

1 **Figure S1.** Plot of the interaction between habitat type, raccoon body weight (kg), hemoplasma infection. [*Footnote for Figure S1: This*
2 *plot shows the relationship (slope) between weight, habitat type, and predicted hemoplasma positivity based on a generalized linear*
3 *model. The weight-hemoplasma positivity relationship for the rural habitat is represented by the black line, and the model predicted*
4 *relationship from the urban habitat is shown by the red line. The slope of the weight-hemoplasma positivity relationship is higher for the*
5 *rural habitat than for the urban one.*]

6 **Figure S2.** Frequency of hemoplasma genotype richness in raccoons in protected and urban barrier island habitats.

7 **Figure S3.** Alignment of the 16S rRNA gene sequences of raccoon hemoplasma genotype 3 and other related hemoplasma
8 sequences that demonstrates nucleotide sequence differences between the species. The primer regions used for the species-specific
9 PCR of this novel genotype are highlighted.

10 **Figure S4.** Alignment of the 16S rRNA gene sequences of raccoon hemoplasma genotype 6 and other related hemoplasma
11 sequences that demonstrates nucleotide sequence differences between the species. The primer regions used for the species-specific
12 PCR of this novel genotype are highlighted.

13 **Figure S5.** Alignment of the 16S rRNA gene sequences of raccoon hemoplasma genotype 4 and other related hemoplasma
14 sequences that demonstrates nucleotide sequence differences between the species. The primer regions used for the species-specific
15 PCR of this novel genotype are highlighted.

16 **Figure S6.** Alignment of the 16S rRNA gene sequences of raccoon hemoplasma genotype 5 and other related hemoplasma
17 sequences that demonstrates nucleotide sequence differences between the species. The primer regions used for the species-specific
18 PCR of this novel genotype are highlighted.

19 **Figure S7.** Alignment of the 16S rRNA gene sequences of raccoon hemoplasma genotype 2 and other related hemoplasma
20 sequences that demonstrates nucleotide sequence differences between the species. The primer regions used for the species-specific
21 PCR of this novel genotype are highlighted.

22 **Table S1.** Oligonucleotide primers used in the study.

23 **Table S2.** Interspecies similarity of the 16S rRNA gene among the hemoplasma genotypes detected in raccoons to all other known
24 hemotropic *Mycoplasma* species.

