

NAME		FUNCTION	GENE	Accession		Coordinates	SIZE (NT)
					PROTEIN		
Maize	MS45	strictosidine synthase	AF360356	LOC_Os03g15710	AAK52489	Chr3:8645330-8645830 (reverse complemented) TIGR	500
RICE			AT3G59530	NP_974462		Chr3:22004091 - 22004688 (TAIR version 6.0)	597
Arabidopsis							
Maize	MS26	cytochrome P450	AF366297	LOC_Os03g07250	AAK52956	Chr3:3680399-3681071 (reverse complemented) TIGR	672
RICE			AT1G69500	NP_177109	XP_470289	Chr1: 26127176-26127762 (TAIR version 6.0)	586
Arabidopsis							
Maize	5126	chalcone and stilbene synthase	AX060770	LOC_Os07g22850	NP_912707	Chr7:12882446-12883053 (reverse complemented) TIGR	607
RICE			AT4G34850	NP_567971		Chr4: 16607608 - 16608354 TAIR v6.0 (11 Nov 2005)	746
Arabidopsis							
Maize	BS7	dihydroflavonol 4-reductase	AF366295	LOC_Os08g40440	AAK52955	Chr8:	
RICE			AT4G35420	NP_195268	BAC78578	Chr4: 16835571 - 16836340 TAIR v6.0 (11 Nov 2005) (reverse complemented)	769
Arabidopsis							

Figure 1. Source information for orthologous promoters.

Figure 2. Complementary suppression constructs determine the progeny phenotype.

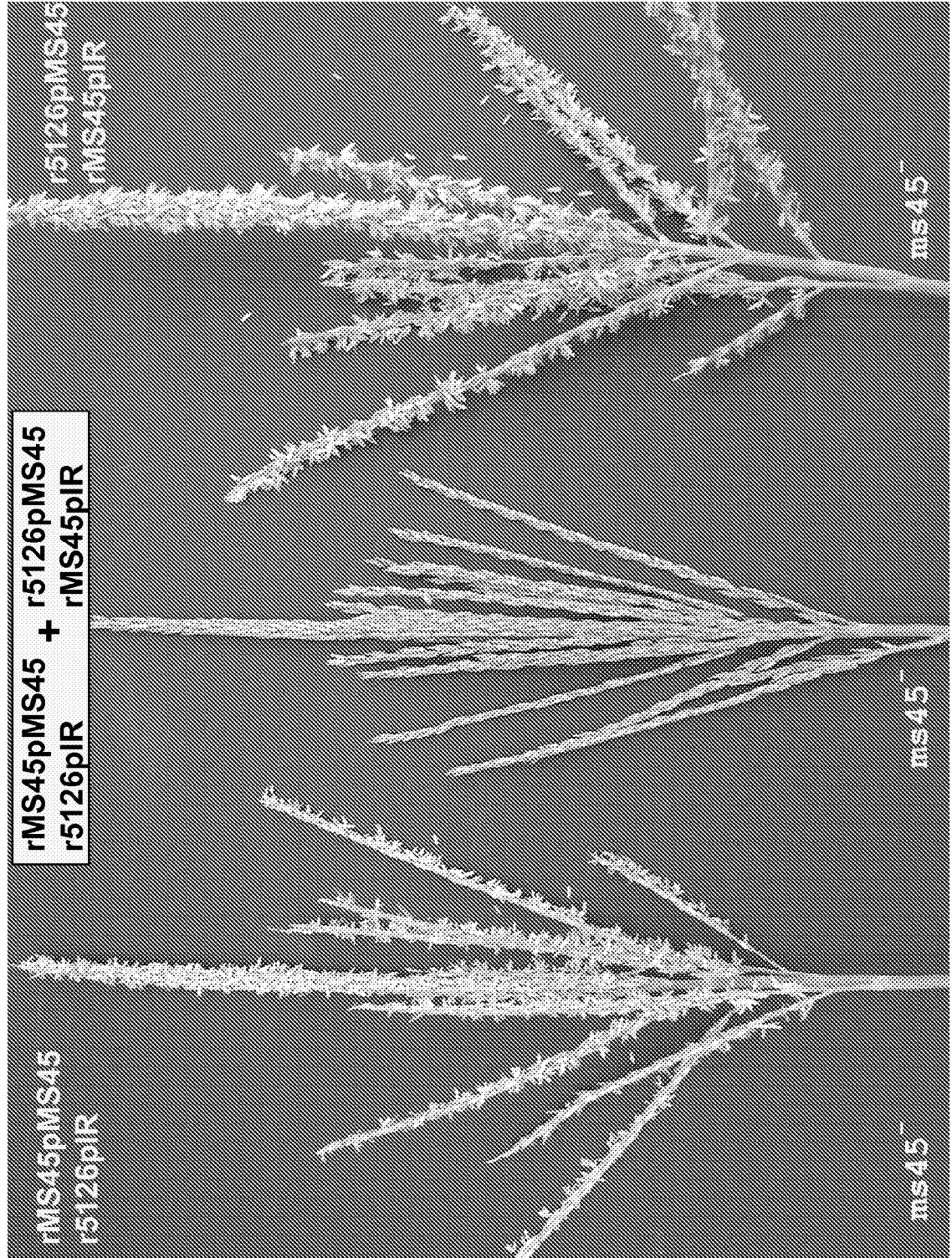
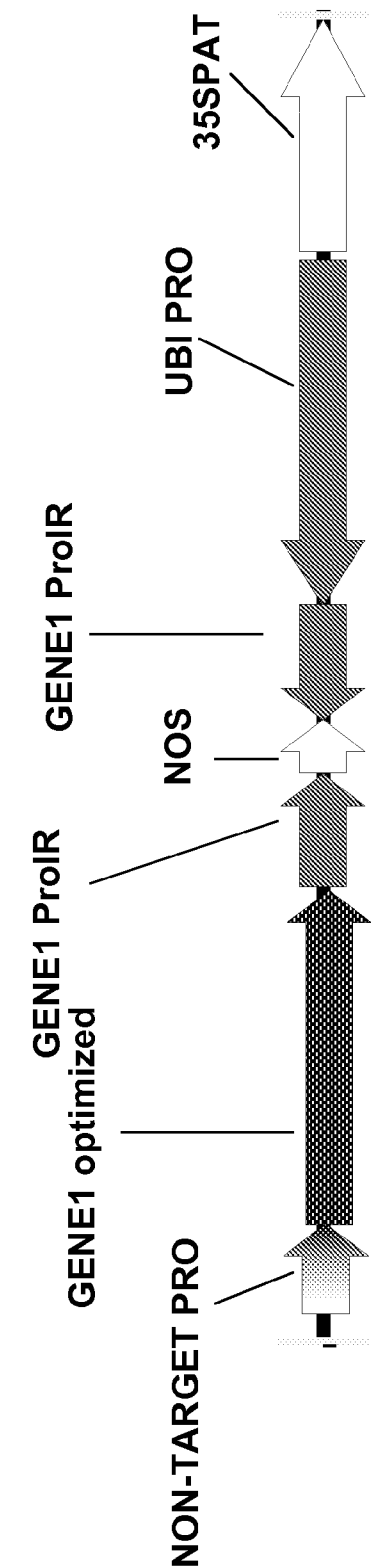


