

Additional file 2. Allele-specific DNA markers that distinguish recessive alleles from dominant functional ones at the maturity loci, *E1*, *E2*, *E3* and *E4*, and a determinate growth habit locus, *Dt1*, in soybean

Locus	Allele	Primer sequence (5' - 3')	Marker type	Restriction enzyme	Sizes of amplified fragments and digested fragments (bp)	Reference
<i>E1</i>	<i>e1-fs/e1-nl</i>	F CACTCAAATTAAGCCCTTTCA R TTCATCTCCTCTTCATTTTGTG	CAPS	<i>Hinf</i> I	<i>E1/e1-as</i> 186 + 36 <i>e1-fs</i> 136 + 46 + 36 <i>e1-nl</i> No amplification	[13], this study
	<i>e1-as</i>	F TCAGATGAAAGGGAGCAGTGTCAAAGAAGT R TCCGATCTCATCACCTTTCC	dCAPS	<i>Taq</i> I	<i>E1/e1-fs/e1-nl</i> 444/443 <i>e1-as</i> 413+31	[13]
<i>E2</i>	<i>e2</i>	F AAGCCTATGCCAGCTAGGTATTT R GAAGCCCATCAGAGGCATGTCTTATT	dCAPS	<i>Dra</i> I	<i>E2</i> 110 <i>e2</i> 27+83	[29]
<i>E3</i>	<i>e3-tr</i>	F TGGAGGGTATTGGATGATGC R1 CTAAGTCCGCCTCTGGTTTCAG R2 CGGTCAAGAGCCAACATGAG R3 GTCCTATACAATTCTTTACGACG	FLP		<i>E3-Misuzudaizu</i> 1,339 <i>E3-Harosoy</i> 558 <i>e3-tr</i> 275	[30]
	<i>e3-fs</i>	F GGGATAGTTCTGATGCTGTTCAA R CCTTGATATCGATAGCATATGTGCT	CAPS	<i>Ale</i> I	<i>E3</i> 552 + 206 <i>e3-fs</i> 759	This study
	<i>e3-ns</i>	F GTTGAAGAGAAGATCACAACA R GATGAACATAATTCCCTAACTGCA	dCAPS	<i>Mfe</i> I	<i>E3</i> 163 <i>e3-ns</i> 140 + 23	This study
	<i>e4-oto</i>	F CCCAGACACTCTTGTGTGAT R CCATACTCTCGGTATCTTTG	CAPS	<i>Sac</i> I	<i>E4</i> 535 <i>e4-oto</i> 439 + 96	[31]
	<i>e4-tsu</i>	F CACCCTAGGAGTTGTGTTGTT R GCGGTTCTGTACAATTGCCTGATA	dCAPS	<i>Eco</i> RV	<i>E4</i> 355 <i>e4-tsu</i> 332 + 23	[31]
<i>E4</i>	<i>e4-kam</i>	F CTTAATAAAGCCATGACTGGTTTG R CTTGAGTTTCAATGAGGTTTCAAC	CAPS	<i>Afl</i> II	<i>E4</i> 494 <i>e4-Kam</i> 286 + 208	[31]
	<i>e4-kes</i>	F CTTAATAAAGCCATGACTGGTTTG R CTTGAGTTTCAATGAGGTTTCAAC	CAPS	<i>Bsp</i> HI	<i>E4</i> 494 <i>e4-Kes</i> 399 + 95	[31]
	<i>e4-SORE-1</i>	F AGACGTAGTGCTAGGGCTAT R1 GCATCTCGCATCACCAGATCA R2 GCTCATCCCTTCGAATTCAG	FLP		<i>E4</i> 1,229 <i>e4-SORE-1</i> 837	[7]
	<i>dt1-ab</i>	F CACACCCACCCACATATAT R GGCAAAACCAGCAGCTACTT	CAPS	<i>Hind</i> III	<i>Dt1</i> 808 <i>dt1-ab</i> 593 + 215	This study
	<i>dt1-tb</i>	F CACACCCACCCACATATAT R GGCAAAACCAGCAGCTACTT	CAPS	<i>Acc</i> I	<i>Dt1</i> 646 + 92 + 70 <i>dt1-tb</i> 738 + 70	This study
	<i>dt1-bb</i>	F GGCTGCTGTCTACTTCAATGTCTAG R GCCACATGTGAAGATCAACTTCCA	dCAPS	<i>Xba</i> I	<i>Dt1</i> 155+21 <i>dt1-bb</i> 176	[33]

CAPS; cleaved amplified polymorphic sequence, FLP; fragment length polymorphism