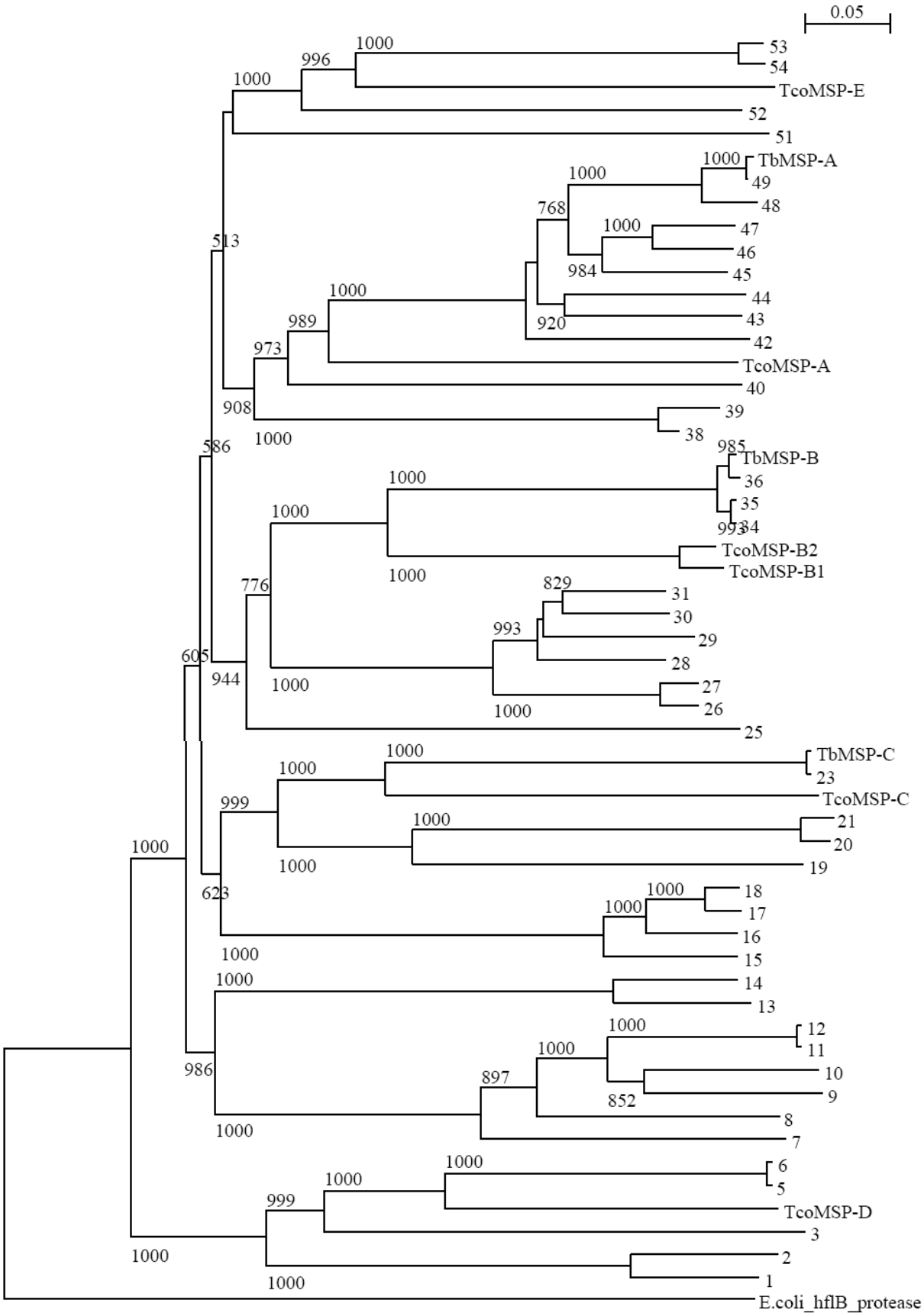
Figure S1. Clustal-W generated bootstrapped phylogenetic tree comparing *T. congolense* putative MSPs with predicted homologues from *T. brucei TREU927, T. brucei gambiense, T. brucei vivax, T. brucei rhodesiense, T. cruzi,* and *Leishmania sp*. (taxid 5658).
Protein sequence alignments of proteins listed in Table 1 were generated using ClustalX ver 2.0.7 (Larkin et al., 2007). Phylogenic trees were generated by ClustalX using the bootstrapped N-J method with 1000 iterations. The unrelated *E. coli* protease HflB was included as an outgroup for alignment. Bootstrap values greater than 500 are indicated at respective branch points. Genetic distance is indicated by the scale bar in the upper right corner. *T. congolense* MSPs are indicated. Numbering follows that used in Table 1 and Figure 3.



Supplementary Figure S1

Supplementary Data: Primary amino acid sequence for analyzed proteins.

*E.coli*_hflB protease = outgroup
MAKNLILWLVIAVVLMSVFQSFGPSESNGRKVDYSTFLQEVNNDQVREARINGREINVTKKDSN
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KGAMSFGKSKARMLTEDQIKTTFADVAGCDEAKEEVAELVEYLREPSRFQKLGGKIPKGVLMVG
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GRQRGAGLGGGHDEREQTLNQMLVEMDGFEGNEGIIVIAATNRPDVLDPALLRPGRFDRQVVVG
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LPEGDAISASRQKLESQISTLYGGRLAEEIIYGPEHVSTGASNDIKVATNLARNMVTQWGFSEK
LGPLLYAEEEGEVFLGRSVAKAKHMSDETARIIDQEVKALIERNYNRARQLLTDNMDILHAMKD
ALMKYETIDAPQIDDLMARRDVRPPAGWEEPGASNNSGDNGSPKAPRPVDEPRTPNPGNTMSEQ
LGDK

1. *T.cruzi* XM_808234
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GIRNMKVFSVFMTAARENIRFHVIFILNKSCSGVGQFVPNFLGNGVRCTADDILTPNKIRTIKI
MVKKACNYLERAILVDPLDEINVIAESCPFLGHSSLRVTEKDYVLFVTANPRSSARGVIAWAHC
CERISTGRPSVGHVNFIPSSFGEYATEKDIHVAMHEITHALGFTDLATNAKSHVGPGGKVVPGF
VRVLRPKLGKAVTLVTSPKVVEVARKHFGCPTLDGVEIEDGGKSGTAGSHWKKRILYEEALVGS
ITSANLFYSSFTLAYLEDLGYYSINYSMAEDNFRWGRNRSCRFLYNKCNDQDEDVDEFCFGKGD
AKKTSCTHDFLGMGSCDIMRHNAVLPVDYRYFTDPRIGGSTPLMDYCPSVQVYSNWNCISEVTA
EVPNFLGNEMGQHSRCFSSNLVTGASPFFSTGFRCFPTVCTKSGQILLRVQGQTVPCPLNGTAG
EADTSHLRGVQGKIVCPAASLLCGDKERNVFSESFHYSSNMIEEPVTADTKRSASEFTKNSSRL
CEERVKCAENITSFFPACRVSAQLILDCFGKDCPLAMRMWIDRTALLEQCRHPKLIAELCLDGW
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2. *T.cruzi* XM806897
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FIPSFFGEYATENDIHVAMHEITHALGFTDLATNAKSHVGPGGKVVPGFARVLRPKLGKVVTLV
TSPKVVEVARKHFGCPTLDGVEIEDGGKSGTAGSHWKKRILYEEALVGSITSANLFYSSFTLAY
LEDLGYYSINYSMAEDNFRWGRNRSCRFLYNKCNDQDEDVDEFCFGNGNAMKTSCTNDFLGMGS
CDIMRHNAVLPVDYRYFTDPRMGGSIPLMDYCPSVQVYSNWNCISEVTAEVPNFLGNEMGQHSR
CFSSNLVTGASPFFSTGFRCFPMVCTKSGQILLRVQGQTVPCPLNGTAGEADTSHLRGVQGKII
CPAAILLCRDKERNISSESFHYSSNMIEEPVTAETKRSASEFTKNSSRLCEERVKCAENINSFF
PACRVSAQRILDCFGRDCPLAMRMWIDRTALLEQCRHPKLIAELCLDGWMGAHRLCAIASSTSA
ATAIYFPIIVVCVMLLAIVFF

