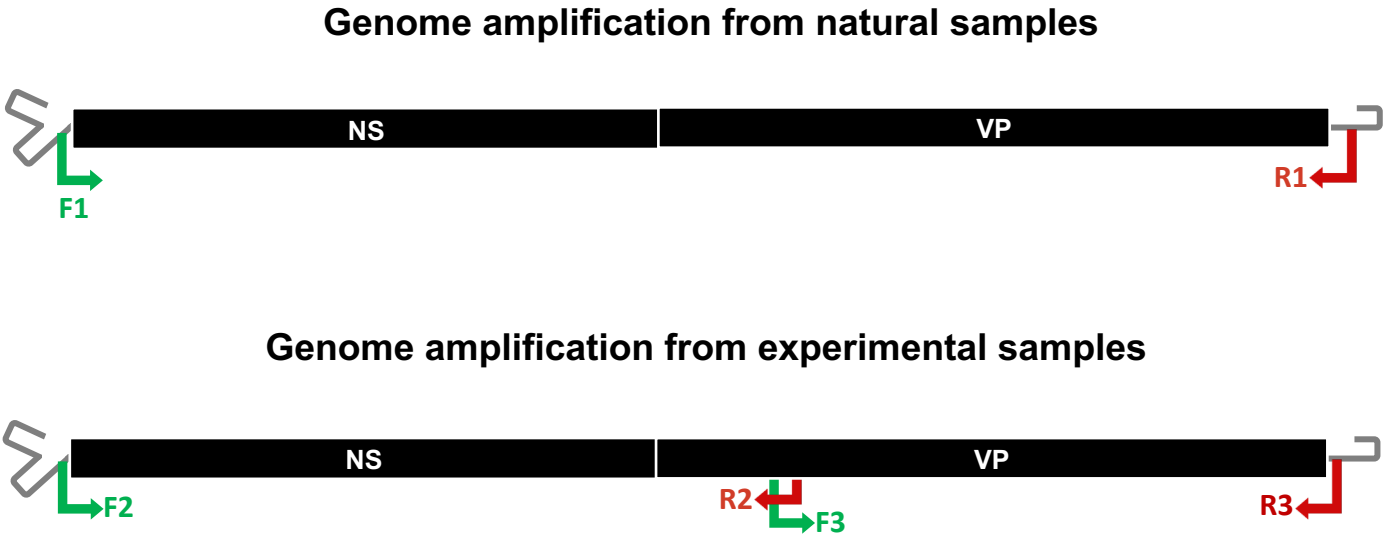
Figure S1.



	Sequence	Reference
F1	ATAAAAGACAAACCATAGACCGTTACTGAC	Pérez *et al.* 2014
R1	CTTAACATATTCTAAGGGCAAACCAACCAA	Pérez *et al.* 2014
F2	CCGTTACTGACATTCGCTTCTTG	This study
R2	GAACTGCTCCATCACTCATTG	This study
F3	CATCCATCAACATCAAGACCAAC	This study
R3	ATAACAAACCTTCTAAATCCTA	This study

Figure S1. Sequences and genomic loci of primers used to amplify parvovirus DNA.

Figure S2.

