

# A multiplex PCR test to identify four common cattle-adapted *Cryptosporidium* species - CORRIGENDUM

## Corrigendum

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The authors apologise for errors in some of the primer sequences contained in [Table 1](#) of the above paper. The corrected Table appears below:

**Table 1.** Primer sequences, size of amplicon and species detected with each primer pair

Primer Pair	Sequence 5'–3'	Fragment Size (bp)	Species Detected
<b>AL1687 (EF)</b> <b>AL1691 (ER)</b>	TTCTAGAGCTAATACATGCG CCCATTTCTTCGAAACAGGA	1370	Genus Specific External
<b>AL1598 (IF)</b> <b>AL3032 (IR)</b>	GG*AAGGGTTGTATTTATTAGATAAAG AAGGAGTAAGGAACAACCTCCA	840	Genus Specific Internal
<b>CaF</b> <b>AL3032 (IR)</b>	GCAAATTACCCAATCCTGAC AAGGAGTAAGGAACAACCTCCA	625	<i>C. andersoni</i>
<b>CrF</b> <b>AL3032 (IR)</b>	TGTTAATTTTTATATA <b>CAATR</b> <sup>†</sup> CTACGG AAGGAGTAAGGAACAACCTCCA	415	<i>C. ryanae</i>
<b>CphF</b> <b>AL3032 (IR)</b>	AGAGTGCTTAAAGCAGGCATA AAGGAGTAAGGAACAACCTCCA	305	<i>C. parvum</i>
<b>CbF</b> <b>AL3032 (IR)</b>	CTTCTTATTG <sup>‡</sup> G <sup>‡</sup> TTCTAGAATAAAA ATG AAGGAGTAAGGAACAACCTCCA	241	<i>C. bovis</i>

\*This base was omitted in the originally published Table

†The degenerate base in the *C. ryanae* primer is shown in bold and underlined

‡These bases were mistakenly written as C in the originally published Table

## Reference

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