25 Table S3. Best fit GLM of hemoplasma infection prevalence in raccoons.

26

Figure S1

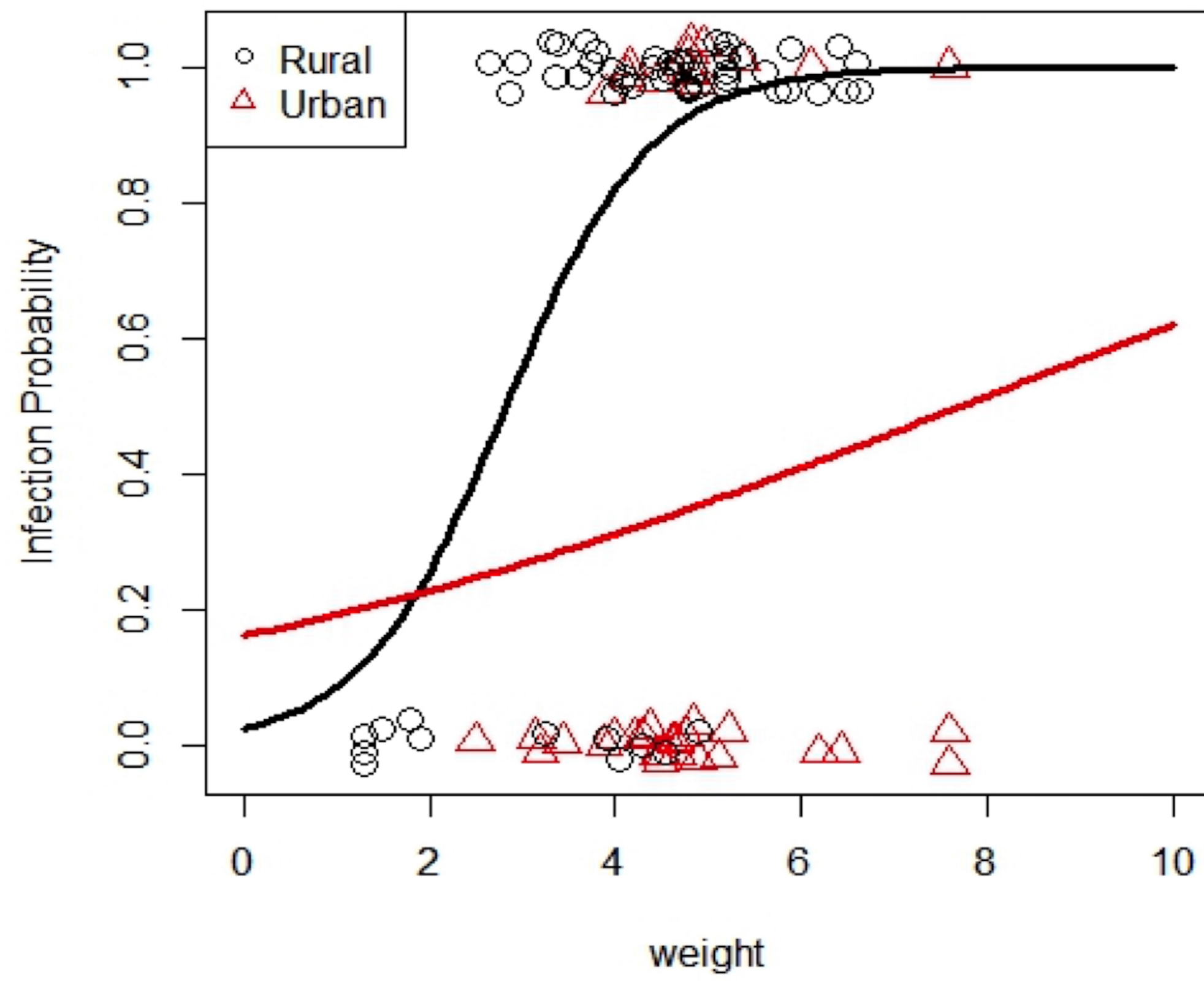


Figure S2

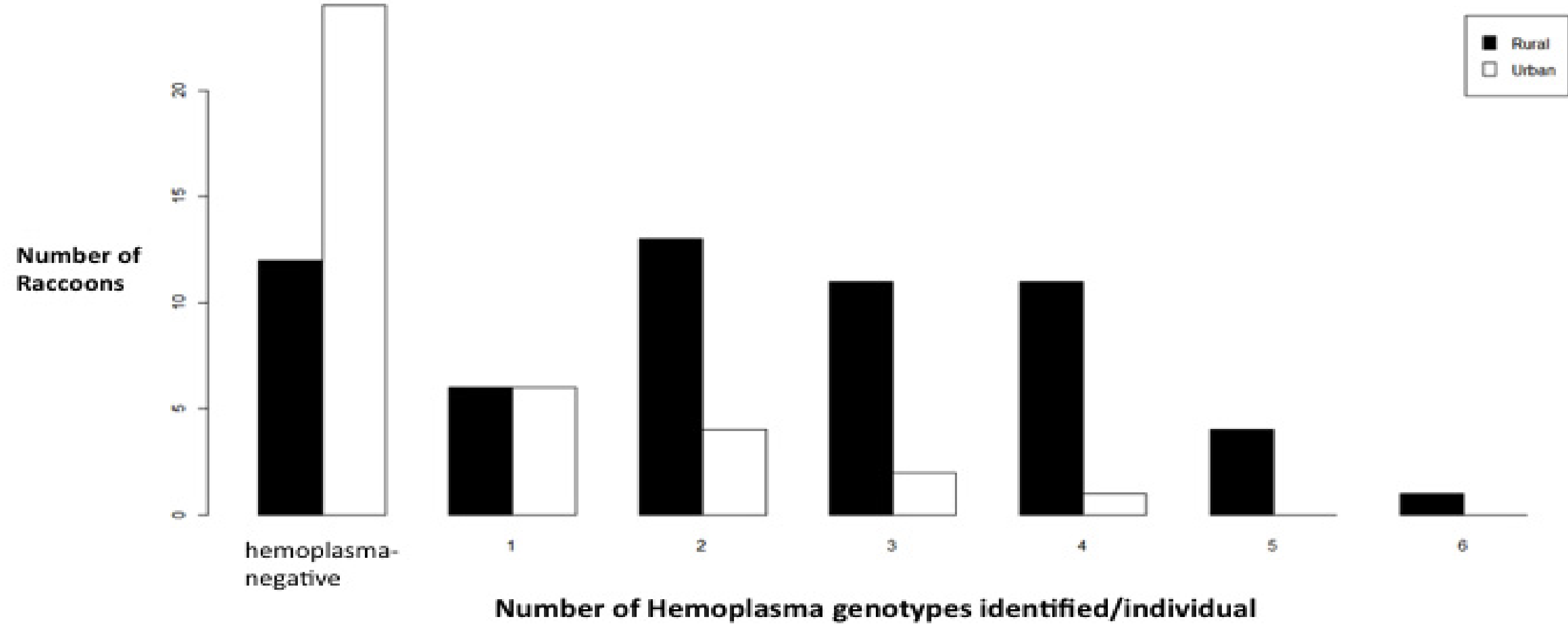


FIG S3: 16S Raccoon Hemoplasma Genotype 3

KC920443_P	CTGTGGTATGCAACACATCAAGTTCGAAAGTAACTTTAGCAATTAAGA---TAGTGGCAACGGGGGCAACACATATCTAACTAATCTGTGTGGAGGATAGCAACCCGAAAGGTTATTAATCTTCATAGTTTATG-GA-ATAAATAA--GGAGGCTCC-180	GCCTTGCAGCAACACGGGATATGCTCTATTAGTAGTTCGGCGGGTAAAGCCCA	231
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KC920445_P	231
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KC920448_P	231
KC920440_P	231
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AF338269_M	231
KF743729_P	231
KF743724_P	231
KF743727_P	231
KF743722_P	231
KF743713_P	231
KC936280_P	231
KF743717_P	231
AB848113_M	231
GU905012_M	231
AF306346_M	231
UB8564_M	231
KF743739_M	231
KF743738_M	231
KF743737_M	231
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AY946266_M	231
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KF743711_P	231
KF743728_P	231
KF743721_P	231
KF743719_P	231
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KF743716_P	231
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HM082963_M	231
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AY171918_M	231
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KF743731_P	231
KF743720_P	231
FJ226566_M	231
AF152879_M	231
KF743735_P	231
DQ522159_M	231

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KF743720_P	480
FJ226566_M	480
AF152879_M	480
KF743735_P	480
DQ522159_M	480

Genomic coordinates and sequence alignments for various samples (e.g., KF743712, KF743725, etc.) across a range of positions (50-950). The sequences are aligned to a reference sequence, with gaps indicated by dashes.

Genomic coordinates and sequence alignments for various samples (e.g., KC920443, KC920441, etc.) across a range of positions (520-950). The sequences are aligned to a reference sequence, with gaps indicated by dashes.

Genomic coordinates and sequence alignments for various samples (e.g., KC920443, KC920441, etc.) across a range of positions (760-1000). The sequences are aligned to a reference sequence, with gaps indicated by dashes.

