

Figure S4. Annotation of methylation peaks normalized to GATC density. Genes *vs.* repeats annotation of peaks located in genes or repeats for each library. Distribution of enriched methylation regions in genes only (red), repeats only (blue), and regions covering both genes and repeats (yellow). Piwi(WT*) refers to a Piwi(WT) DamID-seq dataset from Ilyin *et al.*, 2017.