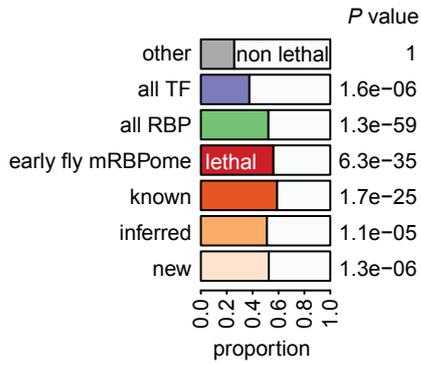
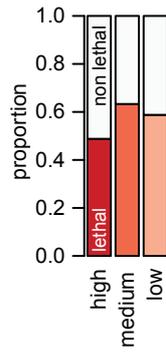


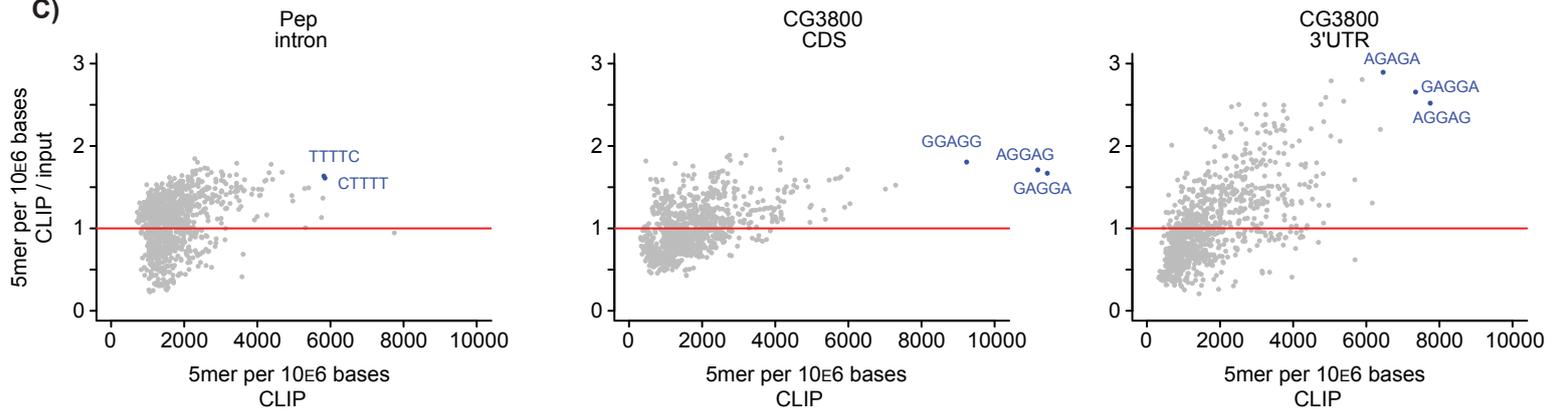
A)



B)



C)



Supplemental Figure S3 A) Intersect with GenomeRNAi v14 database. Proportions of genes, with phenotype description containing “lethal” in at least 1 out of 67 whole fly in vivo screens. (= essential genes) (all TF = Transcription factors in embryonic transcriptome; FPKM > 0; flyTF.org. All RBP = Pfam RBD or GO:RNA-binding. Other categories like in Fig. 2D). P value, one-sided fisher-exact test relative to whole embryonic transcriptome. **B)** Proportion of essential genes in the three RBP enrichment classes high, medium and low as in Fig. 3A. **C)** Like Fig. 3D, CLIP sequencing read 5-mer enrichment in sub-annotation categories, predominantly bound by either Pep (intron) or CG3800 (mRNA exon).