COVID-19 subject 290

2020-08-13

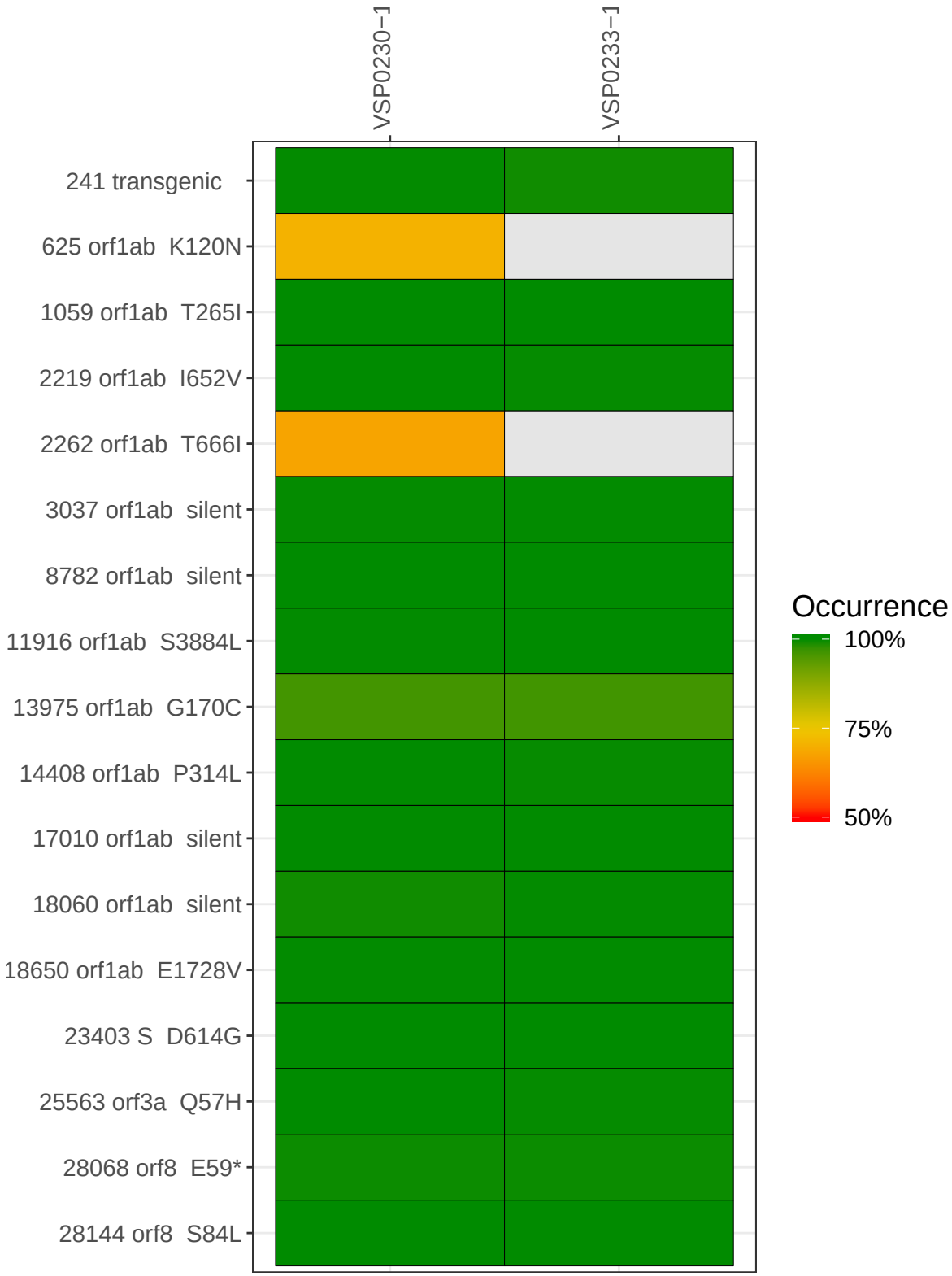
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report.

