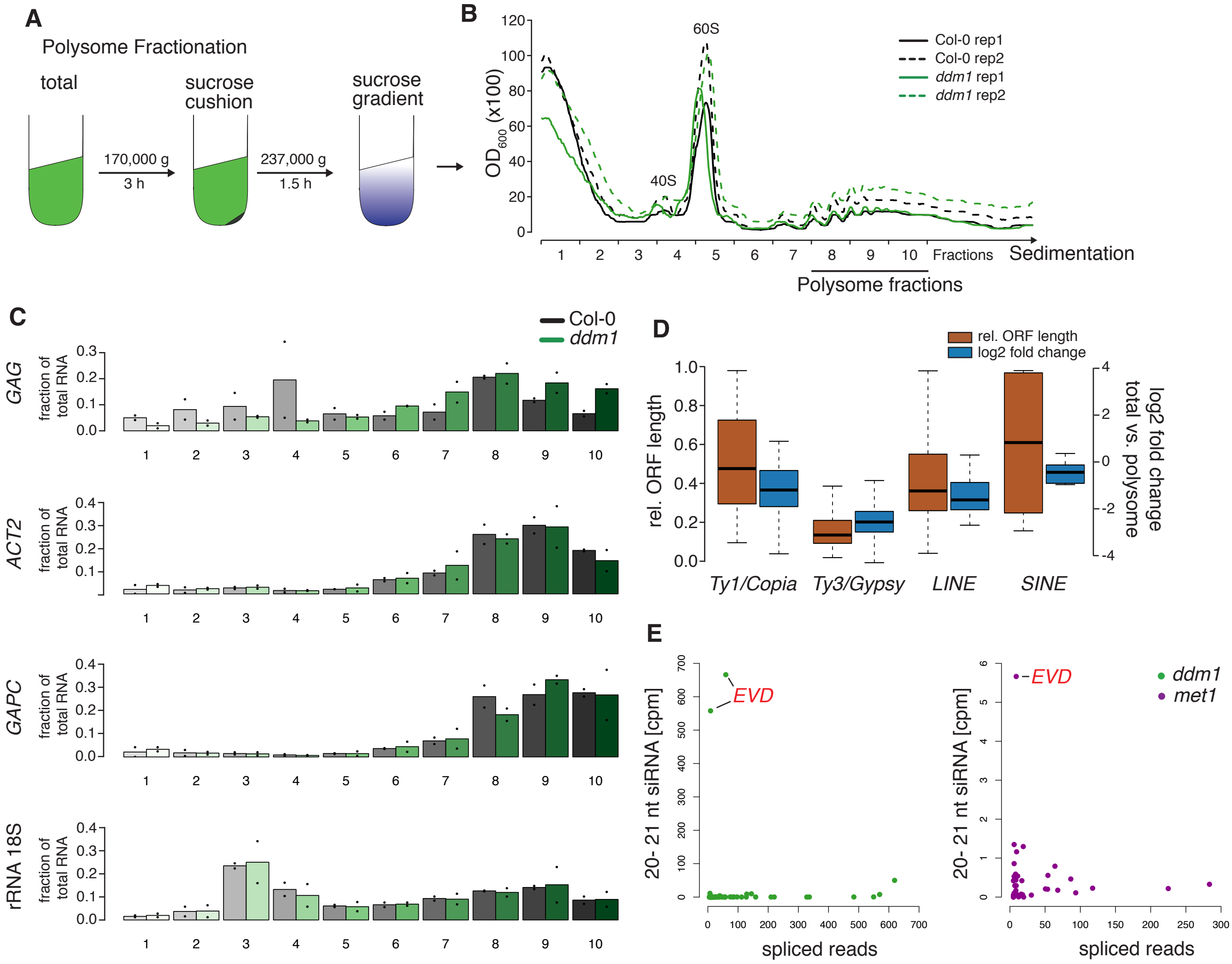

Supplemental Figure S5. Differential polysome association and siRNA production of de-repressed transposons.
(A-B) Two-step polysome fractionation protocol yielding (B) resolvable monosomal and polysomal fractions. (OD600) optical density at 600nm. (C) qRT-PCR analysis of *EVD GAG*, *ACT2* (AT3G18780), *GAPC* (AT3G04120) mRNAs and of the 18S rRNA (AT3G41768) of the ten separated ribosomal fractions (fractions 4-5: monosomes; fractions 8-10: polysomes). Histograms display the mean of two independent replicates indicated by black dots. The values are displayed as the ratio between RNA accumulation found within each individual fraction and total RNA levels across all fractions. (D) ORF-length-dependent polysome association of various retroelement superfamilies in *A. thaliana*. (E) Comparison between levels of spliced reads, reflecting shGAG mRNA abundance, and 20-21-nt siRNAs of upregulated TEs in *ddm1* (green) and *met1* (magenta) backgrounds.