

Table S1. Primer sequences of PCR techniques referred in Table 2.

PCR type	Tarteted genomic region (amplicon size, bp)	Primers Sequences (5'-->3')	Ref
c-PCR, qPCR	LTR on GenBank accession n. M10608 (291 bp)	F: TGACACAGCAAATGTAACCGCAAG R: CCACGTTGGGCGCCAGCTGCGAGA	[1-5]
Semi n-PCR	<i>Pol</i> gene from K1514, EV1, SA-OMVV, CAEV-Cork (1 st round 412 bp & 2 nd round 404 bp)	1 st round F: CARGGIGGIATMATAGAYTCIGG R: ARTGIGTRTARTCIACYTGCCA 2 nd round F: GGGATMATAGAYTCGGGRTATCARGG R: TGGGTRTARTCGACYTGCCARTG	[6]
qPCR	<i>Gag</i> gene on GenBank accession n. M51543 (138 bp)	F: TGGCGCCCAACGTGGGGC R: CTTCAGGCGTCCCCGAAG	[2,3]
n-PCR	<i>gag</i> gene (500 bp) of CAEV-Co GenBank accession n. M33677	1 st round F: CTG GCG GCC CAA CGT GG R: CAC AAG ACC ATG CTG CAT DGCYAC 2 nd round F: GAT AGA GAC ATG GCG AVG CAR G R: AAGACC ATG CTG CAT DGC YAC TGT	[7]
RT-PCR	<i>Gag</i> gene (748 bp)	F: GGGACGCCTGAAGTAAGGTA R: CAAAATCCTCGGACACAAG	[4]
q(RT)-PCR	<i>env</i> gene (114 bp) GenBank accession n. NC_0014	F: TACATGCGCTTAAGTGGG R: TACCTGRGGTYKATACTTAC	[8]

n-PCR	<p><i>env</i> gene (625 bp or 394 bp or 608 bp)</p> <p><i>gag</i> gene (990 bp) of CAEV-Co molecular clone</p>	<p><i>env</i>-PCR</p> <p>1st round</p> <p>F: ACAAAGATGGCTWGCWATGCTTA</p> <p>R: ATGCCAGCAATCCAATTCWTGGT</p> <p>2nd round</p> <p>C1V2</p> <p>F: AGGTAAGTATAAAACCCAGGTAAG</p> <p>R: GGCATCTTTTCTGTACAGGAGACTGCT</p> <p>Or V1V2</p> <p>F: TTGCAAAATGGGGATGTCAACC</p> <p>R: GGCATCTTTTCTGTACAGGAGACTGCT</p> <p>Or V4V5</p> <p>F: GGIACIAAIACWAATTGGAC'</p> <p>R: GCYAYATGCTGIACCATGGCATA</p> <p><i>gag</i>-PCR</p> <p>1st round</p> <p>F: TGGTGARKCTAGMTAGAGACATGG</p> <p>R: GTTATTCCATAGGAGGAGCGGACGGCACCA</p> <p>2nd round</p> <p>F: GGAGCACTTGACAGAAGGAAA</p> <p>R: GATCAGAAGGGTTCAAAATGAA</p>	[9]
Semi n(RT)-PCR	<p><i>pol</i> gene from K1514 for semi-nested (475 bp & 303 bp)</p>	<p>1st round</p> <p>F: DSAAGARAAATTARARGG</p> <p>R: ATCATCCATRTATATBCCAAATTG</p> <p>where B = C, G or T, D = A, G or T, R = A or G, and S = C or G</p> <p>2nd round</p> <p>replacing the F primer with GATTTAACAGAGGCACA</p>	[10]
Semi n(RT)-PCR	<p><i>pol</i> gene from K1514 for semi-nested PCR (475 bp & 303 bp)</p>	<p>pol-PCR</p> <p>1st round</p> <p>F: DSAAGARAAATTARARGG</p> <p>R: ATCATCCATRTATATBCCAAATTG</p> <p>2ndround</p> <p>replacing the F primer with GATTTAACAGAGGCACA</p>	[5]
qPCR	<p><i>gag</i>MA gene from CAEV Co (113 bp)</p> <p>LTR from KV1514</p>	<p>-3'</p> <p><i>Gag</i>MA-PCR for g</p> <p>F: GGGAAAAGGGATTATCCTGAG</p> <p>R: GTTTTAAGGCACCAAYAAACAATTTC</p> <p>CAEV MA probe: TCTGTCAAGTKCTCCCCTCTG-</p> <p>LTR-PCR for s</p> <p>F: GGATACCCCGAGCTCAAAG</p> <p>R: MVVMA R3 TTYAAKGCCCAAYAGACARTT</p> <p>MVV MA probe: TCTGTCAAGGTCTCCTTCCCG</p>	[11]

n-PCR	(101 bp)		
	<i>gag</i> gene	1st round	[12]
	(1 st round	F: AACTGAAACTTCGGGGACGCCTG	
	1191 bp &	R: GTTATCTCGTCCTAATACTTCTACTGG	
	2 nd round	F: AAGGTAAGTGACTCTGCTGTACGC	
	1327 bp)	R: TTTTCTCCTTCTACTATTCCYCC	
		2nd round	
		F: TGGTGAGTCTAGATAGAGACATGG	
		R: CAEV R2 GGACGGCACCACACGTAKCCC	
qPCR	<i>gag</i> gene	For genotype B:	[13–15]
	(524 bp)	F: AAWCCGCCRTGGTGARTCTAGATA	
	strain	R: CSAGYTCAGGATAATCYCKTTTCC	
	K1514	SRLV-B probe: TGGCGAGGCARGTCTCCGG	
		For genotype A:	
		F: TAGAGACATGGCGAAGCAAGG	
		R: GCCCATAGACAGTTCCCTTC	
		MGB-probe: TACCCCGAGCTCAA	
Semi n-qPCR	<i>pol</i> gene	1 st round	[16]
	(1 st round	F: ZNA CARGGAGGAATMA-pdU	
	455 bp &	AGAYICAGGATATCARGG-	
	2 nd round	R: ZNA CCYGAAT-pdU-WGTTTCTAYCCA	
	416 bp)	2 nd round	
		F: CAGGGAGGAATMATAGAYGCAGGATAT	
		R: TCATAATGGGTRTARTCYACYTGCCAATG	
		Probe 1: AAA + T + G + GCATC + A + A + GATG	
		Probe 2: AAG + T + G + GCATC + A + A + GATG	
		Probe 3: AAA + T + G + GCATC + A + G + GATG	

bp: base pairs; s: sheep; g: goat c-PCR: conventional PCR; n-PCR: nested PCR; qPCR: quantitative (real time) PCR; RT-PCR: reverse transcription PCR; F:forward primer; R:reverse primer; IUPAC ambiguity codes: B = C, G or T; D = A, G or T; V = A, C or G; S = C or G; W = A or T; Y = C or T; R = A or G; M = A or C; K = G or T; I = inosine; ZNA5: Zipped nucleic acid primer conjugated with 5 cationic spermine units; pdU: 5-(1-propynyl)-2'-deoxy-uridine; Ref:Reference.

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