Figure 4. Generic complementation/suppression TDNA Vector Design



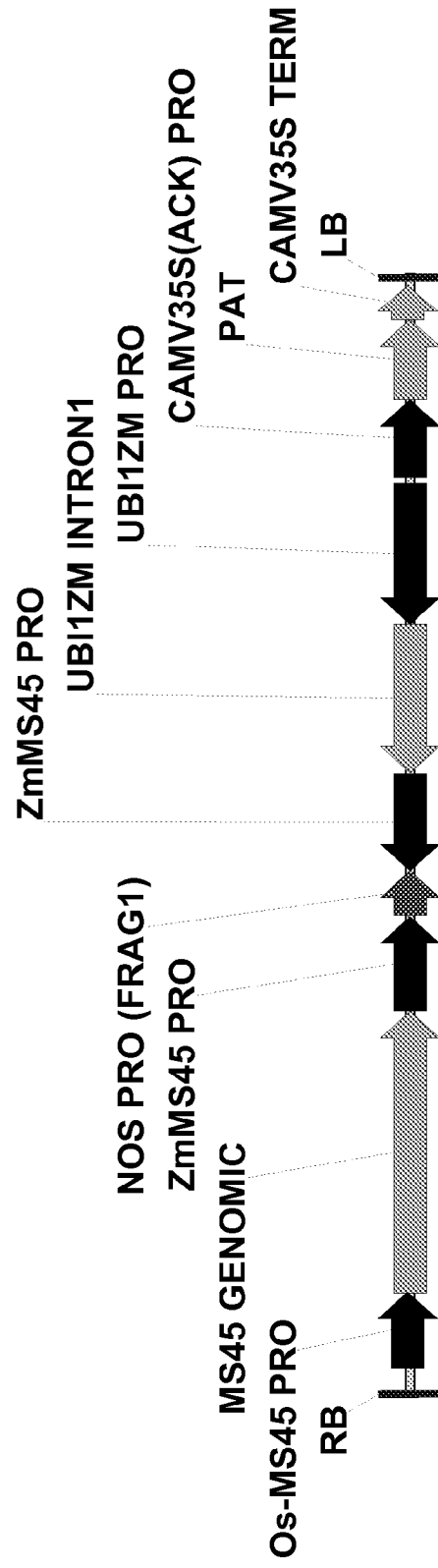


Figure 5. MS45 Complementation/Suppression T-DNA vector design.