3. *T.b.vivax* 1037d01.p1k
MGEKGRGSGTACTGARARPWLLVILLCATVIPRANGSEPLLRGAKRHVCIHDQVALPSHIVHTI
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VLRKCNDQPANVTEFCFRRNLITAECTADHSSLGACDVVTHGMKLPTEFQYFEDPARGGSSAEM
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4. TcoMSPD
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AYVAENDNVSNNTQLNATAPASTEKVEKQPAKKVVRRNLRFYIHYMLERACKSVGEVVPSYIKK
AKTVCTADDVLTNWKKRSLKVMMEAATKFLSSALLVDPLEGVPVTVENCSGLPIPLLVAKDSDY
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5. *T.b.gambiense* 11_v2.orf3
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6. *T.brucei* TREU927XM_823726
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7. *L.braziliensis* XM001562766

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V

8. *L.guyanensis* LEIGP63X

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9. *L.mexicana* X64394

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10. *L.donovani* AJ495007

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11. *L.major* XM001681325
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12. *L.major* XM001681324
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13. *L.major* XM001684283
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14. *L.infantum* XM001470056
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15. *T.cruzi* XM802134
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GLYSALTLAAFEDMGVYVANYSAAELLWWGNNSGCGLLEKKCLTDGITEYPQLFCNEFDDDEKF
FCTYDRLSLGYCRLMRHEEALPQEYRYFADPRVGGDDPCMSRCPYFEAYSNGGCTNGDPSVLPG
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SIVCPQYADVCTAFPNISGYPIPVVDPPLVDDPTSAEGAEGDGGEVPRKRPRRL

16. *T.cruzi* XM807916
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17. *T.cruzi* XM801120
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18. *T.cruzi* XM799438
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IILRQILPAAIQLHAERLSVRPVTGPIVIPQTGLGMCDKFTIPRRHRTVGVAGTDMILYANIFP
TSGPAAWAALCFMLDDGRPVVAAVNFDPRRVAATNGYVRIAAHELGHALGFSVDFFVMLHMISE
VLNVRGSSKVSVISTPKAKAMARQYHNCPTLEGIELEDEGGPATALSHWKKRSMRDELMTSDVG
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19. *T.b.vivax* 942f04.q1k

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AEPSLWGMHSGCGFLRNKCLVNEATAYPAMYCSKSSSLSDEQCTHDRLGIGYCGVFEHNEDIPK
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20. *T.b.vivax* 1924b07q1k

MLQEAPCLAALLHMLCPATERICPLTHCLTSSASHAHKVKNSMTTMHLSFYRLALLYATVVHVL
FPTRNCVAKAVRTHQVTLSAFPSTSAPEKPSARAKLSIPTAAHTPRPNGESVACASDRISLARR
SVPAVLVVPHTAANGTGFIGAQEAGGQGDAEEWRPIQIRAFTRDLNDPQRFCTAAGDRRVSFLG
DDVVCDASSVLTLRKKRFLLERALPLGIKMHSDRLAVRPVDANVALPELESICAAFSVPPEHFV
SNPAVADMYVYVGAMQDASGALAWATTCAVLNDGRPFAGVTNISPWHLKETEEVVRTVTHELGH
ILGFMSNYFRNVDALKKVTTRGGMDRYIVDTEHTRRVTSEHFNCMNVYGIELENVGGDGTAGSH
IDRRFVADDLMTQRSIGGRYTVFSLASFESLGFYRVNYSCAEPSLWGLHSGCGFFHNECFVNGT
TEYPDVFCSRVPVQGDESCTHDRLGIGYCNLFEYTQDIPERYRYFDNPRLGGEILADYCPSVGL
SENRSCEHGNSEEMHGSFIGKGSRCVRGSDLRYKEGAVTAACVEMDCADRILRVRVLGGEWQEC
PEGKSVQPKTNGGLWSGSIICPRHADVCARTECGAFVLEPLTPQENDMEPVSAEIEETHPDVPN
ESSAGAVEGAESEKPEEVVHDDVIPEDAVSEKSAEDSGTTESTWAPCLRHLHSAVPVLFIVFVV
YL

21. *T.b.vivax* 1240d01.p1k

MLQEAPCLAALLHILCPATERICPLTHCLTSSASHAHKVKNSMTTMHLSFYRLALLYATVVHVL
FPTRNCVAKAVRTHQVTLSAFPSTSAPEKPSPHAKLSIPTAAHTPRPNGESVACASDRISLARR
SVPAVLVVPHTAANGTGFIGAQEAGGQGDAEEWRPIQIRAFTRDLNDPQRFCTAAGDRRVSFLG
DDVVCDASSVLTVRKKRFLLERALPLGIKMHSDRLAVHPVDVNVALPELESTCAAFSVPPEHFV
SNPAVADMYVYVGAMQDASGALAWATTCAVLNDGRPFAGVTNISPWHLKETEEVVRTVTHELGH
ILGFMSNYFRNVDALKKVTTRGGMHRYVVDTEHTRRVTSEHFNCTNVYGIELENIGGDGVVDSH
IDRRFVADDLMTQRSIGGRYTVFSLASFESLGFYRVNYSCAEPSLWGLHSGCGFFHNECFVNGT
TAYPDVFCSRVPVQGDESCTHDRLGIGYCNLFECTQDIPERYRYFDNPRLGGEILADYCPSVGL
SENRSCEHGNSEEMHGSFIGKGSRCVRGSDLRYKEGAVAAACVEMDCTDRILRVRVLGGEWQEC
PEGKSVQPKSNGGLWSGSIICPRHADVCARTECGALVLEPLPPQENDMEPVSAEIEETHPDVPN
ESSAGTVEGAESEKSEEVVHDDVIPEDAVPEKSAEDSGTTESTWAPCLRHLYSAVPVLFNVFVV
YL

22. TcoMSPC

MLHQGGFTSRLYLLSAVLFSFFHCAFIASGSDSPGVEEAELGQVRSGWCGHGAHVPPPSEMMVF
DETPPPSRSGRTAGGLITAQIASVNESGVKAKNEFGEYGQEELDDSWQPIRIYASTLDMDDPHR
FCTRPGDVRDTLTGGGNVTCKEADVLTVRKKRIIKQQALPEAIKMHSSRLFVQRLQRKIVLGRN
QIGQCSVFKVPEAHYTNGVDADLLVYVGVRPTIGSIAWAFTCGLLPNGRSVVGSINLSPAFVEE
SDFFIRVIVHELGHVLGFDKGHLVRARVLQEVRGVRGLGQVYVVNSTIAKRVAQKHFNCSDVLG

IEMENEGGNAVEISHLEQRHAYEDVMSPDGQLTRYTAMTLAVFASLGYYRVNFSRAEPTRWGLN
AGCGFLNDRCVVNGTATHPKWFCDREGGEHSHVCSYDHLSLGRCALGRQEGGPPLEYRYFSDDE
LGGTSLFMDYCPVVVPYSHGKCTGAGGGLLRGSATGRNSRCVKGVNLRYSFRDVGDVCVHTDCS
GGRLRIRFLMDFFWKECKAGELVKPSNIFLWSGGVICPTREEVCFEEEDYTLKLKALPRQANDS
EPAF

