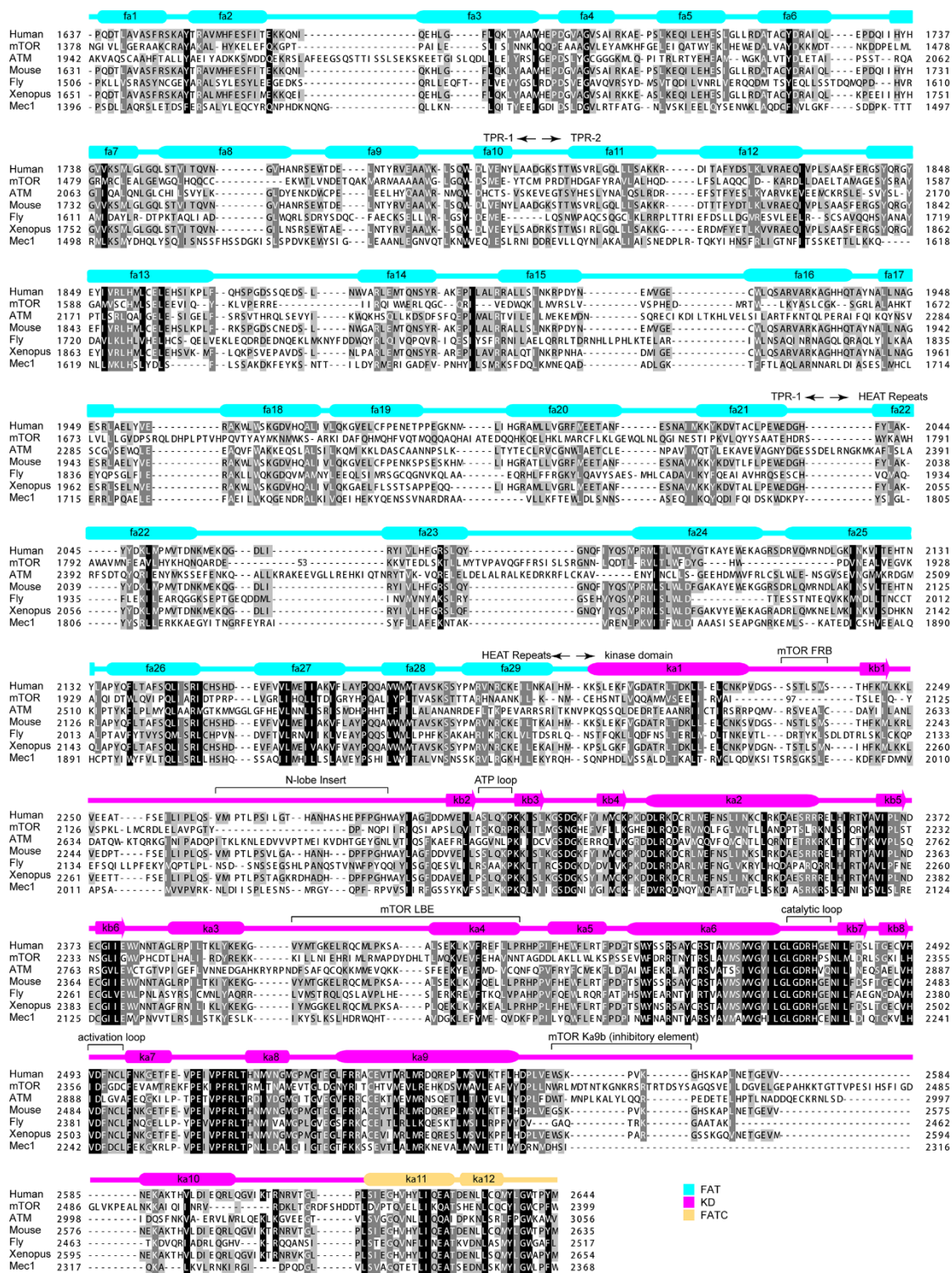


Supplementary information, Figure S4

A



B

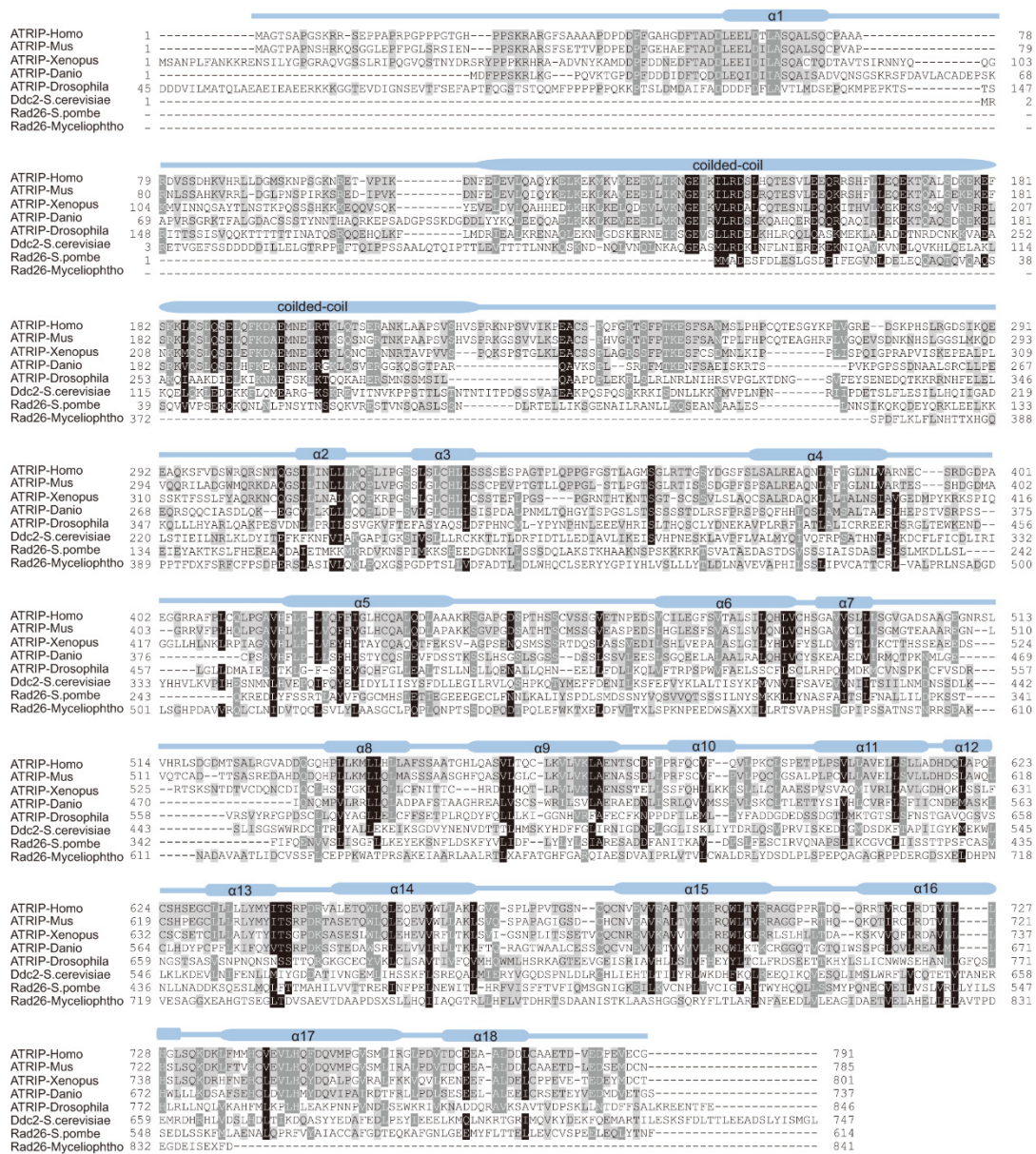


Figure S4 Sequence alignment of ATR across species. (A) The sequence alignment based on the sequence of human ATR (residues 1637-2644). Secondary structure of ATR is shown above the sequence according to the structure. The numbers of each residue are shown after the name in each line. The same color scheme is used as in Figure 1A. The proteins used for alignment include: Human ATR, GI: 157266317; Mouse ATR, GI: 62286489; *Drosophila* ATR, GI: 24642511; *Xenopus laevis* ATR, GI:

90110844; *S. cerevisiae* Tel1, GI: 506876; Human mTOR, GI: 4826730; Human ATM, GI: 71902540. The highly and less conserved residues are indicated under dark and grey background, respectively. (B) The sequence alignment based on the sequence of human ATRIP (residues 1-791). The predicted secondary structure of ATRIP by the PSIPRED Protein Sequence Analysis Workbench is shown above the sequence. The numbers of each sequence are shown after the name in each line. The same color scheme is used as in Figure 1A. The proteins used for alignment include: *Homo Sapiens* ATRIP, GI: 18390347; *Mus musculus* ATRIP, GI: 283436205; *Xenopus laevis* ATRIP, GI: 213625364; *Danio rerio* ATRIP, GI: 558534; *Drosophila melanogaster* ATRIP, GI: 40003; *S. cerevisiae* Ddc2, GI: 74583474; *S. pombe* Rad26, GI:1246743038; *Myceliophtho thermophila* Rad26, GI:11509752. The highly and less conserved residues are indicated under dark and grey background, respectively.