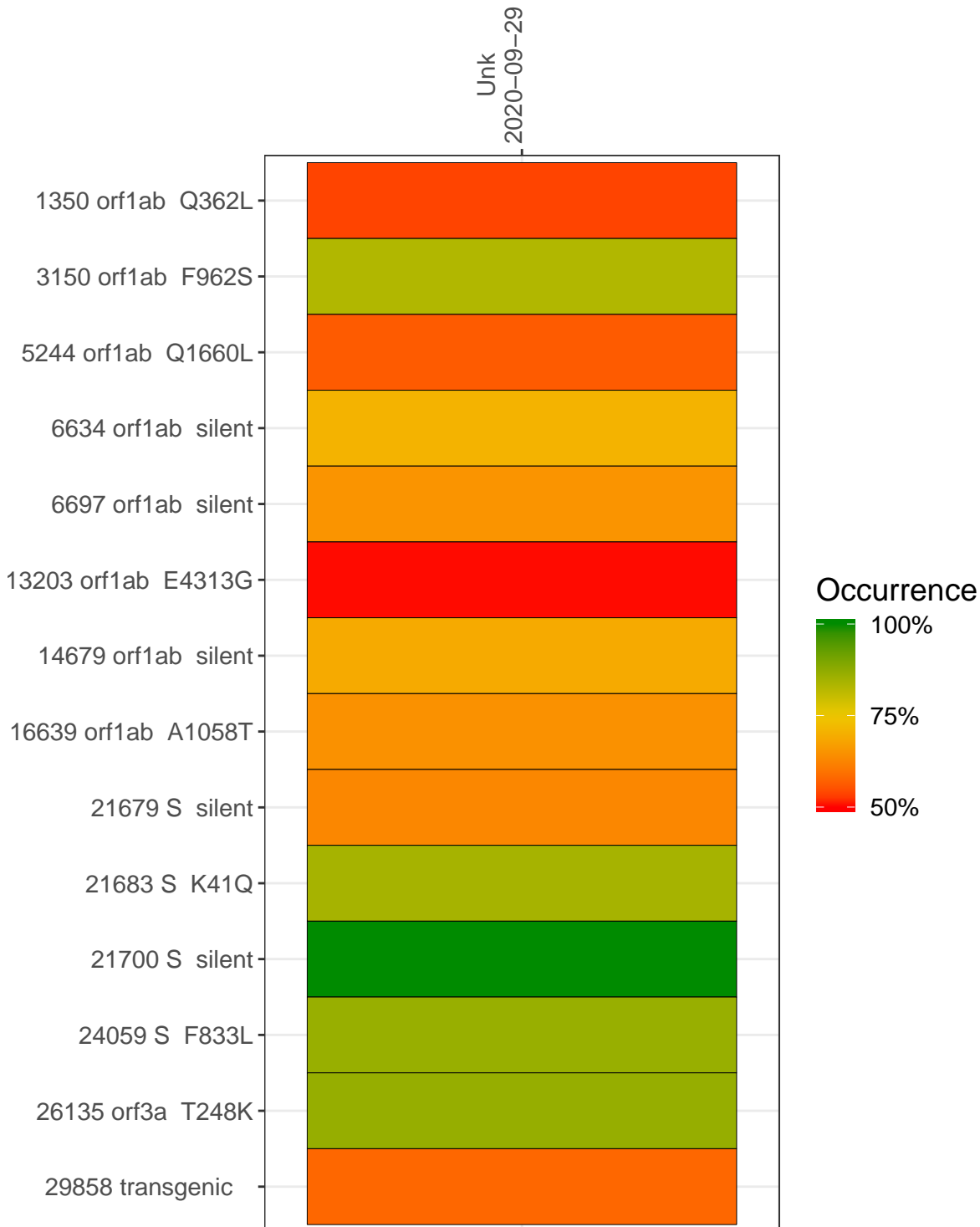# COVID-19 subject SRR11783621

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).

