

TB -----MTEKEDIVQRAKLAEQAERYDDMAAAMKKVETG--- 35
TS -----MSEKEDIVQRAKLAEQAERYDDMAAAMKKVETG--- 35
HC -----MADNKDELVQRAKLAEQAERYDDMAQSMKKVETG--- 36
DI -----MAENKDELVQRAKLAEQAERYDDMAQSMKKVETG--- 36
CE -----MSDGKEELVNRAKLAEQAERYDDMAAAMKKVETG--- 36
BX -----MSDGKDELVQRAKLAEQAERYDDMAQSMKKVETG--- 36
AM -----MSVDKEELVQRAKLAEQAERYDDMAAAMKKVETGV--- 36
HV -----MTDKEEQVQRAKLAEQAERYDDMAAAMKKVETSGA--- 35
HS -----MDKNELVQRAKLAEQAERYDDMAAAMKKVETGGA--- 34
SB -----MTTSWVLQCKDLSNTLVHIAKLAEQAERYDDMAAAMKKVETSG--- 45
HM -----MVDVSSTEWLKDPLRDRESLVYTAKCLEQAERFDDMAICMKEVTFNFDQ--- 49
EG -----MAELLSTEWLKDPLKDRDSYVNTAKCLEQAERFDDMAVCMKEVTRFDK--- 49
EM -----MAAITSWITDSGCKDHASLVSTAKLAEQAERYDDMAVAMKTTAEFGN--- 47
TG MVSTDIASFSSAKKSTRPLLVFHRPARDFFVFLRFPSPFFSGHFSPFLLLSVCPVSTMAEEIKNLRDEYVYKAKLAEQAERYDDMAEAMKNVENCLEQ 100
ET -----MIEDIKTLREHHVYRAKLAEQAERYDDMAEAMKNVENCLEQ 43
GI -----MAEAFTREDYVFMALNENAERYDEMVEVTRKISGMEG--- 38
SM -----MDELREERNIVIAKLCEQAERYDEMVKAMIEATNTET--- 37

TB -----ELTNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICHVDVLGLLDKYLIPKAATPESKVFYFKM 122
TS -----ELTNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICHVDVLGLLDKYLIPKAATPESKVFYFKM 122
HC -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICQDVNLNLLDKYLIPKAGNPESKVFYFKM 123
DI -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICQDVNLNLLDKYLIPKAGNPESKVFYFKM 123
CE -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICQDVNLNLLDKYLIPKAGNPESKVFYFKM 123
BX -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELRDICHVDVLGLLDKYLIPKAGNPESKVFYFKM 123
AM -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELREICQDVNLGLLDKYLIPKASNAESKVFYFKM 123
HV -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELREICQDVNLGLLDKYLIPKASNPESKVFYFKM 122
HS -----ELSNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GSEKKQOMAREYREKVEKELREICQDVNLGLLDKYLIPKASNAESKVFYFKM 121
SB -----NLGNEERNLLSVAYKNVVGARRSARVHIGSEMKAV---NDCTKKQIAEYRKMEKELNTICQVIALLEDYLLPNASPDPSKVFYFKM 132
HM -----ELNNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---DAE-KQNLTKKEYEILQKELNDICTDVLKILIDERLYPKCSNAESKVFYFKM 135
EG -----ELNNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---DPE-KQALTRYEILQKELNACISDVLQILIERIYPSCSNAESKVFYFKM 135
EM -----ELNNEERNLLSVAYKNVVGARRSSWRVSSIIEOKTE---GTP-LADQTDIYLKKVEBELTKICNDVIALLSKNLITEKIGAEAKIFVYFKM 133
TG QPK-----DELSVEERNLLSVAYKNVVGARRASWRVSSIIEOKELSK--QHMQNKAIAEYRKVEBELNKICHDIQLLTDLKLPKTSDESSEKVFYFKM 193
ET NSPPGAKGDELTVEERNLLSVAYKNVVGARRASWRVSSIIEOKELSK--NHMANKALAAEYRKVEBELNKIQEILTLTLTKLPRTDSESEKVFYFKM 141
GI -----ELSDKERNLLSVAYKNVVGARRASWRVSSIIEOKELSK--QHMQNKAIAEYRKVEBELNKICHDIQLLTDLKLPKTSDESSEKVFYFKM 129
SM -----ELTVEERNLLSVAYKNVVGARRSSWRVSSIIEOKELSK--QAGSDEIHITKREKVEKELDEICTSILNLLNCLLPKAVSDESSEKVFYFKM 125

TB KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 222
TS KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 222
HC KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 223
DI KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 223
CE KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 223
BX KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 223
AM KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 223
HV KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 222
HS KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 221
SB KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 231
HM KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 234
EG KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 235
EM KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 233
TG KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 293
ET KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 241
GI KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 228
SM KGDYYRYLAEVATGDDRTNIVENSQAYOEALDVAKSKMQPTHPIRLGLALNFVSFYYEILNAPDRACOLAKQAFDDATAELDTLNEDSYKDSSTLIMQLL 224

TB RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 250
TS RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 250
HC RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 249
DI RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 251
CE RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 248
BX RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 251
AM RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 247
HV RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 246
HS RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 245
SB RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 252
HM RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 255
EG RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 256
EM RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 248
TG RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 323
ET RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 277
GI RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 248
SM RDNLTLWTTDAGGDECEGGGQDQTAAGQ----- 249

Supplementary Figure 1. Sequence of *T. britovi* 14-3-3 aligned with selected 14-3-3 protein isoforms. 14-3-3 in nematodes (magenta) shows 88-96% conservation of sequence. 14-3-3 isoforms in Platyhelminthes (green) and protozoa (orange) share 63-67% and 54-66% similarity with Tb14-3-3, while human (blue), bee (yellow) and barley (brown) 14-3-3 zeta share 86%, 89% and 91% similarity with Tb14-3-3, respectively. TB - *Trichinella britovi* (clade I), TS - *Trichuris suis* (clade I) KFD65230.1, HC - *Haemonchus contortus* (clade V) CDJ94531.1, DI - *Dirofilaria immitis* (clade III) AHJ11155.1, CE - *Caenorhabditis elegans* (clade V) NP_509939.1, BX - *Bursaphelenchus xylophilus* (clade IV) ACZ13351.1, AM - *Apis mellifera* XP_006566159.1, HV - *Hordeum vulgare* BAJ95666.1, HS - *Homo sapiens* NP_001129171.1, SB - *Schistosoma bovis* (zeta) AAT39382.1, HM - *Hymenolepis microstoma* (zeta) CDS31680.1, EG - *Echinococcus granulosus* (zeta) XP_024353113.1, EM - *Echinococcus multicularis* AAM94864.1, TG - *Toxoplasma gondii* XP_002365409.1, ET - *Eimeria tenella* AAD02687.1, GI - *Giardia intestinalis* AAZ91664.1, SM - *Schistosoma mansoni* (epsilon) XP_018645303.1.