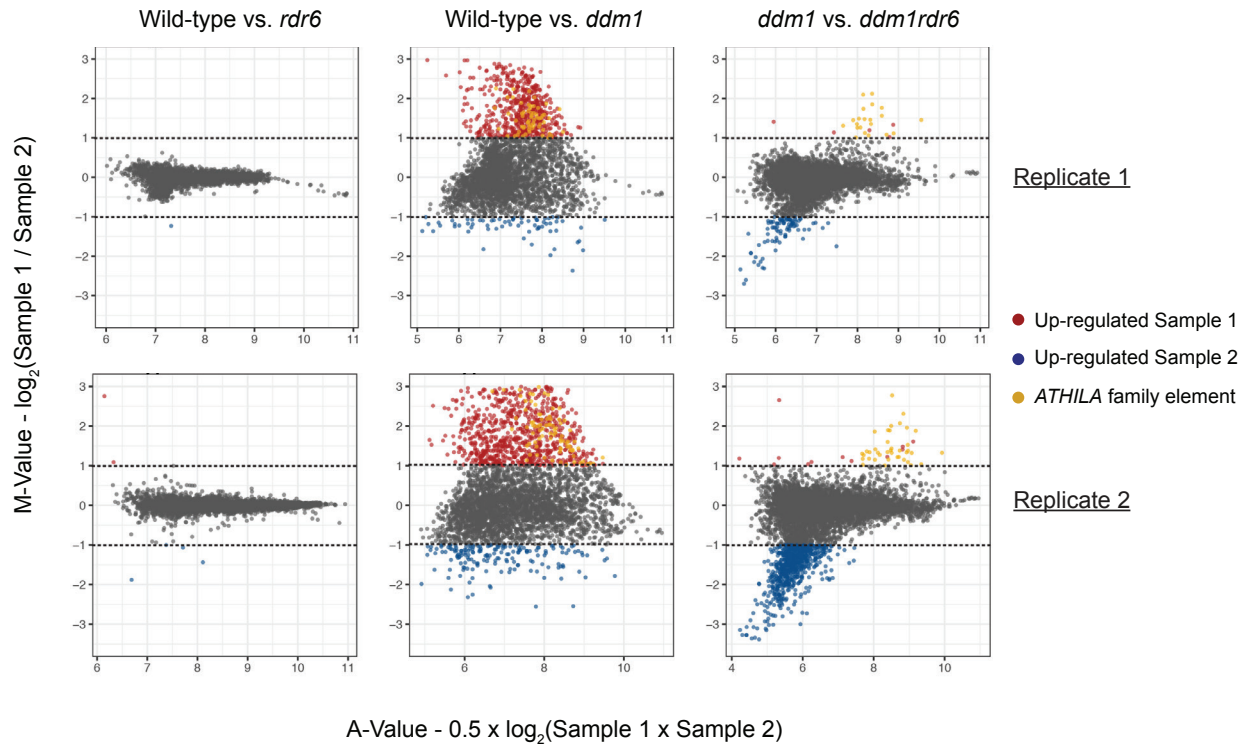
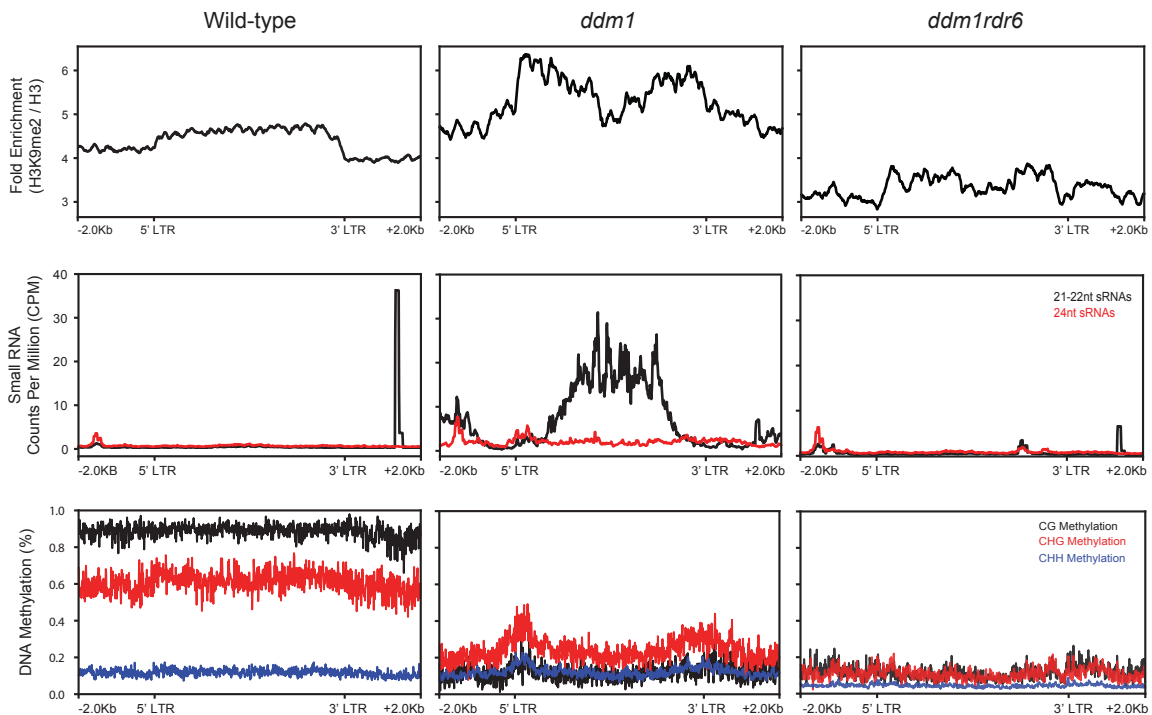


A**B**

Supplemental Figure S6. Meta-analysis of H3K9me2, small RNAs, and DNA methylation. (A) MA plots of H3K9me2 ChIP-seq data for wild-type, *ddm1*, and *ddm1rdr6*. Pairwise comparisons between genotypes revealing global changes in H3K9me2. \log_2 fold changes between Sample 1 and Sample 2 (M-value) are plotted against average read density between samples (A-value). Points represent ChIP-seq peaks that are up-regulated in Sample 1 (red), up-regulated in Sample 2 (blue), or not significantly different (gray). Annotated *ATHILA* family elements that are differentially regulated between samples are highlighted in yellow. (B) Metaplots depicting H3K9me2, small RNAs, and DNA methylation levels at the 73 most significantly affected *ATHILA* family elements across wild type, *ddm1*, and *ddm1rdr6* genotypes. Small RNA and DNA methylation data were obtained from a previously published study (Creasey et al., 2014).