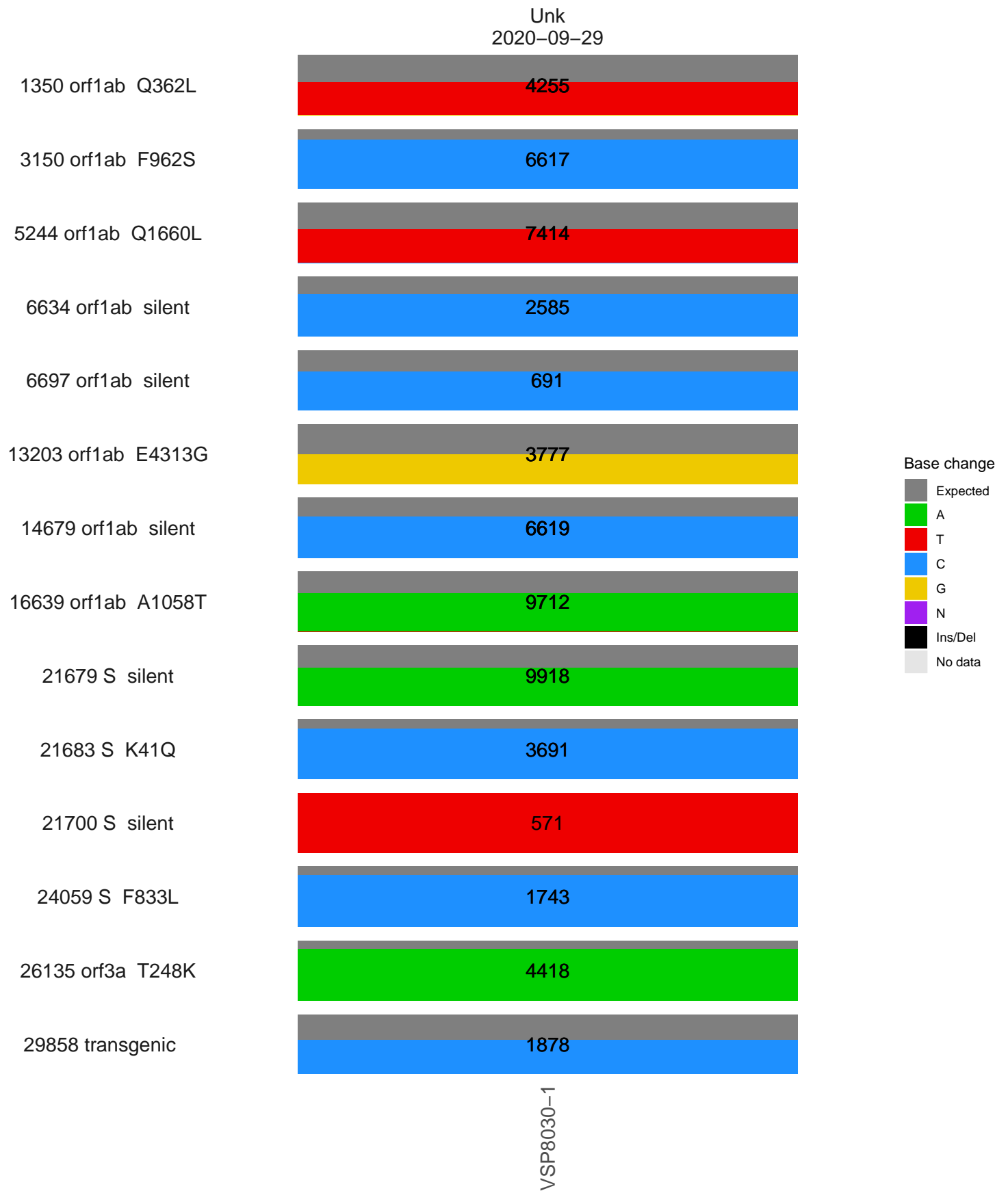Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP8030-1	single experiment	NA	Unk	2020-09-29	7.85	99.3%	99.1%

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

Position	Value
1350 orf1ab Q362L	4255
3150 orf1ab F962S	6617
5244 orf1ab Q1660L	7414
6634 orf1ab silent	2585
6697 orf1ab silent	691
13203 orf1ab E4313G	3777
14679 orf1ab silent	6619
16639 orf1ab A1058T	9712
21679 S silent	9918
21683 S K41Q	3691
21700 S silent	571
24059 S F833L	1743
26135 orf3a T248K	4418
29858 transgenic	1878

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP8030−1

Analyses of individual experiments and composite results.

