

'Jumping genes' help plants adapt to extreme temperature and pathogens

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Epigenetic regulation of TE-ATTS. a Representative genome loci showing Epi-ATE-G isoform production with TE-ATTS events. Tracks (from top to bottom): ChIP-seq data for RNA Pol II phosphorylated at Ser5/Ser2 in CTD repeats (bins per million); ChIP-seq data for IBM2 and EDM2 localization (bins per million); Col-0 ChIP-seq of H3K9me2 (reads per million); methylation levels of Col-0 in CG, CHG, and CHH contexts (0–100%); poly(A) sites obtained from the PlantAPA database; DRS read alignments of Col-0 and indicated mutants; TE and transcript annotations of AtRTD3 and DRS-AtRTD3 in this study and the



orientation of genes and TEs. b Metaplots for ChIP-seq signals of Pol II (Ser2P), IBM2, EDM2, and H3K9me2 over TEs with ATTS (isoform switching with q

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