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 KF743733 PC..ACTA..T.T.G.T..T.....A.....TT.....G.....G..G.GTGGC.T..TA..T..T.....TA..A..AAT.C.C.....GAGTTAAGTC : 1391
 KF743707 PACTA..T.T.G.T..T.....A.....TT.....G.....G..G.GTGGC.T..TA..T..T.....TA..A..AAT.C.C.....GAGTTAAGTC : 1391
 KF743731 PC..ACTA..T.T.G.T..T.....A.....TT.....G.....G..G.GTGGC.T..TA..T..T.....TA..A..AAT.C.C.....GAGTTAAGTC : 1391
 KF743720 PC..ACTA..T.T.G.T..T.....A.....TT.....G.....G..G.GTGGC.T..TA..T..T.....TA..A..AAT.C.C.....GAGTTAAGTC : 1391
 NR_036946A..C.TCAA..A.CGT..T..T..T.....T.....C..A..T..A.....C.....G..AGA.....CGCT..C.....T.G.....C..GG..CTG.....A.GCCCG..GT..G..T..TAA.....GAAACT..C..AGGCA..G..C..GG..C..GGTTAAGTC : 1433
 F0236566 MA..C.TCAA..A.CA..T..T..T.....T.....C..A..T..A.....C.....G..AGA.....CGCT..C.....T.G.....C..GG..CTG.....A.GCCCG..GT..G..T..TAA.....GAAACT..C..AGGCA..G..C..GG..C..GGTTAAGTC : 1446
 AF125879 MAT..AT..A..A..TCA..T..T..T.....T.....C..A..T..A.....C.....G..AGA.....CGCT..C.....T.G.....C..GG..CTG.....A.GCCCG..GT..G..T..TAA.....GAAACT..C..AGGCA..G..C..GG..C..GGTTAAGTC : 1410
 AF125878 MT..AT..A..A..CA..T..T..T.....T.....C..A..T..A.....C.....G..AGA.....CGCT..C.....T.G.....C..GG..CTG.....A.GCCCG..GT..G..T..TAA.....GAAACT..C..AGGCA..G..C..GG..C..GGTTAAGTC : 1411
 DQ522159 MT..AT..A..A..CA..T..T..T.....T.....C..A..T..A.....C.....G..AGA.....CGCT..C.....T.G.....C..GG..CTG.....A.GCCCG..GT..G..T..TAA.....GAAACT..C..AGGCA..G..C..GG..C..GGTTAAGTC : 1416

AF338269	M	T	GCC	G	G	G	G	G	G	T	C	T	G	T	T	A	T	C	G	T	T	C	A	C	TTTA	A	AAAG	CATGATAGGAATGATTAGCCT	C	AAA	T	478
KF743738	M	C	G	G	G	A	G	TC	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CTTGATAGGAATGATTAGCCT	T	AAA	T	484
KF743735	P	C	A	G	G	A	G	TC	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CTTGATAGGAATGATTAGCCT	T	AAA	T	480
AY383241	M	C	GT	G	G	G	G	CC	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CTTGATAGGAATGATTAGCCT	C	AAA	T	477
AY946266	M	C	AG	G	G	A	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	G	AAI	T	470
AY383724	M	C	A	G	G	A	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	G	AAI	T	480
AF338268	M	C	A	G	G	A	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	G	AAI	T	481
EU165512	M	C	A	G	G	A	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AA	AGCGCTAGGAATGAGCGCCCT	G	AAI	T	464
AB858899	M	C	A	G	G	A	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	G	AAI	T	481
AB558897	M	C	A	G	G	AA	G	T	C	G	A	T	G	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	G	AAI	T	481
AY492086	M	C	G	G	A	G	T	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495
BB082863	M	T	AG	GC	TA	G	TA	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	497
DQ157153	M	G	G	G	A	G	T	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495
AY81867	M	G	G	A	G	T	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495	
AY11918	M	G	G	A	G	T	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495	
FJ667774	M	A	G	T	C	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495		
AB820288	M	G	G	A	G	T	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495	
FJ28566	M	C	AGT	C	G	C	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	495		
AF125879	M	T	G	GC	TA	G	TA	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	482
AF125878	M	T	G	GC	TA	G	TA	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	482
DQ523159	M	C	GT	G	TA	G	TA	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	482
DQ523159	M	C	GT	G	TA	G	TA	G	A	T	C	G	A	GA	T	T	A	T	T	C	A	T	C	A	TTTA	A	AAAG	CGCGCTAGGAATGAGCGCCCT	T	AAI	T	482

520	540	560	580	600	620	640	660	680	700	720	740	
CGCGGTAATACATAGTCCGACGATTATCGGATTATGGCGTAAGCAAGCCAGCGGGATGTGTAAGTTCTGTGTTAAATGACACTCAAT	AGTTGTTTGACCCGAATCACTACATGTGAGATGTTGGTAGGAGTTCGGAATTAAGCATTGAGCGGTGGAATGTGATAGTCTTAAAGAACACACAG	AGCGAAGCGGAACCTTAGCCCTTAATGACGCTTAGGCTGAAAGTGTG										
760	780	800	820	840	860	880	900	920	940	960	980	1000
GGGACAAATGGGA	TTAGATACCCGACTAGT	CCACACCGTAACAGTGGGATAGGATGGGG										

