

Supplementary material S1. Additional primers used in inverse nested PCRs to amplify the complete genomes of mongoose associated circoviruses and cycloviruses.

Mongoose associated circovirus	Primer name	Primer sequence (5'-3')	Primer position
Mon-1 and -29	Mon-1-Circo-F1	ACC CGG AAG TCT ACA TCC GGC ATG ¹	nt 590-nt 613 ²
	Mon-1-Circo-R1	CTG GCG CGA GGG ACA TCC AAT CTC ¹	nt 510-nt 487 ²
	Mon-1-Circo-Nested PCR-F2	ACT ACG TGA ATG CTG CTG GAC TGG ¹	nt 629-nt 652 ²
	Mon-1-Circo-Nested PCR-R2	GAT TCT CCA GAT CCG TCC CCC TCG ¹	nt 454-nt 431 ²
Mon-66	Mon-66-Circo-F1	CGA CCT GCT AGC AAT GAA GAA GGC ³	nt 468-nt 491 ⁴
	Mon-66-Circo-R1	GTA GGT CCA TGG TCC GTC CTG TC ³	nt 435-nt 413 ⁴
	Mon-66-Circo-Nested PCR-F2	GAC GAA GGA CAG AGC GAG AAG G ³	nt 496-nt 517 ⁴
	Mon-66-Circo-Nested PCR-R2	TGT CTT CTT TGC TGC AGT AGG CG ³	nt 409-nt 387 ⁴
Mongoose associated cyclovirus			
Mon-20 and -24	Mon-24-Cyclo-F1	GGC AGG CAC GTG GTT TGA ACA G ⁵	nt 456-nt 477 ⁶
	Mon-24-Cyclo-R1	TGC CTT CTC AAT ATG GAT TGC GTC ⁵	nt 417-nt 394 ⁶
	Mon-24-Cyclo-Nested PCR-F2	ATT TGG AGT CCG TCG TAT CTG CTA ⁵	nt 509-nt 532 ⁶
	Mon-24-Cyclo-Nested PCR-R2	TTG ATG GCA CTG AAG CGC ATG G ⁵	nt 380-nt359 ⁶
Mon-32	Mon-32-Cyclo-F1	ACA ACG CTA CGA GAT ATT GCC AC ⁷	nt 385-nt 407 ⁸
	Mon-32-Cyclo-R1	CGT CGG ATC CAT TTG CCT TCT C ⁷	nt 268-nt 247 ⁸
	Mon-32-Cyclo-Nested PCR-F2	CAT ACG CTA TTT CCG TGG CAT CC ⁷	nt 426-nt 448 ⁸
	Mon-32-Cyclo-Nested PCR-R2	GCT TCT TGA TGG TAC TGT AGC GTG ⁷	nt 223-nt 200 ⁸
Mon-58, -60 and -62	Mon-58-Cyclo-F1	CTA AGT CTG GCG AGG TAT GGA TGC ⁹	nt 427-nt 450 ¹⁰
	Mon-58-Cyclo-R1	GTT CCT TTA GCC GGT TCA ATG TGC ⁹	nt 400-nt 377 ¹⁰
	Mon-58-Cyclo-Nested PCR-F2	CGG AGA ACC TAG TAC TCA AGG AGC ⁹	nt 452-nt 475 ¹⁰
	Mon-58-Cyclo-Nested PCR-R2	TCC TAA CGC TTG AGA ATC TCC GGG ⁹	nt 357-nt 334 ¹⁰

The primer sequences were designed manually following multiple alignment/from the partial Rep-encoding ORF sequence/s of Mon-1 and -29 ¹, Mon-66 ³, Mon-20 and -24 ⁵, Mon-32 ⁷, and Mon-58, -60 and -62 ⁹. The partial Rep-encoding ORF (~400 bp) of the mongoose associated circoviruses and cycloviruses were amplified by nested PCR assays using pan-*rep* primers (CV-F1, CV-R1, CV-F2 and CV-R2) as described previously [3].

Nucleotide (nt) position corresponds to that of the complete genome sequence of mongoose associated circovirus Mon-1 and -29 ² and Mon-66 ⁴, and reverse complement of complete genome sequence of mongoose associated cyclovirus Mon-20 and -24 ⁶, Mon-32 ⁸, and Mon-58, -60 and -62 ¹⁰. Following ICTV guidelines [1, 2], the first nt of the nonanucleotide motif was considered as 'position one' of the Mon sequences.