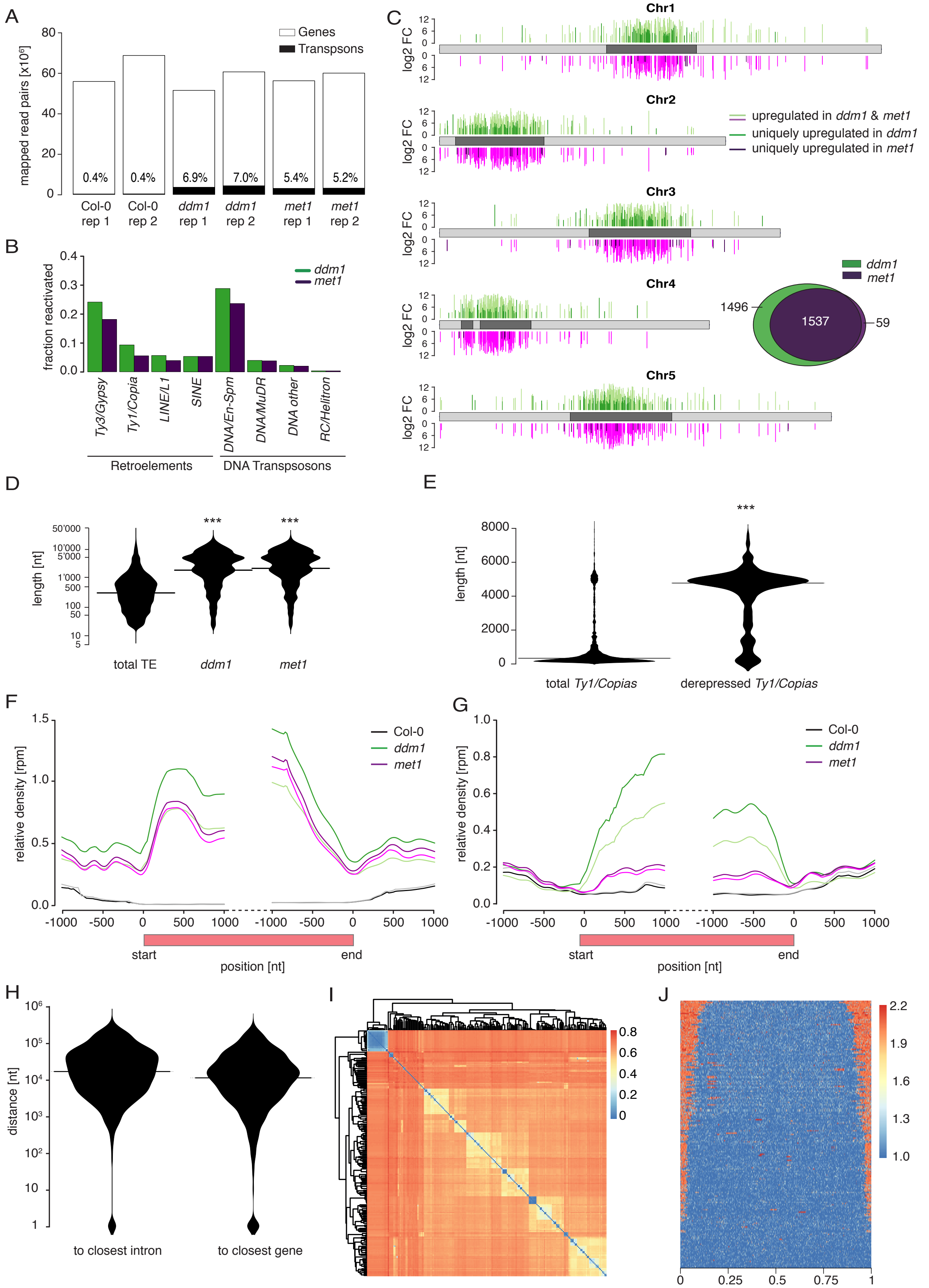

Supplemental Figure S1. Transcriptome analysis of *A. thaliana* TEs.
(A) TE contribution to the global *A. thaliana* transcriptome displayed by the proportion of mapped read pairs from total RNA-seq of genes and transposons. (B) Fractions of transcriptionally reactivated transposon superfamilies compared to total elements in the *A. thaliana* genome. (C) Chromosomal distribution and log2 expression fold change (log2 FC) of transcriptionally reactivated transposons in respect to wild type Col-0 plants. Dark gray bars mark pericentromeric regions and light gray chromosomal arms. The inset graph shows a Venn diagram of those significantly upregulated single TEs in the *ddm1* and *met1* backgrounds. (D) Length distribution of total and de-repressed TEs in *ddm1* and *met1* backgrounds. Solid line: background-specific median values. (E) Length distribution of total versus de-repressed *Ty1/Copia* elements as in (D). (F) Kernel density plot of sequence coverage in reads per million (rpm) around 3' and 5' borders of significantly upregulated transposons. (G) Density plot as in (F) showing sequence coverage of the full-length *Ty1/Copia* elements used for splice junction detection (see Fig. 2A). (H) Distances in nucleotides (nt) between all TEs upregulated in either met1 or ddm1 background and their closest genes and introns. (I) Clustered heatmap showing the inter element dissimilarity of full-length *Ty1/Copia* elements sequences used for splice junction detection. (J) Intra element sequence identity using nine nucleotide long sliding windows of the elements from (I). Identity scores of two around the 3' and 5' borders highlight the presence of long terminal repeats. In all figures: (***) $p < 0.001$ (Wilcoxon rank-sum test).