**Supplementary material**

# Signalling the genome: the ras-like small GTPase family of trypanosomatids

Mark. C. Field

The Molteno Building, Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP

**Correspondence:** Tel: 01223- 333734, email: mcf34@cam.ac.uk

**Running title:** The ras superfamily in trypanosomes

**Key words:** small GTPase/signalling/ras/evolution/trypanosome

**Supplementary material**

## Methods

*Search strategy:* Searches were performed against release 3 of the *T. brucei* and *T. cruzi* databases and against a version of the *L. major* genome database that contained 8306 annotated genes. Sequence retrieval procedures were performed using a combination of keyword search (terms used including; small GTPase, Ras, Rab, Rac, Cdc42 etcetera) and also using tBLASTx or tBLASTp with query sequences to sample the ras-like small GTPase superfamily subdomains at GeneDB (http://www.genedb.org/genedb/tryp/index.jsp) using the BLAST server and text/keyword search facilities. Retrieved sequences were subsequently verified at NCBI nonredundant databases. Protein sequences corresponding to *Homo sapiens* Ras, Ral, Rac, Cdc42 and Wrch, *Mus musculus* TTF and two members of the Rop family from *Arabidopsis thaliana* were used to probe the *T. brucei* database. All sequences returned by BLAST were retrieved from these searches, i.e. no significance cut off was used, and data were than parsed for Rab, Ran or ARF sequences already identified (1, 10). The BLAST results were also parsed for non-GTPase sequences by either database annotation, for example ATPases are frequently retrieved with low significance in these searches, or by reverse BLAST against the nonredundant databases. Redundant entries, i.e. sequences retrieved by more than one query sequence, were also removed. In cases of concern with the gene models, i.e. with assignment of the ATG or TAA codons, comparisons between the three trypanosomatid genomes were used to further support the open reading frame model.

*Alignments, phylogenetic reconstruction and other* in silico *analysis:* Alignments were performed using a local implementation of Clustal X (http://www.embl.de/~chenna/clustal/darwin/) on a Macintosh G5 dual processor computer. Initial dendrogams were also assembled using the Neighbour-Joining algorithm in Clustal X and bootstrapped 10 000 times and analysed with TreeView X (http://darwin.zoology.gla.ac.uk/~rpage/treeviewx/). Additional phylogenetic reconstructions were performed using PAUP* V4b10, again on a Macintosh G5. Reference sequences corresponding to the query sequences, together with representative trypanosome, yeast and *Caenorhabditis elegans* small GTPases

were included to provide annotation and also control sequences for the reconstructions. In some cases excessive N- or C-terminal extensions were removed from the alignments prior to phylogenetic analysis. Dot plot analysis was performed using DotPlot V1.0 running on Windows$^{XP}$ (http://www.microsoft.com) emulation on a G5 Macintosh. Motif searches were performed using the PSSM database (http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi). Original sequences, alignments and phylogenetic trees, including the relevant GeneDB accession numbers, can be obtained from the author or downloaded from http://homepage.mac.com/mfield/lab/publications.html or by email request.

**Acknowledgements**

Mark C. Field's laboratory is supported by project and programme grants from the Wellcome Trust and the British Heart Foundation. Kinetoplastid sequence data were obtained from The Sanger Institute website at http://www.sanger.ac.uk/Projects/T_brucei/, /T_cruzi/ and /L_major and from The Institute for Genomic Research website and the TIGR-Seattle Biomedical Research Institute-Karolinska Institute *T. cruzi* Sequencing Consortium (TSK-TSC). Sequencing of the kinetoplastid genomes was accomplished as part of the Trypanosoma and Leishmania Genome Networks with support by The Wellcome Trust and awards from the National Institute of Allergy and Infectious Diseases, National Institutes of Health. Provision of these data in the public domain is gratefully acknowledged. Original sequences, alignments and phylogenetic trees, including the relevant GeneDB accession numbers, can be obtained from the author or downloaded from http://homepage.mac.com/mfield/lab/publications.html.

**Supplementary material**

**Figure legends**

**Figure S1: Clustal X alignment of the closest ras homologues from *T. brucei*.** The hypothetical polypeptide sequences of Tb11.02.3850 (TbRLP) and Tb11.52.0014 (TbRLJ) are compared against *H. sapiens* N-ras. Despite conservation of the major features of the GTPase domain, the trypanosome sequences are sufficiently divergent as to suggest a lack of functional equivalence between these proteins. GTP binding regions are underlined and prenylation sequences are in bold. Fully conserved residues are in red, residues with conservative substitutions in blue.

**Figure S2: Clustal X alignment of Tb11.52.0014 (TbRLJ) family.** The hypothetical polypeptide sequence of TbRLJ is compared against the orthologues for *Leishmania major* and *Trypanosoma cruzi* together with the top BLAST hit from the non-redundant database, RnRBJ, a small GTPase from *Rattus norvegicus* that possesses a dnaj domain extension within the C-terminus. Despite very good conservation of the major features of the GTPase domain, all of the kinetoplastid proteins lack the dnaj region, suggesting divergent functions. Note that the *L. major* family member contains a number of insertions relative to the remaining sequences, which are of low complexity sequence and which may be intronic sequences. Fully conserved residues are in red, residues with conservative substitutions in blue.

**Figure S3: Clustal X alignment of Tb07.29D18.100 (TbEAR) family.** The hypothetical polypeptide sequence of TbEAR is compared against the orthologues for *Leishmania major* and *Trypanosoma cruzi* together with the top BLAST hit from the non-redundant database, a GTPase from *Rhodospirillum rubrum*. The domain structure is highly unusual, consisting of tandem GTPase domains, which is conserved throughout evolution. Fully conserved residues are in red, residues with conservative substitutions in blue.

**Figure S4: Dot plot analysis of Tb07.29D18.100.** Tb07.29D18.100 was compared against itself using DotPlot Version 1, with stringency of 1.0 and a

residue window of 5.0. Clear homology is present between the N-terminal 220 residues and the C-terminal 230 amino acids.

**Figure S5: Clustal X alignment of the nucleostemin family.** The hypothetical polypeptide sequence of Tb11.02.0240 is compared against the orthologues for *Leishmania major* and *Trypanosoma cruzi* together with the top BLAST hits from the non-redundant database, members of the nucleostemin family from *C. elegans* and *H. sapiens*. Somewhat weaker homology is also seen against a GTPase from *Baccilus subtilis*. Conserved domains are indicated above the alignment. Fully conserved residues are in red, residues with conservative substitutions in blue.

**Figure S6: Clustal X alignment of all *T. brucei* ras-like small GTPases together with a reference set of sequences.** The raw alignment was used in building the large phylogenetic reconstruction shown in Figure 1 following manual trimming of N and C-terminal extensions, and is provided for investigators who may wish to reprocess or reanalyze the data.

**Figure S7: Phylogenetic reconstruction of selected small GTPases from *T. brucei*.** The non-Ran/ARF members of the small GTPase family described here are shown in red, designated by their GeneDB identifiers, together with reference sequences from *H. sapiens*, *S. cerevisiae*, *C. elegans*, *A. thaliana*, *M. musculis* and *T. brucei* in black. Gross family groupings are shown at right. Domain structures of the GTPases are shown iconised: GTPase domain; red oval, prenylation site; blue circle, myristolylation sire; yellow circle, FYVE domain; green rectangle, nucelostemin domains; orange and blue rectangles. Polypeptide extensions lacking clear homology are shown as black lines. The tree was generated with Clustal X and the Neighbour-Joining method, together with 10 000 boostrap replicates. Highly similar trees were obtained used other methods, indicating that the tree is robust.

**Table S1: New small Ras-like GTPases of *T. brucei*.** Structural features, size and a proposed systematic name are given for the new members of the small GTPase family described here.

| GeneDB accession | Size (aa) | Domains[1] | C-terminal extension | Function[2] | Systematic Name |
|---|---|---|---|---|---|
| Tb03.5L5.790 | 183 | | | | TbRX1 |
| Tb05.26C7.80 | 194 | | | **Sar1** | TbSAR1 |
| Tb11.52.0014 | 216 | | | | TbRLJ |
| Tb11.02.3850 | 226 | | | Possible signalling | TbRLP |
| Tb10.6k15.1520 | 339 | | + | **Rag/Gtr1-like** | TbGRP |
| Tb10.70.0590 | 403 | | + | Possible signalling | TbRHP |
| Tb11.02.0820 | 407 | | | **Rag/Gtr1-like** | TbGTR |
| Tb11.02.0240 | 486 | Nuclear targeting, coiled coil, acidic | + | **Nucleostemin** | TbNST |
| Tb04.1D20.300 | 563 | | + | | TbRX2 |
| Tb07.29D18.100 | 576 | Second GTPase | | | TbEAR |
| Tb07.6C8.230 | 577 | FYVE domain | | Membrane transport | TbFRP |
| Tb08.6H23.400 | 632 | | + | | TbRX3 |

1. Excludes the GTPase domain.
2. Strongly suggested from sequence analysis (**bold**) or suggested based on predicted tertiary structure. See main text for details. 3. Citations for previously identified members of the family.

**Table S2: Evoutionary distribution of *T. brucei* GTPases.** Each GTPase sequence was used as a query against multiple genomes from fungi, archae, proteobacteria, plants, apicomplexa and metazoa. A positive hit was scored based on both local areas of homology as well as on similarity throughout the length of the ORF, especially outside of the GTPase domain if relevant. The other classes of GTPase not included here (Rabs, Ran and ARF) are found throughout the eukaryota, but not in prokaryotes. -; no homologue found, +; clear homologue found. In some cases where a borderline similarity/relationship was found the e value is shown.

| GeneDB accession | Systematic name | Proteo-bacteria | Archae | Apicomplexa | Fungi | Plants | Metazoa |
|---|---|---|---|---|---|---|---|
| Tb03.5L5.790 | TbRX1 | - | - | - | - | - | - |
| Tb05.26C7.80 | TbSAR1 | - | - | + | + | + | + |
| Tb11.52.0014 | TbRLJ | - | - | + | + | + | + |
| Tb11.02.3850 | TbRLP | - | - | - | + | + | + |
| Tb10.6k15.1520 | TbGRP | - | - | $e^{-13}$ | + | - | + |
| Tb10.70.0590 | TbRHP | - | - | - | - | - | - |
| Tb11.02.0820 | TbGTR | - | - | + | + | - | + |
| Tb11.02.0240 | TbNST | $e^{-15}$ | $e^{-28}$ | + | + | - | + |
| Tb04.1D20.300 | TbRX2 | - | - | - | - | - | - |
| Tb07.29D18.100 | TbEAR | + | - | + | - | - | + |
| Tb07.6C8.230 | TbFRP | - | - | - | - | - | - |
| Tb08.6H23.400 | TbRX3 | - | - | - | - | - | - |

```
Tb11.02.3850      1 ------------------MRNINLVVLGDGGVGKSSLIIQYVRNRFVVKYEATIEDVY--
HsNRasAAQ94397    1 ------------------MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSY--
Tb11.52.0014      1 MPSHTTSDGSPTTGGDKSGPRIKIVSLGSVGVGKSCLIKQYCEGRFVSKYIPTIGIDYGV

Tb11.02.3850     41 --------QKAVEVDAQPTVLTIVDTSGQDVFGGMRYKYIRKCHGVILVYSVIDAESFSH
HsNRasAAQ94397   41 --------RKQVVIDGETCLLDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNSKSFAD
Tb11.52.0014     61 KRVDVRVPAHLAPSGKISTRVNFWDMSGCEEYLEIRNEFYRATEGVLLVYDVTDAESFFA

Tb11.02.3850     93 IKAIH-------------TQLCRARGSPSIPCVLVGNKVDE------VKHRAVSSEEASK
HsNRasAAQ94397   93 INLYR-------------EQIKRVKDSDDVPMVLVGNKCD-------LPTRTVDTKQAHE
Tb11.52.0014    121 LNQWVKEMEAHVNTKGNDTYVARVDASVPCKVVVCANKIDEVSEGGGRKKRAVSSETGRQ

Tb11.02.3850    134 FAAQFMYPLLEVTAKDHSMAAAVFETLVRSIRGEESWLECRSPNVIFPPAATISEVRDEV
HsNRasAAQ94397  133 LAKSYGIPFIETSAKTRQGVEDAFYTLVREIR----------------------------
Tb11.52.0014    181 WAKEHDYKYFETSACTGAGVEEALETLFKDVVAAFF-------------------------

Tb11.02.3850    194 HQLELPSVDLVDEHEEESPGIANRKKKSGCTML
HsNRasAAQ94397  165 -QYRMKKLNSSDDGTQGCMGLP-------CVVM
Tb11.52.0014        ---------------------------------
```

