```
              1         10        20        30        40        50        60        70        80
              |--------+---------+---------+---------+---------+---------+---------+---------|
   H.sapiens                                 MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
 P.troglodytes                               MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
   M.mulatta                                 MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
   M.musculus                                MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
 R.norvegicus                                MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
    G.gallus                                 MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
 C.l.familiaris                              MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
    B.taurus                                 MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
  X.tropicalis                               MAANKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
    D.rerio                                  MAAAKPKGQNSLALHKVIMVGSGGVGKSALTLQFMY
D.melanogaster                                MSKKPTAGPALHKVIMVGSGGVGKSALTLQFMY
   A.gambiae                                 CGTMSKKPTTGPALHKVIMVGSGGVGKSALTLQFMY
   C.elegans     MDKVSHVLRNGWNWIKLKFLALWHFLFRRKSDEPEFYDPEAMASKKASGTLPPQQQVVHKVIMVGTGGVGKSALTLQFMY
   Consensus     ...................................a...kp....alHKVIMVGsGGVGKSALTLQFMY

              81        90        100       110       120       130       140       150       160
              |--------+---------+---------+---------+---------+---------+---------+---------|
   H.sapiens   DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
 P.troglodytes DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
   M.mulatta   DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
   M.musculus  DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
 R.norvegicus  DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
    G.gallus   DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITELESFAATADFREQILRVKE
 C.l.familiaris DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
    B.taurus   DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESFAATADFREQILRVKE
  X.tropicalis DEFVEDYEPTKADSYRKKVVLDGVEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEQESFAATADFREQILRVKE
    D.rerio    DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITELESFAATADFREQILRVKE
D.melanogaster DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITDDESFQATQEFREQILRVKN
   A.gambiae   DEFVEDYEPTKADSYRKKVVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEDDSFQATQEFREQILRVKN
   C.elegans   DEFVEEYEPTKADSYRKKVVLDGEECSIDILDTAGQEDYSAIRDNYYRSGEGFICVFSILDMESFEATNEFREQILRVKN
   Consensus   DEFVE#YEPTKADSYRKKVVLDGEEvqIDILDTAGQEDYaAIRDNY%RSGEGFlCVFSIt#.#SF.AT.#FREQILRVK#

              161       170       180       190       200       210       220       230       240
              |--------+---------+---------+---------+---------+---------+---------+---------|
   H.sapiens   -DENVPFLLVGNKSDLEDKRQVSVEEAKNRAEQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
 P.troglodytes -DENVPFLLVGNKSDLEDKRQVSVEEAKNRAEQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
   M.mulatta   -DENVPFLLVGNKSDLEDKRQVSVEEAKNRAEQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
   M.musculus  -DENVPFLLVGNKSDLEDKRQVSVEEAKNRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
 R.norvegicus  -DENVPFLLVGNKSDLEDKRQVSVEEAKNRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
    G.gallus   -DENVPFLLVGNKSDLEDKRQVSIEEAKNRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
 C.l.familiaris -DENVPFLLVGNKSDLEDKRQVSVEEAKTRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
    B.taurus   -DENVPFLLVGNKSDLEDKRQVSVEEAKTRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
  X.tropicalis -DENVPFLLVGNKSDLEDKRQVSVEEAKSRADQWNVNYVETSAKTRANVDKVFFDLMREIRARKMEDSKEKNGKKKRKSL
    D.rerio    -DENVPFLLVGNKSDLEDRRQVSADEAKARADQWGVCYVETSAKTRENVDKVFFDLMREIRSRKTEDSKATSGRAKDRC-
D.melanogaster -DESIPFLLVGNKCDLNDKRKVPLSECQLRAQQWAVPYVETSAKTRENVDKVFFDLMREIRSRKTEDSKATSGRAKDRC-
   A.gambiae   -DENIPFLLVGNKCDLNDKRKVPLAECQSRAQQWGVPYVETSAKTRENVDKVFFDLMRQIRSRKTEDSKTTNGRVKDKS-
   C.elegans   SDSSYPIVLVGNKGDMRDQRYVSAELCRQRAEQWGCHYVETSAKRRENVDKVFYDLMREMKRRKGGSQAQTGIDASASSG
   Consensus   .Den!PflLVGNK.D$.DkR.Vs.eec..RA#QWgv.YVETSAKtReNVDKVF%DLMR#ir.RK.edsk.tng..k.ks.

              241       250  254
              |--------+---|
   H.sapiens   AKRI---RERCCIL
 P.troglodytes AKRI---RERCCIL
   M.mulatta   AKRI---RERCCIL
   M.musculus  AKRI---RERCCIL
 R.norvegicus  AKRI---RERCCIL
    G.gallus   AKRI---RERCCIL
 C.l.familiaris AKRI---RERCCIL
    B.taurus   AKRI---RERCCIL
  X.tropicalis AKRI---RERCCIL
    D.rerio    AKRI---RERCCIL
D.melanogaster -KKR---RLKCTLL
   A.gambiae   -KRR---KIKCMPL
   C.elegans   RKKRSGIKKHCTIL
   Consensus   .Krr...r..C.iL
```

S6 Figure. Alignment of RALA protein sequences across various species. Protein reference sequences of RALA homologs as defined by HomoloGene (NCBI, hid=3942) were aligned using MultAlin (http://multalin.toulouse.inra.fr/multalin/multalin.html). Residues comprising the

GTP/GDP-binding region as defined by computational modeling are highlighted in green. For the Consensus row, uppercase represents a residue conserved across all sequences, lowercase represents a residues conserved across at least half of the sequences, and the following symbols represent one of multiple residues: !, I or V; $, L or M; %, F or Y; #, one of N, B, Q, E, B or Z.