

Supplementary Table 2. Retrogene and parental gene pairs features. Presence of 5' UTR, TSS prediction by McPromoter, distribution of detected promoter motifs and cDNA/EST hits are reported.

Table with 11 columns: Retrogene, Location, Predicted by McPromoter, Motif Type (location is based on Ensembl database TSS), Motif Type (location is based on McPromoter Predicted TSS), cDNA/ESTs Hits, Parental Gene, Location, Predicted by McPromoter, Motif Type (location is based on Ensembl database TSS), cDNA/ESTs Hits. Rows include genes like CG2718-RC, CG10838-RA, CG9564-RA, etc., with detailed motif and hit information.

Notes: 1) Bolded genes are the ones with annotated 5' UTR; 2) "Y" means that McPromoter has a detection and "N" means that McPromoter does not have a detection at the criteria level mentioned in Materials and Methods; 3) "NA" means that either no motif enumerated in the text is detected or no cDNA/ESTs hit is found in the library at the criteria level mentioned in Materials and Methods;

cDNA/ESTs libraries. CK: rough endoplasmic reticulum. GH: head library. GM: ovaries. HL: adult heads. LD: 0-22hr embryos. LP: varying stages of larvae and early pupae. SD: non-isogenic Schneider L2 cells. AT: adult testes. UT: adult testes stem cell enriched. RE: Riken embryo. RH: Riken head. Other information about these libraries are available at the website: http://www.fruitfly.org/EST/faq.html