

**Supplemental Fig. S3.** The histone marks examined in this study and their corresponding acting regions for expressed and silent genes in each of the mouse, fly, and worm genomes. The acting regions are represented with boxes and they include the genic regions of: “TSS-1000 to TSS”, “TSS to TSS+500”, “TSS+500 to TTS-500”, “TTS-500 to TTS”, and “TTS to TTS+1000”, from left to right, respectively (as diagrammed at the bottom left of the panel). According to the Extended Data Figure 1 of Ho et al. (2014), genic regions that show opposing trends in scaled ChIP-fold enrichment for a histone mark in expressed genes versus silent genes (“+” denotes increased enrichment; “-” denotes decreased enrichment) were defined as acting regions of the histone marks. Acting regions of a focal active histone mark (or repressive mark) are those showing increased (or decreased) enrichment in the expressed genes and decreased (or increased) enrichment in the silent genes. Common acting regions that exhibited a consistent effect on gene expression in mouse, fly, and worm are marked with a red box, and they were used to produce Figure 2. Acting regions commonly found in two of the three species examined (e.g., fly and worm), are marked with a green box and were used to produce Figure 3A. Species-specific regions that were only found in worm are marked with a blue box and were used to produce Figure 3B.

