

- UNMUTATED ALLELE

5' [...] CTGTGCACCAATTGGTCGAGAACACAGAT**G**AGACCTTC[...] 3'

Fsite198Ab: 5' CTGTGCACCAATTGGTCGAGAACACAG**CTG** 3'
 3' [...] GACACGTGGTTAACCAGCTCTTGTGTCT**ACT**CTGGAAG[...] 5'

214 bp

5' [...] CTGTGCACCAATTGGTCGAGAACACAG**CTGAG**ACCTTC[...] 3'
 3' [...] GACACGTGGTTAACCAGCTCTTGTGTCT**GACT**CTGGAAG[...] 5'

DdeI  ➔ 186 + 28 bp

- MUTATED ALLELE

5' [...] CTGTGCACCAATTGGTCGAGAACACAGAT**GCG**ACCTTC[...] 3'

Fsite198Ab: 5' CTGTGCACCAATTGGTCGAGAACACAG**CTG** 3'
 3' [...] GACACGTGGTTAACCAGCTCTTGTGTCT**ACG**CTGGAAG[...] 5'

214 bp

5' [...] CTGTGCACCAATTGGTCGAGAACACAG**CTGCG**ACCTTC[...] 3'
 3' [...] GACACGTGGTTAACCAGCTCTTGTGTCT**GACG**CTGGAAG[...] 5'

DdeI  ➔ 214 bp

Additional file 2: Figure S1. Representation of the methodology used to analyze codon 198 of the beta-tubulin isotype 1 gene from *Ancylostoma braziliense*. The *Fsite198Ab* primer was designed to add a mutation in the amplicon, regardless of whether there was a mutation at codon 198. The absence of the mutation at codon 198 in combination with the primer-introduced change creates a site for *DdeI*. If the allele is mutated, even the altered primer cannot create a *DdeI* site. Codon 198 is underlined, with the base of interest in bold.