KF743725_P	C	G	C	A	A	C	G	1390
KF743708_P	C	G	C	K	A	C	G	1390
KF743730_P	C	G	C	A	A	C	G	1390
NR_036946	A	C	T	A	A	A	A	1433
KF743710_P	T	A	T	A	A	T	C	1391
KF743733_P	C	A	T	A	A	T	C	1391
KF743707_P	T	A	T	A	A	T	C	1391
KF743731_P	C	T	A	T	A	T	C	1391
KF743720_P	C	T	A	T	A	T	C	1391
GU734681_M	C	G	C	A	A	C	G	1313
EF460765_M	T	G	T	C	A	G	T	1392
KF743726_P	CTCC	AGC	TA	C	C	GA	T	1401
KF743711_P	CTCC	AGC	TA	C	C	GA	T	1401
KF743728_P	CTCC	AGC	TA	C	C	GA	T	1401
KF743721_P	CTCC	AGC	TA	C	C	GA	T	1401
KF743719_P	CTCC	AGC	TA	C	C	GA	T	1410
KF743718_P	CTCC	AGC	TA	C	C	GA	T	1410
KF743716_P	CTCC	AGC	TA	C	C	GA	T	1410
GU562823_M	A	A	C	A	C	A	T	1379
KF743729_P	CC	AACCTA	C	A	A	A	T	1415
KF743724_P	CC	AACCTA	C	A	A	A	T	1415
KF743727_P	CC	AACCTA	C	A	A	A	T	1415
KF743722_P	CC	AACCTA	C	A	A	A	T	1415
KF743713_P	CC	AACCTA	C	A	A	A	T	1415
KC936280_P	CC	AACCTA	C	A	A	A	T	1415
KF743717_P	CC	AACCTA	C	A	A	A	T	1415
AB848713_M	CT	AACCTA	C	A	A	A	T	1393
GU905012_M	CG	AACCTA	C	A	A	A	T	1427
AF306346_M	CT	AACCTA	C	A	A	A	T	1415
US8954_W.H	CG	AACCTA	C	A	A	A	T	1417
KF743739_M	CG	AACCTA	C	A	A	A	T	1419
KC920443_P	CG	AACCTA	C	A	A	A	T	1414
KC920447_P	CG	AACCTA	C	A	A	A	T	1414
KC920446_P	CG	AACCTA	C	A	A	A	T	1414
KC920445_P	CG	AACCTA	C	A	A	A	T	1414
KC920444_P	CG	AACCTA	C	A	A	A	T	1414
KC920442_P	CG	AACCTA	C	A	A	A	T	1414
KC920448_P	CG	AACCTA	C	A	A	A	T	1414
KC920440_P	CG	AACCTA	C	A	A	A	T	1414
KC920439_P	CG	AACCTA	C	A	A	A	T	1414
AF178676_M	CG	AACCTA	C	A	A	A	T	1414
AF338269_M	C	A	A	A	A	A	A	1411
KF743738_M	TCG	AACCTA	C	A	A	A	T	1419
KF743737_M	CG	AACCTA	C	A	A	A	T	1419
AY383241_M	A	CC	AACCTA	C	A	A	T	1419
AY946266_M	CT	AGCCTA	C	A	A	A	T	1411
AY837724_M	CT	AGCCTA	C	A	A	A	T	1414
AF338268_M	CT	AACCTA	C	A	A	A	T	1415
EU165512_M	CG	AACCTA	C	A	A	A	T	1398
AB558899_M	CT	AGCCTA	C	A	A	A	T	1406
AB558897_M	CG	AACCTA	C	A	A	A	T	1406
AY492086_M	TC	CT	AG	CTA	C	A	A	1430
HM092963_M	C	C	A	C	A	C	A	1368
DQ157153_M	C	A	C	A	C	A	T	1368
AY831867_M	C	A	C	A	C	A	T	1384
AY171918_M	G	C	T	C	A	T	A	1391
FJ667774_M	T	A	A	C	A	T	G	1347
AB820288_M	AGC	A	C	A	T	A	G	1373
FJ226566_M	A	C	T	A	A	A	A	1446
AF125879_M	AT	ATCAC	AG	CNA	TGA	C	TCA	1410
AF125878_M	T	ATCAC	AGCCAA	TGA	C	TCA	A	1411
DQ522159_M	T	ATCAC	AGCCAA	TGA	C	TCA	A	1416