**Figure S1**

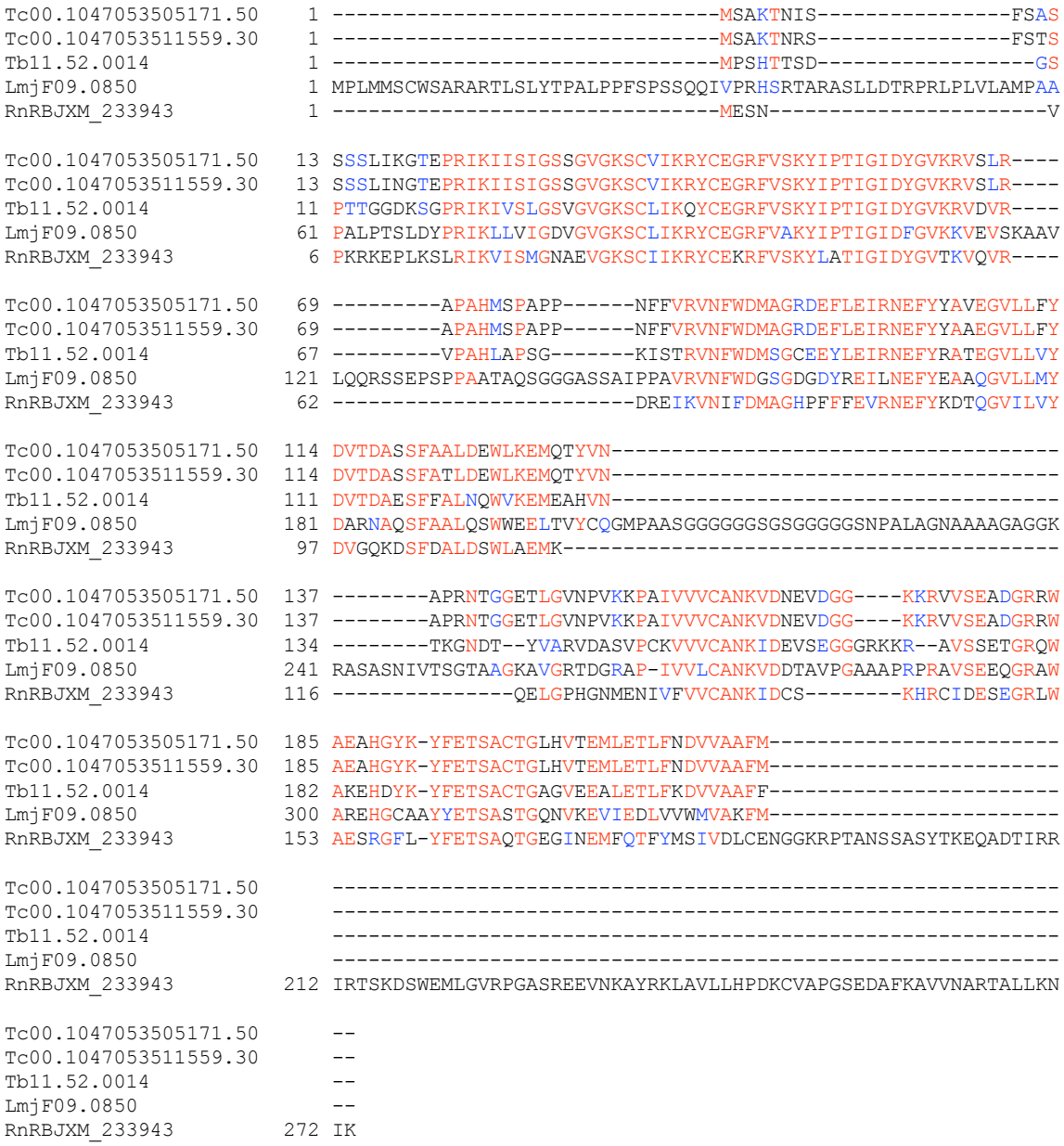
Tc00.1047053505171.50 1 ----------MSAKTNIS----------FSAS
Tc00.1047053511559.30 1 ----------MSAKTNRS----------FSTS
Tb11.52.0014 1 ----------MPSHTTSD----------GS
LmjF09.0850 1 MPLMMSCWSARARTLSLYTPALPPFSPSSQQIVPRHSRTARASLLDTRPRLPLVLAMPAA
RnRBJXM_233943 1 ----------MESN----------V
Tc00.1047053505171.50 13 SSSLIKGTEPRIKIISIGSSGVGKSCVIKRYCEGRFVSKYIPTIGIDYGVKRVSLR----
Tc00.1047053511559.30 13 SSSLINGTEPRIKIISIGSSGVGKSCVIKRYCEGRFVSKYIPTIGIDYGVKRVSLR----
Tb11.52.0014 11 PTTGGDKSGPRIKIVSLGSVGVGKSCLIKQYCEGRFVSKYIPTIGIDYGVKRVDVR----
LmjF09.0850 61 PALPTSLDYPRIKLLVIGDVGVGKSCLIKRYCEGRFVAKYIPTIGIDFGVKKVEVSKAAV
RnRBJXM_233943 6 PKRKEPLKSLRIKVISMGNAEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVQVR----
Tc00.1047053505171.50 69 ---------APAHMSPAPP------NFFVRVNFWDMAGRDEFLEIRNEFYYAVEGVLLFY
Tc00.1047053511559.30 69 ---------APAHMSPAPP------NFFVRVNFWDMAGRDEFLEIRNEFYYAAEGVLLFY
Tb11.52.0014 67 ---------VPAHLAPSG-------KISTRVNFWDMSGCEEYLEIRNEFYRATEGVLLVY
LmjF09.0850 121 LQQRSSEPSPPAATAQSGGGASSAIPPAVRVNFWDGSGDGDYREILNEFYEAAQGVLLMY
RnRBJXM_233943 62 -------------------------DREIKVNIFDMAGHPFFFEVRNEFYKDTQGVILVY
Tc00.1047053505171.50 114 DVTDASSFAALDEWLKEMQTYVN----------
Tc00.1047053511559.30 114 DVTDASSFATLDEWLKEMQTYVN----------
Tb11.52.0014 111 DVTDAESFFALNQWVKEMEAHVN----------
LmjF09.0850 181 DARNAQSFAALQSWWEELTVYCQGMPAASGGGGGGSGSGGGGGSNPALAGNAAAAGAGGK
RnRBJXM_233943 97 DVGQKDSFDALDSWLAEMK----------
Tc00.1047053505171.50 137 --------APRNTGGETLGVNPVKKPAIVVVCANKVDNEVDGG----KKRVVSEADGRRW
Tc00.1047053511559.30 137 --------APRNTGGETLGVNPVKKPAIVVVCANKVDNEVDGG----KKRVVSEADGRRW
Tb11.52.0014 134 --------TKGNDT--YVARVDASVPCKVVVCANKIDEVSEGGGRKKR--AVSSETGRQW
LmjF09.0850 241 RASASNIVTSGTAAGKAVGRTDGRAP-IVVLCANKVDDTAVPGAAAPRPRAVSEEQGRAW
RnRBJXM_233943 116 ---------------QELGPHGNMENIVFVVCANKIDCS--------KHRCIDESEGRLW
Tc00.1047053505171.50 185 AEAHGYK-YFETSACTGLHVTEMLETLFNDVVAAFM----------
Tc00.1047053511559.30 185 AEAHGYK-YFETSACTGLHVTEMLETLFNDVVAAFM----------
Tb11.52.0014 182 AKEHDYK-YFETSACTGAGVEEALETLFKDVVAAFF----------
LmjF09.0850 300 AREHGCAAYYETSASTGQNVKEVIEDLVVWMVAKFM----------
RnRBJXM_233943 153 AESRGFL-YFETSAQTGEGINEMFQTFYMSIVDLCENGGKRPTANSSASYTKEQADTIRR
Tc00.1047053505171.50 ----------
Tc00.1047053511559.30 ----------
Tb11.52.0014 ----------
LmjF09.0850 ----------
RnRBJXM_233943 212 IRTSKDSWEMLGVRPGASREEVNKAYRKLAVLLHPDKCVAPGSEDAFKAVVNARTALLKN
Tc00.1047053505171.50 --
Tc00.1047053511559.30 --
Tb11.52.0014 --
LmjF09.0850 --
RnRBJXM_233943 272 IK

**Figure S2**

```
Tc00.1047053508207.200    1 MRRFCIVNALR-----SSGVVFLTTATPPSTNSTAAANNAMKSSQFALPLNRQIRHGLSS
Tc00.1047053509509.60     1 MRRFCIVNALR-----SSGVVFLTTATPPSTNSTAAANNAMKSSQFALPLNRQIRHGLSS
Tb07.29D18.100            1 MRRCIPASVLRRVLLLQTRLVSTNTQTPPSGCATKIQNESPMNGSFNLPRERQILGGLHA
LmjF26.0270               1 ------------------------------------------------------------
RrGTPaseZP_00270676        1 ------------------------------------------------------------

Tc00.1047053508207.200   56 DWREQVRRSGGVLNDISPALPDSNRTDDQRKRVAGWQPVVKLLGDQRLRVAIVGRMNSGK
Tc00.1047053509509.60    56 DWREQVRRSGGVLNDISPALPDSNRTDDQRKRVAGWQPVVKLLGDQRLRVAIVGRMNSGK
Tb07.29D18.100           61 DWRTQMKRSGSILNDITPALPDTKRTEEQRRRVAGWRPVVKLLGDQRLRIAIVGRMNSGK
LmjF26.0270               1 -------------------MEDTARTDEQRRRVAGWTPVVKTLGDHRLRVAIVGRMNSGK
RrGTPaseZP_00270676        1 ----------------------------------------------MFTVAIIGRPNVGK

Tc00.1047053508207.200  116 SSLFNLLSEDPTMPNRKNIVRDFDGITRDSVEGHAQLEGMHFTIIDTPGMVNG-------
Tc00.1047053509509.60   116 SSLFNLLSEDPTMPHRKNIVRDFDGITRDSVEGHAQLEGMHFTIIDTPGMVNG-------
Tb07.29D18.100          121 SSLFNLLRLEPTVPGRSNVVRDFDGITRDSVEGQAQLEGMHFTIIDTPGMVQG-------
LmjF26.0270              42 SSLFNLLCEDPTMPAKKNIVKDFNGITRDCVEAHAALDDLHFTVIDTPGLLGG-------
RrGTPaseZP_00270676      15 STLFNRLCG-----RRLAIVHDMPGVTRDRREGKASLADLVFRVVDTAGLEEAGPEVLEG

Tc00.1047053508207.200  169 KLVEEAFRTVETADAAIFVTSVDEDLHSAEFDLIHYLQLKCMPTFVLVNKMDLVPLDEED
Tc00.1047053509509.60   169 KLVEEAFRTVETADAAIFVTSVDEDLHSAEFDLIHYLQLKCMPTFVLVNKMDLVPLDEED
Tb07.29D18.100          174 RMVEEAFRTVETADAAIFVTAVDEDIMPEELSLMQYLHLKHMPVVLLANKMDLIQEEEEE
LmjF26.0270              95 KLVEEAFRTVETADAAIFVTAVDEDVSAEEHDLIQYLAAKKMPTCLLVNKMDLVPEEEEA
RrGTPaseZP_00270676      70 RMRQQTDRALSEAHVALMLIDSRAGVTPLDAHFAEILRKAPIPVILVANKCEGGAGKPG-

Tc00.1047053508207.200  229 RVLERYNGLGLGNAIPFSARRKSGMEMLAAVLEPLYHIHSMQKVENDWDIEDLAMQGDES
Tc00.1047053509509.60   229 RVLERYNELGLGNAIPFSARRKSGMEMLAAVLEPLYHIHSMQKVENDWDIEDLAMQGDES
Tb07.29D18.100          234 AVLDRYNSLGFGNAIPFSARRKSGLEMLAAVLEPLYHIHAMHKVENDWDIEDLAMQGDES
LmjF26.0270             155 LVLDVYNRLGLGKAVPFSARKREGLDMLSALLEPLYHIHAMRKVENDWDIEDLAMAGDEA
RrGTPaseZP_00270676     129 --FYESYSMGLGDPVPLSAEHGEGLSLLYEALMPIYDAHMAQEAKDEADAVRAAFLETEA

Tc00.1047053508207.200  289 AMEEIRDRNCA---------------------------------DRFIRIALVGRTNSGKS
Tc00.1047053509509.60   289 AMEEIRDRNCA---------------------------------DRFIRIALVGRTNSGKS
Tb07.29D18.100          294 AMEEIRERNCS---------------------------------DRFIRIAIVGRTNSGKS
LmjF26.0270             215 AMEEIRDRNCT---------------------------------DRYIRVAIVGRTNSGKT
RrGTPaseZP_00270676     187 ASAAKPYIDFASLEPDEVPEDDDSDPSQDPEDDFSVEAFDPRGERPIQMAIIGRPNTGKS

Tc00.1047053508207.200  317 SLINRLVGFERSRAVDEKNSTRDPVELSCIYKGRKVKLIDTAGLTRHRFRADRDFIGRIH
Tc00.1047053509509.60   317 SLINRLVGFERSRAVDEKNSTRDPVELPCIYKGRKVKLIDTAGLTRNRFRADRDFIGRIH
Tb07.29D18.100          322 SLVNRLVGFERNRAVDEKNSTRDPVELPCSYKGRKLKLIDTAGLARHRYRADRDFIGRIH
LmjF26.0270             243 SLVNRLVGYERNRAADESNTTRDPIEIACMYKGRKLKLIDTAGLARQRYRTDREFLSRIH
RrGTPaseZP_00270676     247 TLINRLIGDDRLVTGPEAGVTRDAIEVDWEWGGRRFRLVDTAGLRR-KARVENSLEKLMV

Tc00.1047053508207.200  377 DLSVNEIRYAHVVIVVFDATEGHPNKYDMAVLHSVAAEGRPFLLCANKWDAVLDQSATAE
Tc00.1047053509509.60   377 DLSVNEIRYAHVVIVVFDATEGHPNKYDMAVLHSVAAEGRPFLLCANKWDAVLDQSATAE
Tb07.29D18.100          382 GLSVNEIRFAHVVIVVFDATEGHPNKYDMAVLHSVAAEGRPFLLCANKWDAVLDQSATAE
LmjF26.0270             303 SLSLNEIRYAHVVIVVFDATEGHPNKYDMSILHKVAQEGRPFVLCANKWDAVLDQSATAE
RrGTPaseZP_00270676     306 ADTLNAIRLAEVCVLMLDANMVMD-RQDLTIARLVIDEGRALVIAVNKWDACADRKAALQ

Tc00.1047053508207.200  437 AIDFKIKRQVREVKYSNAVVVSAHTGLNLTLLMDQALLLYDTWNKRVRRAELTRLWRKME
Tc00.1047053509509.60   437 AIDFKIKRQVREVKYSNAVVVSAHTGLNLTLLMDQALLLYDTWNKRVRRAELTRLWRKME
Tb07.29D18.100          442 AIDFKIKRQVREVKYSNAVVVSAHTGLNLTLLMDQALELYDKWNKRVRRAELTRLWRKME
LmjF26.0270             363 AIDFKIKRQVQEVKYSNAVVVSAHTGMNLTLLMDQVLELYDTWNKRVRRSELTKFWRKLE
RrGTPaseZP_00270676     365 RLADRLETSLAQVRGVPFVTLSALEGHGLNRLMDAALEAHAKWNRRVPTSRFNRWLKGMI

Tc00.1047053508207.200  497 KSVIIPY----HVARVGRITQVNTRPPTFLLHLQTKNDENTLPKALQEMMKNTIVEEFDF
Tc00.1047053509509.60   497 KSVIIPY----HVARVGRITQVNTRPPTFLLHLQTKNDENTLPRALQEMMKNTIVEEFDF
Tb07.29D18.100          502 KSVIIPY----HVARIGRITQVNTRPPTFLLQLQTKNDSNTLPKALQEMMKNTLVEEFDF
LmjF26.0270             423 KSVIIPY----HVARVGRITQISTRPPTFLLQLQTKKEESQLPKALQEMMKNAITEEFGF
RrGTPaseZP_00270676     425 DRHPLPMGKHGRRLRIRYGTQAKIRPPTFALFMTRPDD---LPESYVRYLNSGLREDFDM

Tc00.1047053508207.200  553 RGVPIRLIQEVKDSNPDYI
Tc00.1047053509509.60   553 RGVPIRLIQEVKDSNPDYI
Tb07.29D18.100          558 RGVPIRLIQEVKDSNPDYI
LmjF26.0270             479 RGVPLRLVQEVKDSNPDYI
RrGTPaseZP_00270676     482 AGTPIRLLFRATKNPYADK
```