VSP8030-1 | 2020-09-29 | Unk | SRR11783621 | 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.
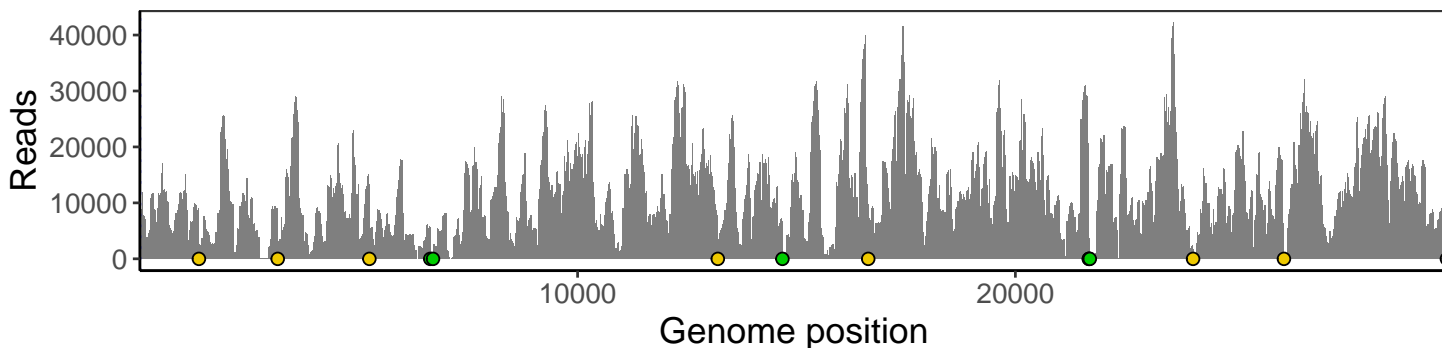
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
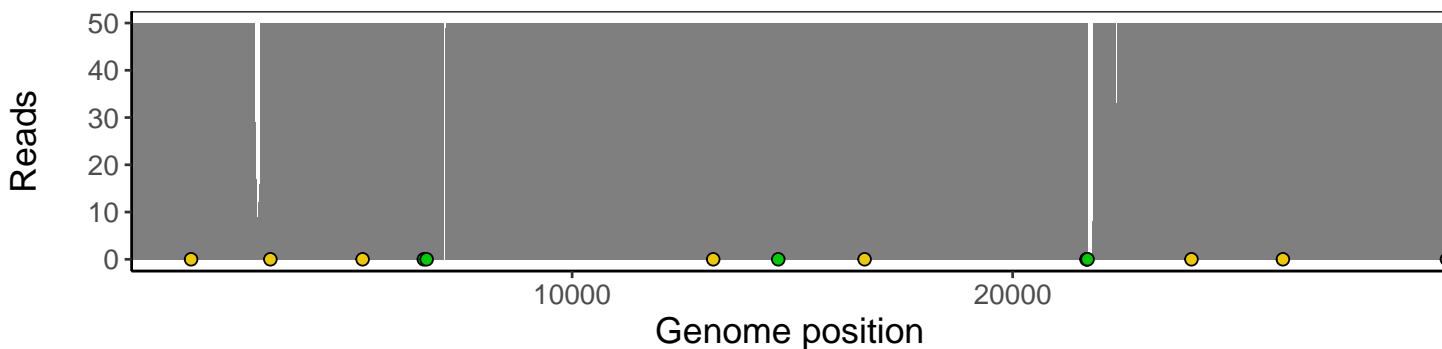
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.