

Fig. S4

Species	Accession	Position	Sequence
Mus		89	MKCYLSRTPDRMPSEHQI-----GSLKKY-Y-----LLNAASLLPVLALERLDGEAVLDLCAAPGGKSVALLLQCAYP-----
Rattus		74	MKCYLSRTADRMPSERHQP-----GRLKTY-Y-----LLNAASLLPVLALVKDGETVLDLCAAPGGKSIALLLQCAYPDTLSPGSPSPSEQC-----LFGKPTIE-----ESSSATI-----LS-----
Homo		89	VKCYLSRTPGRIPSEHQI-----GNLKKY-Y-----LLNAASLLPVLALERLDGEKVLVDLCAAPGGKSIALLLQCACP-----
Rhinolophus		90	MKCYLSRIPSRMPSEHQI-----GNLKKY-Y-----LLNAASLLPVLALERLDGEKVLVDLCAAPGGKSVALLLQCAHP-----
Liparis		197	LQCYIHPRLRFPSQAHRP-----GQLKQY-Y-----LLNAASLLPVLALKVRDGEKVLVDLCSAPGGKAVAIMQCATP-----
Columba		117	LKCYIRRTPGRFPAQKHQA-----GKLKEY-Y-----LLNAASLLPVLALVKDGEDVLDLCAAPGGKSVALLLQCACP-----
Oesophagostomum		18	LRCFDRGVLSDFPPPVKDD-----SGIPSW-W-----LLDGGSLVPVLALGLEKGDSMLDICAAPGGKSLLSLLTKLP-----
Ancylostoma		524	LRCYDRGVLAADFPPPVKDD-----SGIPSW-W-----LLDGGSLVPVLALGLEKGDSLVDVCAAPGGKSLLALLTKLP-----
Chytridiomycetes		151	-----FPSPVMDL-----KNIKTH-Y-----LMDAASVLATDGLDIQAGDIVLDMCAAPGGKSFCMLQRLGP-----
Gossypium		81	-----SYLDGKIY-----GIDAASGAAVSVLNI SPGDHVLDLCAAPGAKLCMMLDLLGD-----
Symbiodinium		107	LPCY-----FLDGASAVAATLLDPAPGASVLDLCAAPGGKSLMLASLLFA-----GRSAAG-----GDSS-----
Cryptosporidium		92	--CI-----FMDAASIIIVSYLLDIDRFSTVLDLCSAPGGKALIIIKRILE-----DIN-----
Theileria		91	PWCYEVTFKALVDPKDYDKI--L FNKN-----IFDANGFVSRINDYIY-----HLDGASAFGAFCLEAKPGDKVLDMCSSPGGKMIIIASNMFNFAMN-GVNGLTN-----GINGSN-----MTTTELI-----DEIKSRMNIIN-----
Marmota		89	LKCYLSRTIDRLPSEHQF-----GNLKKY-Y-----LLNAASLLPVLALERLNGEKALDICAAPGGKSLALLQCAWP-----
Gulo		89	MRCYLSRTPDRMPSEHQI-----GNLKKY-Y-----LLNAASLLPVLALERLDGEKVLVDLCAAPGGKSIALLLQCAYP-----
PVP01_0930100		240	VK ITRNNLLN I LKSN I NA-----EEGANMNNVG I VINDANSNVGSLNEYLYGYMYLQSASSL I PVLELNVNPEDT I LDMCAAPGGKCTFICALQKN-----
PY17X_0920500		261	LK ITRTNLLK I LKNKNI A I-----QDGP TWNVND I TLTDTSSNVGSLNEYLYGYI I QSSSSL I PVLELNVKENELVLDMCAAPGGKCTFICTIQKN-----
PF3D7_1129400		237	LK ITRNNLMK I LKNQNVSV-----QEGESWNHVG I TIKDVNTNVGSLNEYLYGYI I QSSSSLMPVLELNIQEDDMVLDMCAAPGGKCTFMCTLKKN-----
PBANKA_0918800		228	LK ITRTNLLK I LKNKNI A I-----QDGSNWNVND I TLTDTSSNVGSLNEYLYGYI I QSSSSL I PVLELNIKENELVLDMCAAPGGKCTFICTIQKN-----
PF3D7_0704200		104	ESY-----KNLYNYL-----INLNESGIFRQELV-----SMLPVLFLRLKENFFVLDICAAPGSKTAQ I LDYMHITIN-----RRRIKNI LIEKFLKKNMQTL YKNLYPWNVNVDENCNLYYDSFELDSYKINGFIKQEEKNDNTNK IIMNAQNI MNSQDVLLYENNINVQ-----
PF3D7_1111000		157	NSSYNNI INNI HDKNVYYKK-----INIQESELLINDI KYD-----GS IENVET I IY-----YLNPCS ILCAYFLDIKQNEHVLDMCASPGGKSLY I VNKLF GYNI S-PLNRIKNVEI-----IYP-DAVN-----NDKDN I-----NNED-----NNIN-----
PF3D7_1230600		134	NK I SRNELYKTLISKGISVEKCVNSPYGLLLTKNQIL-----KN IHEYKKG YFEIQDEASQ I VSSK I PVHPGDKVLDFY CAGSGGKTLAFSMLMEN-----