**Figure S3**

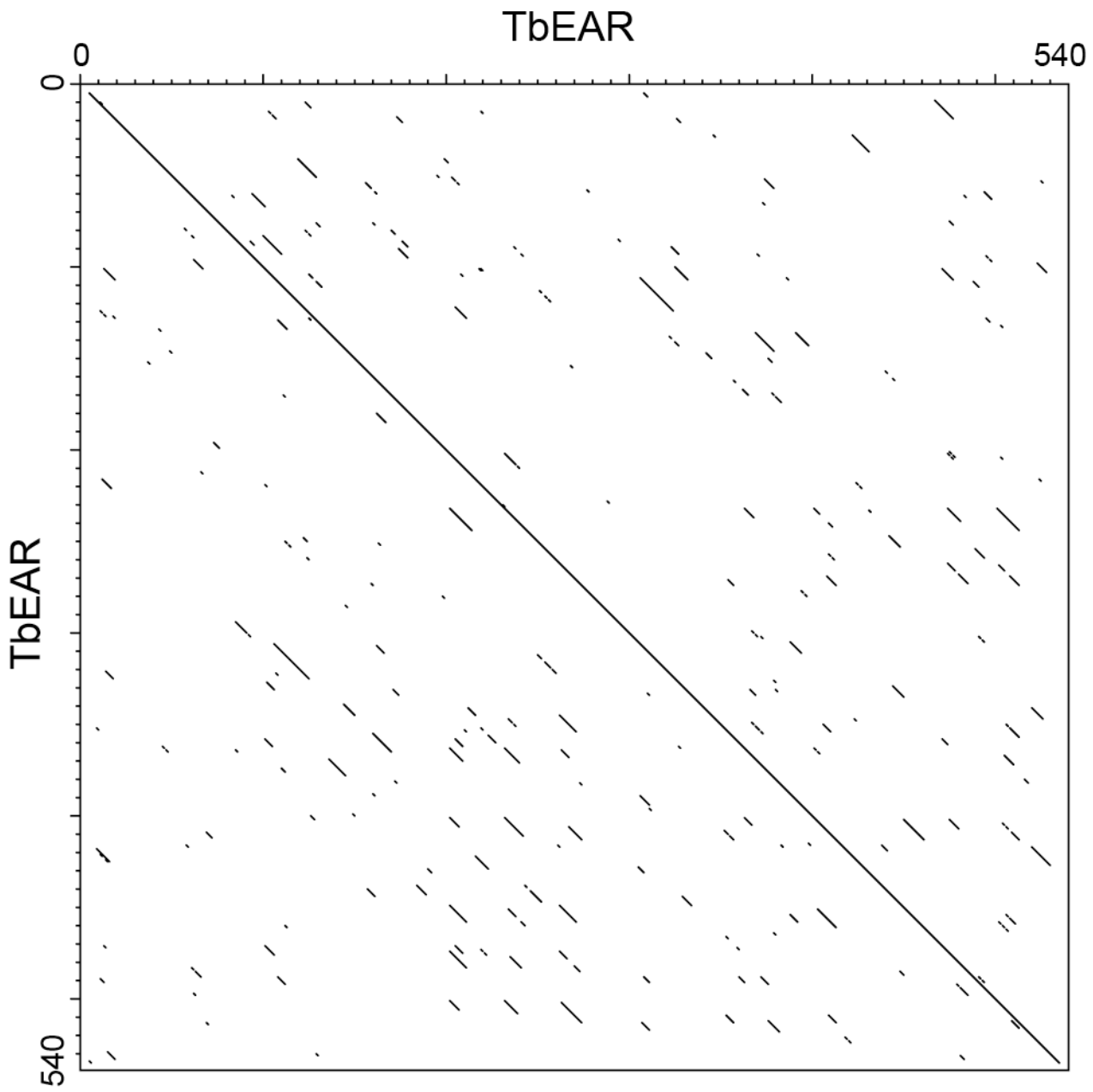


Figure S4

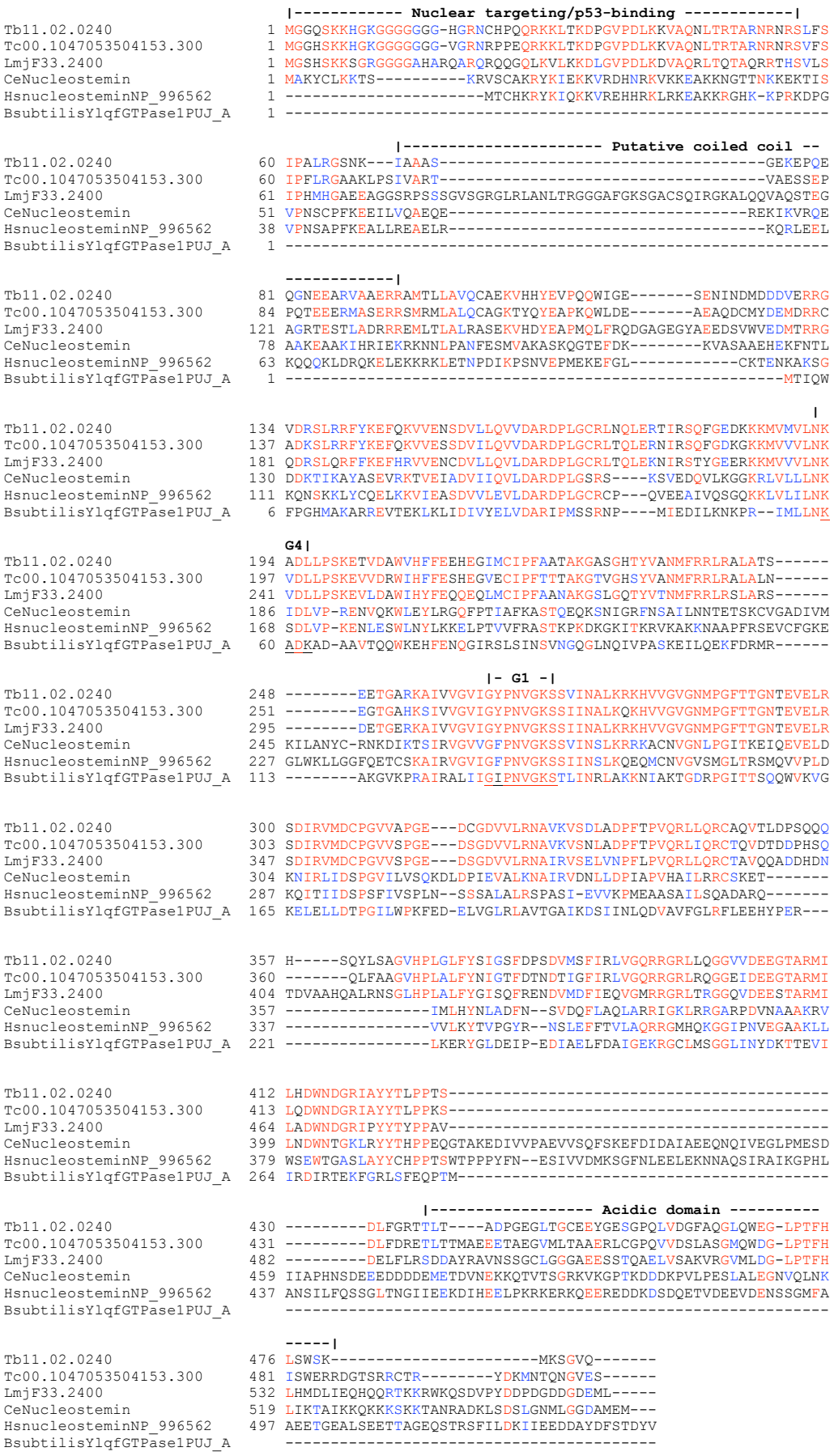
Nuclear targeting/p53-binding
Putative coiled coil
G4
G1
Acidic domain
Tb11.02.0240
Tc00.1047053504153.300
LmjF33.2400
CeNucleostemin
HsnucleosteminNP_996562
BsubtilisYlqfGTPase1PUJ_A