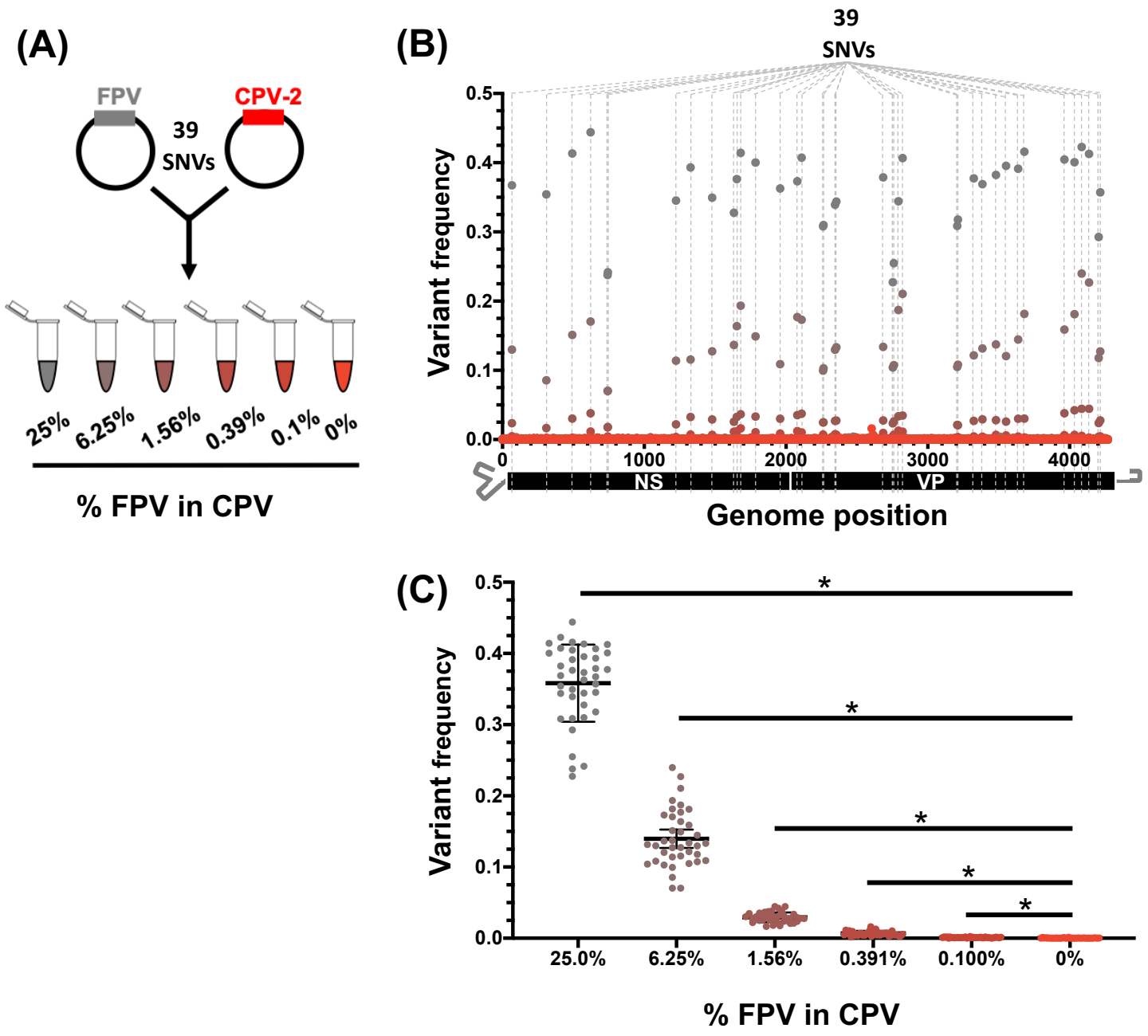


Figure S2. Demonstration of sub-consensus single nucleotide variant (SNV) detection sensitivity across CPV genome. (A) Plasmids containing full length FPV (p292) and CPV-2 (p265) genomes, which differ at 39 sites across the region of analysis were mixed in various proportions based on DNA quantifications and deep sequenced. (B) Position and frequency of dominant sub-consensus SNVs for various plasmid mixtures colored as in "A". Grey dotted lines indicate locations of the 39 mutations that differentiate the two input sequences. (C) Variant frequencies in each mixture for each of the 39 mutations. Asterisk (*) indicate significance ($P<0.05$) between means of spikes and no spike (0% FPV in CPV) control.

Figure S3.

(A)

