

Supplemental Table S1
Sequences homologous to *rMx* and *Mx* in the maize GSS database

Sequence analysis of GenBank GSS database								
ID	5' TSD	5' TIR	3' TIR	3' TSD	Sequence length	% identity to <i>rMx</i> 180-bp end	% identity to <i>Mx</i> 180-bp end	No. CCCGAA + TTCGGG
1a. Sequences adjacent to <i>rMx</i>-like 5' TIR								
<i>rMx</i>	GTGGAGGA	<u>TAG</u> CACTGGGCAT			180	100	76	4 + 1
BZ368767	gtaagagt	<u>TAG</u> CACTGGGCAT			100	91	72	
BZ982159	tgtgtagc	<u>TAG</u> CACTGGGCAT			175	82	69	2 + 0
CG888784	ggtgacgg	<u>TAG</u> CACTGAGCAT			171	82	66	3 + 0
CG088731	cctccagg	<u>TAG</u> CACTGGGCAT			180	80	65	3 + 1
CC356586	ggcgcgaa	<u>TAG</u> CACTGGGCAT			180	75	67	6 + 0
CC369107	ggtggcag	<u>TAG</u> CACTAGGCAT			180	73	53	1 + 0
1b. Sequences adjacent to <i>rMx</i>-like 3' TIR								
<i>rMx</i>			<u>ATG</u> CCCAGTCCTA	GTGGAGGA	180	100	74	7 + 3
BZ672184		same sequence	<u>ATG</u> CCCAGTCCTA	gtaaagac	144			
CG058007			<u>ATG</u> CCCAGTCCTA	gtaaagac	111			
CG110562			<u>ATG</u> CCCAGTCCTA	gtaaagac	180	96	72	5 + 2
CG064758		pairs with BZ368767? they do not overlap.	<u>ATG</u> CCCAGTCCTA	gtaagagt	180	96	72	4 + 3
CG149316			<u>ATG</u> CCCAGTCCTA	ctcacaac	180	81	57	2 + 3

Bold: invariant TIR nucleotides characteristic of either *Mx* or *rMx* type elements
Underline: nucleotides different from consensus TIR

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ID	5' TSD	5' TIR	3' TIR	3' TSD	Sequence length	% identity to <i>rMx</i> 180-bp end	% identity to <i>Mx</i> 180-bp end	No. CCCGAA + TTCGGG
2a. Sequences adjacent to <i>Mx</i> -like 5' TIR								
<i>Mx</i>	cactacac	TCACAGTGGGCAT			180	72	100	6 + 1
ZMMBMa0346A06	gatgagat	TCACAGTGGGCAT			180	71	99	6 + 1
ZMMBTa466O06	gatgagat	ACACAGTGGGCAT	same sequence; A is error					
ZMMBMa0397E15	acttgaag	TCACAGTGGGCAT	same sequence		178	71	95	5 + 1
ZMMBPa0063H11	acttgaag	TCACAGTGGGCAT						
ZMMBTa0640E17	ctagcgag	TCACACCGGGCAT			180	69	92	5 + 1
ZMMBTa403G10	ccaccaat	TCACACTGGGCAT	same TSD as ZMMBTa0786H18		180	63	82	3 + 1
ZMMBTa0543N15	ccaccaat	TCACACTGGGCAT	same sequence					
2b. Sequences adjacent to <i>Mx</i> -like 3' TIR								
<i>Mx</i>			ATGCCCAGCGTGA	cactacac	180	74	100	7 + 3
ZMMBTa066D13		probable seq. Error (end of sequence)	ATGCCCAGCG_GA	end of sequence	179	75	98	7 + 3
ZMMBTa399I15			ATGCCCAGCGTGA	gtttgatc	180	74	97	6 + 4
ZMMBTa376A09		same sequence	ATGCCCAGCGTGA	actaaagg	180	74	96	6 + 3
ZMMBTa442N13			ATGCCCAGCGTGA	actaaagg				
ZMMBTa350F01		same sequence	ATGCCCAACGTGA	gggtatga	180	68	93	5 + 3
ZMMBTa0764K21			ATGCCCAACGTGA	gggtatga				
ZMMBTa0685J03			ATGCCCAGAGTGA	gtgtatcc	180	69	93	4 + 1
ZMMBTa0639F10			ATGCCCAGCGTGA	gtatacac	180	69	91	5 + 3
ZMMBTa0786H18		same TSD as ZMMBTa40	ATGCCCAGCGTGA	ccaccaat	180	64	89	3 + 2
ZMMBTa0599F07		same sequence	ATGCCCAGCGTGA	ccaccaat				

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