Supplemental Figures and Legends

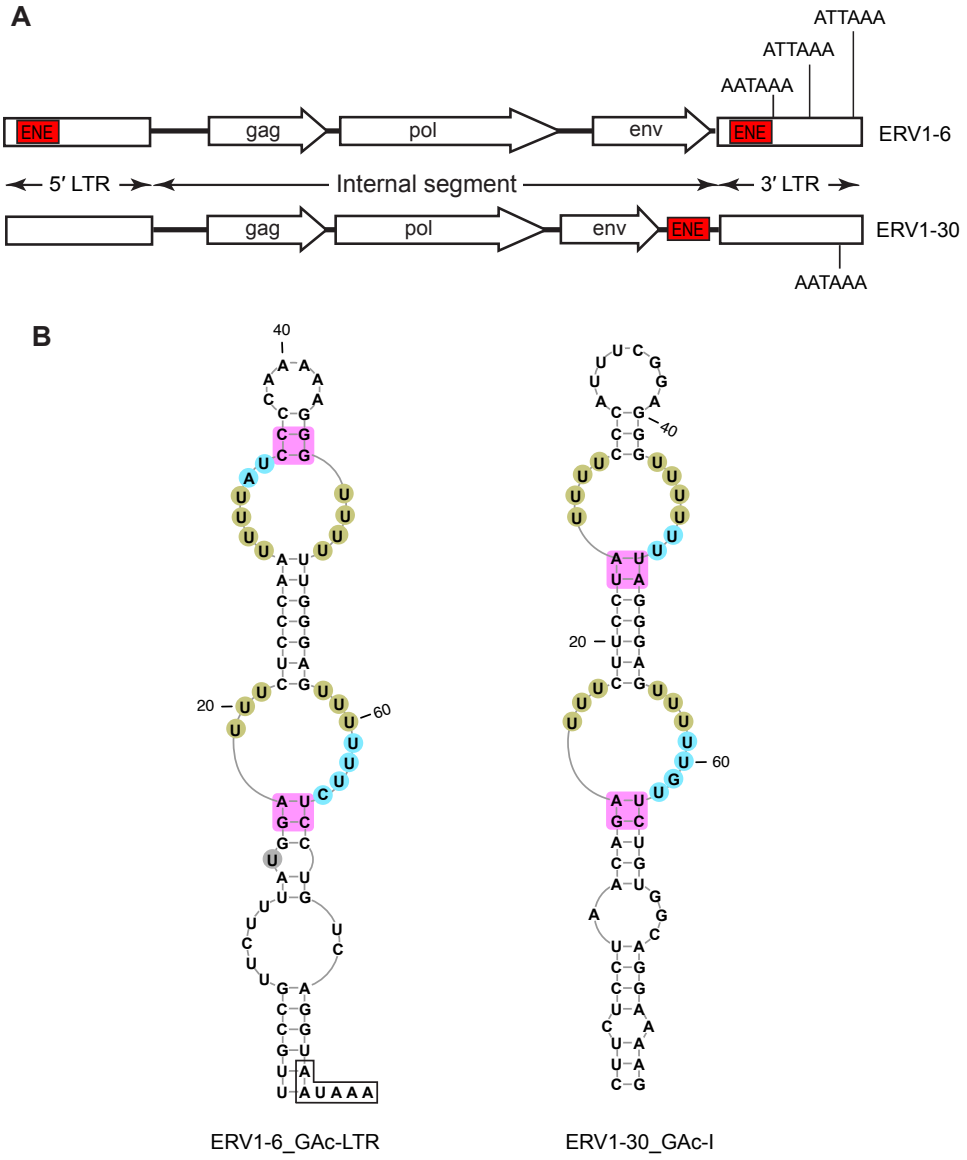

Figure S1. ENEs identified in stickleback ERVs, Related to Figure 2
(A) Schematic of two ERVs with the position of ENEs and possible polyadenylation signals shown. (B) Predicted secondary structures of stickleback ENEs. A polyadenylation signal in ERV1-6_GAc-LTR is boxed. Nucleotide shading is as described in Figure 2.

