

Supplemental Fig. S12. Recalculated intensities of the various active or repressive histone marks indicated on invertebrate-specific (A) and worm-specific (B) acting regions of fly (A) and worm (A, B) genes, when ChIP-seq reads were mapped by TopHat with the parameters “-N 0 -g 0”. Both active and repressive histone marks were compared according to *Predicted Patterns I-III*. For a detailed description of the figure see the legend of Fig. 2.

