

Figure S3. Alignment of Trabid amino acid sequences

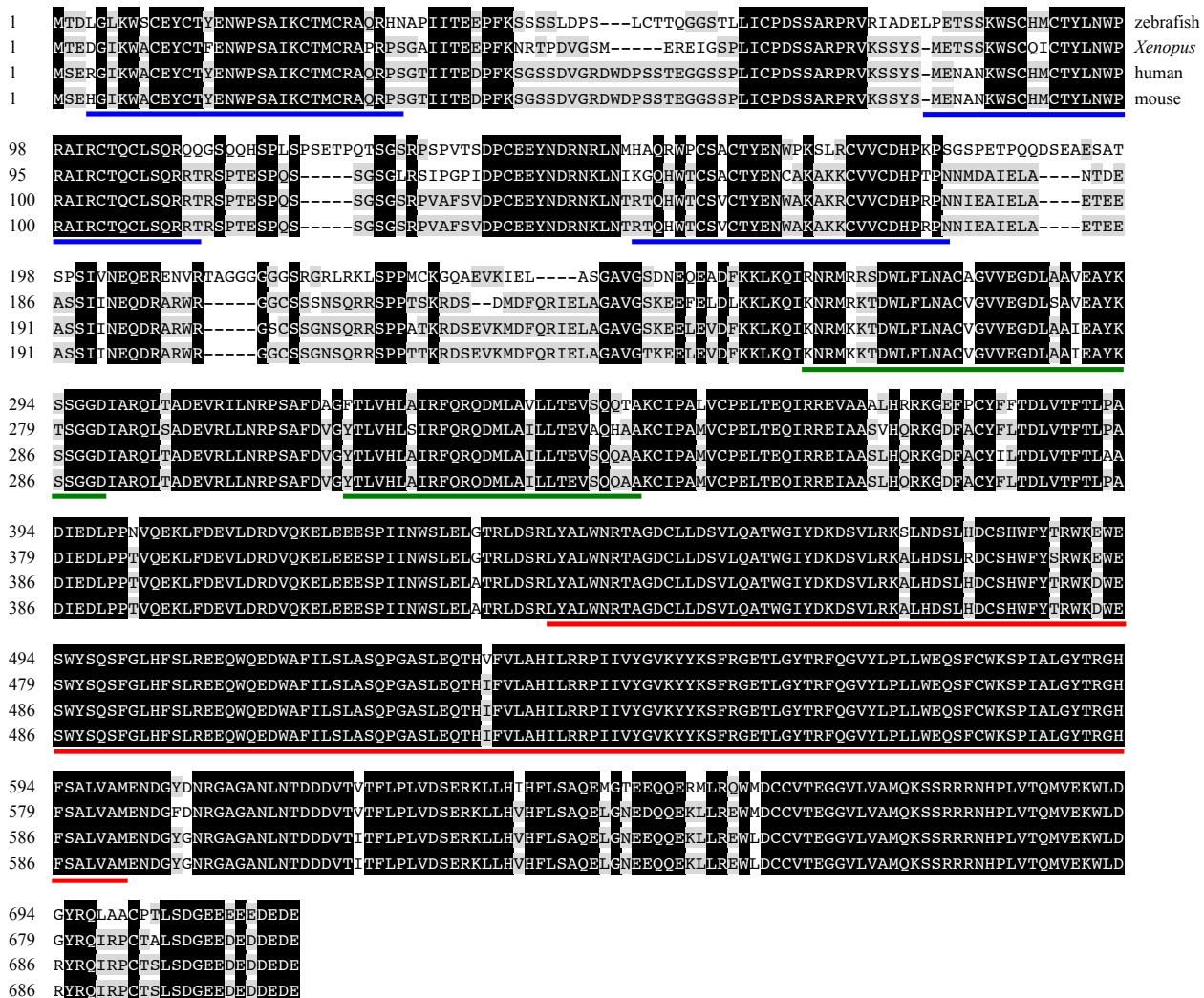


Figure S3. Alignment of Trabid amino acid sequences. Alignment of zebrafish Trabid (*Danio rerio*, our sequence), African clawed frog Trabid (*Xenopus laevis*, NP_001084698), human Trabid (*Homo sapiens*, CAB64449) and mouse Trabid (*Mus musculus*, NP_997185). Zebrafish Trabid bears 78.88%, 80.17% and 80.31% amino acids identity to its counterparts of *Xenopus*, human and mouse, respectively. Blue line indicates the region of Npl4 zinc finger domain (NZF). Green line indicates the region of ankyrin repeat. Red line indicates the region of ovarian tumor protease (OTU) domain.