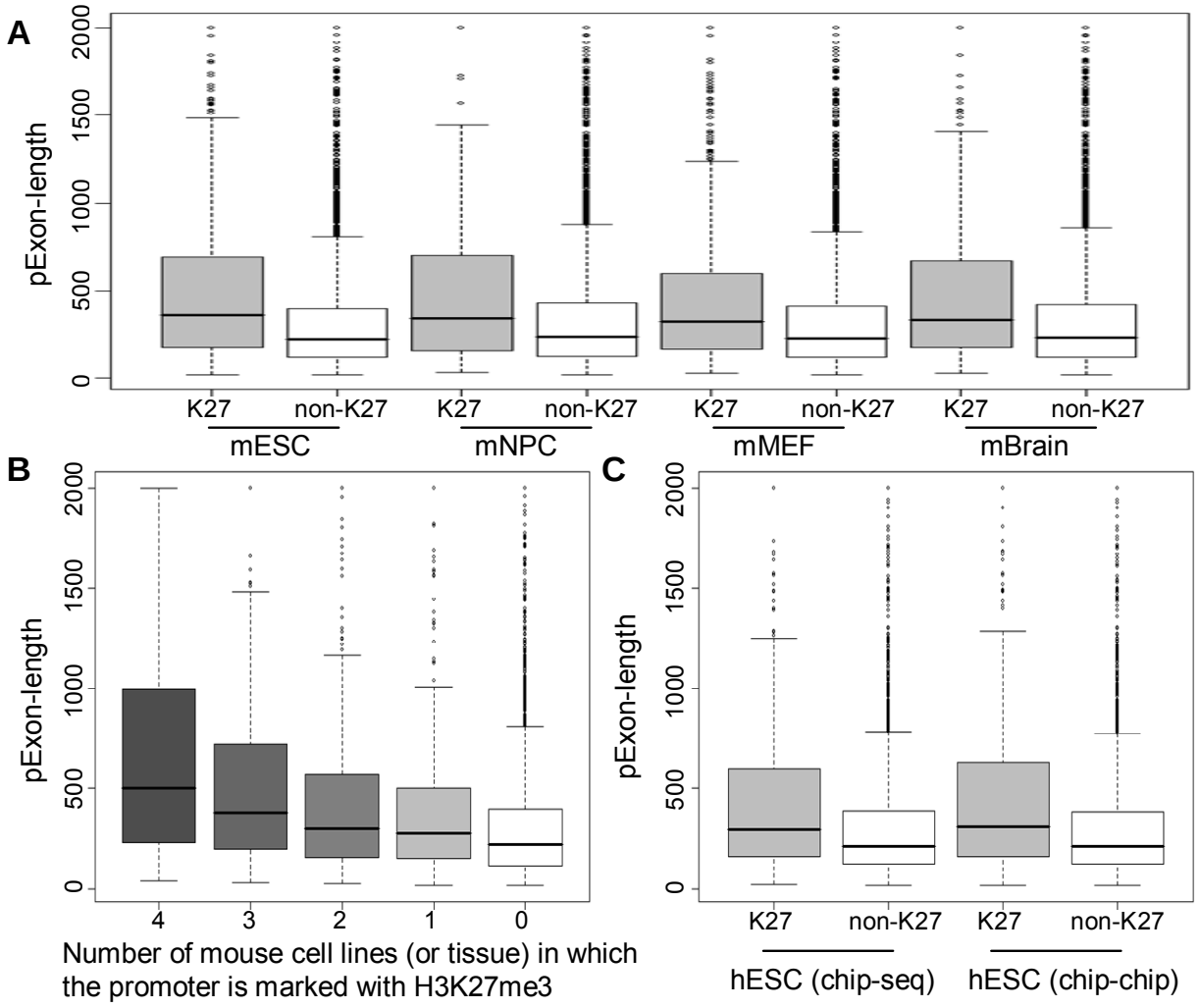
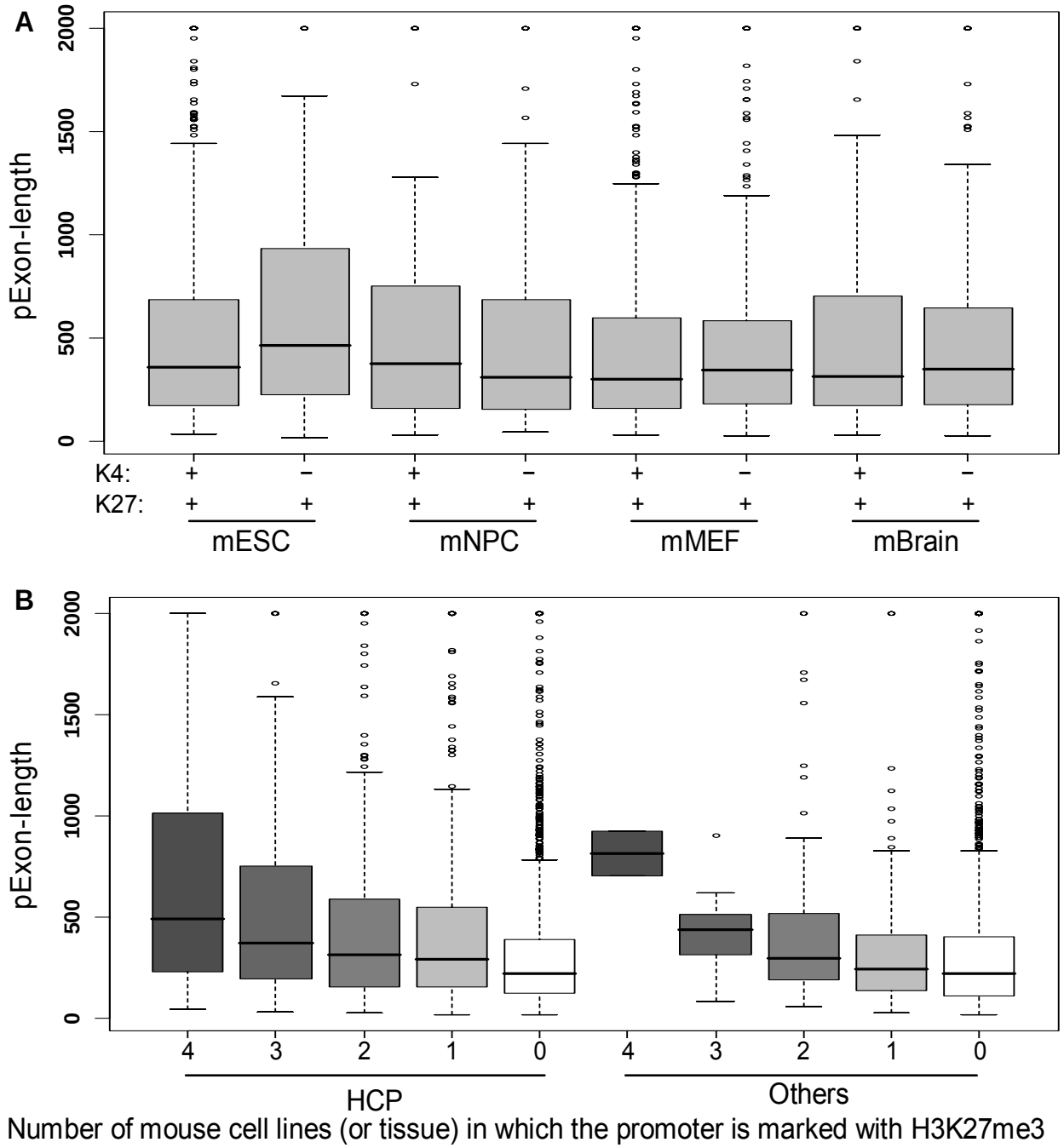
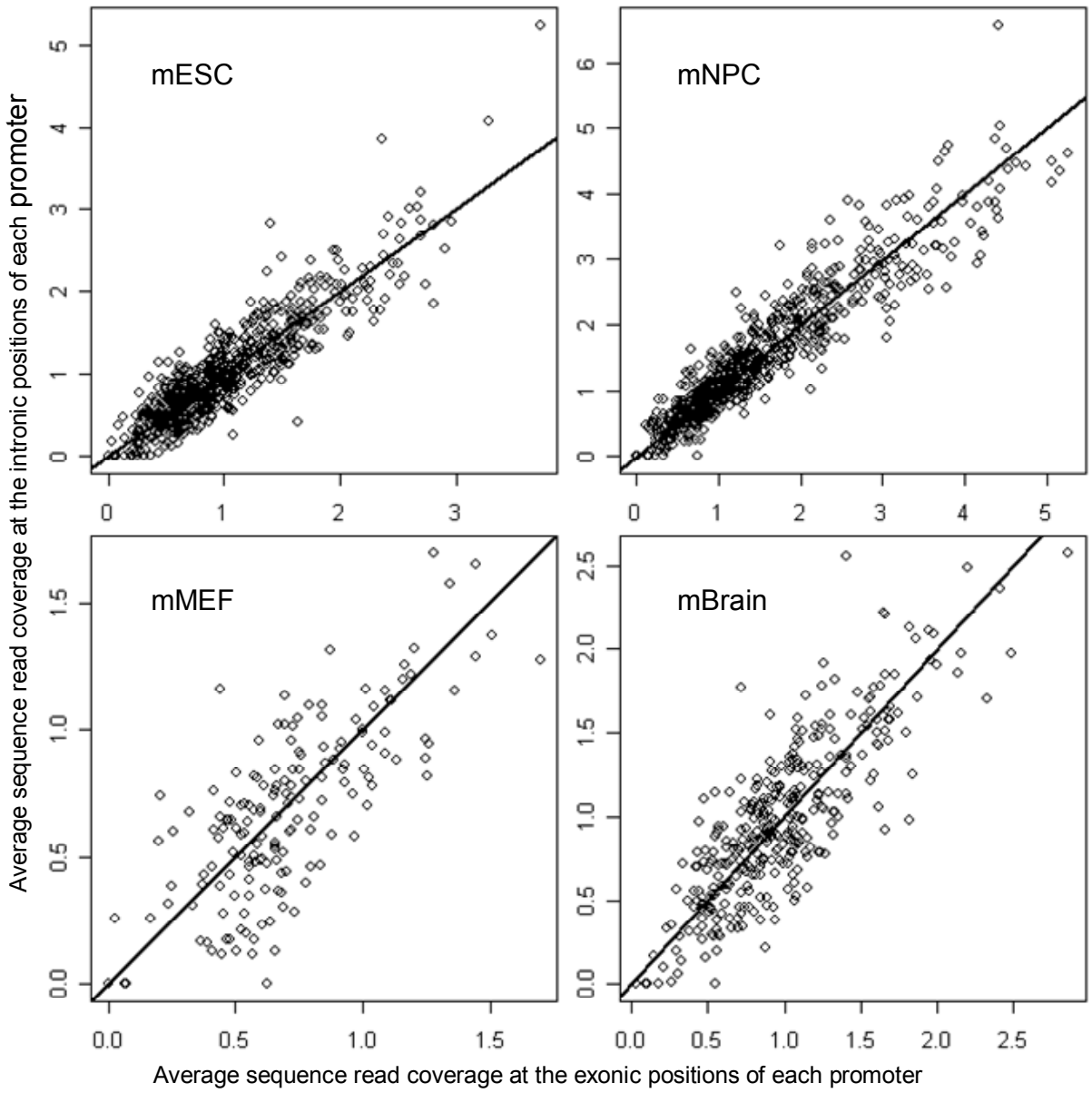


Supplementary Figure 1. The "pExon-length'" of the promoters marked with H3K27me3 and the promoters without H3K27me3 mark. **(A)** and **(B)** are for mouse cell lines and tissue. **(C)** is for human ES cells and the histone modifications were profiled using chip-seq or chip-chip technologies. The "conservative" promoter sets were used.



Supplementary Figure 2. The association between the "pExon-length" and H3K27me3 is independent of H3K4me3 **(A)** and CpG content **(B)**. The "conservative" promoter set was used.



Supplementary Figure 3. H3K27me3 signal at exonic positions vs. H3k27me3 signal at intronic positions. For each promoter marked with H3K27me3 modification, we calculated the sequence read coverage for each exonic and intronic position. The sequence reads were based on the chip-seq data for H3K27me3 modification in the mouse ES cells, NP cells, MEF cells, and brain tissue. Then the average read coverage for the exonic positions and the average read coverage for the intronic positions were calculated respectively and shown in the figure. The straight line is y = x. The "conservative" promoter set was used.