23. *T.b.gambiense* 10_v2
MTQLLGTATFWCIFAAFVSHHLRAHVHVEASATHLEAPEEQWGEEGTGDTPRGWCGSHHSAINP
DDVPIVGTMPPESEAKGTTGGDLISARTASVDKKPKYTNNVDDYGQGEIDSRWKPIRIRAYTQD
LNDPSRFCTMAGDVRSILVSGKTTVCTAGDVLTVRKKRVIVQVAIPKAIKLHTDRLLVRRYHRR
IVLPSSYAGYCSLFKVPKGHYTNGFEGDVSIYVAARPTIGNMAWASVCAMLTDGRPVSGVVNIS
PKYVAETDFFVRVIAHELGHALGFQADILIRRGIMKQKGGIRGLKTSWLVDSEVAKRVARKHFN
CSTAPGIEMENEGGPGVFATHLEQRNAVEDVMAPYGNLNYLTVMSLGVFASMGHYRVNFSRAEK
TRWGLNRGCSFLQEKCLQEGKSKHPDTFCDHLWKSHLFTCTHDRLGLGQCSLGTHRTELPAEFR
YFRNSRVGGKSRFMDHCPMVVQYNSGNCVNGQSKFLRGSEVGKGSRCVKGVNLKFSNKDIGDVC
VRTNCTGKELQIRFLLDHSWQTCKPGATVQPLGRHLWKGSIICPTREEVCFDDEDYKLRLTPLP
KLPTDDNAAVNPRQM

24. TbMSPC
MTQLLGTAIFWCIFAAFVSHHLRAHVHVEASATHLEAPEEQWGEEGTGDTPRGWCGSHHSAINP
DDVPIVGTMPPESEAKGTTGGDLISARTASVDKKPKYTNNVDDYGQGEIDSRWKPIRIRAYTQD
LNDPSRFCTMAGDVRSILVSGKTTVCTAGDVLTVRKKRVIVQVAIPKAIKLHTDRLLVRRYHRR
IVLPSSYAGYCSLFKVPKGHYTNGFEGDVSIYVAARPTIGNMAWASVCAMLTDGRPVSGVVNIS
PKYVAETDFFVRVIAHELGHALGFQADILIRRGIMKQKGGIRGLKTSWLVDSEVAKRVARKHFN
CSTAPGIEMENEGGPGVFATHLEQRNAVEDVMAPYGNLNYLTVMSLGVFASMGHYRVNFSRAEK
TRWGLNRGCSFLQEKCLQEGKSKHPDTFCDHLWKSRLFTCTHDRLGLGQCSLGTHRTELPAEFR
YFRNSRVGGKSRFMDHCPMVVQYNSGNCVNGQSKFLRGSEVGKGSRCVKGVNLKFSNKDIGDVC
VRTNCTGKELQIRFLIDHSWQTCKPGATVQPLGRHLWKGSIICPTREEVCFDDEDYKLRLTPLP
KLPTDDNAAVNPRQM

25. *T.cruzi* XM799266
MCTIFFFFPGLFLFPFFFFCFACSVRCDRISFCMQMSSFYSSSTLPLILLLLLLCVRLCSGLVE
HRCTFDKRTRDGAPLPMVRELPRKGQGAFQAYTASEPEWRPLRIGFFTEDLKNKSRYCTAEGDM
RPDYEGNTVKCEKKHILTEEKRALLINKLLPDSIKLHSDRLLVQPTELFVLPPSLVGACTLFLI
PDSHFAEGITGADFILYVAAGPTHDVNVAWGVPCALRSGGRPAVGALNFGPQHISSRQDLSRAV
AHEIAHALGFSVQLFAESKMVTKLSKIRGKSNVLVVSSEKTREVTRKHFNCDRAPGMELEDEGG
AGTAQSHWERRNAKDEIMAGVAGIGYYSAMTMAAFEDLGYYRANWGMEEVMGWGRNTGCDFLEE
KCVNNGTTKYPDMFCVDGSFLFQCTSDHLALGVCGLFHFGRDLHPVYRYFKYPFMGGSPNELTD
YCPVIMPSGEGACTNTLNNFTGCRVGPNSRCVESDLLRFNSVTIGAICVEVSCEHKGVASIRYV
GDDTWYPCPEGHRLKPGPPFTRGHIICPRYTDICTTLASAVLKPTLDNNTFQNLLTPVEGPVQR
SLSKPLEMKKTDARKKHFGVDAGSVAVTPSLPWLLLCSLLGALLGI

26. *T.cruzi* XM802023
MHQLLNPFISFLKVSQLTSIQTAKVHCERPKRKKHTRMRHTLLFQVLLLCCVSGSVAVAEHHCI
SDEVENKVGPRTTAVVLELPTRGGGMMRALTASAPEWAPIRFQVFTEDLNDPSKHCTAEKQIRP
DFIGGTLECNKRDILTKEKRSIIINSLLPRAFRMHTDRLLVRPLTGRVIVPWYFSGVCAQFTIP
SSHHIEGVSGADMYLYVSAGPTRYSTLAWATACSQLIDGRPVVGVVNYGPSFVTNSENSVRVSV

HEVAHALGFSVWLLQERNMLKEVLNVRGKAKVLQVSSPKTVEKTREHFNCVNATGMELEDEGGE
GTALSHWERRNAKDELMAGISGIGYYTSLTMAALEDTGFYKANWGMEEPMSWGNNSGCALLTEK
CLMNGVTQYPEMFCTAETTLISCTSDRLALGYCTIYLYTAELLQQYQYFSNLKLGGSNSSLMDL
CPYVQPYSNTRCSNGEASIMHGSRVGPRSKCLKGDGLVDFMGRIGDVCAEVSCEKGEVSVRYLG
DDTWRQCPEGSSITPTGLFTGGKILCPKYDDVCIIFDPLRGGGDVSSLLSVFPSISVILLVFIF
ISMY

27. *T.cruzi* XM798784
MHQLLNPFISFLKVSQLTSIQTAKVHCERPKRKKHTRMRHTLLFQVLLLCCVSGSVAVAEHHCI
SDEVENKVGPRTTAVVLELPTRGGGMMRALTASAPEWAPIRFQVFTEDLNDPSKHCTAEKQIRP
DFIGRNLECNKRDILTKEKRSIIINSLLPRAFRMHTDRLLVRPLTGRVIVPGYSSGVCAQFTIP
SSHQTEGVSGADMYLYVSAGPTQGSTLAWATTCLKLPDGRPVVGVVNYGPRSVTDSENSVRVSA
HEVAHALGFAVWLLQERNMLKEVLNVRGKAKVLQVSSPKTVEKTREHFNCVNATGMELEDEGGE
GTASSHWERRNTKDELMAGISGIGYYTSLTMAALEDTGFYKANWGMEEPMSWGNNSGCALLTEK
CLMNGVNKYSEMFCTAETTLISCTSDRLALGYCTIYLYTAELPQQYQYFSNLKLGGSNSSLMDL
CPYVQPYSNTRCSNGEASIMHGSRVGPRSKCLKGDGLVDFMGRIGDVCAEVSCEKGEVSVRYLG
DDTWRQCPEGSSITPTGLFTGGKILCPKYDDVCIIFDPLRGGGDVSSLLSVFPSISVILLVLIF
ISMY

