Figure S11

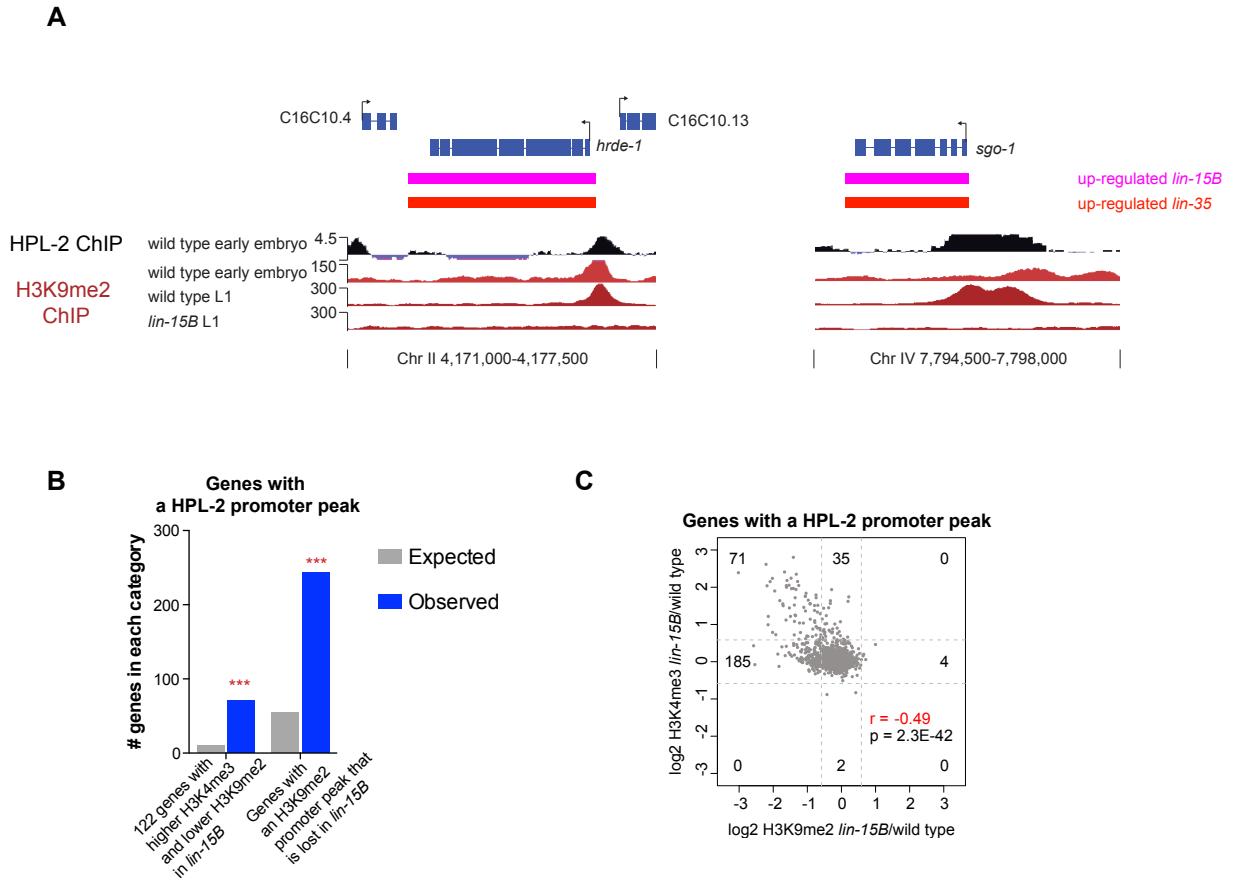

Figure S11: Analysis of HPL-2 binding compared to H3K9me2. (A) HPL-2 ChIP-chip and H3K9me2 ChIP-seq in wild type in early embryos and L1s, and in *lin-15B* mutant L1s, visualized on the UCSC genome browser at two genes *hrde-1* and *sgo-1* that are upregulated in synMuv B mutants. We found H3K9me2 broadly at the promoters of genes up-regulated in *lin-15B* mutants in early embryos in a similar pattern as in L1s. The vertical lines and arrows indicate the location of the transcript start site (TSS) and the direction of transcription. Locations of up-regulation in *lin-15B* (pink) and *lin-35* (red) are shown above are shown above ChIP signal tracks. ChIP signals shown are ChIP-chip z-scored log2 fold changes IP/Input and ChIP-seq reads scaled to 15 million total reads (see Materials and Methods). (B) Enrichment analysis of genes with a HPL-2 peak expected and observed among the 122 genes that showed reduced H3K9me2 promoter signal and increased H3K4me3 promoter signal in *lin-15B* mutants, and genes that have a called H3K9me2 promoter peak in wild type that is lost in *lin-15B* mutants. Significant over-enrichment (red) was determined by the hypergeometric test (*p-value < 0.01, **p-value < 1x10-5, ***p-value < 1x10-10). (C) Scatter plots of log2 fold change of the H3K9me2 signal over the TSS in *lin-15B* mutant/wild type vs. log2 fold change of the H3K4me3 signal over the TSS in lin-15B mutant/wild type. The signal was calculated within 250bp upstream and downstream of the transcript start site (TSS) at 20°C. Shown are genes with a HPL-2 peak. Dotted lines represent 1.5 fold cutoffs; the numbers of genes above and below the cutoffs are indicated. The r value shows the Pearson correlation between log2 fold change in H3K9me2 and in H3K4me3 for genes with a HPL-2 promoter peak. 71 of 122 genes with at least a 1.5 fold decrease in H3K9me2 and a 1.5-fold increase in H3K4me3 in lin-15B mutant/wild type have a HPL-2 peak in their promoter (p-value = 2.4*10^-42, hypergeometric test)