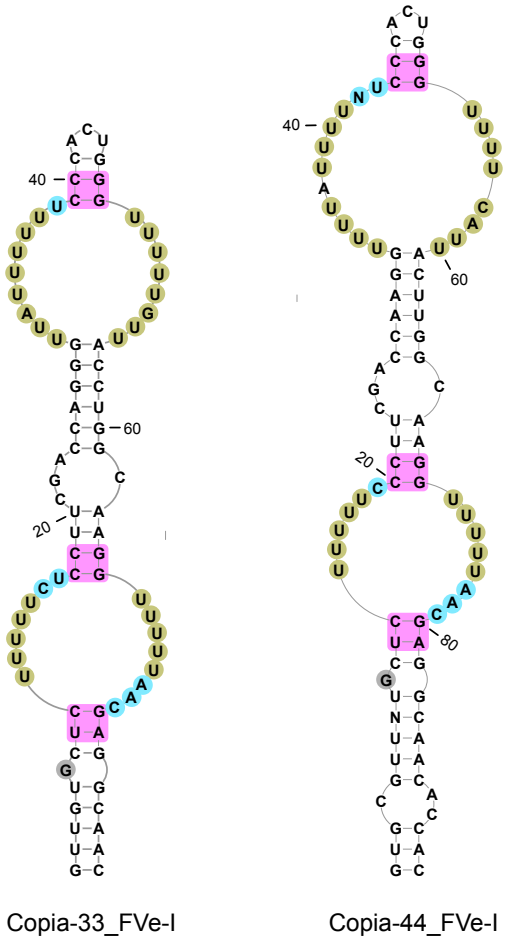

Figure S2. ***Fragaria*** **ENEs, Related to Figure 2**
Nucleotide shading is as described in Figure 2. Note that the upper domain of Copia-33_FVe-I may form an A•A-G triple, while that of Copia-44_FVe-I may include two noncanonical triples , U•A-C and U•A-A, with an A bulge.

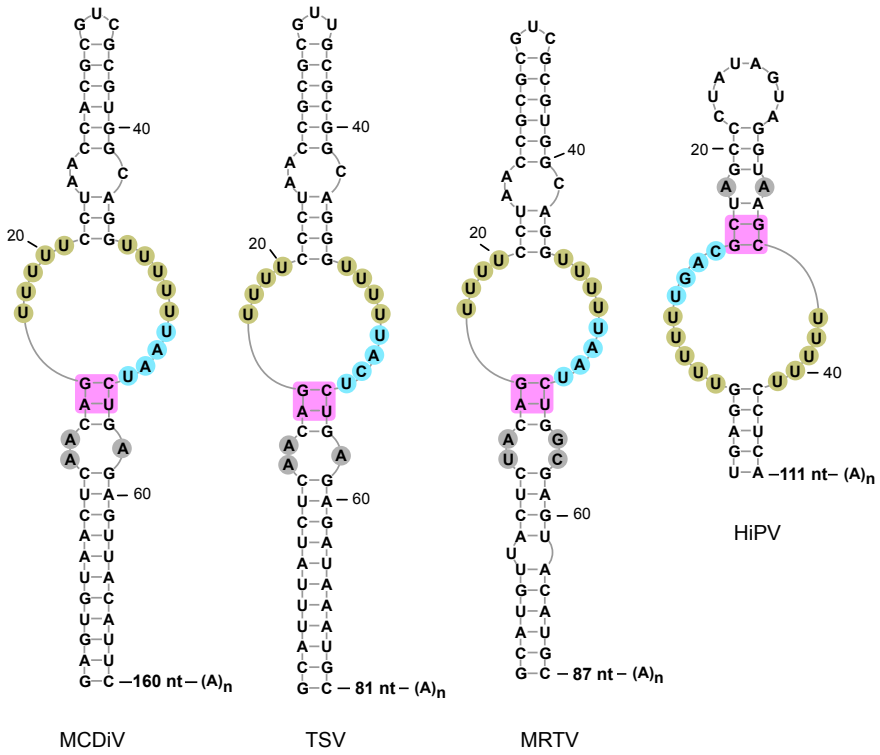

Figure S3. ENEs from Dicistroviruses, Related to Figure 3
Nucleotide shading is as described in Figure 2.

Supplemental Tables

Table S1. hAT transposons included in the phylogenetic tree shown in Figure 7
TEs with experimentally-demonstrated transposition activity are in bold.

TE name	Organism	Evidence for introns in the tranposase gene	References
Ac	*Zea mays*	cDNA sequencing	(Kunze et al., 1987)
Crypt1	*Cryphonectria parasitica*	RT-PCR	(Linder-Basso et al., 2001)
Dart	*Oryza sativa*	RT-PCR	(Fujino et al., 2009; Smith et al., 2012)
Folyt1	*Fusarium oxysporum*	RT-PCR	(Gomez-Gomez et al., 1999)
Mx	*Zea mays*	predicted	(Xu and Dooner, 2005)
restless	*Tolypocladium inflatum*	cDNA sequencing	(Kempken and Kuck, 1996)
Tag1	*Arabidopsis thaliana*	cDNA sequencing	(Liu and Crawford, 1998)
Tag2	*Arabidopsis thaliana*	cDNA sequencing	(Henk et al., 1999)
Tam3	*Antirrhinum majus*	cDNA sequencing	(Hehl et al., 1991)
TCUP	*Zea mays*	RT-PCR	(Smith et al., 2012)
Thelma13	*Silene latifolia*	cDNA sequencing	(Pritham et al., 2003)
Br1	*Brassica rapa*	Bioinformatics prediction	This paper
hAT-3	*Sorghum bicolor*	Bioinformatics prediction	This paper
ZhAT3	*Zea mays*	Bioinformatics prediction	This paper
hAT-15	*Zea mays*	Bioinformatics prediction	This paper
Mn1	*Morus notabilis*	Bioinformatics prediction	This paper
Si1	*Setaria italica*	Bioinformatics prediction	This paper
TWIFB1	*Oryza sativa*	EST-based annotation	(Itoh et al., 2007)
TWIFBIG	*Oryza sativa*	Bioinformatics prediction	This paper

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