FIG S7: 16S Raccoon Hemoplasma Genotype 2

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          20          40          60          80          100          120          140          160          180          200          220          240
KF743728_P CGTGGTGTATGCATCAACAGTCAAGTCTCGACGAAAGAAAGT-----TTTTCTCTTTTGTGGCAAAAGGGGGGCAAGTAACTATTAACTTACTCGCAGCAGAAATTAACCTCCCGAAAGGGTGGCTAATGTCCCATATGTTTGTAG-GA-----ATAAATTAAG-----GGGAGCGTTCCCGAAGGCTCGACCTGCAACGCAAGATATGTCTATTAGGTAGTTGGCGGGGTAATGCCCAACCA
KF743724_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743727_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743722_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743713_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC936280_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743717_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB848131_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
GU905012_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF306346_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
UR8594_W.B -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743739_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920443_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920441_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920447_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920446_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920445_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920444_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920442_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920448_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920440_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KC920439_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF178676_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF338269_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743738_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743737_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY383241_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY946266_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
SF743724_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF338268_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
EU165512_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB558899_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB558897_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY492086_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743726_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743711_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743728_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
SF743721_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743719_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743718_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743717_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
GU562823_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
HMU82963_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
DS157153_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY831867_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY171918_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
F1667774_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB820288_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB848714_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AY529659_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF548631_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743714_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AB71559596_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743709_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743723_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743722_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743705_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743710_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743725_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743708_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743730_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
GU734688_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743706_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743734_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743735_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743736_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743704_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF74407185_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743710_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743733_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743707_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
KF743731_P -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF1252879_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----
AF9251159_M -----GCGAAGGCGAGTCCAGCAGTCCATCAAGG-----

          260          280          300          320          340          360          380          400          420          440          460          480          500
KF743728_P GCCTTTGATGGGTAGCTGGAGCTGAGAGTGGGAAGCGGCCAATGGGATGAGATATGGCCCATATTCTCTCGGAAGCAGCAGTGAAGAAATTTTCACAAATGGACGAAGTCTGATGGACGAATACCAGCTGAACACGGAAGGCTTCCT--GATTTAAATGCTTTTTATTTGGGAATAAAG--CTTAGACAGAAATGGTGGAGCTTGATGTAATAAATGAAATAGTAGACACTAACTATGTTGCCAGGAG
KF743724_P -----
KF743727_P -----
KF743722_P -----
KF743713_P -----
KC936280_P -----
KF743717_P -----
AB848131_M -----
GU905012_M -----
AF306346_M -----
UR8594_W.B -----
KF743739_M -----
KC920443_P -----
KC920441_P -----
KC920447_P -----
KC920446_P -----
KC920445_P -----
KC920444_P -----
KC920442_P -----
KC920448_P -----
KC920440_P -----
KC920439_P -----
AF178676_M -----
AF338269_M -----
KF743738_M -----
KF743737_M -----
AY383241_M -----
AY946266_M -----
SF743724_M -----
AF338268_M -----
EU165512_M -----
AB558899_M -----
AB558897_M -----
AY492086_M -----
SF743726_P -----
KF743711_P -----
KF743728_P -----
SF743721_P -----
KF743719_P -----
KF743718_P -----
KF743717_P -----
GU562823_M -----
HMU82963_M -----
DS157153_M -----
AY831867_M -----
AY171918_M -----
F1667774_M -----
AB820288_M -----
AB848714_M -----
AY529659_M -----
AF548631_M -----
KF743714_P -----
AB71559596_M -----
KF743709_P -----
KF743723_P -----
KF743722_P -----
KF743705_P -----
KF743710_P -----
KF743725_P -----
KF743708_P -----
KF743730_P -----
GU734688_P -----
KF743706_P -----
KF743734_P -----
KF743735_P -----
KF743736_P -----
KF743704_P -----
AF74407185_M -----
KF743710_P -----
KF743733_P -----
KF743707_P -----
KF743731_P -----
AF1252879_M -----
AF9251159_M -----

          260          280          300          320          340          360          380          400          420          440          460          480          500

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Genomic coordinates and sequence alignments for various samples (e.g., KF743712, KF743725, etc.) with corresponding reference sequences and quality scores.

