Tco MTSPTVPNPMSTVPMTEM----TE-ANGTTNPPIPDAGERTAV---NFDTEQCK-TKEIL 51

Tbr1 MSD--EKINVHQYPSETDVRGLKARNGGACEVPFEENN-EPIPNRSANPQEKNE--NELV 55

Tsu1 MSS--EPVNVHRYTAEGDRSGLKDRHGKTCEVCVGDESAAAVPSAVYNPQEQSGDGPEVK 58

Tsu2 MQN--QPDAMTH-STAVQMV-NKNPEDGTGGADTERSDEMTAP--------TTRTGDAQK 48

Tbr2 MQS--QPDNVAY-PMELQAV-NKDGT---VEVRVQGNVDNSSN--------ERWDADVQK 45

Tbr3 MQS--QPDNVAY-PMELQAV-NKDGT---VEVRVQGNDDSS----------------NRK 37

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Tco -AGEGEAPHGPMDINYWPLRNLRMDFREYVGEFLGTFVLLFMGNGVVATTLLDNNLGFLS 110

Tbr1 GDNADNEAHDAVDVNYWAPRQLRLDYRNYMGEFLGTFVLLFMGNGVVATTILDKDLGFLS 115

Tsu1 AGGGEAEVQNAADVNNWAPRRLRLDYRDYMGEFLGTFVLLFMGNGVVATTMLDDGLGFLS 118

Tsu2 CETTNTPKEGAGGINYWAPRELRLKYRDYMGELLGTFVLLLMGNGVVATVVVDGKLGFLS 108

Tbr2 HEVAEAQEKPVGGINFWAPRELRLNYRDYVAEFLGNFVLIYIAKGAVITSLLVPDFGLLG 105

Tbr3 HEVAEAQEEVPGGINFWAPRELRLNYRDYMGELLGTFVLLFMGNGVVATVIIDGKLGFLS 97

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Tco ITFGWGIAVTMGLYVSLGTSSGHLNPAVTVANAFFGGFPWKKVPGYIAMQMLGAFVGAAC 170

Tbr1 ITLGWGIAVTMGLYISLGISCGHLNPAVTLANAVFGCFPWRRVPGYIAAQMLGAFVGAAC 175

Tsu1 ITLGWGIAVTMGLYISLGTSCGHLNPAVTVANAVFGCFPWKKVAGYIAMQMLGAFVGAAC 178

Tsu2 ITLGWGIAVTMALYISLGISSGHLNPAVTVGNAVFGDFPWRKVPGYIAAQMFGAFLGAAC 168

Tbr2 LTIGIGVAVTMALYVSLGISGGHLNSAVTVGNAVFGDFPWRKVPGYIAAQMLGTFLGAAC 165

Tbr3 ITLGWGIAVTMALYVSLGISSGHLNPAVTVGNAVFGDFPWRKVPGYIAAQMLGAFLGAAC 157

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Tco AYGVYADLLNKKVSDG----EIEDYAGMFSTYPRDGNSLFSCIFGEFICTAMLTFCVCGI 226

Tbr1 AYGVYADLLKQHSGG-LVGFGDKGFAGMFSTYPREGNRLFYCIFSEFICTAILLFCVGGI 234

Tsu1 AYGVFADLLKQHSGG-LIPFGDKGFAGMFSTYPRDGNRLFYCIFGEFICTAMLLFCVSGI 237

Tsu2 AYGVFADLLKEYCGGKLLAFGAKGIAGVFSTYPKEANSVFACVFGEFICTAILLFCVCGI 228

Tbr2 AYGVFADLLKAHGGGELIAFGEKGIAWVFAMYPAEGNGIFYPIFAELISTAVLLLCVCGI 225

Tbr3 AYGVFADLLKAHGGGELIAFGEKGTAGVFSTYPRDSNGLFSCIFGEFICTAMLLFCVCGI 217

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Tco FDTHNAPATGHEPLAVGALVFAIGNNVGYATGYAINPARDFGPRVFSAILYGSTVFTRGD 286

Tbr1 FDPNNSPAKGHEPLAVGALVFAIGNNIGYASGYAINPARDFGPRVFSAILFGSEVFTTGN 294

Tsu1 FDANNSPAKGHEPLAVGALVFAIGNNIGYATGYAINPARDFGPRLFSAILFGSEVFTAGN 297

Tsu2 FDPNNSPAKKHEPLAVGSLIFAIGNNIGYSTGYAMNPARDFAPRVFSALLLGGEVFSHGN 288

Tbr2 FDPNNSPAKGYETVAIGALVFVMVNNFGLASPLAMNPSLDFGPRVFGAILLGGEVFSHAN 285

Tbr3 FDPNNSPAKGHEPLAVGALVFAIGNNIGYSTGYAINPARDFGPRVFSSFLYGGKVFSHAN 277

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Tco YYFWVPLFIPLLGGIFGIILYKYFVPH 313

Tbr1 YYFWVPLFIPFLGGIFGLFLYKYFVPY 321

Tsu1 YYFWVPLFIPFLGGIFGLLLYKYFVPH 324

Tsu2 YYFWVPLFIPFLGAIFGLFLYKYFVPH 315

Tbr2 YYFWVPLVVPFFGAILGLFLYKYFLPH 312

Tbr3 YYFWVPLVIPLFGGIFGLFLYKYFVPH 304

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**Figure 1-figure supplement 1.** Sequence alignment and individual sequences of the *T. congolense*, *T. b. brucei* and *T. suis*. The *T. brucei* and *T. congolense* sequences were obtained from tritrypDB, *T. suis* sequences (Kelly S, Gibson W and Carrington M. The genome of *Trypanosoma suis*. In preparation). The alignment was produced with Clustal Omega. The yellow highlighting indicates the N-terminus of the sequences used to determine non-synonymous v synonymous ratios.