28. *T.cruzi* XM815532
MRHTLLFQALLLCCVSGSVAVAEHHCISDEIEKKVGPRTTAVVLELPTRESGMMRAMTASDSEW
APIRFQVFTEDLNDPSKYCTAEGQIRPDFTGGTVECKEKDILTEEKKSIMLKSLIPQALKMHTD
RLLVKPLTVNVIVPTFYSGICAQFTIPSSHHTEGVSGADMYLYVSAAPIKSSTLAWATTCSRAV
TGRPIIGVMNYGPNFVTDSEYSVRTLAHEIAHALGFTFGIMKERKMVKEVKGVRGKAAVFQVSS
PKTVEKTREHFNCMSATGMELEDEGGERTASSHWKRRNAKDELMAGVSGIGYYTALTMAAFEDT
GFYKANWGMEEPMSWGNNSGCALLTEKCVINGVTKYPEMFCTAESSLLLCTSDRLALGHCAMEL
YDAPLPPQFQYFSNPKLGGVPGFLMDFCPYIETYVNTGCSNGDETVMSGSRVGPRSKCLKGDGL
ADSEGLVGDVCAELSCDKGEVSVRYLGDDAWHKCPEGSSITPTGLFMQGRILCPKYDDVCIVFD
TINGGGDVSSLLSAFPPIPLILLVLIFISMC

29. *T.cruzi* XM815930
MCISAVTITHWYNILLSLHQLCNPFIYSVKVIHSTSIQAAKLCAVKGPKEKTHTRMRQTLLFLV
LLLCCVSGSVAVAAHRCISEKIEKKVGPRTTAVVLELPTRGGGMIRALTASAPEWAPIRFQFFT
EDLNDPSRYCTAEGQIRPDFTGGTLECKGEDILTEEKKSIILKSLVPRALKMHADRLLVEPLTG
RVIVPKYSSGVCAQFTIPSSHHTVGVFGADMYLYVSAGPTQDSTLAWAHFCTELPDGRPVVGVM
DYGPSSVTDSEYGVRALAHEIAHALGFTLEIMEKRNMLKEFEGVRGKAAVVQVSSPKTVEKTRE
HFNCVSATGMELEDEGGNETALSHWKRRNAKDELMAGIPGIGYYTALTMAAFEDTGFYKANWGM
EEPMSWGNNSGCALLTEKCVINGVTKYPEMFCTARSSPLLCTSDRLALGHCAMKLYDAPLPPQY
QYFPNPKLGGVPDLLMDFCPYIRPNIKTRCSNGDKALMRGSRVGPRSKCLKGDGLADSEGFVGD
VCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITPTGLFMKGRILCPKYDDVCIFFDTINGGGDAS
SLLSAFPPIPLVMLLLIFISMC

30. *T.cruzi* XM812094
MRHTMLLLVLLLCCVSGSVAVAEHHCISDEIEKKVGSRTTAVVLELPTRESGMMRALTASAPEW
APVRFQLFTEDLNDPSRYCTAEGQIRPDFTGGTVECKERDILTEEKKSIILNSLIPRALKMHTD
RLLVEPLMGRVIVPEFLSGACAQFTIPSSHHTEGVFGADMYLYVSAAPIKGSTLAWAVACSALP
DGRPVVGVVNYGPRSVTDSEHSVRALVHEIAHALGFTLEIMEERNMLKEFLNVRGKASVLQVSS

PKTVEKTREHFNCVTATGMELEDEGGERTASSHWKRRNAKDELMAGLSGIGYYTALTMAALEDT
GFYKANWGMEEPMSWGNNSGCALLTEKCVMNGVTKYPEMFCTAESRLLSCTSDRLALGYCALKL
YDAPLPPQFQYFSNPKLGGSPDLLMDFCPYIEEYANAGCSDGNATDMRGSRVGPTSKCLKGDGL
ADFMGFIGDVCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITPTGLFMKGRILCPKYDDVCIVID
TINGTGDVSSLLSAFPPIPLIILVLIFISMF

31. *T.cruzi* XM798806
MRHTMLLLVPLLCCVSGSVAVAEHHCISDEIEKKVGPRTTAVVLELPTRGGGMIRALTASDPDW
APIRFQFFTEDLNDPSRYCTAEGQIRPDFTGGTVECKREDILKEEKKSIILKSLVPRALKMHTD
RLLVRPLMGRVIVPEFLSGVCAQFTIPSSHQIEGVTGADMYLYVSAAPVKGSALAWATSCSALP
DGRPVVGVVNYGPSSVTDSEYSVRVVVHEIGHALGFAVEIMEERNMLKEVKGVRGKAKVLQVSS
PKTVEKTREHFNCVNATGMELEDEGGERTASSHWKRRNAKDELMAGNEGIGYYTALTMAAFEDT
GFYRANWGKEEPMSWGNNSGCALLTEKCVINGVTKYPEMFCTAESRLFSCTSDRLGLGHCTIEL
YDAPLPPQYQYFSNPKLGGSPGFFMDFCPYIEAYFNTWCTDGEADVMRGSRVGPTSKCLKGDGL
ADFMGRIGDVCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITPTGLFTGGRILCPKYDDVCIVFN
TINGTGDVSSLLSAFPPIPLVMLVLIFISMC

32. TcoMSPB1
MILISPNASTRKTLTHQAMTPMRSSLALLLLTLLHRVLGSSVPPSPRCISDEVTARAGPPVRLA
TRNIAHSQTGADSEWSNIRIVTFTKDIEDERKHCTAEGQKRPTFFGDTADCTSDDVLTAAKKGL
VITRLIPSAVQLHVDRLLVKPEAEPLVLPKFDGKVCSSFTVPASHNTEGVPDADMVMYAAAGPM
PAGAAAWATTCIVFDDDRPAAGVMNLGVASISLTETSIRTVAHEIAHSLGFTFYSMSNAKAVTR
VPGVRGKKEVVLVSSPRTLQKTREHYKCPAAAGMELEDEGGSGTAMSHWERRNAKDEFMSGISG
PGRYTALTMAAFEDLGYYRGAWGMEEPMGWGNSSGCELLTEKCLVEGVTAYPAMFCNGSEVGLT
CTSDGFALGKCLTVQYESELPAEYQYFSDTKLGGSAHTLMDYCPYIFGYSNTRCSDGDIRHMYG
SVIGPSSKCLKGNKLLDNESRPVGDVCADVRCDNGTVSVRYLGNSEWHPCPAGGAVTPTETFTG
GTILCPKYEEVCIVAAVVTKSDTTNPFASVAQPLLLALLVAAVSSS

33. TcoMSPB2
MTPMRSSLALLLLTLLHRVLGSSVPPSPRCISDEVAARAGPPVRLATRNIAHSQTGADSEWSNI
RIVTFTKDIEDERKHCTAEGQKRPTFFGDTADCTSDDVLTAAKKDLVITRLIPSAVQLHVDRLL
VKPEAEPLVLPKFDGKVCSSFTVPASHNAEGVPDADMAMYAAAGPMPAGVAAWATTCIVFDDDR
PAAGVMNLGVASISLTETSIRTVAHEIAHSLGFSFYFMSNAKTVTRVPGVRGKKEVVLVSSPRT
LQKTREHYKCPAAAGMELEDEGGSGTAMSHWERRNAKDEFMSGISGPGRYTALTMAAFEDLGYY
RSVWGMEEPMGWGNSSGCELLTEKCLVEGVTAYPAMFCNGSEVGLTCTSDGSALGECFTVQYES
ELPAEYQYFSDTKLGGSAHTLMDYCPYIFGYSNTRCSDGDIRRMYGSVIGPSSKCLKGNKLLDN
ESRPVGDVCADVRCDNGTVSVRYLGNSEWQLCPAGGAVTPTETFTGGTILCPKYEEVCIVAAVV
TKLNTTNSFASVAQPLLLALLVAAVSSS

