

Supplemental Fig. S9. Recalculated intensities of the various active or repressive histone marks indicated on common acting regions of mouse **(A)**, fly **(B)**, and worm **(C)** genes are shown, when ortholog sets with a $\bar{d}_5 > 1$ were excluded from the analyses. 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.

