgenic
566
VSP8026−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

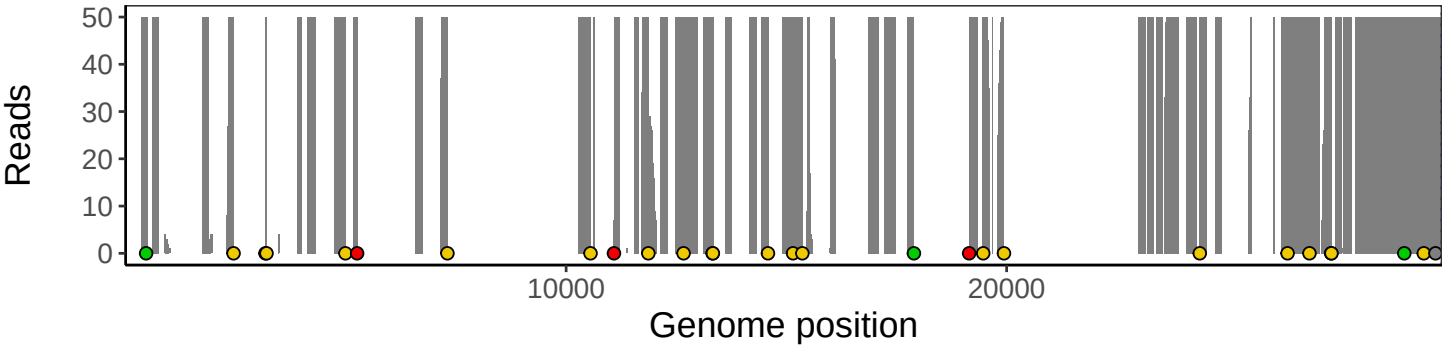
Analyses of individual experiments and composite results.

VSP8026-1 | 2020-09-29 | Unk | SRR11783580 | 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.