34. *T.brucei* TREU927XM841902
MFNTITDVTLLFSLFPLFLPCVKRKRLMMLPACVIPMHGALKLAILLMLVWCCSLCLAKSGGRC
MFDEIAAKAGRPRVLALRRTKAGMENVKYDRTGSVDPEWQHIRIVVFAEDMKDRSRYCTSAGQE
RPTFFGETATCSQEDILTAAKRDIAVTKLLPSAVQMHMDRLLVDPITEPLVFPPFDGSVCSEFK
VPSSHFSEGVPDADMVMYAAAGPTPEGVAAWATGCITLDDGRAVAGVTNLGPGSISLSETSIRT
AAHEIAHALGFDFEAMNDAGMVQRIPGVRGKVDVTLISSPRTLQKAREHYNCPDAPGMELEDEG
GSGTALSHWERRNAKDEIMSGISSPGRYTALTMAAFEDLGYYRGAWGSEEPMGWGNNSGCELLN
ESCLVNGVTAHPDMFCNETVSKLVCNSERDGLGRCNVIKHENPLPPQYHYFSDPSRGAPSHLLM

DYCPSIDAFSNTPCADGETKFMRGSLIGPSSMCLKAEGLRDSQGVIGDVCADVRCDGGEVSIRY
LGDDAWHPCPEGSHIKPTTTFTDGVIVCPTYSEVCIKATVVVRPSSASYRSSVPQSLLLTLFAI
VYAAC

35. *T.b.gambiense* 08_v2
MFNTVTDVTLLFSLFPLFLPCMKRKRLMVLPACVIPMHGALKLAILLMLVWCCSLCLAKSGGRC
MFDEIAAKAGRPRVLALRRTKAGMENVKYDRTGSVDPEWQHIRIVVFAEDMKDRSRYCTSAGQE
RPTFFGETATCSQEDILTAAKRDIAVTKLLPSAVQMHMDRLLVDPITEPLVFPSFDGSVCSEFK
VPSSHFSEGVPDADMVMYAAAGPTPEGVAAWATGCITLDDGRAVAGVTNLGPGSISLSETSIRT
AAHEIAHALGFDFEAMNDAGMVQRIPGVRGKVDVTLISSPRTLQKAREHYNCPDAPGMELEDEG
GSGTALSHWERRNAKDEIMSGISSPGRYTALTMAAFEDLGYYRGAWGSEEPMGWGNNSGCELLN
ESCLVNGVTAHPDMFCNETVSKLVCNSERDGLGRCNVIKHENPLPPQYHYFSDPSRGAPSHLLM
DYCPSIDAFSNTPCADGETKFMRGSLIGPSSMCLKAEGLRDSQGVIGDVCADVRCDGGEVSIRY
LGDDAWHPCPEGSHIKPTTTFTDGVIVCPTYSEVCIKATVVVRPSSASYRSSVPQSLLLTLFAI
VYAAC

36. *T.brucei* TREU927XM841905
MLTTHFRCCISPRVSGAYSLFPLFLPCIKRKRLMMLPACVIPMHGALKLAILLMLVWCCSLCLA
KSGDRCMFDEIAAKAGRPRVLALRRTKAGMENVKYDRTGSVDPEWQHIRIVVFAEDMKDRSRYC
TSAGQERPTFFGETATCSQEDILTAAKRDIAVTKLLPSAVQMHMDRLLVDPITEPLVFPPFDGS
VCSEFKVPSSHFSEGVPDADMVMYAAAGPTPEGVAAWATGCITLDDGRAVAGVTNLGPGSISLS
ETSIRTAAHEIAHILGFNFRAMNDAGMVQRIPGVRGKVDVTLISSPRTLQKAREHYNCPDAPGM
ELEDEGGSGTALSHWERRNAKDEIMSGISSPGRYTALTMAAFEDLGYYRGAWGSEEPMGWGNNS
GCELLNESCLVNGVTAHPDMFCNETVSKLVCNSERDGLGRCNVIKHENPLPPQYHYFSDPSRGA
PSHLLMDYCPSIDAFSNTPCADGETKFMRGSLIGPSSMCLKAEGLRDSQGVIGDVCADVRCDGG
EVSIRYLGDDAWHPCPEGSHIKPTTTFTDGVIVCPTYSEVCIKATVVVRPSSASYRSSVPQSLL
LTLFAIVYAAC

37. TbMSPB
MLTTHFRCCISPRVSGAYSLFPLFLPCIKRKRLMMLPACVIPMHGALKLAILIMLVWCCSLCLA
KSGGRCMFDEIAAKAGRPRVLALRRTKAGMENVKYDRTGSVDPEWQHIRIVVFAEDMKDRSRYC
TSAGQERPTFFGETATCSQEDILTAAKRDIAVTKLLPSAVQMHMDRLLVDPITEPLVFPPFDGS
VCSEFKVPSSHFSEGVPDADMVMYAAAGPTPEGVAAWATGCITLDDGRAVAGVINLGPGSISLS
ETSIRTAAHEIAHALGFDFEAMNDAGMVQRIPGVRGKVDVTLISSPRTLQKAREHYNCPDAPGM
ELEDEGGSGTALSHWERRNAKDEIMSGISSPGRYTALTMAAFEDLGYYRGAWGSEEPMGWGNNS
GCELLNESCLVNGVTAHPDMFCNETVSKLVCNSERDGLGRCNVIKHENPLPPQYHYFSDPSRGA
PSHLLMDYCPSIDAFSNTPCADGETKFMRGSLIGPSSMCLKAEGLRDSQGVIGDVCADVRCDGG
EVSIRYLGDDAWHPCPEGSHIKPTTTFTDGVIVCPTYSEVCIKATVVVRPSSASYRSSVPQSLL
LTLFAIVYAAC

38. *T.b.vivax* 1393e12.p1k
MLVLFALLGVTGWCCTGGIAMPGCMFDSLMDKNGQSLPIAQEVLPTGPDALAAATAASTSTLPV
WATIRIMVSTRDMTDPSKICTHAGQSRPDFLGAYKKCSAAAVLTAKKHENLLKRVVPGAVKMHT
DRLEVRPVRGRIVVPLFSGLCANFHIPRDHRTRGVGGADTILYGAAGPVGGWSAWALACAALGD
GRPFAGVFNVGPESLDIVDTSTRTVAHEIAHALGFSISIASNLGMVKDVNVRGKGFVKMVTTRN
VVRVARQLYNCSELVGMELEDEGGAGTKHSHWERRNAMDEMMAGARMVTGGYYSALTMAFFEDT
GLYRAKWGAEEHTRWGRNAGCGFLSEKCVKNGTTHFPDMFCTEPARRHEFKCTHDRMALGVCTI

QRHNKRLPSHASYFDSPDIGGASYFMDYCPIIHTSEAFTCLYGTRLQRWGSRVGRHSRCVEGDG
LRLQGGGLTTGNICVETACGAGVLHVRFVGDDEWYACPEGSYLSPRKHFSGGRILCPSKGDVSP

39. *T.b.vivax* 797h07.q1k
MPCRAVCSTVSWIRMAISPIAQEVLPTGPDALAAATAASTSTLPVWATIRIMVSTRDMTDPSKI
CTHAGRSRPDFLGAYKKCSAAAVLTAKKHENLLKRVVPGAVKMHTDRLEVRPVRGRIVVPLFSG
LCANFHIPRDHRTRGVGGADTILYGAAGPVGGASAWALPCAALGDGRPFVGVFNVGPESLDIVD
TATRTVAHEIAHALGFSISIASNLGMVKDVNVRGKGFVKMVTTRNVVRVARQLYNCSELVGMEL
EDEGGAGTKHSHWERRNAMDEMMAGVKMATGGYYSALTMAFFEDTGLYRAKWGAEEHTRWGRNA
GCGFLSEKCVKNGTTHFPDMFCTEPARRHEFKCTHDRMALGVCTIQRHNKRLPSHASYFDSPDI
GGASYFMDYCPIIHTSEAFTCLYGTRLQRWGSRVGRHSRCVEGDGLRLQGGGLTTGNICVETAC
GAGVLHVRFVGDDEWYACPEGSYLSPRKHFSGGRILCPSKGDVCPPDGTVGAAAGHGPQLTSAS
SNSTANEPLGGEAGQSRNASRTGEQSGTARPDPPAANTTANHTGRGRNAQPPPTAPNRSSMKST
AAPEGQHNASSRMGRANGTRPTAPAKHKPCSTCSQKRGDHKVAAGARVRHSRTAGGQRAK