**Figure S5**

CLUSTAL X (1.82) multiple sequence alignment

```
TbARF1C                          --------------------------------------------------
TbARF1B                          --------------------------------------------------
TbARF1D                          --------------------------------------------------
TbARF1A                          --------------------------------------------------
TbARF1A_Tb09.211.4460            --------------------------------------------------
HsARF1NM_001658                  --------------------------------------------------
ScARF1YDL192w                    --------------------------------------------------
TbARF1E                          --------------------------------------------------
TbARL3_embl.27                   --------------------------------------------------
TbARL1_167.t00109                --------------------------------------------------
TbARL1B_09.160.5300              --------------------------------------------------
TbARL3B_92.m00269                --------------------------------------------------
TbARL3C_06.4F7.880               --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790     --------------------------------------------------
TbRABX1                          --------------------------------------------------
TbRABX2                          --------------------------------------------------
TbRAB21                          --------------------------------------------------
TbRAB1A                          --------------------------------------------------
HsRab1ANM_004161                 --------------------------------------------------
ScYpt1YFL038c                    --------------------------------------------------
TbRAB18                          --------------------------------------------------
TbRAB2                           --------------------------------------------------
TbRAB4                           --------------------------------------------------
TbRAB11                          --------------------------------------------------
TbRAB6                           --------------------------------------------------
TbRAB5B                          --------------------------------------------------
TbRAB5A                          --------------------------------------------------
TbRAB7                           --------------------------------------------------
Tb08.6H23.400                    --------------------------------------------------
Tb04.1D20.300                    --------------------------------------------------
HsNRasAAQ94397                   --------------------------------------------------
ScRas1YOR101w                    --------------------------------------------------
CeRas1C44C11.1                   --------------------------------------------------
HsRalANM_005402                  --------------------------------------------------
HsRanNM_006325                   --------------------------------------------------
TbRAN                            --------------------------------------------------
HsRac2CAB45265                   --------------------------------------------------
CeRac1C09G12.8                   --------------------------------------------------
HsCdc42NM_001791                 --------------------------------------------------
CeCdc42R07G3.1                   --------------------------------------------------
ScCdc42YLR229c                   --------------------------------------------------
HsRhoCAAM21119                   --------------------------------------------------
CeRho-1CE25369                   --------------------------------------------------
AtRop4ARAC5AT1G75840             --------------------------------------------------
AtRop10ARAC8AT3G48040            --------------------------------------------------
HsWrch-1AAK83340                 --------------------------------------------------
MmTTFXP_359315                   --------------------------------------------------
ScGtr1RagYML121W                 --------------------------------------------------
Tb11.02.0820                     --------------------------------------------------
TbRAB1B                          --------------------------------------------------
TbRAB23                          --------------------------------------------------
TbRABX3                          --------------------------------------------------
Tb05.26C7.80                     --------------------------------------------------
TbRAB28                          --------------------------------------------------
Tb11.02.3850                     --------------------------------------------------
Tb11.52.0014                     --------------------------------------------------
Tb10.70.0590                     --------------------------------------------------
Tb03.5L5.790                     --------------------------------------------------
```

```
TbARF2like_TRYP10.0.000567_68      --------------------------------------------------
Tb07.6C8.230                       --------------------------------------------------
Tb10.6k15.1520                     --------------------------------------------------
Tb07.29D18.100                     MRRCIPASVLRRVLLLQTRLVSTNTQTPPSGCATKIQNESPMNGSFNLPR
HsnucleosteminNP_996562            --------------------------------------------------
Tb11.02.0240                       --------------------------------------------------


TbARF1C                            ------------------------------MGQWLAS----------AFK
TbARF1B                            ------------------------------MGQWLAS----------AFK
TbARF1D                            ------------------------------MGQWLAS----------AFK
TbARF1A                            ------------------------------MGQWLAS----------AFK
TbARF1A_Tb09.211.4460              ------------------------------MGQWLAS----------AFK
HsARF1NM_001658                    ------------------------------MGNIFAN----------LFK
ScARF1YDL192w                      ------------------------------MGLFASK----------LFS
TbARF1E                            ------------------------------MGNVLS-----------WFE
TbARL3_embl.27                     ------------------------------MGLLEFL----------LKI
TbARL1_167.t00109                  ------------------------------MGALVSQIK-------SLLG
TbARL1B_09.160.5300                ------------------------------MGQLIS----------GLWS
TbARL3B_92.m00269                  ----------------------------------MLKG----------IRS
TbARL3C_06.4F7.880                 ----------------------------------MLKG----------IRS
TbARL6_10.70.3000|08.5H5.790       --------------------------------------------------
TbRABX1                            ------------------------------MITAASPGGDCD---------
TbRABX2                            ----------------------------------MKEEP--------------
TbRAB21                            ------------------------------MRSSVP--------------
TbRAB1A                            ------------------------------MSTEYD--------------
HsRab1ANM_004161                   --------------------------MSSMNPEYD--------------
ScYpt1YFL038c                      ------------------------------MNSEYD--------------
TbRAB18                            ------------------------------MAQGDN--------------
TbRAB2                             ----------------------------------MQQHH--------------
TbRAB4                             ------------------------------MSERYQ--------------
TbRAB11                            ------------------------------MEDMN---------------
TbRAB6                             ------------------------------METNSAPVASTKKGGDGVTA
TbRAB5B                            ------------------------MSVKTVAAPTK--------------
TbRAB5A                            ------------------------MSVSATPYKRQDA------------
TbRAB7                             ------------------------------MAPNRQ--------------
Tb08.6H23.400                      ----------------MRVEDPKSLDAVADAEESVKVEAPLEGRNTREE
Tb04.1D20.300                      ----------------MRPEFP---GLVEAATETECTEASTEPEDEQWE
HsNRasAAQ94397                     ------------------------------------MT-----------
ScRas1YOR101w                      ------------------------------MQGNKSTIR----------
CeRas1C44C11.1                     ------------------------------MGGRSNSATTAAQ-------
HsRalANM_005402                    ------------------------------MAANKPKGQNS---------
HsRanNM_006325                     ------------------------------MAAQGEPQ------------
TbRAN                              ------------------------------MQASSTADCV----------
HsRac2CAB45265                     --------------------------------------------------
CeRac1C09G12.8                     --------------------------------------------------
HsCdc42NM_001791                   --------------------------------------------------
CeCdc42R07G3.1                     --------------------------------------------------
ScCdc42YLR229c                     --------------------------------------------------
HsRhoCAAM21119                     --------------------------------------------------
CeRho-1CE25369                     --------------------------------------------------
AtRop4ARAC5AT1G75840               --------------------------------------------------
AtRop10ARAC8AT3G48040              -------------------------------------------------M
HsWrch-1AAK83340                   --------MPPQQGDPAFPDRCEAPPVPPRRERGGRGGRGPGEPGGRGRA
MmTTFXP_359315                     --------------------------------------------------
ScGtr1RagYML121W                   --------------------------------------------------
Tb11.02.0820                       MLICYSLLFDRFVCLFVCFSLFPVSSFVFPFPILLFISEIIFELLLANPV
TbRAB1B                            ------------------------------MRVETLRS------------
TbRAB23                            ------------------------------MLKRGGLN------------
TbRABX3                            --------------------------------------------------
Tb05.26C7.80                       ------------------------------MGLFSWFWDMLS-------F
```

```
TbRAB28                          ------------------------------MSSDSSDSE----------
Tb11.02.3850                     --------------------------------------------------
Tb11.52.0014                     ------------------------------MPSHTTSDGSP------TTG
Tb10.70.0590                     ------------------------------MNLRGDGS---------AQK
Tb03.5L5.790                     --------------------------------------------------
TbARF2like_TRYP10.0.000567_68    ------------------------------MLPSSPLG------------
Tb07.6C8.230                     --------------------MDHIDLAEEREMGNGDPIMVLNVSVPYSAN
Tb10.6k15.1520                   -------------------------------------------------M
Tb07.29D18.100                   ERQILGGLHADWRTQMKRSGSILNDITPALPDTKRTEEQRRRVAGWRPVV
HsnucleosteminNP_996562          --------------MTCHKRYKIQKKVREHHRKLRKEAKKRGHKKPRKDP
Tb11.02.0240                     ----MGGQSKKHGKGGGGGGGHGRNCHPQQRKKLTKDPGVPDLKKVAQNL


TbARF1C                          SLVGKQEVRILMVGLDAAGKTTILYKLKLGE--IVTT-------------
TbARF1B                          SLVGKQEVRILMVGLDAAGKTTILYKLKLGE--IVTT-------------
TbARF1D                          SLVGKQEVRILMVGVDAAGKTTILYKLKLGE--IVTT-------------
TbARF1A                          SLVGKQEVRILMVGLDAAGKTTILYKLKLGE--IVTT-------------
TbARF1A_Tb09.211.4460            SLVGKQEVRILMVGLDAAGKTTILYKLKLGE--IVTT-------------
HsARF1NM_001658                  GLFGKKEMRILMVGLDAAGKTTILYKLKLGE--IVTT-------------
ScARF1YDL192w                    NLFGNKEMRILMVGLDGAGKTTVLYKLKLGE--VITT-------------
TbARF1E                          GLFSKKDATILMVGLDAAGKTTILWKLKLNE--VQQT-------------
TbARL3_embl.27                   RPFSRRTRRILMLGLDNAGKTRLLRRICEEE--VSDT-------------
TbARL1_167.t00109                ILPADRKIRVLVLGLDNAGKTSILYRLQLGN--VTST-------------
TbARL1B_09.160.5300              VFNPNRHYKLLILGLNNAGKTSILYHLQLGH--SIAT-------------
TbARL3B_92.m00269                RAKRDNEPRVLIVGLDNAGKTTVLNALGEDE--VPVEGKVSHAA------
TbARL3C_06.4F7.880               RAKRDNEPRVLIVGLDNAGKTTVLNALGEDE--VPVEGKVSHAA------
TbARL6_10.70.3000|08.5H5.790     MGQSKTKLQVVMCGLDNSGKTTIINQVKPAQ--SSSK-------------
TbRABX1                          -----YIFKIIVIGDSGVGKSSLTVRLSEDV--FYKDYAS----------
TbRABX2                          ------AYKIIVIGDVGVGKSNISSRFCDSI--YYDDIVP----------
TbRAB21                          ------SYKVVLLGEGRVGKTSLISRFVNDT--FDAQQRS----------
TbRAB1A                          -----HLFKLLLIGDSGVGKSCLLLRFADDS--YTESYIS----------
HsRab1ANM_004161                 -----YLFKLLLIGDSGVGKSCLLLRFADDT--YTESYIS----------
ScYpt1YFL038c                    -----YLFKLLLIGNSGVGKSCLLLRFSDDT--YTNDYIS----------
TbRAB18                          -----SPVKIVLLGESGVGKSSLLLSFSLGT--FDGDVRS----------
TbRAB2                           -----YVFKYIIIGDSGVGKSCLLLQFTDKR--FEPLHDL----------
TbRAB4                           -----QLMKLIVVGDSGTGKSSLLHRFVEDT--FSEERAQ----------
TbRAB11                          -----LTFKVVIVGDSGVGKSNLMTRYTADE--FSQDTPA----------
TbRAB6                           ETAPVVKHKIVLLGDQAVGKTSLITRFMYDT--FDQQYQA----------
TbRAB5B                          ------KYKIVLLGDSGVGKSSLVQRLAKNE--WCDNQNS----------
TbRAB5A                          -----ITARTVLLGESAVGKSSIALRFARNE--FSSNQET----------
TbRAB7                           ------LLKIIILGDSGVGKTALVHQYVNKN--FDNRYKA----------
Tb08.6H23.400                    KDEQMFVFKIAVVGDYNVGKTSIVKRLLDIP--YENISPLPQAENKQTRA
Tb04.1D20.300                    DEEQMFVFKVAIVGDYSVGKTSMVKRLLDIP--YEKIASSSSAPQ-----
HsNRasAAQ94397                   ------EYKLVVVGAGGVGKSALTIQLIQNH--FVDEYDP----------
ScRas1YOR101w                    ------EYKIVVVGGGGVGKSALTIQFIQSY--FVDEYDP----------
CeRas1C44C11.1                   ---QNAVLRIVVVGGGGVGKSALTIQFIQRY--FVQDYDP----------
HsRalANM_005402                  ----LALHKVIMVGSGGVGKSALTLQFMYDE--FVEDYEP----------
HsRanNM_006325                   -----VQFKLVLVGDGGTGKTTFVKRHLTGE--FEKKYVA----------
TbRAN                            -----ATFKLVLVGDGGTGKTTFVKRHLTGE--FEKRYVA----------
HsRac2CAB45265                   --MQAI--KCVVVGDGAVGKTCLLISYTTNA--FPGEYIP----------
CeRac1C09G12.8                   --MQAI--KCVVVGDGAVGKTCLLISYTTNA--FPGEYIP----------
HsCdc42NM_001791                 --MQTI--KCVVVGDGAVGKTCLLISYTTNK--FPSEYVP----------
CeCdc42R07G3.1                   --MQTI--KCVVVGDGAVGKTCLLISYTTNK--FPSEYVP----------
ScCdc42YLR229c                   --MQTL--KCVVVGDGAVGKTCLLISYTTNQ--FPADYVP----------
HsRhoCAAM21119                   --MAAIRKKLVIVGDGACGKTCLLIVFSKDQ--FPEVYVP----------
CeRho-1CE25369                   --MAAIRKKLVIVGDGACGKTCLLIVFSKDQ--FPDVYVP----------
AtRop4ARAC5AT1G75840             -MSASRFIKCVTVGDGAVGKTCMLISYTSNT--FPTDYVP----------
AtRop10ARAC8AT3G48040            ASSASKFIKCVTVGDGAVGKTCMLICYTSNK--FPTDYIP----------
HsWrch-1AAK83340                 GGAEGRGVKCVLVGDGAVGKTSLVVSYTTNG--YPTEYIP----------
MmTTFXP_359315                   --MLSS-IKCVLVGDSAVGKTSLLVRFTSET--FPEAYKP----------
ScGtr1RagYML121W                 -MSSNNRKKLLLMGRSGSGKSSMRSIIFSNY--SAFDTRR----------
```

```
Tb11.02.0820                        KLMHEQIQKLLLMGPARAGKTSMRSIIFDNY--LPRDTLR----------
TbRAB1B                             --TPDYIFKIILVGDSYVGKTRFLKNLVGAIG-FGDQCVT----------
TbRAB23                             ------GVKVIVIGDENVGKSSLLRRFVTGT--FSNQYNK----------
TbRABX3                             -MTNGNSVKVILLGDSAVGKSKLVERFLMQRY-VPVQMS-----------
Tb05.26C7.80                        LGFTNKTGKILFLGLDNAGKTTLLGKLATDQV-HVHR-------------
TbRAB28                             --KRLLAYKVIVVGDGAVGKTSLIRRYCVAD--YGSNYKQ----------
Tb11.02.3850                        ----MRNINLVVLGDGGVGKSSLIIQYVRNR--FVVKYEA----------
Tb11.52.0014                        GDKSGPRIKIVSLGSVGVGKSCLIKQYCEGR--FVSKYIP----------
Tb10.70.0590                        YASVPTLYNVVVLGCERVGKSTFIDQVMKGT--FRSDYVP----------
Tb03.5L5.790                        --MVNLRLQVAVVGAPTVGKTAFVQMLHSNGTTFPKNYLM----------
TbARF2like_TRYP10.0.000567_68       AKDKLTKITIGTFGIENAGKTTIISALGGNIEKNPMP-------------
Tb07.6C8.230                        SSDRKSNVSSPLLSKCASKQTSGVMWLTKPT--LDPSCIRLCPLR-----
Tb10.6k15.1520                      TSSFLAHPKVLLMGLRKSGKTSIQKVVFEGMQPHHCVDLT----------
Tb07.29D18.100                      KLLGDQRLRIAIVGRMNSGKSSLFNLLRLEPTVPGRSNVVR---------
HsnucleosteminNP_996562             GVPNSAPFKEALLREAELRKQRLEELKQQQKLDRQKELEKKR--------
Tb11.02.0240                        TRTARNRNRSLFSIPALRGSNKIAAASGEKEPQEQGNEEAR---------
                                                          .

TbARF1C                             -------------------------------------------------
TbARF1B                             -------------------------------------------------
TbARF1D                             -------------------------------------------------
TbARF1A                             -------------------------------------------------
TbARF1A_Tb09.211.4460               -------------------------------------------------
HsARF1NM_001658                     -------------------------------------------------
ScARF1YDL192w                       -------------------------------------------------
TbARF1E                             -------------------------------------------------
TbARL3_embl.27                      -------------------------------------------------
TbARL1_167.t00109                   -------------------------------------------------
TbARL1B_09.160.5300                 -------------------------------------------------
TbARL3B_92.m00269                   -------------------------------------------------
TbARL3C_06.4F7.880                  -------------------------------------------------
TbARL6_10.70.3000|08.5H5.790        -------------------------------------------------
TbRABX1                             -------------------------------------------------
TbRABX2                             -------------------------------------------------
TbRAB21                             -------------------------------------------------
TbRAB1A                             -------------------------------------------------
HsRab1ANM_004161                    -------------------------------------------------
ScYpt1YFL038c                       -------------------------------------------------
TbRAB18                             -------------------------------------------------
TbRAB2                              -------------------------------------------------
TbRAB4                              -------------------------------------------------
TbRAB11                             -------------------------------------------------
TbRAB6                              -------------------------------------------------
TbRAB5B                             -------------------------------------------------
TbRAB5A                             -------------------------------------------------
TbRAB7                              -------------------------------------------------
Tb08.6H23.400                       NGAEKGDDKSGNSANVSAEGANKYEAEVNSAQNGANTRTDCNDKADVALM
Tb04.1D20.300                       ---PPGSSREGE-------------------------------------V
HsNRasAAQ94397                      -------------------------------------------------
ScRas1YOR101w                       -------------------------------------------------
CeRas1C44C11.1                      -------------------------------------------------
HsRalANM_005402                     -------------------------------------------------
HsRanNM_006325                      -------------------------------------------------
TbRAN                               -------------------------------------------------
HsRac2CAB45265                      -------------------------------------------------
CeRac1C09G12.8                      -------------------------------------------------
HsCdc42NM_001791                    -------------------------------------------------
CeCdc42R07G3.1                      -------------------------------------------------
ScCdc42YLR229c                      -------------------------------------------------
HsRhoCAAM21119                      -------------------------------------------------
CeRho-1CE25369                      -------------------------------------------------
```

```
AtRop4ARAC5AT1G75840              --------------------------------------------------
AtRop10ARAC8AT3G48040             --------------------------------------------------
HsWrch-1AAK83340                  --------------------------------------------------
MmTTFXP_359315                    --------------------------------------------------
ScGtr1RagYML121W                  --------------------------------------------------
Tb11.02.0820                      --------------------------------------------------
TbRAB1B                           --------------------------------------------------
TbRAB23                           --------------------------------------------------
TbRABX3                           --------------------------------------------------
Tb05.26C7.80                      --------------------------------------------------
TbRAB28                           --------------------------------------------------
Tb11.02.3850                      --------------------------------------------------
Tb11.52.0014                      --------------------------------------------------
Tb10.70.0590                      --------------------------------------------------
Tb03.5L5.790                      --------------------------------------------------
TbARF2like_TRYP10.0.000567_68     --------------------------------------------------
Tb07.6C8.230                      --------------------------------------------------
Tb10.6k15.1520                    --------------------------------------------------
Tb07.29D18.100                    --------------------------------------------------
HsnucleosteminNP_996562           --------------------------------------------------
Tb11.02.0240                      --------------------------------------------------


TbARF1C                           ------------IPTIGFNVETVEYKN-----------------LKFTM
TbARF1B                           ------------IPTIGFNVETVEYKN-----------------LKFTM
TbARF1D                           ------------IPTIGFNVETVEYKN-----------------LKFTM
TbARF1A                           ------------IPTIGFNVETVEYKN-----------------LKFTM
TbARF1A_Tb09.211.4460             ------------IPTIGFNVETVEYKN-----------------LKFTM
HsARF1NM_001658                   ------------IPTIGFNVETVEYKN-----------------ISFTV
ScARF1YDL192w                     ------------IPTIGFNVETVQYKN-----------------ISFTV
TbARF1E                           ------------VPTLGFNVQTVEYRN-----------------VKFHL
TbARL3_embl.27                    ------------FPTQGFNIQNITADE-----------------LKFVV
TbARL1_167.t00109                 ------------VPTVGFNLETLTHKN-----------------ITFEV
TbARL1B_09.160.5300               ------------QPTLGGNVEQLSISHGS-----------NNNKIEVSC
TbARL3B_92.m00269                 -----------PEGPTQGFNIKTLTRGN-----------------KRAKL
TbARL3C_06.4F7.880                -----------PEGPTQGFNIKTLTRGN-----------------KRAKL
TbARL6_10.70.3000|08.5H5.790      -----------HITATVGYNVETFEKGR-----------------VAFTV
TbRABX1                           ------------TIAIDFRMHQMTYMDK------------RVR---LQI
TbRABX2                           ------------TIGVDFKYCHTTTLEK------------HARTILLQI
TbRAB21                           ------------TTQASMYSSVNVPLLN------------SDKTVNLNV
TbRAB1A                           ------------TIGVDFKIRTLDIDG---------------KVIKLQI
HsRab1ANM_004161                  ------------TIGVDFKIRTIELDG---------------KTIKLQI
ScYpt1YFL038c                     ------------TIGVDFKIKTVELDG---------------KTVKLQI
TbRAB18                           ------------TIGIDFRTKDVSVVDSM----------GRQKKLKLHL
TbRAB2                            ------------TIGVEFGARVVTIKE---------------KNIKLQI
TbRAB4                            ------------TIGVEFGSKIIELSG---------------RRIKLQI
TbRAB11                           ------------TIGVEFMTKSIKIEG---------------RDAKVQI
TbRAB6                            ------------TIGIDFFSKTLHINN---------------RATRLHV
TbRAB5B                           ------------TGRRVFLRYVCTVGDTA---------------VNFDI
TbRAB5A                           ------------TIGAAFLSRSVTVSATLQSGGGGAVANAASGTIKFEI
