Supplementary Table S1. Primers used in three overlapping nested PCR assays to amplify the complete genomes of *Porcine circovirus 3* (PCV3) strains from the Dominican Republic.

Nested PCR reaction		Primer name	Primer sequence † (5′-3′)	Primer position ‡
A	First PCR	PCV3-F-A	TGAGTGGATATACCGGGCAGTG	nt 88-nt 109
		PCV3-R-A	TCCGATGAATACCACTCCTCCG	nt 1011-nt 990
	Second PCR	PCV3-FN-A	GTGTTTTGATGCCGCAGGAC	nt 127-nt 146
		PCV3-RN-A	CCACAAAATTAACAAACCCACCC	nt 946-nt 924
B	First PCR	PCV3-F-B	GGGTTTGCGTGATTTTTGCGG	nt 645-nt 665
		PCV3-R-B	AAACACAGCCGTTACTTCACCC	nt 1570-nt 1549
	Second PCR	PCV3-FN-B	GATGGGGTTGGGTAAACCGC	nt 669-nt 688
		PCV3-RN-B	TTCTGGCGGGAACTACCAGC	nt 1539-nt 1520
C	First PCR	PCV3-F-C	ATGCGAGGGCGTTTACCTGTG	nt 1238-nt 1258
		PCV3-R-C	CTTCACCGAGCTGAGTCGCC	nt 420-nt 401
	Second PCR	PCV3-FN-C	CCACCGGAGGGGTCAGATTT	nt 1309-nt 1328
		PCV3-RN-C	GTACCCTTGCAAGTGTGGGG	nt 381-nt 362

† The primer sequences were determined from conserved regions among PCV3 genomes.

‡Nucleotide (nt) positions are those of reference PCV3 strain PCV3/CN/Fujian-5/2016 (GenBank accession number KY075986).