40. *T.b.vivax* 899g05.p1k
MSHRFLLLLMVITSHATSTDDTSAPRCMFDEAIRSNSEFKLPVVRLSPPGPVGVLEATTAGESS
EVWDTIRFQVFKRDIEDSSKYCTQVGQVRSNFMNAMVHCSADSVLTPEKKYTMLTGVIPTAVKM
HTDRLMVKPLNTSLKVPKIPGGMCGNYNIPPEHHTAGVPGADMVLYGSAGPMGMAAAWAAPCAL
LDYHTGRPIFGVFNIGPEAISTVDGTARVLAHEIAHALGFGHHIMVMLGMVANLTNVRGKPHSQ
GLKTPKVVEVGQLFFGCSTITSVELEDEGGSGTVNSHWEARNLKEEMMTGVKSTGGGFYSAFTM
AFFEDTGLYKAKWGAEESMNWGYNAGCRFLEEKCVVNGKSNFPEWFCDSMLHYGERACTADRRG
LGNCRLGRVTKGLQSHHQYFGNEGLVGVAPLMDFCPIVEAYSNTGCIDGDANMMLGSRIGPNSR
CVKGVDIKVSGYSNLFGDVCVDVDCNSSNVRLRLANDDEWRECTEGTPVTSNKSFASGHVICPK
KSDVCQSRQTSRGLISFSSSDTCRCSLAWFGVLQAILWAFLRPLRSASW

41. TbMSPA
MAVIMFPRYIIPCLLGLISCGDVTEGNIPPHRCDFGKLMKNMSMRDLPVVDEPPVPKGDLVHAI
VISSMAGWQPIREKVFKSDIKNPKKYCGNVGETRSNFRGIYYKCKTESVLTEKKKSLLDAVIPD
ALKMHSDRLMVQPVKGRITVYREQSFCRNFNIPREHRTKGVSDADMVLYGAAGPMGSPAAWAVP
CAKLRNGRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGEGFDIMNERKLVASKSGIRGKGPV
WVVKSPTVVKKAQEFYGCNRITGVELEDEGGRGTVRSHWERRIAMEEMMAGIKGSDGGRYSVLT
MALFEDMGFYKAKWGTEEDMHFGKGRGCDFLKKKCIENGRSNFPDVFCTSATKKGENVCTSDRG
GLGSCAIYLYRTPIPQQYRYFSRVNKGGPNELLDFCPYIRLFSNTGCTDGHPHAMWGSRIGPNS
RCVKATGLKLKNVIVAIADICVEVNCEPDTLQVRFVDDEKWYDCPEGRNVTSNVTFSSGYIQCP
KKSELCASKVLKQVTVASAVVSPGSDGSSEGSSEGSSEGSSEGSFEGPSPVDSSEVPSAESSEE
YSEESSEAPSPVDSEETEHLGTGATSWALHSSYFMWNLLLFVSCFSL

42. *T.brucei* TREU927XM823758
MAVIMFPRYIIPFLLGLILCGDVSEGNIPPHRCDFGKLMKNMSVREPPVVDEPPVPKGDLVHAI
ATSSTAGWHPIRVQVFDFDIKNRNKYCEKEGQVRSNFRDAYYECTTASVLTKEKKALLAVVIPD
ALKMHTDRLMVQPVHDPIKVYEKQTFCNNFSIPRDHYTTGVSGADMVLYGAAGPMGSPAAWAGP
CSRVSGQRPTVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMEELKLVEKKSGIRGKNDV
WVVTSPTVVKKAQEFYGCNEIKGVELEDEGGDGTKNSHWERRIAMEEMMTGLKSSDGGRYSVLT
MALFEDMGFYRAKWGNEEDMHFGKGRGCDFLEKRCVENGRSNFPDVFCTSKARDTEIFCTSDRG
GLGSCAIQTHESPIPEQYRYFADEKKGGPAELLDYCPYIRLFSNTGCTDGNPNVMLGSRVGPNS
RCVKGTRLRLQKKKGVPLADICVEVNCESDILQVRFVGDNRWYDCPEGRNVTSNVTFSSGSIQC

PEKSELCASKILRRITVPSAVAFPVTSPGPSTGPFAAPFAETYEGASPTSSTGASEDFSEEYSE
ESSHEDSEGSSPMTRQLTGTSSWSAYSSYLMWNMLLFVSCFSLL

43. *T.b.gambiense* 1167d01.p1k
MAVIMFPRYITPCLLGLILCGDVSEGNIPPHRCDFGKLMKNMSVREPPVPKGDLVHAIATSSAE
VWHPIRFKVFKSDIDDPNKYCERVGETRSDFRGRNLMCTSYSVLTKEKKSLLDVVITDALKMHS
DRLMVQPVHGPITVHRNQTFCNNFNIPEHHRTTGVSGADMVLYGAAGPMGSPAAWAGPCSRYRG
QRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFKIMEERNLVEKRNNIRGKNDVWVVKSP
TVVKKAQEFYGCDKITGVELEDEGGEGTINSHWERRIAMEEMMTGVKGSDGGRYSVLTMALFED
MGFYKAIWGTEEDMHFGKGRGCEFLEKKCVENGRSNFPDVFCTPEAAKGNNICTSDRGGLGSCA
IYLYTPALPAYYRYFGDERKGGPKELLDYCPYIRLFSNGGCTNGDADVMKGSRIGPKSRCVKGT
GLQIKKGNLIYIVDDICVEVNCEPDTLQVRFVDDEKWYDCPEGSNVTSTVTFYKGSILCPKKSE
LCASKVMKQVTTISPVTASGASVGDSAGTWAGDSPDASPVASPGPLGEPSAVPIEGSSTVSSPV
TEDGTGASSWSAYSSYLMWNMLLFVSCFSLL

44. *T.b.rhodesiense* MSPA2
MAVIMFPRYVIPCLLGLILCGDVSEGNIPPHRCDFGKLMKNMSVREPPVPKGDLVHAIVTSSTA
GWQPIRFKVFDFDIKDPEKYCGREGEYRPNFKGNKLLCTADSVLTPQKKKSLLDAVIPDALKMH
SDRLMVQPVQGPITVHRNQTFCNNFNIPEEHRTTGVSGADMVLYGAAGPMGSPAAWAGPCSRYK
DHRPTVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMKERNLVEQRNDIRGKNDVWVVKS
QTVVKKAQEFYGCDKITGVELEDEGGEGTINSHWERRIAMEEMMTGVKGSDGGRYSVLTMALFE
DMGFYRAKWGTEEDMHFGKGRGCDFLEKKCVENGKSNFPDVFCTSETKPGENVCTADRGGLGSC
AIYSYTPALPVRYQYFADITKGGPDDLLDYCPYVRLFSNGGCTNGDSEIMIGSRIGPNSRCVEG
AGLQVRRGNLIYIIHDICVEVNCEPDILQIRFVDDNQWHNCPEGSKVTSTVALYNGSILCPKKS
ELCASKEVKQVTTASPVVSPGPSTGASAKAPPGSSPVSSPGASAEPSAGPSAGPSEMPLAETKE
VTGTSWALHSCYFMWNMLLFVSCFPLL