TbRAB7                            ------------TIGADFLTRDVEIDGKL---------------VTLQI
Tb08.6H23.400                     TKNVLEPLPATTPTVGTDFFSRVVRSVRPG-------------QHVRLQF
Tb04.1D20.300                     VSNSLQPLHTTTPTVGTDFFSRVVRNVRAG-------------QHVRLQL
HsNRasAAQ94397                    ------------TIEDSYRKQVVIDGET----------------CLLDI
ScRas1YOR101w                     ------------TIEDSYRKQVVIDDKV----------------SILDI
CeRas1C44C11.1                    ------------TIEDSYTKQCFVDEDL----------------CKLEI
HsRalANM_005402                   ------------TKADSYRKKVVLDGEE----------------VQIDI
HsRanNM_006325                    ------------TLGVEVHPLVFHTNRGP---------------IKFNV
TbRAN                             ------------TVGVDVHPLTFHTNRGK---------------ICFNC
HsRac2CAB45265                    ------------TVFDNYSANVMVDSKP----------------VNLGL
CeRac1C09G12.8                    ------------TVFDNYSANVMVDGRP----------------INLGL
```

```
HsCdc42NM_001791                    ------------TVFDNYAVTVMIGGEP----------------YTLGL
CeCdc42R07G3.1                      ------------TVFDNYAVTVMIGGEP----------------YTLGL
ScCdc42YLR229c                      ------------TVFDNYAVTVMIGDEP----------------YTLGL
HsRhoCAAM21119                      ------------TVFENYIADIEVDGKQ----------------VELAL
CeRho-1CE25369                      ------------TVFENYVADIEVDGKQ----------------VELAL
AtRop4ARAC5AT1G75840                ------------TVFDNFSANVVVDGNT----------------VNLGL
AtRop10ARAC8AT3G48040               ------------TVFDNFSVNVVVEGIT----------------VNLGL
HsWrch-1AAK83340                    ------------TAFDNFSAVVSVDGRP----------------VRLQL
MmTTFXP_359315                      ------------TVYENTGVDVFMDGIQ----------------ISLGL
ScGtr1RagYML121W                    ------------LGATIDVEHSHLRFLGN----------------MTLNL
Tb11.02.0820                        ------------LAITISHEESRVRLLNN----------------MYVNL
TbRAB1B                             ------------TLSVDVVNHYVIVDGKT---------------VQVLM
TbRAB23                             ------------TVGVEYMEKSVCLRQRS-------------TTVNSFL
TbRABX3                             ------------TYALTLFHYDFVTEDDE--------------AIDVDI
Tb05.26C7.80                        --------------PTFHPNVEELTLGG-----------------IKLKT
TbRAB28                             ------------TIGLDFYSKEVLLPGKQ--------------DVKMEI
Tb11.02.3850                        ------------TIEDVYQKAVEVDAQP----------------TVLTI
Tb11.52.0014                        ------------TIGIDYGVKRVDVRVPAHLAP------SGKISTRVNF
Tb10.70.0590                        ------------TTLETFIHRTTVDGRN----------------YVLHL
Tb03.5L5.790                        ------------TLGCDFIVKEVPVDDDN--------------TVEMII
TbARF2like_TRYP10.0.000567_68       ---------------TVGFTPTRFQTDR-----------------CDLCI
Tb07.6C8.230                        ------------RWVPDTQVSTCMAHGCN---------------VAFSM
Tb10.6k15.1520                      --------------TTVQPEKSTVCSYDF----------------VNFEV
Tb07.29D18.100                      --------------DFDGITRDSVEGQAQLEG-------------MHFTI
HsnucleosteminNP_996562             -----------KLETNPDIKPSNVEPMEKEFG------------LCKTEN
Tb11.02.0240                        ------------VAAERRAMTLLAVQCAEKVHHYEVPQQWIGESENIND


TbARF1C                             WDVGGQ--------------DVLRPLWRHYYQNTNGIIFVVDSNDK----
TbARF1B                             WDVGGQ--------------DVLRPLWRHYYQNTNGIIFVVDSNDK----
TbARF1D                             WDVGGQ--------------DVLRPLWRHYYQNTNGIIFVVDSNDK----
TbARF1A                             WDVGGQ--------------DVLRPLWRHYYQNTNGIIFVVDSNDK----
TbARF1A_Tb09.211.4460               WDVGGQ--------------DVLRPLWRHYYQNTNGIIFVVDSNDK----
HsARF1NM_001658                     WDVGGQ--------------DKIRPLWRHYFQNTQGLIFVVDSNDR----
ScARF1YDL192w                       WDVGGQ--------------DRIRSLWRHYYRNTEGVIFVVDSNDR----
TbARF1E                             WDVGGQ--------------KLLRSLWKHYYEGANAIIFVVDSNDR----
TbARL3_embl.27                      WDVGGQ--------------KSLRSYWRHYFDHTDALVFVIDSADM----
TbARL1_167.t00109                   WDLGGQ--------------ANIRPFWRCYFTDTDAVIYVVDSTDK----
TbARL1B_09.160.5300                 WDLGGQ--------------EQLRDSWRLYYDQTDAVIFVVDAADP----
TbARL3B_92.m00269                   CDLGGQ--------------RALRDYWQDYYSNTDCIMYVVDSSDH----
TbARL3C_06.4F7.880                  CDLGGQ--------------RALRDYWQDYYSNTDCIMYVVDSSDH----
TbARL6_10.70.3000|08.5H5.790        FDMGGA--------------KKFRGLWETYYDNIDAVIFVVDSSDH----
TbRABX1                             WDTAGQ--------------ERFQSVATAFYRGANGVMLCFDLTHR----
TbRABX2                             WDTSGQ--------------DRFVSLTTAYYRNCHGALICFDLTNR----
TbRAB21                             WDTAGQ--------------ERFHALGPIYYRNANGAILVYDVTDA----
TbRAB1A                             WDTAGQ--------------ERFRTITSSYYRGAHGIIIVYDTTDM----
HsRab1ANM_004161                    WDTAGQ--------------ERFRTITSSYYRGAHGIIVVYDVTDQ----
ScYpt1YFL038c                       WDTAGQ--------------ERFRTITSSYYRGSHGIIIVYDVTDQ----
TbRAB18                             WDTAGQ--------------ERFRTLTSSYYRGAHAVVLVYDVNEP----
TbRAB2                              WDTAGQ--------------ESFRSITRSYYRGACGALLVYDVTRR----
TbRAB4                              WDTAGQ--------------ERYKSVTRSYYRGAVGCLIVYDITER----
TbRAB11                             WDTAGQ--------------ERFRAISRSIYHGAKGAMLVYDITNQ----
TbRAB6                              WDTAGQ--------------ERFRSLIPSYIRNSAATVVVYDITSR----
TbRAB5B                             WDTAGQ--------------ERYKSLASMYYRGAAAALVVYEIPSW----
TbRAB5A                             WDTAGQ--------------ERYRSLAPIYYRGACGALVVYDITSA----
TbRAB7                              WDTAGQ--------------ERFQSLGSAFYRGADACVLVFDLTDS----
Tb08.6H23.400                       WDTAGL--------------ERYASVHDSTFRRASALIVVFDVRNR----
Tb04.1D20.300                       WDTAGL--------------ERYASVDKSTFRCASAAIVVFDVKNR----
HsNRasAAQ94397                      LDTAGQ--------------EEYSAMRDQYMRTGEGFLCVFAINNS----
ScRas1YOR101w                       LDTAGQ--------------EEYSAMREQYMRTGEGFLLVYSVTSR----
CeRas1C44C11.1                      LDTAGQ--------------EEFSTMREQYLRTGSGFLIVFAVTDR----
```

```
HsRalANM_005402                  LDTAGQ-------------EDYAAIRDNYFRSGEGFLCVFSITEM----
HsRanNM_006325                   WDTAGQ-------------EKFGGLRDGYYIQAQCAIIMFDVTSR----
TbRAN                            WDTAGQ-------------EKFGGLRDGYYIEGQCAIIMFDVTSR----
HsRac2CAB45265                   WDTAGQ-------------EDYDRLRPLSYPQTDVFLICFSLVSP----
CeRac1C09G12.8                   WDTAGQ-------------EDYDRLRPLSYPQTDVFLVCFALNNP----
HsCdc42NM_001791                 FDTAGQ-------------EDYDRLRPLSYPQTDVFLVCFSVVSP----
CeCdc42R07G3.1                   FDTAGQ-------------EDYDRLRPLSYPQTDVFLVCFSVVAP----
ScCdc42YLR229c                   FDTAGQ-------------EDYDRLRPLSYPSTDVFLVCFSVISP----
HsRhoCAAM21119                   WDTAGQ-------------EDYDRLRPLSYPDTDVILMCFSIDSP----
CeRho-1CE25369                   WDTAGQ-------------EDYDRLRPLSYPDTDVILMCFSIDSP----
AtRop4ARAC5AT1G75840             WDTAGQ-------------EDYNRLRPLSYRGADVFILAFSLISK----
AtRop10ARAC8AT3G48040            WDTAGQ-------------EDYNRLRPLSYRGADVFVLAFSLISR----
HsWrch-1AAK83340                 CDTAGQ-------------DEFDKLRPLCYTNTDIFLLCFSVVSP----
MmTTFXP_359315                   WDTAGN-------------DAFRSIRPLSYQQADVVLMCYSVANH----
ScGtr1RagYML121W                 WDCGGQDVFM---------ENYFTKQKDHIFQMVQVLIHVFDVEST----
Tb11.02.0820                     WDCGGQQQYV---------AEYLNRQRECIFRNVGVLLFVFDISSMSREE
TbRAB1B                          YDTCGQ-------------ERFRAMTAQFYRDAHGAIMVYDTTQIG---
TbRAB23                          WDTAGE-------------TVSSVKDIYYLDAAVAILVFSTDSS----
TbRABX3                          WDTAGQ-------------ERFSTMHPAYYHEAHACILVFDVTRK----
Tb05.26C7.80                     IDMGGH-------------LEARRLWKDYFTKVDGVVFIVDAANP----
TbRAB28                          WDIGGQ-------------QIGGTMIDNYIMGAHAIFFVYDVTNK----
Tb11.02.3850                     VDTSGQ-------------DVFGGMRYKYIRKCHGVILVYSVIDA----
Tb11.52.0014                     WDMSGC-------------EEYLEIRNEFYRATEGVLLVYDVTDA----
Tb10.70.0590                     CDSSGS-------------EAFVRHRLLYLARADGVLLFYSTTDK----
Tb03.5L5.790                     FDVSGQ-------------REYEPMVSSYLQNTAVFIVMYDVSNK----
TbARF2like_TRYP10.0.000567_68    FDLGGG-------------ANFRGIWVHYFHDCHGFMFVIDSAADD---
Tb07.6C8.230                     FNRRHHCRVCGRVFCSACCSETVNALVQSALEVQSNPIEACGGVDKTSLP
Tb10.6k15.1520                   WDFPGQTDPFDLN-------NTVHYDVGVLLENCGAIVFVMDCGELID--
Tb07.29D18.100                   IDTPGMVQG------------RMVEEAFRTVETADAAIFVTAVDEDIMP-
HsnucleosteminNP_996562          KAKSGKQNSK----------KLYCQELKKVIEASDVVLEVLDARDPLG--
Tb11.02.0240                     MDDDVERRGVDR------SLRRFYKEFQKVVENSDVLLQVVDARDPLG-C
                                                                          .

TbARF1C                          ----------ERVGKARQELEKMLS--------EDELRNAV---------
TbARF1B                          ----------ERVGKARQELEKMLS--------EDELRNAV---------
TbARF1D                          ----------ERVGKARQELEKMLS--------EDELRNAV---------
TbARF1A                          ----------ERVGKARQELEKMLS--------EDELRNAV---------
TbARF1A_Tb09.211.4460            ----------ERVGKARQELEKMLS--------EDELRNAV---------
HsARF1NM_001658                  ----------ERVNEAREELMRMLA--------EDELRDAV---------
ScARF1YDL192w                    ----------SRIGEAREVMQRMLN--------EDELRNAA---------
TbARF1E                          ----------DRVMEVRSELTKLLG--------EPLLSSAT---------
TbARL3_embl.27                   ----------ERIEEARTELHYILE--------EEKLVGVP---------
TbARL1_167.t00109                ----------DRMGVAKHELCNLLD--------EDELRGSL---------
TbARL1B_09.160.5300              ----------SRFPAARSVLHKILAN-------EPQLRQAV---------
TbARL3B_92.m00269                ----------RRLEESHAAFVDVLK----------GIEGAP---------
TbARL3C_06.4F7.880               ----------RRLEESHAAFVDVLK----------GIEGAP---------
TbARL6_10.70.3000|08.5H5.790     ----------LRLCVVKSEIQAMLKH-------EDIRRELPG---GGRVP
TbRABX1                          ----------PSFLHL-EHWMERVR------------QQS-----LPGIP
TbRABX2                          ----------SSFEGI-DAWFERLR------------SHC-----PVLPP
TbRAB21                          ----------DTLEKV-RLWIRELR------------AVV-----GDQIQ
TbRAB1A                          ----------ESFNNV-KTWLSEID------------KFA-----SENVN
HsRab1ANM_004161                 ----------ESFNNV-KQWLQEID------------RYA-----SENVN
ScYpt1YFL038c                    ----------ESFNGV-KMWLQEID------------RYA-----TSTVL
TbRAB18                          ----------QTFHAL-RKWIDEAD------------AFCRLDGVEEAVV
TbRAB2                           ----------DTFTHL-QTWLEDAR------------SNA-----NTAIV
TbRAB4                           ----------TSYESV-PQWLNDVR------------QLA-----GPDVV
TbRAB11                          ----------TSFDSI-STWLQELR------------AFV-----PATCS
TbRAB6                           ----------SSFLST-FKWIHEVR------------AAR-----GDDVI
TbRAB5B                          ----------ETFERA-KHWVRELA------------TNS------PETI
TbRAB5A                          ----------ESLKKA-QMWMRELR------------ANAD-----PTLL
TbRAB7                           ----------ESFSHI-NSWLEEFR------------AQA------GQRE
```

```
Tb08.6H23.400                          ----------ESFAHV-TSQHLKRA-----------MQYN--PDISGRH
Tb04.1D20.300                          ----------ESFAHV-TSQHLDLV-----------MRYN--PDISGRH
HsNRasAAQ94397                         ----------KSFADI-NLYREQIK-----------RVKD----SDDVP
ScRas1YOR101w                          ----------NSFDEL-LSYYQQIQ-----------RVKD----SDYIP
CeRas1C44C11.1                         ----------NSFEEV-KKLHELIC-----------RIKD----RDDFP
HsRalANM_005402                        ----------ESFAAT-ADFREQIL-----------RVKE----DENVP
HsRanNM_006325                         ----------VTYKNV-PNWHRDLV-----------RVC------ENIP
TbRAN                                  ----------NTYKNV-PNWHRDIT-----------RVC------DNIP
HsRac2CAB45265                         ----------ASYENVRAKWFPEVR-----------HHCP------STP
CeRac1C09G12.8                         ----------ASFENVRAKWYPEVS-----------HHCP------NTP
HsCdc42NM_001791                       ----------SSFENVKEKWVPEIT-----------HHCP------KTP
CeCdc42R07G3.1                         ----------ASFENVREKWVPEIS-----------HHCS------KTP
ScCdc42YLR229c                         ----------PSFENVKEKWFPEVH-----------HHCP------GVP
HsRhoCAAM21119                         ----------DSLENIPEKWTPEVK-----------HFCP------NVP
CeRho-1CE25369                         ----------DSLENIPEKWTPEVR-----------HFCP------NVP
AtRop4ARAC5AT1G75840                   ----------ASYENVAKKWIPELR-----------HYAP------GVP
AtRop10ARAC8AT3G48040                  ----------ASYENVFKKWIPELQ-----------HFAP------GVP
HsWrch-1AAK83340                       ----------SSFQNVSEKWVPEIR-----------CHCP------KAP
MmTTFXP_359315                         ----------NSFLNLKNKWISEIR-----------SNLP------CTP
ScGtr1RagYML121W                       ----------EVLKD-IEIFAKALK-----------QLRK---YSPDAK
Tb11.02.0820                           SDVFGGKTSEQNLRDTFQYFREAVQ-----------HVRT---YSPQAK
TbRAB1B                                -----------SFDNI-EVWFSQLN-----------SFG-----CENTS
TbRAB23                                ----------ESFARI-EMWKRCVE-----------RVCG------SIP
TbRABX3                                ----------ATYKNL-EKWLGELR-----------NYR------EHIP
Tb05.26C7.80                           ----------ERFQEAKQELDMLLQ----------TEELAK-------TP
TbRAB28                                ----------DSFKNI-EDWHSCVRDSL-A---KHARETAEEGAAAVEPL
Tb11.02.3850                           ----------ESFSHIKAIHTQLCR-----------ARGS-----PSIP
Tb11.52.0014                           ----------ESFFAL-NQWVKEMEAHVNT---KGNDTYVARVDASVPCK
Tb10.70.0590                           ----------ESLASV-VGWVKELR-----------EARHNIGVKAAMP
Tb03.5L5.790                           ----------VTFEAC-ARWVNQVR-----------TNSK------ESV
TbARF2like_TRYP10.0.000567_68          ----------AVVEESLNALRTVAQH----------KHVR------GKP
Tb07.6C8.230                           SGRVSGTDIANGEDNISQQQQQGQVQFMNP---TTVAAYRVCFACHYEVQ
Tb10.6k15.1520                         ----------DSHARLVETVCAAYDRDPEL---SVEVFIHKVDKLSEDHQ
Tb07.29D18.100                         ----------EELSLMQYLHLKHMPVVLLAN-KMDLIQEEEEEAVLDRYN
HsnucleosteminNP_996562                --CRCPQVEEAIVQSGQKKLVLILNKSDLVP-KENLESWLNYLKKELPTV
Tb11.02.0240                           RLNQLERTIRSQFGEDKKKMVMVLNKADLLPSKETVDAWVHFFEEHEGIM


TbARF1C                                LLVFAN----------KQDLPNAMST--------TEVTEKLGLQS-----
TbARF1B                                LLVFAN----------KQDLPNAMST--------TEVTEKLGLQS-----
TbARF1D                                LLVFAN----------KQDLPNAMST--------TEVTEKLGLQS-----
TbARF1A                                LLVFAN----------KQDLPNAMST--------TEVTEKLGLQS-----
TbARF1A_Tb09.211.4460                  LLVFAN----------KQDLPNAMST--------TEVTEKLGLQS-----
HsARF1NM_001658                        LLVFAN----------KQDLPNAMNA--------AEITDKLGLHS-----
ScARF1YDL192w                          WLVFAN----------KQDLPEAMSA--------AEITEKLGLHS-----
TbARF1E                                LLVFCN----------KQDLPNRLTP--------GELVDKLGFREQG---
TbARL3_embl.27                         LLLFAN----------KQDIPEAASQ--------EEVMSSLNLAD-----
TbARL1_167.t00109                      LLIFAN----------KQDVVGAVSE--------AGVAEQLGVGA-----
TbARL1B_09.160.5300                    LLVLAN----------KQDMEGAVSP--------ADLIESLGLAA-----
TbARL3B_92.m00269                      VLVFAN----------KQDLATAKDA--------QAIAECLHLHD-----
TbARL3C_06.4F7.880                     VLVFAN----------KQDLATAKDA--------QAIAECLHLHD-----
TbARL6_10.70.3000|08.5H5.790           FLFFAN----------KMDAAGAKTA--------AELVEILDLTT-----
TbRABX1                                CLLVGC----------KSDEARTS----------------RQVSKE----
TbRABX2                                LILVGC----------KLDLVECSELHKEGTSL----GICRQVEKS----
TbRAB21                                LVVCAN----------KSDLEQER-----------------EVSEE----
TbRAB1A                                KLLVGN----------KCDLV-----------------TKKAVDT-----
HsRab1ANM_004161                       KLLVGN----------KCDLT-----------------TKKVVDY-----
ScYpt1YFL038c                          KLLVGN----------KCDLK-----------------DKRVVEY-----
TbRAB18                                YLLVGNKID-------KCEVGGGA--------------TGMAVPK-----
TbRAB2                                 IMLIGN----------KCDLE-----------------KKREVSR-----
TbRAB4                                 VMLIGN----------KSDMS-----------------KNRAVQH-----
```

```
TbRAB11                          IFLIGN----------KCDLE----------------HLRVIKK-----
TbRAB6                           IALVGN----------KCDVQ----------------EKREVSA-----
TbRAB5B                          VILVGN----------KSDLRGTS--------------GCVSSE------
TbRAB5A                          IILVGN----------KKDMESLR--------------QVSYE------
TbRAB7                           CVLIGN----------KSDLTERR--------------QVTSRTAEAWCE
Tb08.6H23.400                    IFIVGN----------KVDLVDNS--------------EPEDMDR-----
Tb04.1D20.300                    IFVVGN----------KVDLIDNT--------------EVEDMDR-----
HsNRasAAQ94397                   MVLVGN----------KCDLP----------------TRTVDT-----
ScRas1YOR101w                    VVVVGN----------KLDLEN----------------ERQVSY-----
CeRas1C44C11.1                   IILVGN----------KADLEN----------------ERHVAR-----
HsRalANM_005402                  FLLVGN----------KSDLED----------------KRQVSV-----
HsRanNM_006325                   IVLCGN----------KVDIKD----------------RKVKA-----
TbRAN                            IVLVGN----------KVDCAE----------------RQVKA-----
HsRac2CAB45265                   IILVGT----------KLDLRDDKDTIEKLKEKKLAPITYP---------
CeRac1C09G12.8                   IILVGT----------KADLREDRDTVERLRERRLQPVSQT---------
HsCdc42NM_001791                 FLLVGT----------QIDLRDDPSTIEKLAKNKQKPITPE---------
CeCdc42R07G3.1                   FLLVGT----------QVDLRDDPGMLEKLAKNKQKPVSTD---------
ScCdc42YLR229c                   CLVVGT----------QIDLRDDKVIIEKLQRQRLRPITSE---------
HsRhoCAAM21119                   IILVGN----------KKDLRQDEHTRRELAKMKQEPVRSE---------
CeRho-1CE25369                   IILVGN----------KRDLRSDPQTVRELAKMKQEPVKPE---------
AtRop4ARAC5AT1G75840             IILVGT----------KLDLRDDKQFFIDHPG--AVPITTN---------
AtRop10ARAC8AT3G48040            IVLVGT----------KMDLREDRHYLSDHPG--LSPVTTS---------
HsWrch-1AAK83340                 IILVGT----------QSDLREDVKVLIELDKCKEKPVPEE---------
MmTTFXP_359315                   VLVVAT----------QTDQRE-------VGPHRASCINAI---------
ScGtr1RagYML121W                 IFVLLH----------KMDLVQLDKREELFQIMMKNLSETSSEFGFP---
Tb11.02.0820                     VFVLLH----------KMDVIQQKLRSSIFESRKREILKEVENVGGSGG-
TbRAB1B                          KILVGN----------KCDLPE-----------------RRAVEIG----
TbRAB23                          MVLCQT----------KFDLAR----------------QAAVVA------
TbRABX3                          CIVACN----------KIDTDPSVVN-------------------------
Tb05.26C7.80                     FIILGN----------KIDLPRAVSED--------HLITAMGLTGLSTG-
TbRAB28                          IVLVGN----------KADLPN-----------------RQVSD-----
Tb11.02.3850                     CVLVGN----------KVDEVK-----------------HRAVSS-----
Tb11.52.0014                     VVVCAN----------KIDEVSEGGG-----------RKKRAVSS-----
Tb10.70.0590                     ILLVGTK---------RDDRRSRVVTMPEAEAVARSCLSALSLKMQHMNR
Tb03.5L5.790                     GILIAN----------KSDLSD-----------------KAEVTD-----
TbARF2like_TRYP10.0.000567_68    VLVLAN----------KKDLKSSR--------------GVEIVSEG----
Tb07.6C8.230                     LVVSRRDRNGEVRRKCRGELKMLQWSLLVRVLSYLTMEELLGVSLVSSDF
Tb10.6k15.1520                   ADLLTSLQR-------RVEAEARQRLNATAQLRLNFNLTSIYDHSVFQAF
Tb07.29D18.100                   SLGFGNAIPFSARRKSGLEMLAAVLEPLYHIHAMHKVENDWDIEDLAMQG
HsnucleosteminNP_996562          VFRASTKPKDKGKITKRVKAKKNAAPFR-----SEVCFGKEGLWKLLGGF
Tb11.02.0240                     CIPFAATAKGASG---HTYVANMFRRLRALATSEETGARKAIVVG-----


TbARF1C                          ------------------VRQRNWYIQGCCATTAQGLYEGLDWLSANIKK
TbARF1B                          ------------------VRQRNWYIQGCCATTAQGLYEGLDWLSANIKK
TbARF1D                          ------------------VRQRNWYIQGCCATTAQGLYEGLDWLSANIKK
TbARF1A                          ------------------VRQRNWYIQGCCATTAQGLYEGLDWLSVNIKK
TbARF1A_Tb09.211.4460            ------------------VRQRNWYIQGCCATTAQGLYEGLDWLSVNIKK
HsARF1NM_001658                  ------------------LRHRNWYIQATCATSGDGLYEGLDWLSNQLRN
ScARF1YDL192w                    ------------------IRNRPWFIQATCATSGEGLYEGLEWLSNSLKN
TbARF1E                          -----------AAGLGPLLRERQWYVQGCCAQTGEGLFEGLDWLCSHLPD
TbARL3_embl.27                   ------------------TINRPWHIELCSAETGEGLSSGLSWVVDTLKK
TbARL1_167.t00109                ------------------LSCRTWTIVKSSAKTGEGILEGMDWLCDKLRE
TbARL1B_09.160.5300              ------------------VNDRTWTLMGCSASKGDSLREAMSWIAQRIGD
TbARL3B_92.m00269                ------------------FRDRKWHIQGCSAKTGAGLEEGVAWILSTCAP
TbARL3C_06.4F7.880               ------------------FRDRKWHIQGCSAKTGAGLEEGVAWILSTCAP
TbARL6_10.70.3000|08.5H5.790     -----------------LMGDHPFVIFASNALKGTGVHEGFSWLQETASR
TbRABX1                          ------------EAMAWAKQHG-MSYIDTSAKEKENVQSAFQKIAQEIFE
TbRABX2                          ------------EADAWAKRHGCLCYFETSSRNNTNVSEAFQHLGTYIVN
TbRAB21                          ------------KGRRFAKDHG-AQHLSTSARTGMNVAEAFQTLATAIAS
TbRAB1A                          ------------QMAQEFADSLGIPFLETSAKESSNVETAFIEMAKNIKK
```

```
HsRab1ANM_004161                    ----------TTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKK
ScYpt1YFL038c                       ----------DVAKEFADANKMPFLETSALDSTNVEDAFLTMARQIKE
TbRAB18                             ----------EDAQQLARDRHMLLAFTSAKTRVGVEQAFDEVARSAYE
TbRAB2                              ----------EEGEAFARKHNLVFMETSAKTAQNVDDAFLKTAAMIYD
TbRAB4                              ----------NEASLFALENKLLHFETSASTGEFVTDAFLKVAKTGLS
TbRAB11                             ----------EVADRFARENGLSFLETSALEKTNVDKAFEWLAKSVYD
TbRAB6                              ----------DEAQKRADENRLIFVEVSAKTGTNVKSLFRKVAEAIPV
TbRAB5B                             ----------EAATYARELNLL-FSEASAKDGSGVSEVFMQIAQRLVA
TbRAB5A                             ----------DGAAVAQEEDVNGFFEVSAKENVNVEEVFAKLARLLLE
TbRAB7                              SLKNGEGGDASLGAAAGEETMGSIQYFEASAKANVGVEEAFLTVSKAALA
Tb08.6H23.400                       ------FVTQSELQSGLFSAFPDVHYYETSAQTNYGVWEVLHGLCQSLPD
Tb04.1D20.300                       ------LVTQHELQFELFSAFPDVQYYEVSTLTNYGLREMLHGLCHTLLN
HsNRasAAQ94397                      ----------KQAHELAKSYGIPFIETSAKTRQGVEDAFYTLVREIR-
ScRas1YOR101w                       ----------EDGLRLAKQLNAPFLETSAKQAINVDEAFYSLIRLVRD
CeRas1C44C11.1                      ----------HEAEELAHRLSIPYLECSAKIRKNVDEAFFDIVRLVR-
HsRalANM_005402                     ----------EEAKNRAEQWNVNYVETSAKTRANVDKVFFDLMREIR-
HsRanNM_006325                      ----------KSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIG
TbRAN                               ----------KMITFHRKKGLQYYDISAKSNYNFEKPFLWLAKKLAN
HsRac2CAB45265                      ----------QGLALAKEIDSVKYLECSALTQRGLKTVFDEAIRAVLC
CeRac1C09G12.8                      ----------QGYVMAKEIKAVKYLECSALTQRGLKQVFDEAIRAVLT
HsCdc42NM_001791                    ----------TAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALE
CeCdc42R07G3.1                      ----------VGEKLAKELKAVKYVECSALTQKGLKNVFDEAILAALD
ScCdc42YLR229c                      ----------QGSRLARELKAVKYVECSALTQRGLKNVFDEAIVAALE
HsRhoCAAM21119                      ----------EGRDMANRISAFGYLECSAKTKEGVREVFEMATRAGLQ
CeRho-1CE25369                      ----------QGRAIAEQIGAFAYLECSAKTKDGIREVFEKATQAALQ
AtRop4ARAC5AT1G75840                ----------QGEELKKLIGSPIYIECSSKTQQNVKAVFDAAIKVVLQ
AtRop10ARAC8AT3G48040               ----------QGEELRKHIGATYYIECSSKTQQNVKAVFDAAIKVVIK
HsWrch-1AAK83340                    ----------AAKLCAEEIKAASYIECSALTQKNLKEVFDAAIVAGIQ
MmTTFXP_359315                      ----------EGKRLAQDVRAKGYLECSALSNRGVQQVFECAVRTAVN
ScGtr1RagYML121W                    --NLIGFPTSIWDESLYKAWSQIVCSLIPNMSNHQSNLKKFKEIMNALEI
Tb11.02.0820                        --DVQFFATSIYDDTLYLAYSNIVRSLIPHCDVLTRAMEKLLVSCNASEV
TbRAB1B                             ----------RARALADKLGVPFIETSAMTGAGVAVAVEALVRMIMR
TbRAB23                             ----------EEVEKLAVKLQLPLFRVSTKDGFNVTQLFEYVAAMCVS
