Supplemental material

Figure S1. Schematic position on their target of PCR primers used for the molecular diagnosis of congenital toxoplasmosis in France (2002-2005) for the two main DNA targets (B1 gene and rep529). A. Nucleotide sequence of the B1 gene (GenBank Accession # AF179871) from (7). Primer sequences from Pelloux et al. (28) red and (>), Robert et al. (30) blue and (–), Burg et al. (7) brown and (#), Lin et al. (26) purple and (~), Foudrinier et al. (20) blue and (.), Costa et al. (14) green and (:), Bretagne et al. (6) brown and (<), and unpublished primer pair from Morin and Miegeville pink and (<>) are located under the B1 sequence. The primer sequences are in capital letters; where two primers overlap, this is indicated by an uppercase to lowercase letter change in the overlapping segment. **B.** Nucleotide sequence of the rep529 element (GenBank Accession # AF146527 from Homan et al. (23) and AF487550 (in bold) from Reischl et al. (29)). Primer sequences from Homan et al. (23) red > signs, Reischl et al. (29) green * signs, Cassaing et al. (8) blue - signs, and Fekkar et al. (18) brown # signs, are located under the rep529 sequence. The three mismatches between both sequences are underlined (C/T 137, A/G 160, C/T 391) and two gaps are double-underlined (G and A are lacking in AF487550 in position 277 and 370 respectively). Primers from Reischl et al. (29), Cassaing et al. (8) and Fekkar et al. (18) were designed on one mismatch (C/T 391) and the forward primer from Cassaing et al. (8) was designed on region 269 to 287 that encompasses one of the gaps. It is noteworthy that three unpublished primer sequences (one for B1 and two for rep529) remain and are not shown.

A. B1 gene

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   1 gaattcgttcgacagaaagggagcaagagttgggactaaatcgaagctgagatgctcaaagtcgaccgcgagatgcacccgcagAAGAAGGGCTGACTCG
                                                                                Pelloux  AAGAAGGGCTGACTCG

 101 AACCAGATGTgctaaaggcgtcattgctgttcTGTCCTATCGCAACGGAGTTCTtcccagacgtggatttccgttggttCCGCCTCCTTCGTCCGTCGTA
     AACCAGATGT>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
                                                                             Robert CCGCCTCCTTCGTCCGTCGTA

 201 atatcaggccttctgttTCTGTTCGCTGTCTGTCTAGGGcacccttactgcaagagaagtatttgaggtcatatcgtcccatgaagtCGACCACCTGTTTC
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
     --------------------------------------------------------------------------------------CGACCACCTGTTTC

 301 CTCTCTTCActgtcacgtacgacatcgcattcaagggaagagatccagcagatctcgttcgtgtattcgaGACAAGAGAGGTCCGCCCcacaagacggc
     >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>GACAAGAGAGGTCCGCCC Pelloux
     CTCTCTTCA Robert

 401 tgaagaatgcaacattcttgtgctgcctcctctcatggcaaatgccagaagaagggtacgtgttgcatcataacaagagctgtatttcccgctggcaaat
 501 acaggtgaaatgtacctccagaaaagccacctagtatcgtgcggcaatgtgccacctcgcctcttgggagaaaaagaggaagagacgctgccgctgtttt
 601 gcaaatgaaaaggattcattttcgcagtacaccaggagttggattttgtagagcgtctctcttcaagcagcgtattgtcgagtagatcagaaaGGAACTG
                                                                                             Burg GGAACTG

 701 CATCCGTTCATGAGtataagaaaaAAATGTGGGAATGAAAGAGACGCTAATGTgtttgcataggttgcagtcactgacgagcTCCCCTCTGCTGGCGAAA
     CATCCGTTCATGAG######################################################################################
                                                                                  Lin  TCCCCTCTGCTGGCGAAA
       Morin and Miegeville  AAATGTGGGAATGAAAGAGACGCTAATGT<><><><><><><><><><><><><><><><><><><><><><><<

 801 AGTgaaattcatgagtatctgtgcaACTTTGGTGTATTCGCAGATTGGTCGCctgCAATCGATAGTTGAccacgaacgcTTTAAAGAacaggagaagaag
     #####################################################################CCACGAACGCTTTAAAGA Burg
     AGT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CAATCGATAGTTGACCACGAACGCT Lin
     <><><><><><><><><><><><><ACTTTGGTGTATTCGCAGATTGGTCGC Morin and Miegeville