Species	Position	Sequence	Conservation	Annotations
Mus	156	SVFVTLNHNS	156	YAG
Rattus	172	SVFVTLNHNS	172	YAG
Homo	156	SVFVTLNHNS	156	YAG
Rhinolophus	157	SVFVTLNHNS	157	YAG
Liparis	264	SVFVTLNHNS	264	YAG
Columba	184	SVFVTLNHNS	184	YAG
Oesophagostomum	85	SVFVTLNHNS	85	YAG
Ancylostoma	591	SVFVTLNHNS	591	YAG
Chytridiomycetes	207	SVFVTLNHNS	207	YAG
Gossypium	130	SVFVTLNHNS	130	YAG
Symbiodinium	162	SVFVTLNHNS	162	YAG
Cryptosporidium	139	SVFVTLNHNS	139	YAG
Theileria	207	SVFVTLNHNS	207	YAG
Marmota	156	SVFVTLNHNS	156	YAG
Gulo	156	SVFVTLNHNS	156	YAG
PVP01_0930100	332	SVFVTLNHNS	332	YAG
PY17X_0920500	353	SVFVTLNHNS	353	YAG
PF3D7_1129400	329	SVFVTLNHNS	329	YAG
PBANKA_0918800	320	SVFVTLNHNS	320	YAG
PF3D7_0704200	255	SVFVTLNHNS	255	YAG
PF3D7_1111000	282	SVFVTLNHNS	282	YAG
PF3D7_1230600	224	SVFVTLNHNS	224	YAG