TbRABX3                             ----------KAFAFVEKHNLSLFYVSAADGTNVVQLLESAISEAVK
Tb05.26C7.80                        ----------KQNKVTDPAVRPLEVFMCSVVKKVGYGDAFRWISQYLQN
TbRAB28                             ----------ADHMKMAEMHRMESCVVSACSGERVNALFTQLAATLSG
Tb11.02.3850                        ----------EEASKFAAQFMYPLLEVTAKDHSMAAAVFETLVRSIRG
Tb11.52.0014                        ----------ETGRQWAKEHDYKYFETSACTGAGVEEALETLFKDVVA
Tb10.70.0590                        KKVVEAEG---FAKLVRDAISSTLPVVEVSALRTNEVLHALRIMILMISN
Tb03.5L5.790                        ----------RQGKDLANANKMKFYKISTLRGVGITEPIDEIARHYVD
TbARF2like_TRYP10.0.000567_68       ----------LLEELFGDVSLYHLVPSCGIEEDPELEKGVDWLLTKIQK
Tb07.6C8.230                        YFMSRDNVIWYRYNMTRCLREEELQRMLSTTLGSRNSTRRQRLPQKQLGE
Tb10.6k15.1520                      S---------SVVQKLMKLQIPYITELLQILNSNSNLDLSYLFLSRSKIF
Tb07.29D18.100                      D-------ESAMEEIRERNCSDRFIRIAIVGRTNSGKSSLVNRLVGFERN
HsnucleosteminNP_996562             QETCSKAIRVGVIGFPNVGKSSIINSLKQEQMCNVGVSMGLTRSMQVVPL
Tb11.02.0240                        ----------VIGYPNVGKSSVINALKRKHVVGVGNMPGFTTGNTEVEL


TbARF1C                             SM----------------------------------K----------
TbARF1B                             SM----------------------------------K----------
TbARF1D                             SM----------------------------------K----------
TbARF1A                             SM----------------------------------K----------
TbARF1A_Tb09.211.4460               SM----------------------------------K----------
HsARF1NM_001658                     QK-------------------------------------------------
ScARF1YDL192w                       ST-------------------------------------------------
TbARF1E                             TH-------------------------------------------------
TbARL3_embl.27                      RR----------------------------------PSLRPDGQV-----
TbARL1_167.t00109                   RG----------------------------------VVTADS--------
TbARL1B_09.160.5300                 RR----------------------------------PASS----------
TbARL3B_92.m00269                   -------------------------------------------------
TbARL3C_06.4F7.880                  -------------------------------------------------
```

```
TbARL6_10.70.3000|08.5H5.790      QS---------------------------------GKAGTKR-------
TbRABX1                           DM---------------------------------KERTGKGLSPS-----
TbRABX2                           NT---------------------------------TP-TVEG---------
TbRAB21                           SA---------------------------------GATGGGGSGGGGSNNN
TbRAB1A                           RV---------------------------------AAQGANSGATA-----
HsRab1ANM_004161                  RM---------------------------------GPGATAGGAEK-----
ScYpt1YFL038c                     SM---------------------------------SQQNLNETTQKK----
TbRAB18                           KM---------------------------------MSKSESR---------
TbRAB2                            NV---------------------------------ESGVLDAGAVS-----
TbRAB4                            -------------------------------------LGTDDND-----
TbRAB11                           HV---------------------------------VAPVDSAATGKRPPLN
TbRAB6                            VE---------------------------------ICEKGTVPLGKR----
TbRAB5B                           S----------------------------------NNNNTVHSG-----
TbRAB5A                           HG---------------------------------LGANSGPGSLS-----
TbRAB7                            KK---------------------------------ATAEEGVALPQ-----
Tb08.6H23.400                     NY---------------------------------AATTSGEAKEEKAAVT
Tb04.1D20.300                     DH---------------------------------TTCEEGNIKENGPTPA
HsNRasAAQ94397                    ---QY-----------------------------------RMKKLN-------
ScRas1YOR101w                     DGGKYNSMNRQLD-------NTNEIRDSELTSSATADREKKNNGSYVLDN
CeRas1C44C11.1                    ---KYQH----------------------------DERMPIHPHD-----
HsRalANM_005402                   ------------------------------------ARKMEDSKEKN----
HsRanNM_006325                    DP---------------------------------NLEFVAMPALAP----
TbRAN                             DP---------------------------------NLTLVEAPMLDP----
HsRac2CAB45265                    PQ---------------------------------PTRQQKRACSLL----
CeRac1C09G12.8                    P----------------------------------PQRAKKSKCTVL----
HsCdc42NM_001791                  P----------------------------------PEPKKSRRCVLL----
CeCdc42R07G3.1                    P----------------------------------PQQEKKKKCNIL----
ScCdc42YLR229c                    P----------------------------------PVIKKSKKCAILSCRH
HsRhoCAAM21119                    V----------------------------------RKNKRRRGCPIL----
CeRho-1CE25369                    Q----------------------------------KKKKKSK-CMIL----
AtRop4ARAC5AT1G75840              PP-KQK-----------------------------KKKKNKNRCVFL----
AtRop10ARAC8AT3G48040             PAVKQKE----------------------------KKKKQKPRSGCLSNIL
HsWrch-1AAK83340                  YSDTQQQ----------------------------PKKSKSRTPDKMKNLS
MmTTFXP_359315                    QARRRNR----------------------------RKLFSINECKIF----
ScGtr1RagYML121W                  ILFERTTFLVICS-------S---------NGENSNENHDSSDNNNVLLD
Tb11.02.0820                      ALYERGTFLCLTY-------VSKIDAAAADNGSLIAEDDGSNRGDRCSGT
TbRAB1B                           QQ---------------------------------PVPLASQWAGSKSG--
TbRAB23                           EAPGG------------------------------ECGRTGKLKSEADGNG
TbRABX3                           YK---------------------------------KSPKKDDLMSQVLGFI
Tb05.26C7.80                      S-------------------------------------------------
TbRAB28                           VR---------------------------------LPEDALNLEERVVAN-
Tb11.02.3850                      EESWLECR-------------------------SPNVIFPPAATISEVR
Tb11.52.0014                      AFF--------------------------------------------------
Tb10.70.0590                      FS---------------------------------KRRLPAPVTLTSSIEFA
Tb03.5L5.790                      AY---------------------------------QKRIEQLTQMR----
TbARF2like_TRYP10.0.000567_68     EY-----------------------------------THIDKLVES-----
Tb07.6C8.230                      LTFGTDFDSITSAGAAKPTISLNARYNFTQFLDFTRRREATRCKGLSCFS
Tb10.6k15.1520                    LSVDERNR-------------------------VKTRTYEICSDAIEVM
Tb07.29D18.100                    RAVDEKNSTRDPVELP----------CSYKGRKLKLIDTAGLARHRYRAD
HsnucleosteminNP_996562           DKQITIIDSPSFIVSPLNSSSALALRSPASIEVVKPMEAASAILSQADAR
Tb11.02.0240                      RSDIRVMDCPG------------------VVAPGEDCGDVVLRNAVKVS


TbARF1C                           -------------------------------------------------
TbARF1B                           -------------------------------------------------
TbARF1D                           -------------------------------------------------
TbARF1A                           -------------------------------------------------
TbARF1A_Tb09.211.4460             -------------------------------------------------
HsARF1NM_001658                   -------------------------------------------------
ScARF1YDL192w                     -------------------------------------------------
TbARF1E                           -------------------------------------------------
```

```
TbARL3_embl.27                    --------------------------------------------------
TbARL1_167.t00109                 --------------------------------------------------
TbARL1B_09.160.5300               --------------------------------------------------
TbARL3B_92.m00269                 --------------------------------------------------
TbARL3C_06.4F7.880                --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790      --------------------------------------------------
TbRABX1                           --------------------------------------------------
TbRABX2                           --------------------------------------------------
TbRAB21                           NSASGAGGSVFFESEGSSAWAPKRRKRRGLLRIEDDMPGEDD--------
TbRAB1A                           --------------------------------------------------
HsRab1ANM_004161                  --------------------------------------------------
ScYpt1YFL038c                     --------------------------------------------------
TbRAB18                           --------------------------------------------------
TbRAB2                            --------------------------------------------------
TbRAB4                            --------------------------------------------------
TbRAB11                           --------------------------------------------------
TbRAB6                            --------------------------------------------------
TbRAB5B                           --------------------------------------------------
TbRAB5A                           --------------------------------------------------
TbRAB7                            --------------------------------------------------
Tb08.6H23.400                     --------------------------------------------------
Tb04.1D20.300                     --------------------------------------------------
HsNRasAAQ94397                    --------------------------------------------------
ScRas1YOR101w                     SLTNAGTGSSSKSAVNHNGETTKRTDEKNYVNQNNNNEGNTKYSSNGNGN
CeRas1C44C11.1                    --------------------------------------------------
HsRalANM_005402                   --------------------------------------------------
HsRanNM_006325                    --------------------------------------------------
TbRAN                             --------------------------------------------------
HsRac2CAB45265                    --------------------------------------------------
CeRac1C09G12.8                    --------------------------------------------------
HsCdc42NM_001791                  --------------------------------------------------
CeCdc42R07G3.1                    --------------------------------------------------
ScCdc42YLR229c                    YPRWMSQQVGNSIRRKLVIVGDGACGKTCLLIVFSKGQFPEVYVPTVFEN
HsRhoCAAM21119                    --------------------------------------------------
CeRho-1CE25369                    --------------------------------------------------
AtRop4ARAC5AT1G75840              --------------------------------------------------
AtRop10ARAC8AT3G48040             CGKN----------------------------------------------
HsWrch-1AAK83340                  KSWWKKYCCFV---------------------------------------
MmTTFXP_359315                    --------------------------------------------------
ScGtr1RagYML121W                  --------------------------------------------------
Tb11.02.0820                      --------------------------------------------------
TbRAB1B                           --------------------------------------------------
TbRAB23                           --------------------------------------------------
TbRABX3                           KE------------------------------------------------
Tb05.26C7.80                      --------------------------------------------------
TbRAB28                           --------------------------------------------------
Tb11.02.3850                      --------------------------------------------------
Tb11.52.0014                      --------------------------------------------------
Tb10.70.0590                      TPPSLTPCFTSFDERPGSAFFRMRSPIRALGERSNIAVGGTTSPSAVVVK
Tb03.5L5.790                      --------------------------------------------------
TbARF2like_TRYP10.0.000567_68     --------------------------------------------------
Tb07.6C8.230                      VGMRDLLSSPIKIALIGPCGVGKTSLMREWGRQRRPGDNSARFAVTPPTV
Tb10.6k15.1520                    MG------------------------------------------------
Tb07.29D18.100                    RDFIGRIHGLSVNEIRFAHVVIVVFDATEGHPNKYDMAVLHSVAAEGRPF
HsnucleosteminNP_996562           QVVLKYTVPGYRNSLEFFTVLAQRRGMHQKGGIPNVEGAAKLLWSEWTGA
Tb11.02.0240                      DLADPFTPVQRLLQRCAQVTLDPSQQQHSQYLSAGVHPLGLFYSIGSFDP


TbARF1C                           --------------------------------------------------
TbARF1B                           --------------------------------------------------
TbARF1D                           --------------------------------------------------
```

```
TbARF1A                          --------------------------------------------------
TbARF1A_Tb09.211.4460            --------------------------------------------------
HsARF1NM_001658                  --------------------------------------------------
ScARF1YDL192w                    --------------------------------------------------
TbARF1E                          --------------------------------------------------
TbARL3_embl.27                   --------------------------------------------------
TbARL1_167.t00109                --------------------------------------------------
TbARL1B_09.160.5300              --------------------------------------------------
TbARL3B_92.m00269                --------------------------------------------------
TbARL3C_06.4F7.880               --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790     --------------------------------------------------
TbRABX1                          ------------GGAGGAGNGVRLAGNE--GQKGSKRGGCC---------
TbRABX2                          ------------HGDKAIGNIVRLNTST--HTK--KRKWRC---------
TbRAB21                          ------EVANLVSGGGGKHSTVNLSSNPNVAAATPRRNRCCS--------
TbRAB1A                          ------------GGRPLLTGNNRPATNSGGQK-----SGCC---------
HsRab1ANM_004161                 ------------SNVKIQS---TPVKQSGG--------GCC---------
ScYpt1YFL038c                    ---------EDKGNVNLKG---QSLTNTGG--------GCC---------
TbRAB18                          -----------YSGVNLSK---TSDPTSGA--------VCC---------
TbRAB2                           -------------GKQGTGPGVARVSRTGGKKSEDSESGCFC--------
TbRAB4                           -------------GENGH----AETLYDGPKR-----FSCAC--------
TbRAB11                          ------AGAAAKKPVNLSPSNSNQP---AGKAS----GGCC---------
TbRAB6                           -----------RDPFLLTPSQQQKDGEGAGWRE----GGCC---------
TbRAB5B                          -------------GVLGGQ----PNSTRRSSG------CCG---------
TbRAB5A                          -------------GPRGAQRLEPPTRQQKKEG------GCAC--------
TbRAB7                           -------------SIRLGQ-----QRPSTKKS------DCAC--------
Tb08.6H23.400                    ------ERDPLHSLLPLCYEPETTLDEGTVAEDPALTADGTLASLSSPSS
Tb04.1D20.300                    ------ERGPLHSHLPLNFDTGTTMDGETGTDGTLFTTDGVMASAPSLYS
HsNRasAAQ94397                   -------------------------SSDDGTQGCMGLPCVVM-------
ScRas1YOR101w                    RSDISRGNQNNALNSRSKQSAEPQKNSSANARKESSGGCCIIC-------
CeRas1C44C11.1                   ----------------------DRKLESPIKLKKKKNCRIQ-------
HsRalANM_005402                  ----------------------GKKKRKSLAKRIRERCCIL--------
HsRanNM_006325                   ------------PEVVMDPALAAQYEHDLEVAQTTALPDEDDDL------
TbRAN                            ------------NVQPLTAEQLQALQEEARAVENVVLPMGEDD-------
HsRac2CAB45265                   --------------------------------------------------
CeRac1C09G12.8                   --------------------------------------------------
HsCdc42NM_001791                 --------------------------------------------------
CeCdc42R07G3.1                   --------------------------------------------------
ScCdc42YLR229c                   YVADVEVDGRRVELALWDTAGQEDYDRLRPLSYPDSNVVLICFSIDLPDS
HsRhoCAAM21119                   --------------------------------------------------
CeRho-1CE25369                   --------------------------------------------------
AtRop4ARAC5AT1G75840             --------------------------------------------------
AtRop10ARAC8AT3G48040            --------------------------------------------------
HsWrch-1AAK83340                 --------------------------------------------------
MmTTFXP_359315                   --------------------------------------------------
ScGtr1RagYML121W                 ------PKRFEKISNIMKNFKQSCTKLKSGFKTLILNNNIYVSELS---S
Tb11.02.0820                     ------ESRTTKVSETVKHFKLSCMNNATSLEGYQMTTTTFTALLHPFTS
TbRAB1B                          -----------HRNAVNLERPRRENGTGRRSERSQRNDNCCCQ-------
TbRAB23                          -----------STGAGNAGKSSKSGGAGKKSSKKSKKKKCSVM-------
TbRABX3                          --------------------------------------------------
Tb05.26C7.80                     --------------------------------------------------
TbRAB28                          ----------LQLLPEDCVGPGVSGPGGGKECGKKKKGKCAVM-------
Tb11.02.3850                     -------DEVHQLELPSVDLVDEHEEESPGIANRKKKSGCTML-------
Tb11.52.0014                     --------------------------------------------------
Tb10.70.0590                     RTPSLVGVAVASRRNSAARRNTVDAVRGPTECEDGSAPWCSDVVLVGGTE
Tb03.5L5.790                     --------------------------------------------------
TbARF2like_TRYP10.0.000567_68    --------------QTLEVKMEAEQKRKKLLEE-----------------
Tb07.6C8.230                     TFNQFDKTVFLTGGLTARAQLRVFDISGHPRFRELTRFVCASCHAVVICY
Tb10.6k15.1520                   ------MNRIYSKGKEQGEGDEEEVSSGARGTEAEVYAGANIVIKLSSDD
Tb07.29D18.100                   LLCANKWDAVLDQSATAEAIDFKIKRQVREVKYSNAVVVSAHTGLNLTLL
HsnucleosteminNP_996562          SLAYYCHPPTSWTPPPYFNESIVVDMKSGFNLEELEKNNAQSIRAIKGPH
Tb11.02.0240                     SDVMSFIRLVGQRRGRLLQGGVVDEEGTARMILHDWNDGRIAYYTLPPTS
```

```
TbARF1C                          --------------------------------------------------
TbARF1B                          --------------------------------------------------
TbARF1D                          --------------------------------------------------
TbARF1A                          --------------------------------------------------
TbARF1A_Tb09.211.4460            --------------------------------------------------
HsARF1NM_001658                  --------------------------------------------------
ScARF1YDL192w                    --------------------------------------------------
TbARF1E                          --------------------------------------------------
TbARL3_embl.27                   --------------------------------------------------
TbARL1_167.t00109                --------------------------------------------------
TbARL1B_09.160.5300              --------------------------------------------------
TbARL3B_92.m00269                --------------------------------------------------
TbARL3C_06.4F7.880               --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790     --------------------------------------------------
TbRABX1                          --------------------------------------------------
TbRABX2                          --------------------------------------------------
TbRAB21                          --------------------------------------------------
TbRAB1A                          --------------------------------------------------
HsRab1ANM_004161                 --------------------------------------------------
ScYpt1YFL038c                    --------------------------------------------------
TbRAB18                          --------------------------------------------------
TbRAB2                           --------------------------------------------------
TbRAB4                           --------------------------------------------------
TbRAB11                          --------------------------------------------------
TbRAB6                           --------------------------------------------------
TbRAB5B                          --------------------------------------------------
TbRAB5A                          --------------------------------------------------
TbRAB7                           --------------------------------------------------
Tb08.6H23.400                    IKSRDVRKDTKASEDELFSPRECADEDDVCHGGADAADNLKSARGRGSNG
Tb04.1D20.300                    LGSMVTVRSAQIAESGWFTPRERGSEGDTCACDKYMTEEVKESPTHGPSG
HsNRasAAQ94397                   --------------------------------------------------
ScRas1YOR101w                    --------------------------------------------------
CeRas1C44C11.1                   --------------------------------------------------
HsRalANM_005402                  --------------------------------------------------
HsRanNM_006325                   --------------------------------------------------
TbRAN                            --------------------------------------------------
HsRac2CAB45265                   --------------------------------------------------
CeRac1C09G12.8                   --------------------------------------------------
HsCdc42NM_001791                 --------------------------------------------------
CeCdc42R07G3.1                   --------------------------------------------------
ScCdc42YLR229c                   LENVQEKWIAEVLHFCQGVPIILVGCKVDLRNDPQTIEQLRQEGQQPVTS
HsRhoCAAM21119                   --------------------------------------------------
CeRho-1CE25369                   --------------------------------------------------
AtRop4ARAC5AT1G75840             --------------------------------------------------
AtRop10ARAC8AT3G48040            --------------------------------------------------
HsWrch-1AAK83340                 --------------------------------------------------
MmTTFXP_359315                   --------------------------------------------------
ScGtr1RagYML121W                 NMVCFIVLKDMNIPQELVLENIKKAKEFFQ--------------------
Tb11.02.0820                     CTYVLIFSEDTSVNVELHRINVLSARWNFEQFLLSGDSIAEEMRKVL---
TbRAB1B                          --------------------------------------------------
TbRAB23                          --------------------------------------------------
TbRABX3                          --------------------------------------------------
Tb05.26C7.80                     --------------------------------------------------
TbRAB28                          --------------------------------------------------
Tb11.02.3850                     --------------------------------------------------
Tb11.52.0014                     --------------------------------------------------
Tb10.70.0590                     PEPFSALHENGYCVSEGPPNQTETQSTLLRSLSHDGEVHACGLERQKKRE
Tb03.5L5.790                     --------------------------------------------------
TbARF2like_TRYP10.0.000567_68    --------------------------------------------------
```

```
Tb07.6C8.230                    DPQRKSSLMEAKAIIADVETKLGVQPVIVCGLIPPADAGRGGSAVEVSAE
Tb10.6k15.1520                  CIYVKELPNSLTLVSMVKNESFRNRILIDHNISAFYNAAYSIFRRN----
Tb07.29D18.100                  MDQALELYDKWNKRVRRAELTRLWRKMEKSVIIPYHVARIGRITQVNTRP
HsnucleosteminNP_996562         LANSILFQSSGLTNGIIEEKDIHEELPKRKERKQEEREDDKDSDQETVDE
Tb11.02.0240                    DLFGRTTLTADPGEGLTGCEEYGESGPQLVDGFAQGLQWEGLPTFHLSWS


TbARF1C                         ------------------------------------------------
TbARF1B                         ------------------------------------------------
TbARF1D                         ------------------------------------------------
TbARF1A                         ------------------------------------------------
TbARF1A_Tb09.211.4460           ------------------------------------------------
HsARF1NM_001658                 ------------------------------------------------
ScARF1YDL192w                   ------------------------------------------------
TbARF1E                         ------------------------------------------------
TbARL3_embl.27                  ------------------------------------------------
TbARL1_167.t00109               ------------------------------------------------
TbARL1B_09.160.5300             ------------------------------------------------
TbARL3B_92.m00269               ------------------------------------------------
TbARL3C_06.4F7.880              ------------------------------------------------
TbARL6_10.70.3000|08.5H5.790    ------------------------------------------------
TbRABX1                         ------------------------------------------------
TbRABX2                         ------------------------------------------------
TbRAB21                         ------------------------------------------------
