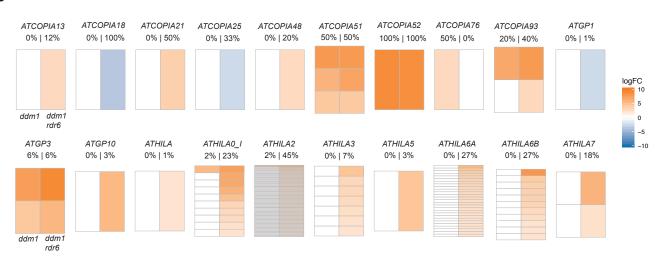


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Supplemental Figure S2. Genome-wide analyses of VLP DNA products in *ddm1* **and** *ddm1rdr6***.** (A) 3 replicate libraries of short sequencing reads (Illumina) and long sequencing reads (Oxford Nanopore) from VLP DNA samples were aligned to the Arabidopsis genome. Peaks of read alignments unique to *ddm1* and *ddm1rdr6* correspond to LTR retrotransposon loci that produce VLP DNA, whereas wild-type (WT) samples share DNase-insensitive background regions. Dashed lines indicate *EVADE*. Density of transposable elements (TE) and genes is shown. (B) Heat maps of log2 fold changes of VLP DNA enrichment in *ddm1rdr6* for LTR retrotransposons. Each *ddm1* and *ddm1rdr6* genotype was compared to WT to calculate fold changes from short-read replicate samples. The percentages of significantly enriched TEs within the family for each genotype are shown above the heatmaps.