 901 atcgtgaaagaatacgagaagaggtacacagagatagaagtcgctgcggagacagcgaagactgcggatgacttcactcccgtcgcaccagcagcagagg
1001 agtgccgggcaagaaaatgagatgcctagaggagacacagcgtgttatgaacaaatctattgaggtttcgcgaagaggagggaacatattatatacagaa
1101 gaagaacaagagacgtgccgcatgtcgctaagccatcggaagggatgctcagaaaatggcacagtatcacattacagttccgttgattcgtctgatggtg
1201 acgaaaggggaagaatagttgtcgcaccaaaactggctagttgttattttgaagaagacgagagatggagtgaaccaccaaaaatcggagaaaatcgatg
1301 gtgtcacgtttttttgtcagacttcactttgtgcagaagcattgcccgtccaaactgcaacaactgctctagcgtgttcgtctccattccgtacagtcttc
1401 aaaaatacaaaagagaacattccagcaacttctgcctttgttcttttagcctcaatagcaggatgacgcctccctcctatctttcagccaacccagcaaa
1501 caccgacgaactctctgtagagtaacaaagagaaggcaaaacgcgccatcacgaacactcgcagagatgatacagagacgtgtcatcaggacaaggttgg
1601 tcgcttaatttctgtatatagcatttttagaatgcacctttcggacctcaacaaccgtgcaaaaggatcgccacctggtgtctcTTCAAGCGTCAAAAC
                                                                              Foudrinier  TTCAAGCGTCAAAAC

1701 GAACTATctgtatatctctcaaGGAGGACTGGCAACCTGGtgtcgacaacagaacagctgcagtccggaaatagaaagccatgaggcactccAACGGGCG
     GAACTAT.............................................................................................
                                                                                           Bretagne  AACGGGCG
                     Costa GGAGGACTGGCAACCTGG::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

1801 AGTAGCACCTGAGGAGAtacaaaCTGCTAAACGGTCCGGGTGAAACAAtagagagtactggaacgtcgccgctacTGCCCAgttgtCATGCCATcgacgt
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     ...........................................................................TGCCCAGTTGTCATGCCAT
     AGTAGCACCTGAGGAGA<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<GTTGTCATGCCATCGACGT
     :::::::::::::::::::::::CTGCTAAACGGTCCGGGTGAAACAA  Costa

1901 AGACCCAgaaatgaggcgagaaattaatattgttagtaaagcattcaaaaagttccggtcgagaggctaaaccacaaaagtgcaaaccatgcgcagccat
     AGACCCA  Bretagne

2001 cagcttaacaaaagcagttggtgatggttgcctcgagttccttctgaaaatggattacttcatcaacgagcccaccacgcagaatcatgctttcccagtg
2101 ctaaagcgtttctaaagtagccgcacaatgcggaatgctaaggggatcgcctacgtagcacatgttgtgcctcacccccccagctcgtgcgctcattctcc
2201 tttcgtgcgcggct
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B. rep529

```
  1 CTGCAGGGAGGAAGACGAAAGTTGttttttatttttttttctttttgtttttctgattttgttttttttgactcgggcccagctgcgtctgtcgggat
    CTGCAGGGAGGAAGACGAAAGTTG Homan >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

101 gagaccgcggagccgaagtgcgttttctttttttgacttttttttgtttttcacaggcaagctcgcctgtgcttggagccacagaagggacagaagtcg
    >> Homan >>>>>>>>>>>>>>>>>>>>>>>>>>>t>>>>>>>>>>>>>>>>>>>>>>g>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

201 aaggggactacagacgcgatgccgctcctccagccgtcttggAGGAGAGATATCAGGACTGTAGatgaAGGCGAGGGTGAGGATGAgggggtggcgtggt
    >> Homan >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>->>>>>>>>>>>>>>>>>>>>>>>
                                     Reischl  AGGAGAGATATCAGGACTGTAG************-***********************
                                                              Cassaing  AGGCGAGG-TGAGGATGA--------------

301 tgggaagcgacgagagtcggagagggagaagatgtttccggcttggctgcttttcctggagggtggaaaaAGAGACACCGGAatgCGATCCAgacgagac
    >> Homan >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>->>>>>>>>>>>>>>>>>>>>t>>>>>>>>>
    *********************************************************************-****************GATCTAGACGAGAC
    ---------------------------------------------------------------------*------------ATGCGATCCAGACGAGAC
                                                                  Fekkar  AGAGACACCGGAATGCGATCT#########

401 gaCGCtttcctcgtggtgatggcggagagaattgaagagtggagaagagggcgagggagacagAGTCGGAGGCTTGGACGAAgggaggaggaggggtagg
    >> Homan >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
    GACGC Reischl
    GA Cassaing
###################################################################AGTCGGAGGCTTGGACGAA Fekkar

501 agaggAATCCAGATGCACTGTGTCTGCAG
    >>>>>AATCCAGATGCACTGTGTCTGCAG  Homan
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