TbRAB1A                         ------------------------------------------------
HsRab1ANM_004161                ------------------------------------------------
ScYpt1YFL038c                   ------------------------------------------------
TbRAB18                         ------------------------------------------------
TbRAB2                          ------------------------------------------------
TbRAB4                          ------------------------------------------------
TbRAB11                         ------------------------------------------------
TbRAB6                          ------------------------------------------------
TbRAB5B                         ------------------------------------------------
TbRAB5A                         ------------------------------------------------
TbRAB7                          ------------------------------------------------
Tb08.6H23.400                   TVATVMADPIDGDGIDVDVDVDVEGEDEDVIADAAAEPECTVNSSKHVDP
Tb04.1D20.300                   TDTTLVAEDVDG-----------------------HEETACSHMHMDP
HsNRasAAQ94397                  ------------------------------------------------
ScRas1YOR101w                   ------------------------------------------------
CeRas1C44C11.1                  ------------------------------------------------
HsRalANM_005402                 ------------------------------------------------
HsRanNM_006325                  ------------------------------------------------
TbRAN                           ------------------------------------------------
HsRac2CAB45265                  ------------------------------------------------
CeRac1C09G12.8                  ------------------------------------------------
HsCdc42NM_001791                ------------------------------------------------
CeCdc42R07G3.1                  ------------------------------------------------
ScCdc42YLR229c                  QEGQSVADQIGATGYYECSAKTGYGVREVFEAATRASLMGKSKTNGKAKK
HsRhoCAAM21119                  ------------------------------------------------
CeRho-1CE25369                  ------------------------------------------------
AtRop4ARAC5AT1G75840            ------------------------------------------------
AtRop10ARAC8AT3G48040           ------------------------------------------------
HsWrch-1AAK83340                ------------------------------------------------
MmTTFXP_359315                  ------------------------------------------------
ScGtr1RagYML121W                ------------------------------------------------
Tb11.02.0820                    ------------------------------------------------
TbRAB1B                         ------------------------------------------------
TbRAB23                         ------------------------------------------------
TbRABX3                         ------------------------------------------------
Tb05.26C7.80                    ------------------------------------------------
TbRAB28                         ------------------------------------------------
```

```
Tb11.02.3850                    --------------------------------------------------
Tb11.52.0014                    --------------------------------------------------
Tb10.70.0590                    LSGRRREVGCTGSCVIM---------------------------------
Tb03.5L5.790                    --------------------------------------------------
TbARF2like_TRYP10.0.000567_68   --------------------------------------------------
Tb07.6C8.230                    EATEISSRERGSLLCAWHEGKILFEHVVQCLLDCIALGTSAISFTAPVSP
Tb10.6k15.1520                  --------------------------------------------------
Tb07.29D18.100                  PTFLLQLQTKNDSNTLPKALQEMMKNTLVEEFDFRGVPIRLIQEVKDSNP
HsnucleosteminNP_996562         EVDENSSGMFAAEETGEALSEETTAGEQSTRSFILDKIIEEDDAYDFSTD
Tb11.02.0240                    KMKSGVQ-----------------------------------------


TbARF1C                         --------------------------------------------------
TbARF1B                         --------------------------------------------------
TbARF1D                         --------------------------------------------------
TbARF1A                         --------------------------------------------------
TbARF1A_Tb09.211.4460           --------------------------------------------------
HsARF1NM_001658                 --------------------------------------------------
ScARF1YDL192w                   --------------------------------------------------
TbARF1E                         --------------------------------------------------
TbARL3_embl.27                  --------------------------------------------------
TbARL1_167.t00109               --------------------------------------------------
TbARL1B_09.160.5300             --------------------------------------------------
TbARL3B_92.m00269               --------------------------------------------------
TbARL3C_06.4F7.880              --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790    --------------------------------------------------
TbRABX1                         --------------------------------------------------
TbRABX2                         --------------------------------------------------
TbRAB21                         --------------------------------------------------
TbRAB1A                         --------------------------------------------------
HsRab1ANM_004161                --------------------------------------------------
ScYpt1YFL038c                   --------------------------------------------------
TbRAB18                         --------------------------------------------------
TbRAB2                          --------------------------------------------------
TbRAB4                          --------------------------------------------------
TbRAB11                         --------------------------------------------------
TbRAB6                          --------------------------------------------------
TbRAB5B                         --------------------------------------------------
TbRAB5A                         --------------------------------------------------
TbRAB7                          --------------------------------------------------
Tb08.6H23.400                   NKSSPVKEEGEEDAVAVHSERSAPGDGVVDKKVKCN----GSDGEVETED
Tb04.1D20.300                   TALLSCKEE--ERDITLYSVCSALESGVVDNSVAEASNGSGSIDALNMGD
HsNRasAAQ94397                  --------------------------------------------------
ScRas1YOR101w                   --------------------------------------------------
CeRas1C44C11.1                  --------------------------------------------------
HsRalANM_005402                 --------------------------------------------------
HsRanNM_006325                  --------------------------------------------------
TbRAN                           --------------------------------------------------
HsRac2CAB45265                  --------------------------------------------------
CeRac1C09G12.8                  --------------------------------------------------
HsCdc42NM_001791                --------------------------------------------------
CeCdc42R07G3.1                  --------------------------------------------------
ScCdc42YLR229c                  NTTEKKKKKCVLL------------------------------------
HsRhoCAAM21119                  --------------------------------------------------
CeRho-1CE25369                  --------------------------------------------------
AtRop4ARAC5AT1G75840            --------------------------------------------------
AtRop10ARAC8AT3G48040           --------------------------------------------------
HsWrch-1AAK83340                --------------------------------------------------
MmTTFXP_359315                  --------------------------------------------------
ScGtr1RagYML121W                --------------------------------------------------
Tb11.02.0820                    --------------------------------------------------
```

```
TbRAB1B                          --------------------------------------------------
TbRAB23                          --------------------------------------------------
TbRABX3                          --------------------------------------------------
Tb05.26C7.80                     --------------------------------------------------
TbRAB28                          --------------------------------------------------
Tb11.02.3850                     --------------------------------------------------
Tb11.52.0014                     --------------------------------------------------
Tb10.70.0590                     --------------------------------------------------
Tb03.5L5.790                     --------------------------------------------------
TbARF2like_TRYP10.0.000567_68    --------------------------------------------------
Tb07.6C8.230                     LGVPVDSEEFSVNRSTAQELLRITMCPSAIDVLLD---------------
Tb10.6k15.1520                   --------------------------------------------------
Tb07.29D18.100                   DYI-----------------------------------------------
HsnucleosteminNP_996562          YV-----------------------------------------------
Tb11.02.0240                     --------------------------------------------------


TbARF1C                          --------------------------------------------------
TbARF1B                          --------------------------------------------------
TbARF1D                          --------------------------------------------------
TbARF1A                          --------------------------------------------------
TbARF1A_Tb09.211.4460            --------------------------------------------------
HsARF1NM_001658                  --------------------------------------------------
ScARF1YDL192w                    --------------------------------------------------
TbARF1E                          --------------------------------------------------
TbARL3_embl.27                   --------------------------------------------------
TbARL1_167.t00109                --------------------------------------------------
TbARL1B_09.160.5300              --------------------------------------------------
TbARL3B_92.m00269                --------------------------------------------------
TbARL3C_06.4F7.880               --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790     --------------------------------------------------
TbRABX1                          --------------------------------------------------
TbRABX2                          --------------------------------------------------
TbRAB21                          --------------------------------------------------
TbRAB1A                          --------------------------------------------------
HsRab1ANM_004161                 --------------------------------------------------
ScYpt1YFL038c                    --------------------------------------------------
TbRAB18                          --------------------------------------------------
TbRAB2                           --------------------------------------------------
TbRAB4                           --------------------------------------------------
TbRAB11                          --------------------------------------------------
TbRAB6                           --------------------------------------------------
TbRAB5B                          --------------------------------------------------
TbRAB5A                          --------------------------------------------------
TbRAB7                           --------------------------------------------------
Tb08.6H23.400                    ATDVECFPQEDNAAPPSVQNTARFGGNSLQARASSFANGGDGVLSCSRAA
Tb04.1D20.300                    ETGVESTRQQTSAAPPSVENTARFVGGSQRLHNSMSMDSYFGSLSHSWAA
HsNRasAAQ94397                   --------------------------------------------------
ScRas1YOR101w                    --------------------------------------------------
CeRas1C44C11.1                   --------------------------------------------------
HsRalANM_005402                  --------------------------------------------------
HsRanNM_006325                   --------------------------------------------------
TbRAN                            --------------------------------------------------
HsRac2CAB45265                   --------------------------------------------------
CeRac1C09G12.8                   --------------------------------------------------
HsCdc42NM_001791                 --------------------------------------------------
CeCdc42R07G3.1                   --------------------------------------------------
ScCdc42YLR229c                   --------------------------------------------------
HsRhoCAAM21119                   --------------------------------------------------
CeRho-1CE25369                   --------------------------------------------------
AtRop4ARAC5AT1G75840             --------------------------------------------------
```

```
AtRop10ARAC8AT3G48040           --------------------------------------------------
HsWrch-1AAK83340                --------------------------------------------------
MmTTFXP_359315                  --------------------------------------------------
ScGtr1RagYML121W                --------------------------------------------------
Tb11.02.0820                    --------------------------------------------------
TbRAB1B                         --------------------------------------------------
TbRAB23                         --------------------------------------------------
TbRABX3                         --------------------------------------------------
Tb05.26C7.80                    --------------------------------------------------
TbRAB28                         --------------------------------------------------
Tb11.02.3850                    --------------------------------------------------
Tb11.52.0014                    --------------------------------------------------
Tb10.70.0590                    --------------------------------------------------
Tb03.5L5.790                    --------------------------------------------------
TbARF2like_TRYP10.0.000567_68   --------------------------------------------------
Tb07.6C8.230                    --------------------------------------------------
Tb10.6k15.1520                  --------------------------------------------------
Tb07.29D18.100                  --------------------------------------------------
HsnucleosteminNP_996562         --------------------------------------------------
Tb11.02.0240                    --------------------------------------------------


TbARF1C                         --------------------------------------------------
TbARF1B                         --------------------------------------------------
TbARF1D                         --------------------------------------------------
TbARF1A                         --------------------------------------------------
TbARF1A_Tb09.211.4460           --------------------------------------------------
HsARF1NM_001658                 --------------------------------------------------
ScARF1YDL192w                   --------------------------------------------------
TbARF1E                         --------------------------------------------------
TbARL3_embl.27                  --------------------------------------------------
TbARL1_167.t00109               --------------------------------------------------
TbARL1B_09.160.5300             --------------------------------------------------
TbARL3B_92.m00269               --------------------------------------------------
TbARL3C_06.4F7.880              --------------------------------------------------
TbARL6_10.70.3000|08.5H5.790    --------------------------------------------------
TbRABX1                         --------------------------------------------------
TbRABX2                         --------------------------------------------------
TbRAB21                         --------------------------------------------------
TbRAB1A                         --------------------------------------------------
HsRab1ANM_004161                --------------------------------------------------
ScYpt1YFL038c                   --------------------------------------------------
TbRAB18                         --------------------------------------------------
TbRAB2                          --------------------------------------------------
TbRAB4                          --------------------------------------------------
TbRAB11                         --------------------------------------------------
TbRAB6                          --------------------------------------------------
TbRAB5B                         --------------------------------------------------
TbRAB5A                         --------------------------------------------------
TbRAB7                          --------------------------------------------------
Tb08.6H23.400                   RGKSGEDSKADENPQVTSHRKRIDDMLKRIDEDAGVEDFSEGGRRVEQMQ
Tb04.1D20.300                   TGRNANAISSDDHPEASSHRRRIDDMLRRIDRDAELENSPESRHVAEDVD
HsNRasAAQ94397                  --------------------------------------------------
ScRas1YOR101w                   --------------------------------------------------
CeRas1C44C11.1                  --------------------------------------------------
HsRalANM_005402                 --------------------------------------------------
HsRanNM_006325                  --------------------------------------------------
TbRAN                           --------------------------------------------------
HsRac2CAB45265                  --------------------------------------------------
CeRac1C09G12.8                  --------------------------------------------------
HsCdc42NM_001791                --------------------------------------------------
```

```
CeCdc42R07G3.1                  --------------------------------------------------
ScCdc42YLR229c                  --------------------------------------------------
HsRhoCAAM21119                  --------------------------------------------------
CeRho-1CE25369                  --------------------------------------------------
AtRop4ARAC5AT1G75840            --------------------------------------------------
AtRop10ARAC8AT3G48040           --------------------------------------------------
HsWrch-1AAK83340                --------------------------------------------------
MmTTFXP_359315                  --------------------------------------------------
ScGtr1RagYML121W                --------------------------------------------------
Tb11.02.0820                    --------------------------------------------------
TbRAB1B                         --------------------------------------------------
TbRAB23                         --------------------------------------------------
TbRABX3                         --------------------------------------------------
Tb05.26C7.80                    --------------------------------------------------
TbRAB28                         --------------------------------------------------
Tb11.02.3850                    --------------------------------------------------
Tb11.52.0014                    --------------------------------------------------
Tb10.70.0590                    --------------------------------------------------
Tb03.5L5.790                    --------------------------------------------------
TbARF2like_TRYP10.0.000567_68   --------------------------------------------------
Tb07.6C8.230                    --------------------------------------------------
Tb10.6k15.1520                  --------------------------------------------------
Tb07.29D18.100                  --------------------------------------------------
HsnucleosteminNP_996562         --------------------------------------------------
Tb11.02.0240                    --------------------------------------------------


TbARF1C                         ----------------------------------
TbARF1B                         ----------------------------------
TbARF1D                         ----------------------------------
TbARF1A                         ----------------------------------
TbARF1A_Tb09.211.4460           ----------------------------------
HsARF1NM_001658                 ----------------------------------
ScARF1YDL192w                   ----------------------------------
TbARF1E                         ----------------------------------
TbARL3_embl.27                  ----------------------------------
TbARL1_167.t00109               ----------------------------------
TbARL1B_09.160.5300             ----------------------------------
TbARL3B_92.m00269               ----------------------------------
TbARL3C_06.4F7.880              ----------------------------------
TbARL6_10.70.3000|08.5H5.790    ----------------------------------
TbRABX1                         ----------------------------------
TbRABX2                         ----------------------------------
TbRAB21                         ----------------------------------
TbRAB1A                         ----------------------------------
HsRab1ANM_004161                ----------------------------------
ScYpt1YFL038c                   ----------------------------------
TbRAB18                         ----------------------------------
TbRAB2                          ----------------------------------
TbRAB4                          ----------------------------------
TbRAB11                         ----------------------------------
TbRAB6                          ----------------------------------
TbRAB5B                         ----------------------------------
TbRAB5A                         ----------------------------------
TbRAB7                          ----------------------------------
Tb08.6H23.400                   EEAS--DQRKKEKSPVKLSRCFCFGSKGGGSKRSGC
Tb04.1D20.300                   YGATPVDHGNEKPSKVNLSSCSCFGSKGDRSKRSGC
HsNRasAAQ94397                  ----------------------------------
ScRas1YOR101w                   ----------------------------------
CeRas1C44C11.1                  ----------------------------------
HsRalANM_005402                 ----------------------------------
```

```
HsRanNM_006325                  ------------------------------------
TbRAN                           ------------------------------------
HsRac2CAB45265                  ------------------------------------
CeRac1C09G12.8                  ------------------------------------
HsCdc42NM_001791                ------------------------------------
CeCdc42R07G3.1                  ------------------------------------
ScCdc42YLR229c                  ------------------------------------
HsRhoCAAM21119                  ------------------------------------
CeRho-1CE25369                  ------------------------------------
AtRop4ARAC5AT1G75840            ------------------------------------
AtRop10ARAC8AT3G48040           ------------------------------------
HsWrch-1AAK83340                ------------------------------------
MmTTFXP_359315                  ------------------------------------
ScGtr1RagYML121W                ------------------------------------
Tb11.02.0820                    ------------------------------------
TbRAB1B                         ------------------------------------
TbRAB23                         ------------------------------------
TbRABX3                         ------------------------------------
Tb05.26C7.80                    ------------------------------------
TbRAB28                         ------------------------------------
Tb11.02.3850                    ------------------------------------
Tb11.52.0014                    ------------------------------------
Tb10.70.0590                    ------------------------------------
Tb03.5L5.790                    ------------------------------------
TbARF2like_TRYP10.0.000567_68   ------------------------------------
Tb07.6C8.230                    ------------------------------------
Tb10.6k15.1520                  ------------------------------------
Tb07.29D18.100                  ------------------------------------
HsnucleosteminNP_996562         ------------------------------------
Tb11.02.0240                    ------------------------------------
```