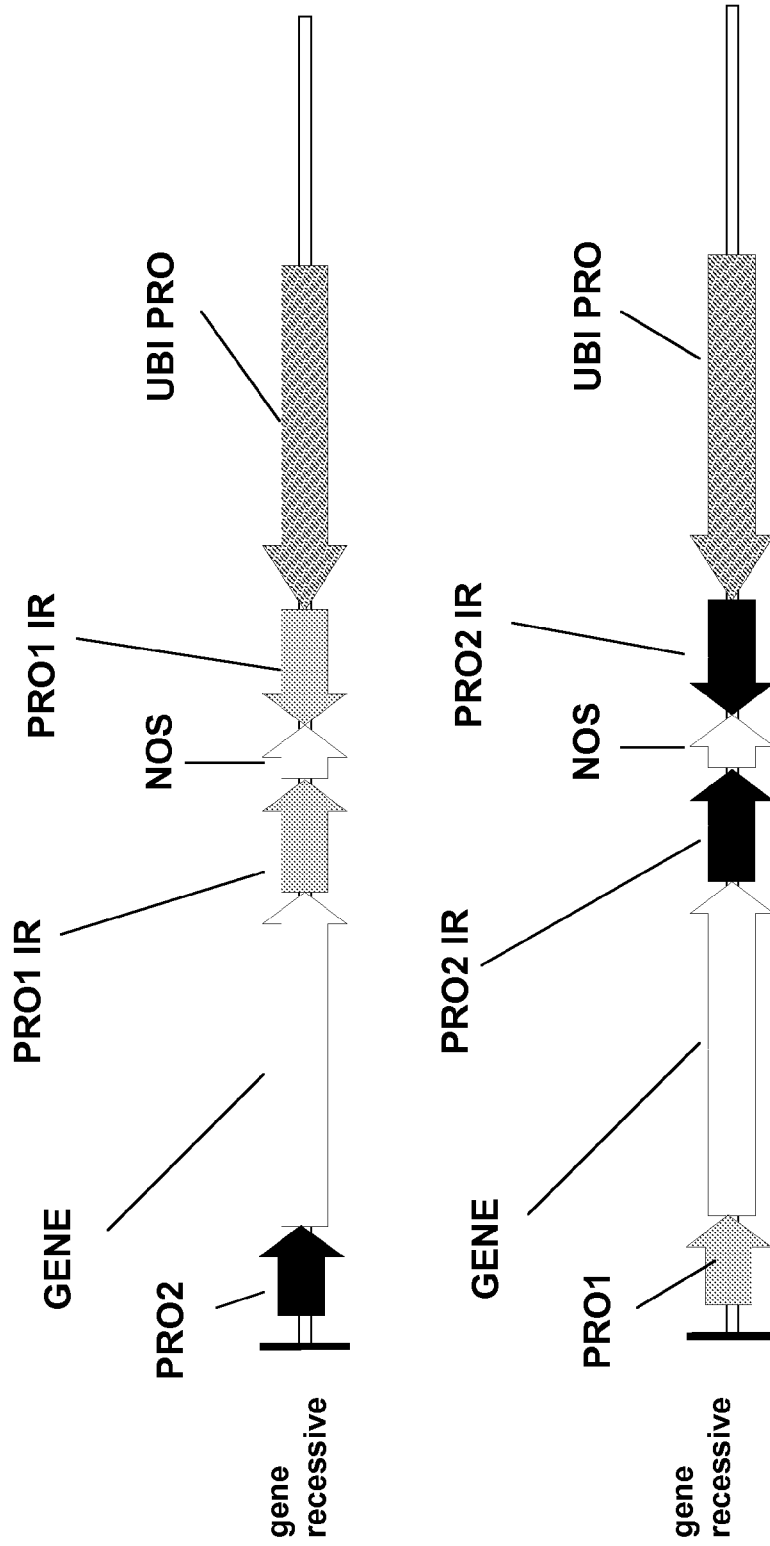


Figure 6. Maintenance of recessive lethals using a complementation/suppression T-DNA vector design