45. *T.brucei* TREU927XM823757
MTVIMFPRYIIPFLLGLILCGDVTEGNIPPHRCDFGKLMKNMSMRDLPVVGEPPVPKGDLVHAI
VTSSTAGWQPIRFKVFKSDIEDRSKYCGSVGETRSNFRGTNYQCNTDSLLTKEKKSLLSVVIPD
ALKMHTDRLMVQPVQGPIKVPKLQSFCNNFNIPQDHYTTGVSGADMVLYGAAGPMGSPAAWAGP
CSRLKGKRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMEELKLVEKRNEIRGKNGV
WVVKSQTVVKKARLFYGCDTLTGMELEDEGGEGTVKSHWERRIAMEEMMAGLKSSDGGRYSVLT
MALFEDMGFYKAKWGTEEDMHFGKGRGCDFLEKRCVEDGKSNFPDVFCTSETKQGENICTSDRT
GLGSCAISTYKSSLPTHYQYFSQSNRGGPGELLDYCPYIRVFSNTGCTNGDPKTMWGSRIGPNS
RCVKATGLKLKNVIVAMADICVEVNCKPDILQVRFVGDDQWHNCPEGRNVTSNVTFSSGSIQCP
KKSELCASKVVKQTTSAQKGQGKGASSWSAYSCYLMWNMLLFVSCFSLL

46. *T.gambiense* 11_v2_orf2
MAVIMYPRYVIPFLLGLILCGDVTEGNIPPHRCDFGKLMKNMSVREPSSGGEPRVPKGDLVHAI
VTSSTAGWHPIRFKVFKSDIEDPNKYCGSVGQTRSNFRGTNYQCNTDSLLTKEKKTLLDAVIPD
ALKMHSDRLMVQPVHGPIKVPQLQSFCKNFNIPQDHYTTGVSGADMVLYGAAGPMGSPAAWAGP
CSRLSGKRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMKELKLVAQKRGIRGKNDV
WVVTSPTVVEKARLFYGCDRITGMELEDEGGDGTKNTHWERRIAMEEMMAGLKSSDGGRYSVLT
MALFEDMGFYRAKWGTEEDMHFGKGRGCDFLEKRCVENGRSNFPDVFCTSETKPGENVCTSDRG
GLGSCAIHLHSSALPKHYQYFSQSNRGGPGELLDFCPYIRVFSNTGCSNGLREAMWGSRIGPNS

RCMKATGLKLKKGIVPIGDICVEVNCESDTLRVRFVDDDRWHNCPEGSNVTSNVTFSSGSIQCP
KKSEFCSSKVLKQVASPEPSPATRQGTGTSWSAYSSYLMWNMLLFVSCFSPIMI

47. *T.gambiense* 2537b02.p1k
MTVIMFPRYITPCLLGLILCGDVTEGNIPPHRCDFGKLMKNMSVRDLPVVGEPPVPKGDLVHAI
VTSSSAGWQPIRFKVFKLDINDRRKYCGGVGETRSNFKGINYQCTDKSLLTPQKKSLLAVVIPD
ALKMHSDRLMVQPVHGPIKVPQLQSFCKYFNIPEHHYTKGVSDADMVLYGAAGPMGSPAAWAGP
CAKLRNGRPTVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMEELKLVEKRNDIRGKNDV
WVVKSPTVVKKARLFYGCNEIKGMELEDEGGDGTKNTHWERRIAMEEMMAGMKSSDGGRYSVLT
MALFEDMGFYRAKWGTEEDMHFGKGRGCDFLEKRCVENGKSNFPDVFCTSETKKGENVCTSDRT
GLGSCAIHLHSSALPKHYQYFSQSNRGGPGELLDFCPYIRVFSNTGCSNGLREAMWGSRIGPNS
RCMKATGLKLKKGIVPIGDICVEVNCESDTLRVRFVDDDRWHNCPEGSNVTSNVTFSSGSIQCP
KKSEFCSSKVLKQVASPEPSPATRQGTGTSWSAYSSYLMWNMLLFVSCFSPIMI

48. *T.brucei* TREU927XM823755
MTVIMFPRYVIPCLLGLILCGDVTEGNIPPHRCDFGKLMKNMSMRDLPVVDEPPVPKGDLVHAI
VTSSMAGWQPIRFKVFKSDIEDPKKYCGNVGETRSNFRGIYYKCKTESLLTSQKKSLLDAVIPD
ALKMHSDRLMVQPVKGRITVHREQSFCKNFNIPREHRTTGVSDADMVLYGAAGPMGSPAAWAVP
CAKLRDGRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMNERKLVASKSGIRGKGPV
WVVKSQTVVKKAQEFYGCNDITGVELEDEGGRGTVRSHWERRIAMEEMMAGIKGSDGGRYSVLT
MALFEDMGFYKARWGTEEDMHFGKGRGCDFLQHTRIESGKSNFPDVFCTSATKKGENVCTADRG
GLGSCAIYLYRTPIPQQYRYFSRVNKGGPNELLDFCPYIRLFSNTGCTDGHPHAMWGSRIGPNS
RCVKATGLKLKNVIVAIADICVEVNCEPDTLQVRFVDDDQWYDCPEGRNVTSNVTFSSGYVRCP
KKSELCASKVLKRVTVPSAVASEGSSEGSSEGSSEGSSEGSSEGSSAESSEESSEESSEAPSPV
DSEETEHGTGAASWAVHSSYFMWNMLLFVSFSL

49. *T.b.rhodesiense* MSPA1
MAVIMFPRYIIPCLLGLISCGDVTEGNIPPHRCDFGKLMKNMSMRDLPVVDEPPVPKGDLVHAI
VTSSMAGWQPIRFKVFKSDIKNPKKYCGNVGETRSNFRGIYYKCKTESVLTEKKKSLLDAVIPD
ALKMHSDRLMVQPVKGRITVYREQSFCRNFNIPREHRTKGVSDADMVLYGAAGPMGSPAAWAVP
CAKLRNGRPVVGVFNIGPEVLTSHDSSMRVTAHEIAHALGFGFDIMNERKLVASKSGIRGKGPV
WVVKSPTVVKKAQEFYGCNRITGVELEDEGGRGTVRSHWERRIAMEEMMAGIKGSDGGRYSVLT
MALFEDMGFYKAKWGTEEDMHFGKGRGCDFLKKKCIENGRSNFPDVFCTSATKKGENVCTSDRG
GLGSCAIYLYRTPIPQQYRYFSRVNKGGPNELLDFCPYIRLFSNTGCTDGHPHAMWGSRIGPNS
RCVKATGLKLKNVIVAIADICVEVNCEPDTLQVRFVDDEKWYDCPEGRNVTSNVTFSSGYIQCP
KKSELCASKVLKQVTVASAVVSPGSDGSSEGSSEGSSEGSSEGSFEGPSPVDSSEVPSAESSEE
YSEESSEAPSPVDSEETEHGTGATSWALHSSYFMWNLLLFVSCFSL

50. TcoMSPA
MEAREVWRRVAEWLVAVLLGSTCVCTASHEGFVHRCTFDAMMQNASNKALPVAIEVPHVPGDVL
RAFTASSSDNWGPIRFTVFKSDISNSEKYCTKAGEVRSNFRGTNIVCSEESVLTERKKSLLEEV
IPAALKMHSDRLTVKRTSNLIKIPQVTGFCTNFHIPAEHRTTGLTAVDMVLYGAAGPMGGKSAW
AGPCAVLEDGRPFVGVFNIGPEILISVDASVRTMTHEIAHALGFGFDILQKLKLVEVRNNIRGK
PKTYVVTSPNVVNVARKYHNCDSITGVELEDEGFEGTVNSHWERRNLMPELMAGLMEHGGGLYS
AFTMALFEDMGFYRAIWGREEQMRWGNGVGCAFLDKKCIEGGKSNFPDMFCTEEGRKGGATCTH
DRMGLGRCRIGTTGSSLPRHYQYFSEPNRGGVSPLMDYCPVVAGFSNADCANGDPGVMWGGRTG