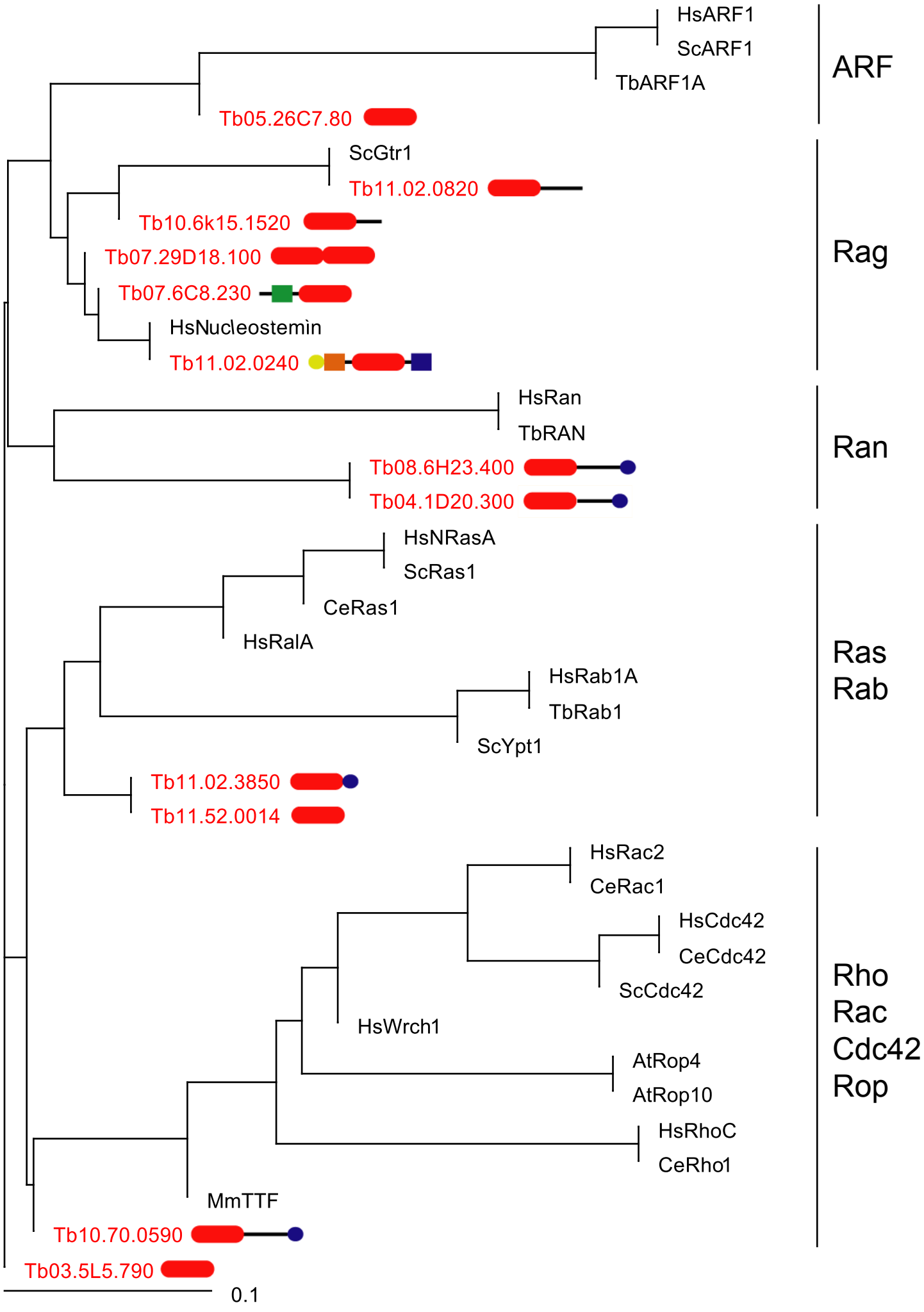
HsARF1
ScARF1
TbARF1A
ARF
Tb05.26C7.80
ScGtr1
Tb11.02.0820
Tb10.6k15.1520
Tb07.29D18.100
Tb07.6C8.230
HsNucleostemin
Tb11.02.0240
Rag
HsRan
TbRAN
Ran
Tb08.6H23.400
Tb04.1D20.300
HsNRasA
ScRas1
CeRas1
HsRalA
HsRab1A
TbRab1
ScYpt1
Ras
Rab
Tb11.02.3850
Tb11.52.0014
HsRac2
CeRac1
HsCdc42
CeCdc42
ScCdc42
HsWrch1
AtRop4
AtRop10
HsRhoC
CeRho1
Rho
Rac
Cdc42
Rop
MmTTF
Tb10.70.0590
Tb03.5L5.790
0.1

Figure S7