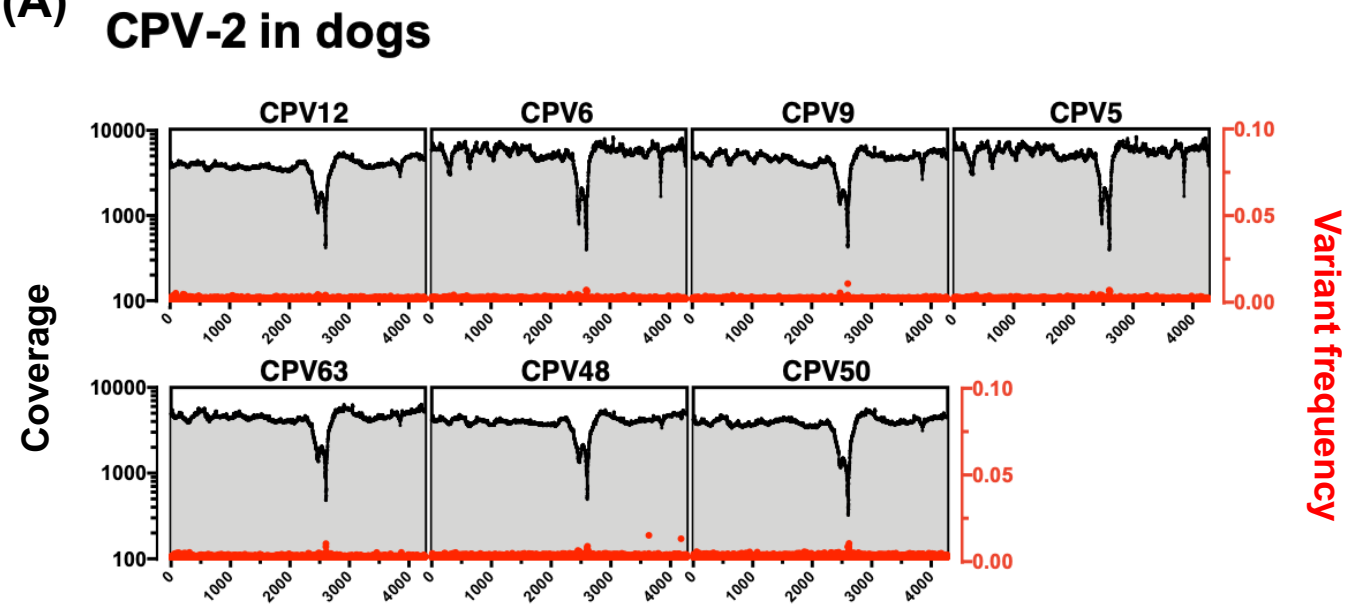

CPV-2 in dogs
CPV12
CPV6
CPV9
CPV5
CPV63
CPV48
CPV50
Coverage
Variant frequency
10000
1000
100
0.10
0.05
0.00
0
1000
2000
3000
4000

Figure S3.

(B)