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0230-1	single experiment	11750	NP-OP	06/29/2020	27.24	99.8%	99.8%
VSP0233-1	single experiment	27900	NP-OP	07/01/2020	29.87	99.8%	99.8%

Variants shared across samples

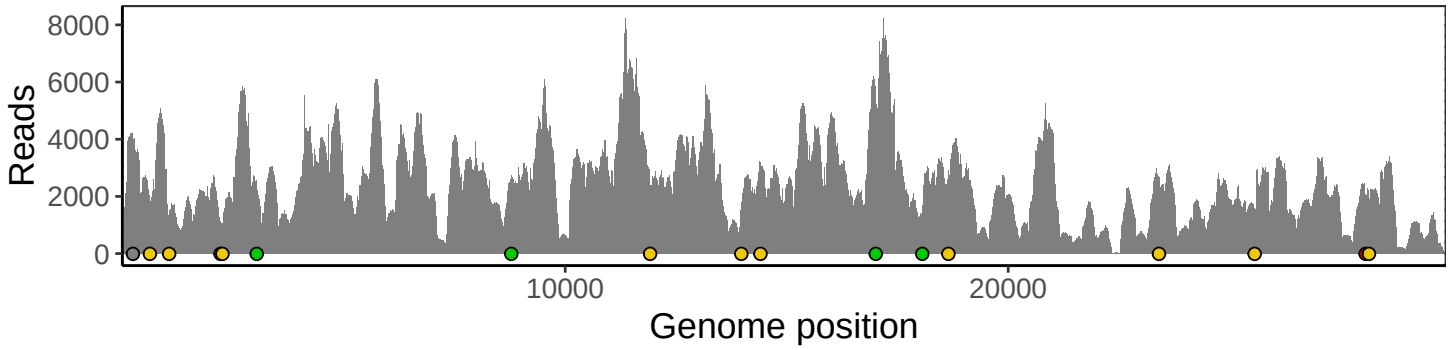
The heat map below shows how variants are shared across subject samples. The quality scores are PHRED scaled values [Q = -10log10(error rate)] where a score of 30 represents a probabilty of 99.9% that a variant is called correctly and a score of 50 represents a probabilty of 99.999% Gray tiles denote that 10 or more reads covered the variant position and the reference base was observed. Tiles are ommited if there are less than 10 reads covering a variant position.



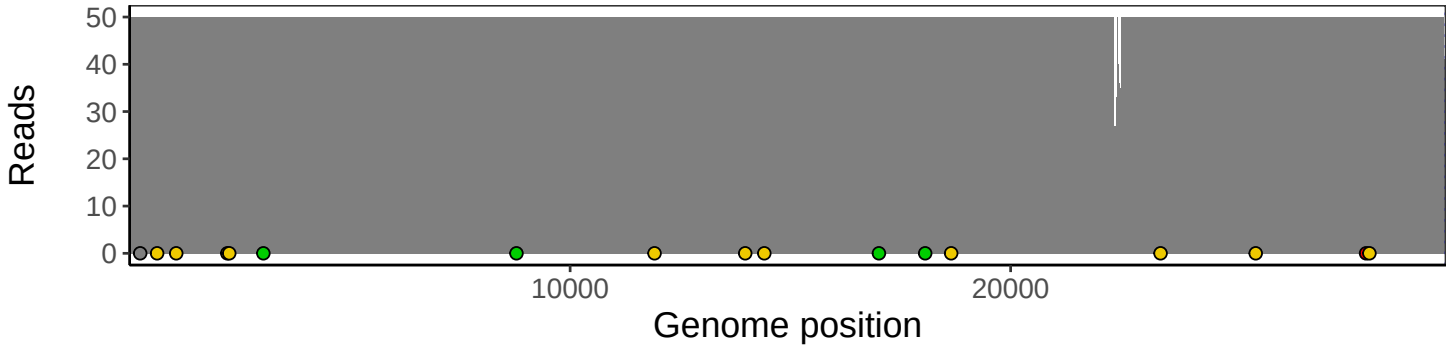
Analyses of individual experiments and composite results.

