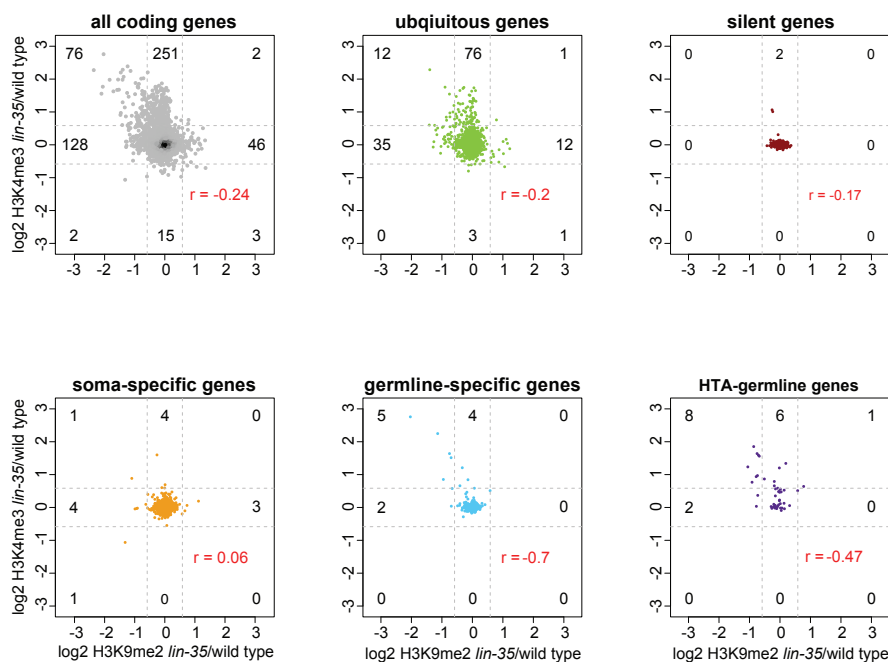
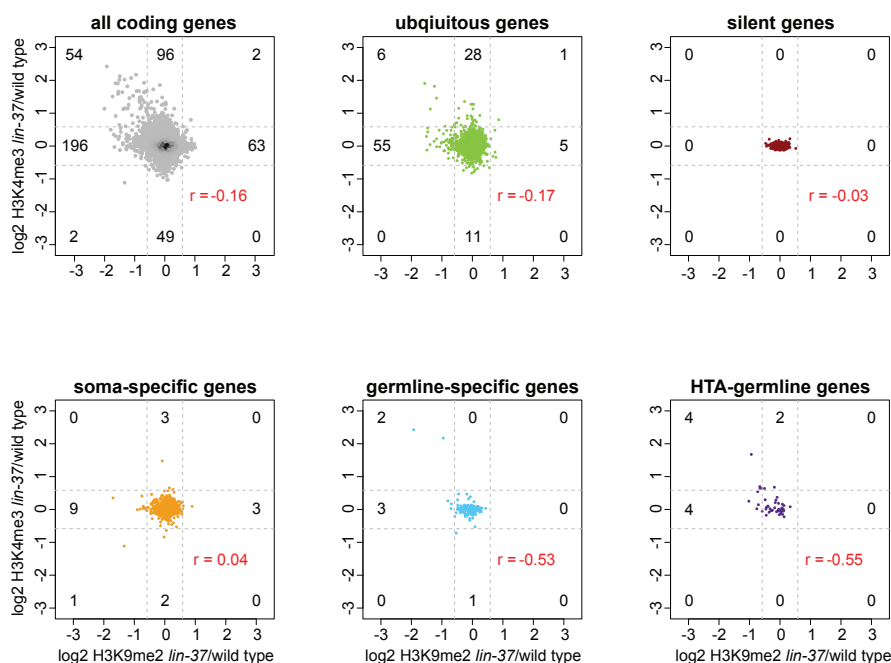


Figure S10

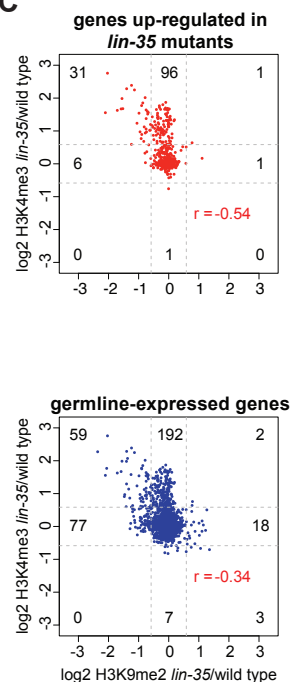
A



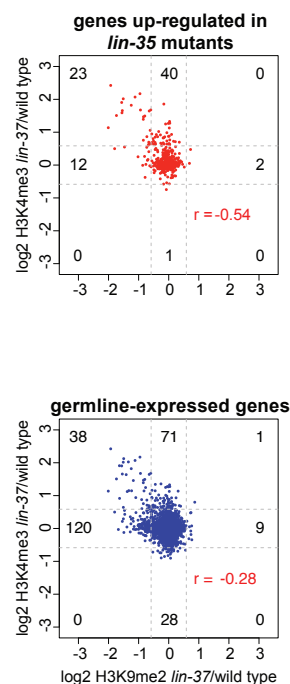
B



C



D



**Figure S10: H3K4me3 vs H3K9me2 in *lin-35* and *lin-37* mutants.** (A-D) Scatter plots of log2 fold change of the H3K9me2 signal in (A, C) *lin-35* mutant/wild type vs. log2 fold change of the H3K4me3 signal in *lin-35* mutant/wild type within 250 bp upstream and downstream of the transcript start site (TSS) at 20°C or (B, D) *lin-37* mutant/wild type vs. log2 fold change of the H3K4me3 signal in *lin-37* mutant/wild type within 250 bp upstream and downstream of the TSS at 20°C. (A, B) All coding genes and genes with ubiquitous, silent, soma-specific, germline-specific, or HTA-germline expression. (C, D) Genes up-regulated in *lin-35* mutants and germline-expressed genes. Dotted lines represent 1.5-fold cutoffs; the numbers of genes above and below the cutoffs are indicated. The r value shows the Pearson correlations between changes in H3K9me2 and changes in H3K4me3 for each set of genes.