Table 2. Complete and partial plant MLEs identified in GenBank (September 2001 release) and animal MLEs included in phylogenetic analyses

MLE clade/species	Name	Acc	Chr	Position	Size, bp	TIRs, bp
DD39D plant MLEs						
Glycine max	*Soymar1*	AF078934	ND	1-3491	3,491	40
Oryza sativa	*Osmar1*	AF172282	11	227526-232784	5,259	26
	Osmar2	AP000836	1	36040-41604	5,565	31
	Osmar2b	AP003294	1	104503-109697	5,195	31
	Osmar3	AL442115	4	76624-78029*	ND	ND
	Osmar4	AP003574	6	44316-49338	3,226	29
	Osmar5	AP002864	6	9230-9480*	ND	ND
Arabidopsis thaliana	*Atmar1*	AF262043	5	65593-66782*	ND	ND
	Atmar2	AC007662	2	4197-3071*	ND	ND
	Atmar3	AF272705	5	54282-55498*	ND	ND
	Atmar4	AC006423	1	83021-83759*	ND	ND
	Atmar5	AB005236	5	20260-19674*	ND	ND
	Atmar6	AL161498	4	88528-89423*	ND	ND
	Atmar7	AC006436	2	30673-29880*	ND	ND
	Atmar8	AC005169	2	50179-50773*	ND	ND
	Atmar9	AL161513	4	138936-138204*	ND	ND
DD37D animal MLEs						
Caenorhabditis elegans	*Ce37mar1*	AC006622	4	9089-10370	1,282	24
Sarcophaga peregrina	*Sp37mar1*	AB054644	ND	21-1179	1,158	25
Bombyx mori	*Bmmar1*	U47917	ND	1-1307	1,307	28
DD34D animal MLEs						
Drosophila mauritiana	*Mos1*	X78906	ND	1-1293	1,293	28
Ceratitis capitata	*Ccmar1*	U40493	ND	1-1268	1,268	30
Homo sapiens	*Hsmar1*	U52077	#	1-1287	1,287	30
	Hsmar2	U49974	#	1-1301	1,301	31

Acc, GenBank accession number; Chr, chromosome number; ND, non determined. The ends of several rice elements were defined by identification of terminal inverted repeats (TIRs) highly similar to those of *Soymar1* and *Osmar1* in the DNA flanking the putative transposase. In some other cases (*), eNDs of MLEs were not determined, and coordinates thus refer to regions similar to MLE transposases; #, consensus sequence. *Soymar1, Osmar1, Bmmar1, Mos1, Ccmar1, Hsmar1, and Hsmar2* were previously described (see text for references).