

Supplemental Fig. S11. Recalculated intensities of the various active or repressive histone marks indicated on common acting regions of mouse (A), fly (B), and worm (C) 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.