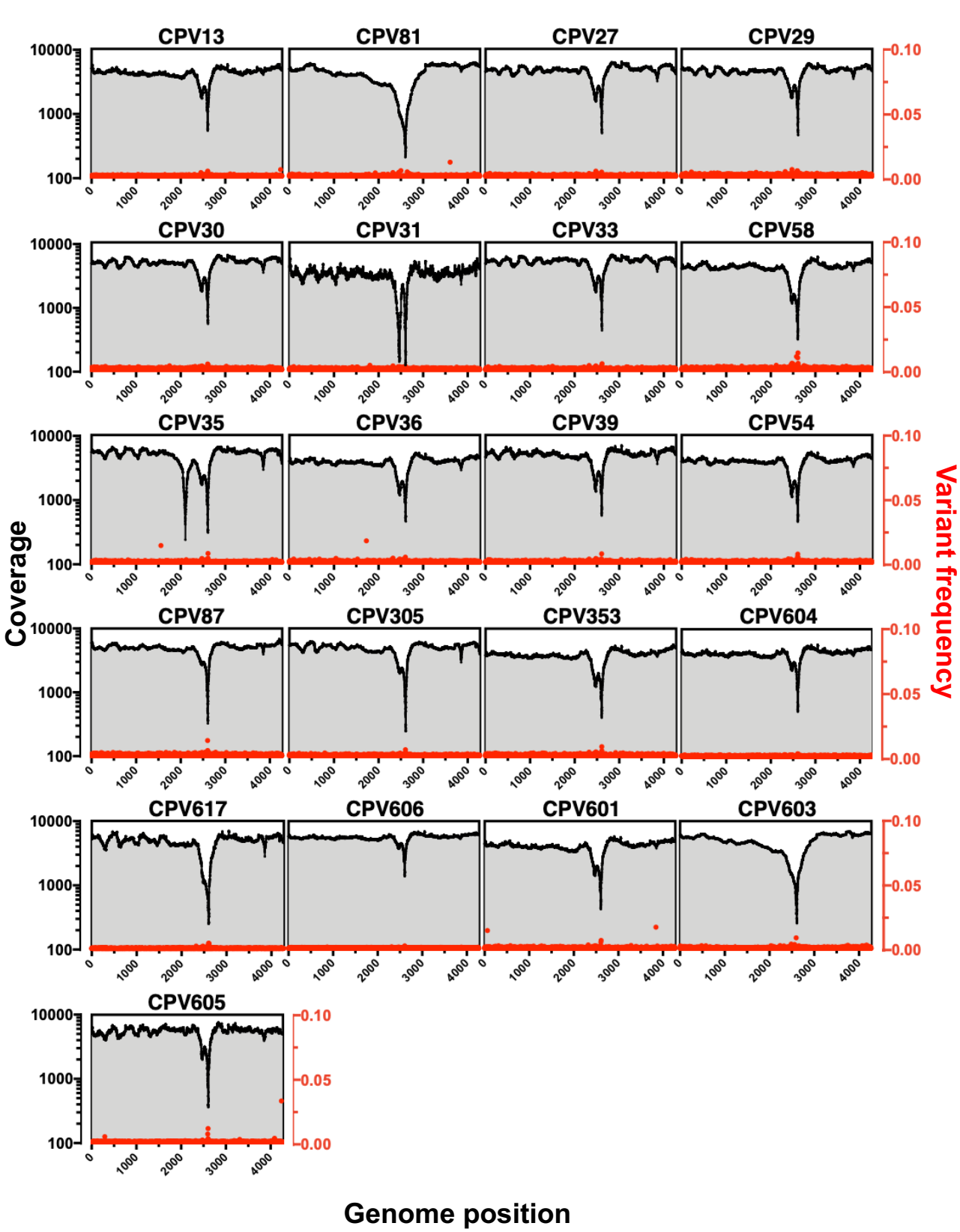

CPV-2a in dogs
CPV13
CPV81
CPV27
CPV29
CPV30
CPV31
CPV33
CPV58
CPV35
CPV36
CPV39
CPV54
CPV87
CPV305
CPV353
CPV604
CPV617
CPV606
CPV601
CPV603
CPV605
Coverage
Variant frequency
Genome position

Figure S3.

(C)

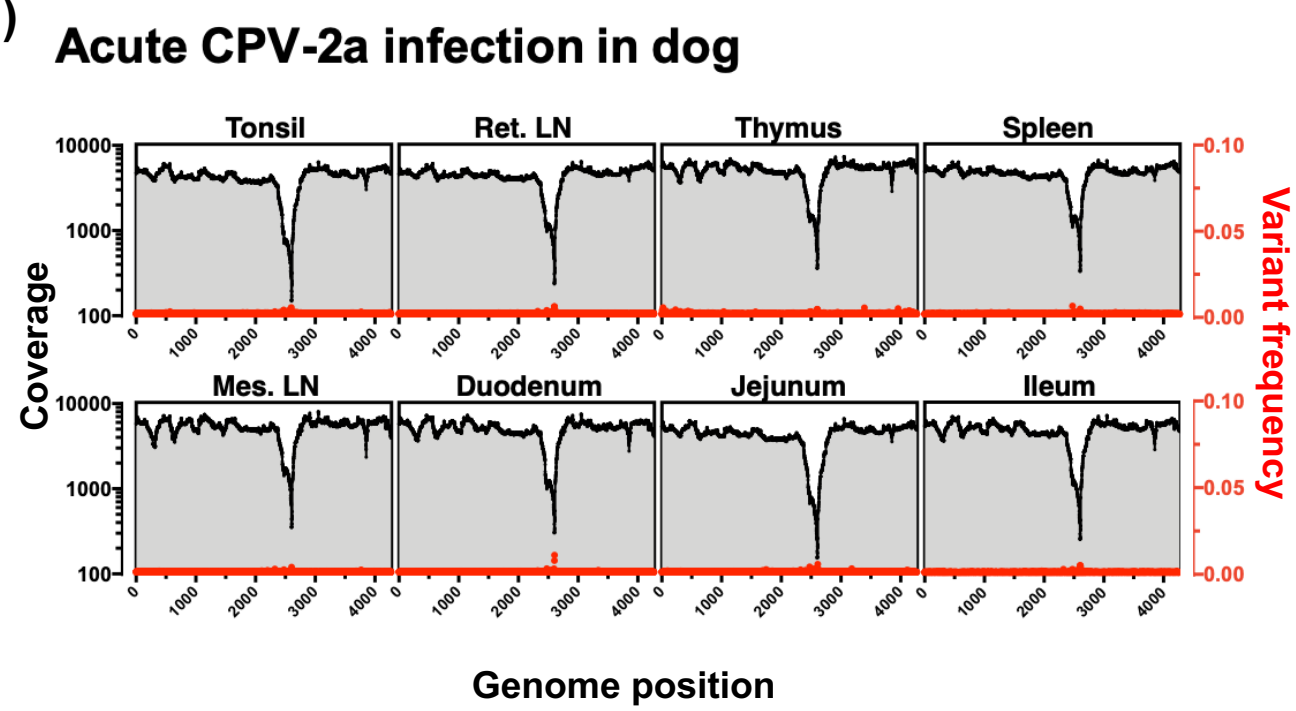

Acute CPV-2a infection in dog
Tonsil
Ret. LN
Thymus
Spleen
Mes. LN
Duodenum
Jejunum
Ileum
Coverage
10000
1000
100
Variant frequency
0.10
0.05
0.00
0
1000
2000
3000
4000
Genome position

Figure S3.