Mus	207	-----KVLVDAPCSNDRSWLFSSDSQKAAYRIH-QRKNLPVLQVELVRS AIK-ALRPGGLLVYSTCTLSKAENQDVIS-----EVL TSDSN---
Rattus	235	-----KVLVDAPCSNDRSWLFSSDSQKATYRIC-QRNNLPALQVGLLRSAIK-ALRPGGLLIYSTCTLSKAENQDVIS-----EIL TSDSN---
Homo	207	-----KVLVDAPCSNDRSWLFSSDSQKASCRIS-QRRNLP LLQI ELLRSAIK-ALRPGGILVYSTCTLSKAENQDVIS-----EILNSHGN---
Rhinolophus	208	-----KVLVDAPCSNDRSWLFSSDSQKAACRIS-QRRNLPVLQI ELLRSAVK-ALRPGGLLVYSTCTLSKAENQDVIS-----EILNSCSN---
Liparis	315	-----KVLVDAPCSNDRSWLYCGN-QQGEQRLK-ERARLPALQTQLLKSALS-AVRPGGVVYSTCTLS SFENC AVVE-----TVLNECFE---
Columba	235	-----KVLVDAPCSNDRSWLFSSDIQQATHRLI-QRKEL SCLQFQLLRSAIK-ALRPGGSLVYSTCTLSKAENSDVIN-----LILHSCSN---
Oesophagostomum	136	-----T-KKAVI I VTVLQVIADVPCSTDR L AVNQDEGNMFSPQMTNERLNL PQLQTK I L INALR-SVKVGGSVVYSTCTLSSI QNEAVVE-----NGVAIAEQKFG
Ancylostoma	642	-----TYDKA-----SVIADVPCSTDR L AVNQDDGNMYS PQMTNERLNL PQLQTK I L INALR-SVKVGGSVVYSTCTLSSI QNEAVVE-----NGVAIAEEKFG
Chytriomycetes	257	-----TY-----LKVLC DAPCSSE RHVLH-DEAF LLQWSPS-RTKNSAKRQLRLLAHALRTALDDGGRVVYATCSISRYENDMVVE-----KVLKRSPIY---
Gossypium	194	FREWTSRRPWKERKRAAKARETMSLQSVTMSENPEL I FYGRHSGVVGLSKNKLYKTMSDLEVSSCSYD-----KVLVDAECTHDCSVKH I QKFENWGWTIL-QRRVLDAL--KLLRNGFR-LLKVGGLLVYSTCTSLTVAQNE DIVE-----KFLKENTS---
Symbiodinium	222	-----RVLVDAPCTSDRHLVQQGQSALAHWAAGAVKAN-AERQLELLRAAAV-LVKGGLVLVYTCALAE AENDGVVS-----KFLKKFGQDFE
Cryptosporidium	204	-----KILVDAPCSSDRHL ILSNDFK--HWS I KLA KRN-SERQTE I INNAIG-LLQDDG I ILYCTCTLNE IENDYTVER I CN NLE I STNDCFKLM-----LNI I KEFN NRYN
Theileria	271	-----KIL I DAPCSSERHL I H---KNLSWSVKS I KEN-SKRQLKLLQTAIS-LLKSGGT I ILYCTCALDPI ENEMVIN-----TILKAYDD---
Marmota	207	-----KVLVDAPCSNDRSWLFSSDPCKATCRIH-QRRNLPVLQME LLRSAIK-ALRPGGVLVYSTCTLSKAENQDVIN-----ETLNSYSN---
Gulo	207	-----KVLVDAPCSNDRSWLFSSDPCKAAWRIS-QRRNLP I LQLELLRSAIK-ALRPGGLLVYSTCTLSKAENQDVIS-----EILNSYTN---
PVP01_0930100	380	-----KILLDAPCSGTGVV---NKNKGARRKT LKE I RELAQKORKLLSNAIS-LVKNGGIVVYSTCS I TVEENEQVIN-----YILKKRDVN---
PY17X_0920500	401	-----KILLDAPCSGTGVV---NKNKNARRKT I KE I RDLAQKORKLLNNAID-LVKNGGIV IYSTCS I TVEENEQVIN-----YILKKRDVN---
PF3D7_1129400	377	-----KILLDAPCSGTGVV---NKNKTARRKT I KE I RDLAQKOK I LLNNAIN-LLKNGGIVVYSTCS I SVEENEQVIN-----YILKKRDVN---
PBANKA_0918800	368	-----KILLDAPCSGTGVV---NKNKNARRKT I KE I RDL S QKORKLLNNAID-MVKNGGIV IYSTCS I TVEENEQVIN-----YILKKRDVN---
PF3D7_0704200	427	-----SILCDVPCS GDGTLRKDRNWIN-WNP N-NAYNL FQM QVN I LKRSIE-LTKENGY I VYSTCSLNP I ENEA VICE I FNSVE--NLDCLKL INFQNE LLTKLNYEKAVKQWV---
PF3D7_1111000	415	-----KILLDVPCSTDEHL I KOGTKE LNKWS I H-VIKNNSDIQLQL I NAFT-LLHTGGV I IYSTCALSYLENDYVI-----EKFLKKYK---
PF3D7_1230600	271	-----VV IVDAPCTGTALR--RNPEMKYKFTNNKLYDYVKTQRE I FENALL-YLKNKGK I VY I TCS I LDAENVHQAK-----YFCQKHNL---

Fig. S2