Detailed genomic coordinates and sequence alignments for a larger region, including sample identifiers like KF743729, KF743724, and various reference sequences.

Continuation of genomic coordinates and sequence alignments, showing sample identifiers and reference sequences for coordinates up to 1000.

KC920445	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
KC920444	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
KC920442	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
KC920448	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
KC920440	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
KC920439	PG.....G.....CC.....T.....A..A.TC..C...G-----G.....	1414
AF178676	MG.....A.....G.....T.....A.....C.....G-----A.....	1414
AF338269	MC.....T.....T.....G.....G.....T.....C.....A.....G-----T.....A.....	1411
KF743738	MT.....G.....G.....GG.....T.....A.....C.....G-----T.....A.....	1419
KF743737	MG.....G.....GG.....T.....A.....C.....G-----T.....A.....	1419
AY383241	MA.....T.....G.....C.....T.....CA.....AC.....C.....G-----T.....	1419
AY846266	MT.....G.....C.....T.....CA.....AC.....C.....G-----T.....	1414
AY837724	MT.....G.....C.....T.....CA.....AC.....C.....G-----T.....	1414
AF338268	MG.....A.....T.....TC.....CA.....C.....C.....G-----T.....	1415
EUI65512	MT.....G.....T.....TC.....CA.....A.....C.....G-----T.....	1398
AB558899	MT.....G.....G.....T.....CA.....C.....A.....G-----T.....C.....	1406
AB558897	MG.....T.....TC.....CA.....A.....C.....G-----T.....	1406
AY492086	MTC.....GT.....G.....T.....C.....G.....CC.....A.....T.....CA.....A.....A.TC.....C.....G-----G.....	1400
KF743726	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1400
KF743711	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1401
KF743728	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1401
KF743721	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1401
KF743719	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1410
KF743718	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1410
KF743716	PCT.....G.....T.....C.....G.....CC.....T.....A.....A.TC.....C.....G-----G.....	1410
GU562823	MA.....TA.....TC.....T.....C.....G.....G.....GG.....GG.....C.....TA.....A.....A.T.G.....G.....AAATC.....CC.....	1379
HMU82963	MC.....TA.....G.....C.....C.....T.....G.....G.....GG.....GG.....T.....CA.....A.....C.....C.T.G.....A.....AATT.....CC.....	1388
DQ157153	MG.....G.....C.....G.....G.....GG.....GG.....T.....CA.....A.....C.....C.T.G.....T.....A.....AA.....C.....C.....	1368
AY831867	MA.....TC.....T.....C.....G.....G.....GG.....GG.....T.....CA.....A.....C.....C.T.G.....T.....A.....AA.....C.....C.....	1384
AY171918	MTA.....G.....C.....C.....T.....T.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.T.....T.....A.....AA.....ATC.....CC.....	1391
F0667774	MTTA.....TTC.....T.....G.....G.....GG.....GG.....GT.....TA.....AC.....A.....T.....G.....TA.....AA.....C.....C.....	1347
AB820288	MTA.....G.....TC.....T.....C.....G.....G.....GG.....GG.....T.....CA.....A.....C.....C.T.G.....A.....AATT.....CC.....	1373
AB848714	MA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
AY529641	MA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1385
AF548631	MA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1385
KF743714	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
AB725596	MA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1357
KF743709	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743723	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743735	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743732	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743705	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743712	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743725	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743708	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