VSP0230-1 | 06/29/2020 | NP-OP | 290no-q | 11750 genomes | single experiment

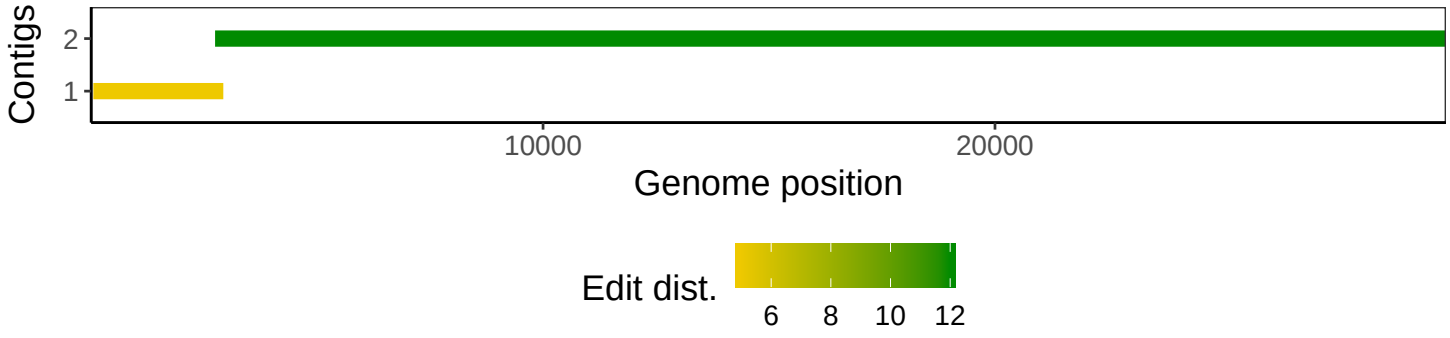
The plot below shows the number of reads covering each nucleotide position in the reference genome (USA-WA1-2020). Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

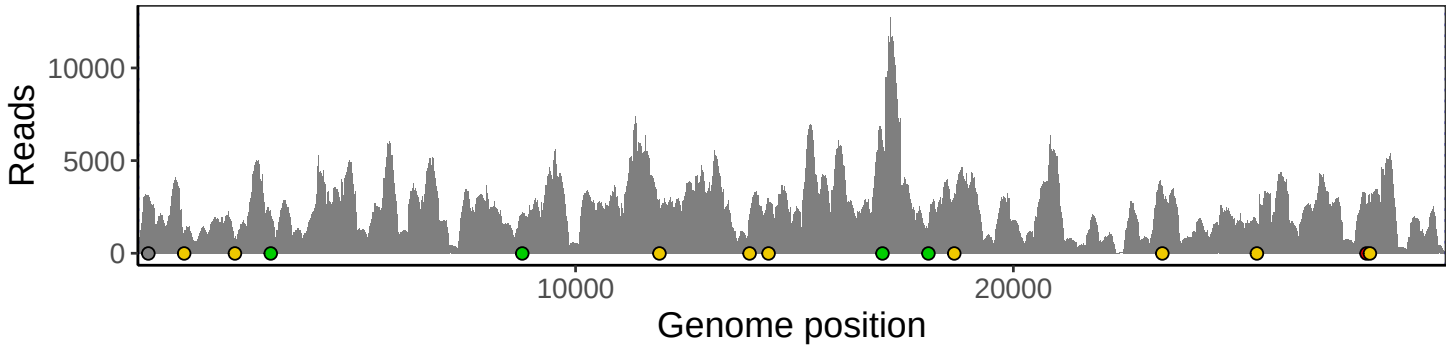


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

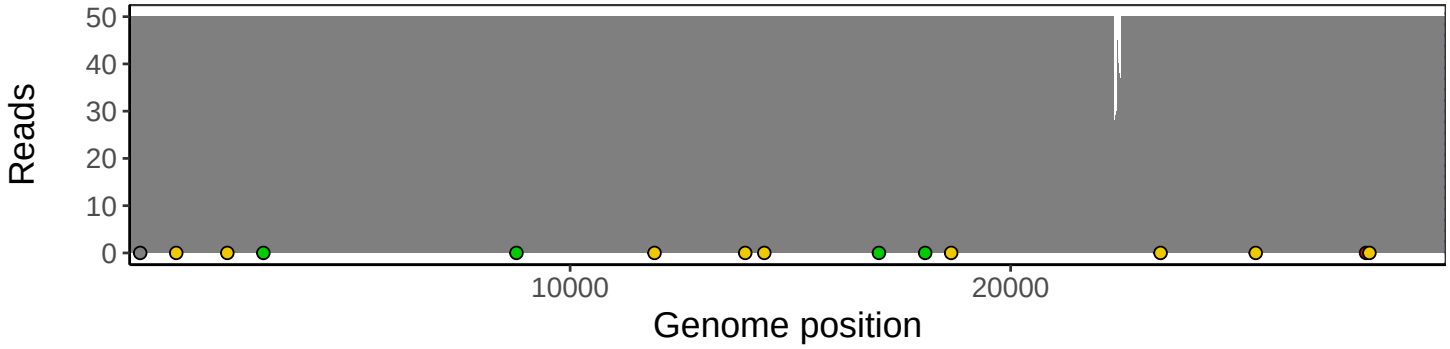


VSP0233-1 | 07/01/2020 | NP-OP | 290no-q | 27900 genomes | single experiment

The plot below shows the number of reads covering each nucleotide position in the reference genome (USA-WA1-2020). 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.