(D)

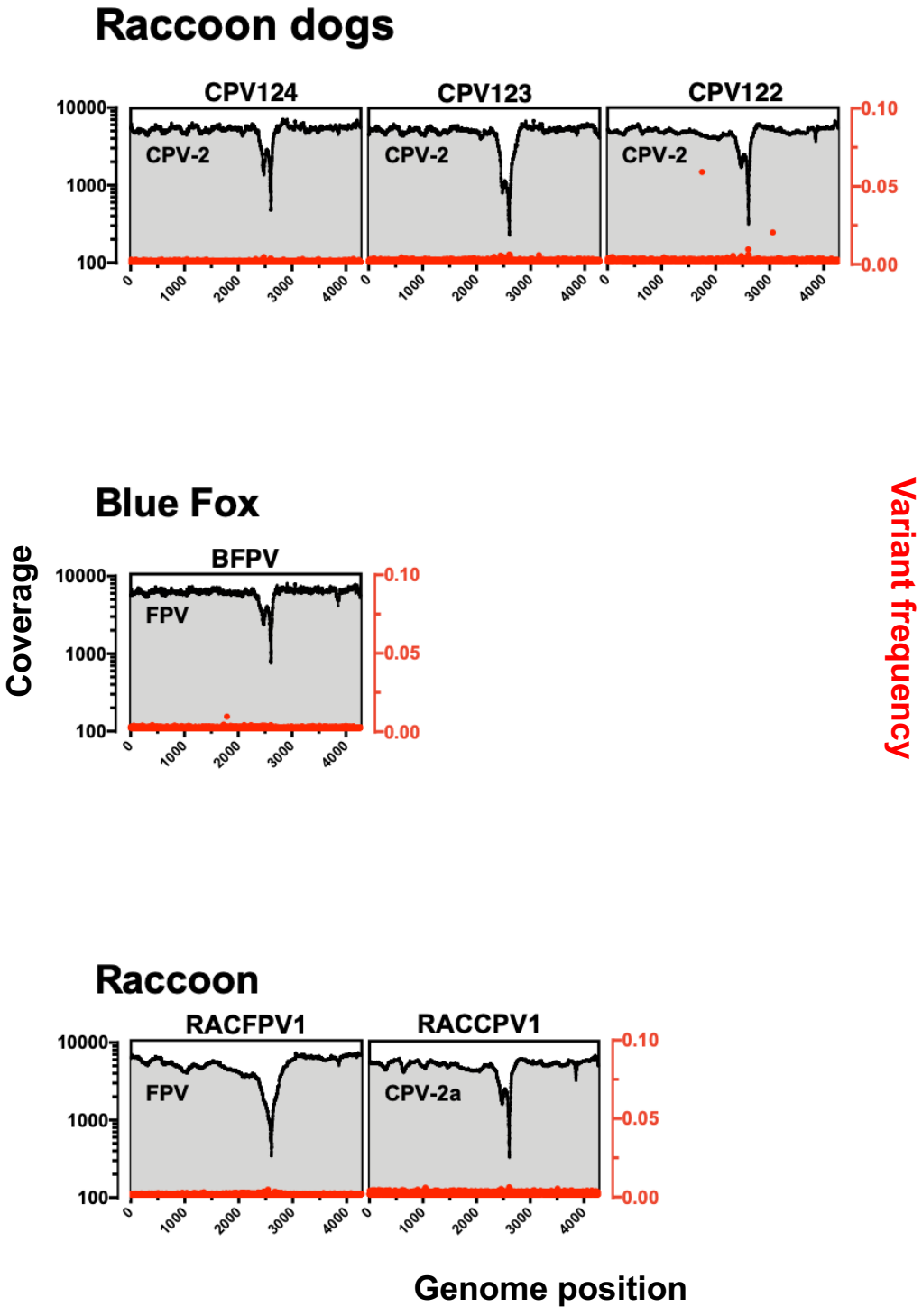


Figure S3. Individual genome-wide coverage and minor variant plots for natural samples deep sequenced in this study. (A) CPV-2 viruses collected from dogs, (B) CPV-2a viruses collected dogs, (C) CPV-2a acute infection in an induvial dog collected from different tissues, (D) CPV-2, CPV-2a, and FPV (as indicated in each plot area) viruses collected from non-dog hosts. No variants were observed outside of the y-axis frequency range of 0.10.