KF743730	PA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1390
GU734681	MA.....T.....TTCC.....T.....GG.....CC.....C.....G.....G.....GG.....GG.....T.....CA.....A.....A.TC.....T.....G.....TA.....G.....AAC.....C.....	1313
KF743706	PTA.....T.....TTCC.....T.....G.....C.....C.....G.....G.....GG.....GG.....GT.....A.....ATAC.....T.....G.....TA.....A.....AAC.....C.....	1391
KF743734	PTA.....T.....TTCC.....T.....G.....C.....C.....G.....G.....GG.....GG.....GT.....A.....ATAC.....T.....G.....TA.....A.....AAC.....C.....	1391
KF743715	PTA.....T.....TTCC.....T.....G.....C.....C.....G.....G.....GG.....GG.....GT.....A.....ATAC.....T.....G.....TA.....A.....AAC.....C.....	1391
KF743736	PTA.....T.....TTCC.....T.....G.....C.....C.....G.....G.....GG.....GG.....GT.....A.....ATAC.....T.....G.....TA.....A.....AAC.....C.....	1391
KF743704	PTA.....T.....TTCC.....T.....G.....C.....C.....G.....G.....GG.....GG.....GT.....A.....ATAC.....T.....G.....TA.....A.....AAC.....C.....	1391
EP460765	MTA.....T.....TT.G.....T.....G.....TC.....C.....G.....G.....GG.....GG.....T.....A.....AT.....C.....T.....G.....A.....G.....AAC.....C.....G.....	1392
KF743710	PTA.....T.....TT.G.....T.....T.....T.....C.....G.....G.....GG.....GG.....T.....A.....ATAC.....T.....G.....TA.....A.....AAT.....C.....C.....	1391
KF743733	PTA.....T.....TT.G.....T.....T.....T.....C.....G.....G.....GG.....GG.....T.....A.....ATAC.....T.....G.....TA.....A.....AAT.....C.....C.....	1391
KF743707	PTA.....T.....TT.G.....T.....T.....T.....C.....G.....G.....GG.....GG.....T.....A.....ATAC.....T.....G.....TA.....A.....AAT.....C.....C.....	1391
KF743731	PTA.....T.....TT.G.....T.....T.....T.....C.....G.....G.....GG.....GG.....T.....A.....ATAC.....T.....G.....TA.....A.....AAT.....C.....C.....	1391
KF743720	PTA.....T.....TT.G.....T.....T.....T.....C.....G.....G.....GG.....GG.....T.....A.....ATAC.....T.....G.....TA.....A.....AAT.....C.....C.....	1391
NB_036946	MA.....C.....T.....AA.....GT.....T.....TG.....T.....C.....A.....TCA.....C.....G.....CGA.....CGCT.....C.....T.....G.....C.....GG.....CTG.....T.....A.....GCC.....GT.....G.....TAA.....GAACT.....C.....AGCA.....G.....C.....GG.....C.....G.....	1433
F2245866	MA.....C.....T.....AA.....A.....A.....T.....TG.....T.....C.....A.....TCA.....C.....T.....G.....CGA.....CGCT.....C.....T.....G.....C.....GG.....TTG.....T.....A.....GCC.....G.....G.....AGT.....A.....CTTCGGAGCGACT.....AGGCA.....G.....CCGA.....C.....G.....G.....	1446
AF125879	MAT.....ATCA.....GT.....A.....T.....TG.....T.....C.....A.....TCA.....C.....GC.....GT.....A.....TATC.....AA.....A.....CGCAA.....T.....A.....GC.....AA.....TGG.....A.....A.....CG.....CT.....GAT.....AT.....	1410
AF125878	MT.....ATCA.....G.....A.....T.....TG.....T.....C.....A.....TCA.....C.....GC.....GT.....A.....TATC.....AA.....A.....CGCAA.....T.....A.....GC.....AA.....TGG.....A.....A.....CG.....CT.....GAT.....AT.....	1411
DQ522159	MT.....ATCA.....G.....A.....T.....TG.....T.....C.....A.....TCA.....C.....GC.....GT.....A.....TATC.....AA.....A.....CGCAA.....T.....A.....GC.....AA.....TGG.....A.....A.....CG.....CT.....GAT.....AT.....	1416

Table S3. Best fit GLM of hemoplasma infection prevalence in raccoons

Variables	Estimate	Standard error	Z value	Pr(> z)
Intercept	-3.66	1.42	-2.6	0.01*
Body weight (kg)	1.30	0.37	3.46	0.005***
habitat (urban)	2.01	2.08	0.967	0.33
Body weight (kg)* habitat (urban) interaction	-1.08	0.48	-2.25	0.025

Significance codes: 0 '***', 0.001 '**', 0.01 '*', AICc=95.2