PNSRCVEAHGIQLIGIVVSVGDICVEVDCSSALLGVRFVGDDNWYPCKKGDHVTSNKSFMGGYI
VCPERSQVCLARQLKIESVTAKSDKKKDGGTLSGRSGDPLLRALTLYLPLACQLFFESLR

51. *T.b.vivax* 1124g05.p1k
MEQRSSASAPRLLCAHVLVTLLSAVAMATTDNYKMLNESDYGCLVGDLPGDDYASIPAIKPVPR
QVGLVEAVTASATSPEWKPARFKVFTKDLDDPRKYCTEVGQIRSSFSLGNVRCTEEDVFTSAKK
TILLNHNIPLGIKKHADRLSVQPITGVIKVAEFRSLTCREFTVPAEHRITGLTDVDTVFYAAAA
PVRGFSAWAVICATHDGGRPLVGAFNIGPPSIAATLRAVNLVAHELAHALGFHDKVISARNMSR
YVQDVRGKRLVRVVNTPKVVEAARRHFKCDSLHGMELEDEGSSGTVGSHWKRRNAMDDLMCGVQ
GTMGSFYSTLTMAFFEDSGFYKVSWGTEEPMGWGYGAGCSFLEKKCVENDTSNFPEWFCDSITP
ERQKLCTADRRGLGKCQMAKFKEELPAHLQYFTNRSQGGGRSLMDCCPLVVAHSRTMCADGTAR
ILPGSRLGSTSRCVKGEGLLPGSASHPVGDICVEICCRLPTLGVRFAGDNTWYQCPAGERLAPR
KGFKGGHIICPTRSQVCPRDSRDIFPIGGDVSQLIPHVDPPSIKTCLSATGSFESPEDCANTRV
IPSDLQADLLTCPSSRSRTMLNVVPTACLSNIGCTIILTRFMLLARPALWGDL

52. *T.b.vivax* 1764g03.p1k
MRGTHIYFVLLLTLSLSPQRTGGYGALDHTPDPRCLFGDQWQNNSVERLPVVREIPVATGGLQQ
AFIQEDEEPQWLPIRIMFFTFDLRNSSRYCTVSGTTRPNYRGGTAICTVNDILTDDKKAMLSAQ
ILPQATKMHADRLLIKRRIQSVFVPTFRDNVCNSFTIPVAHRSKGVNQTDMILYVASGPSSTGG
ASIAQACATLSNGRPIIGAINFAPGAIVRSGVSVRMAAHEIAHVLGFNYNTMKNLNMITRLSNI
RGKSIVTVVNSTKVLEVARTYYGCDSLAGVELEDGGGRGVAGSHWERRIAMDDLMAVNVGLSAY
SVLTMAFFEDTGFYKVVWEKGERMVWGRNAGCEFINEKCVTNNRTKYPNMFCTEPTDEKLYCTY
DRQALGHCTLKNHKKTLRPEFQYFGDANIGGSDADAMDFCPIIAPYRDSYCTNGEQQLLLGSRI
GPHSRCIKGDGLQIHSEEVGDVCAEVQCSKGTVSLRYVGDDKWYACPEGGYLTPTSFSGGRLVC
PKWEEVCYDGLRPNVLSAVALLIWWCVGVVLVS

53. TcoMSPE
MHRSLCPTPHCRSTASIYSPPRLHESTRVRMKENSFTVARALGACVSKWVIFILLSALFLCNVA
CQDRDHSLNDTAVVVENDTAVNITNASEEDIAVVEGGTEKMVNGWTSLRVVVSTNDLDNPKRCC
TLSGQERPDFMGGVAPCGEQDVLTTEKRLTLTEYTIPGAIRLHYERLGVSMRMDNIIVPDFLSA
VCSSFTVPESHRSVGVSGADVILYVAAGPTGRADYAHTRVCALLPSGRPAVGVINFSPSAISRS
RSSLRAAAHEIAHILGFNNEVMRRLKMISTKVHRGKNSTFVITPKVVEVARKYYACKNMDGMQL
EDGGNDDVRDSHWKRLFVKDDLMAAVVGASYYSALTLAFFHDTGFYRVKWAMAERMRWGNGTGC
GLMNGKCMKNNITMFLDMFCNESVSTKLHCTYERQAIGRCALNTYGAPLDPDKQYFTRSWIGGN
QDNLMDYCPIVEPYKDSYCEDGRQQLLPGSRVGPNSRCVKGDRLVAFSREVGDVCAEVYCGRDA
VSIRYSGDDSWHVCPEGEYITPTKTFSSGRIICPKREEVCYNTDMSPPFDPHASVALLFLLTSS
RRII

54. *T.brucei* TREU927XM823843
MTTFPPVVYCTADATVSPSPAVCLLTAGCRRPCCSWRIALKVSFSQTPIAQCFSYNLLSFALCL
RLCVAMRLRTQVVGIGQLRTSFTSRICMGRRSNSVFFHLWLSFASLCLGNSDSSEGSPPVSNGT
SPVVLSDQSVANMEANDSQWKPIRIVVSAKDLDDSLKYCVVAGVPRPDFMGGTLRCKTGDVLTN
EKRLILTEHALPSAIHLHAERLLVGMEIDNIVVPEFDSPACKSFTVPIHHRSVGVPQADIILYV
ASGPAPHDGPAYATTCASLLSGRPIAGAINFSPSAITESYLYIRTVAHEIAHVLGFNFEAMKQL
NMVGTKNIRGKSSVKVVKTPNVVKVARQYYGCGKITGMELEDNGDDSVRNSHWKRRIARDDLMT
AIMGVSHYSELTLAFFLDTGFYRVNWEKGERMRWGHGAGCSFIEGKCMENNETNFPDMFCNDSA
ETLSCTHDRQALGRCTVHSYAVPIEESVRYFTMSWVGGSDNNLMDYCPVVEPYTDSYCRDGRRE

LLPGSRIGESSRCVKGEGLVAFTTHVGDICVEIHCGKRRGVSIRYSGDDSWHVCPEGGHVTPDK
TFSEGRIVCPKWEEVCDDNAMTLSCLAAVFAIFVSALSLVV

55. *T.gambiense* 11_v2_orf1
MTTFPPVVYCTADATVSLSPAVCLLAAGCRRPCCSWRIVLKVNFSQTPIAQCFSYNLLSFALCL
RLCVAMRLRTQVVGIGQLRTSFTSRICMGRRSNSVFFHLWLSFASLCLGNSDSSEGSPPVSNGT
SPVVLSDQSVANMEANDSQWKPIRIVVSAKDLDDSLKYCVVAGVPRPDFMGGTLRCKTGDVLTN
EKRLILTEHALPSAIHLHAERLLVGMEIDNIVVPEFDSPACKSFTVPIHHRSVGVPQADIILYV
ASGPAPHDGPAYATTCASLLSGRPIAGAINFSPSAITESYLYIRTVAHEIAHVLGFNFEAMKQL
NMVGTKNIRGKSSVKVVKTPNVVKVARQYYGCGKITGMELEDNGDDSVRNSHWKRRIARDDLMT
AIMGVSHYSELTLAFFLDTGFYRVNWEKGERMRWGHGAGCSFIEGKCMENNETNFPDMFCNDSA
ETLSCTHDRQALGRCTVHSYAVPIEESVRYFTMSWVGGSDNNLMDYCPVVEPYTDSYCRDGRRE
LLPGSRIGESSRCVKGEGLVAFTTHVGDICVEIHCGKRRGVSIRYSGDDSWHVCPEGGHVTPDK
TFSEGRIVCPKWEEVCDDNAMTLSCLAAVFAIFVSALSLVV