

Table 1 Suppl. The sequences of adaptors, pre-amplification primers, and selective amplification primer combinations in MSAP analysis.

Primers		Sequences
Adapters	<i>Eco</i> RI-adaptor I	5'-CTCGTAGACTGCGTACC-3'
	<i>Eco</i> RI-adaptor II	5'-AATTGGTACGCAGTCTAC-3'
	<i>Hpa</i> II/ <i>Msp</i> I –adaptor I	5'-GATCATGAGTCCTGCT-3'
	<i>Hpa</i> II/ <i>Msp</i> I –adaptor II	5'-CGAGCAGGACTCATGA-3'
Pre-selective primers	E0	5'-GACTGCGTACCAATTC-3'
	H/M0	5'-ATCATGAGTCCTGCTCGG-3'
Selective primers	HM 1	5'-ATCATGAGTCCTGCTCGGTTA-3'
	HM 2	5'-ATCATGAGTCCTGCTCGGTTC-3'
	HM 3	5'-ATCATGAGTCCTGCTCGGTGA-3'
	HM 4	5'-ATCATGAGTCCTGCTCGGTGT-3'
	HM 5	5'-ATCATGAGTCCTGCTCGGTGC-3'
	HM 6	5'-ATCATGAGTCCTGCTCGGTAC-3'
	HM 7	5'-ATCATGAGTCCTGCTCGGTTC-3'
	HM 8	5'-ATCATGAGTCCTGCTCGGTCA-3'
	E1	5'-GACTGCGTACCAATTCAAC-3'
	E2	5'-GACTGCGTACCAATTCAAG-3'
	E3	5'-GACTGCGTACCAATTCACA-3'
	E4	5'-GACTGCGTACCAATTCAC-3'
	E5	5'-GACTGCGTACCAATTCACC-3'
	E6	5'-GACTGCGTACCAATTCACG-3'
	E7	5'-GACTGCGTACCAATTCAGC-3'
	E8	5'-GACTGCGTACCAATTCAGG-3'

Table 2 Suppl. Cytosine methylation patterns at the CCGG sites between hybrids and their parent lines (Z - Zheng58, C - Chang7-2).

Class	Band pattern displayed in MSAP gel													
	maternal		paternal		hybrid		Z×C	C×Z						
	parent		parent		(F1)			leaf	root	embryo	endosperm	leaf	root	embryo
	H	M	H	M	H	M	leaf	root	embryo	endosperm	leaf	root	embryo	endosperm
A1	+	+	+	+	+	+	183	93	439	341	181	93	422	338
A2	-	+	-	+	-	+	113	45	56	18	114	45	32	7
A3	+	-	+	-	+	-	120	57	19	32	120	57	19	6
Total for monomorphic loci							416	195	514	391	415	195	473	351
B1	+	+	-	-	+	+	2	4	30	13	1	4	22	11
B2	-	+	-	-	-	+	0	0	9	6	0	0	18	4
B3	-	-	-	+	-	+	6	2	3	0	7	2	7	0
B4	-	-	+	+	+	+	24	7	34	16	24	7	40	18
B5	+	-	-	-	+	-	1	1	6	3	1	1	4	1
B6	-	+	-	+	+	+	0	0	5	8	0	0	26	19
B7	-	+	-	-	+	+	0	0	4	0	0	0	3	1
B8	-	+	+	-	+	+	0	0	3	1	0	0	3	1
B9	+	+	+	-	+	+	0	0	30	16	0	0	26	12
B10	+	-	+	+	+	+	0	0	14	7	0	0	18	13
B11	+	-	-	-	+	+	0	0	1	0	0	0	2	0
B12	-	-	-	-	-	+	0	0	0	0	0	0	0	0
Total for de-methylation loci							33	14	139	70	33	14	169	80
							66.00 %	73.68 %	(45.28 %)	(37.84 %)	82.50 %	73.68 %	50.30 %	41.45 %
C1	-	-	+	+	-	-	2	0	5	1	1	0	3	0
C2	+	-	-	-	-	-	0	0	5	3	0	0	4	3
C3	+	+	+	+	-	+	0	1	5	3	0	1	3	5
C4	-	+	-	+	-	-	0	0	0	0	0	0	1	0
C5	-	+	-	-	-	-	0	0	3	0	0	0	2	0
C6	-	-	-	+	-	-	1	0	4	1	0	0	0	0
C7	+	+	+	+	+	-	0	0	1	0	1	0	11	2
C8	+	+	-	-	-	+	0	0	1	0	0	0	1	1
Total for hyper-methylation loci							3	1	24	8	2	1	24	11
							6.00 %	5.26 %	7.82 %	4.32 %	5.00 %	5.26 %	7.14 %	5.70 %
D1	-	+	+	+	+	+	0	0	41	32	0	0	54	37
D2	+	+	-	+	+	+	0	1	65	57	0	1	61	47
D3	+	+	-	+	-	+	0	0	10	6	2	0	13	10
D4	-	+	+	+	-	+	14	3	14	8	3	3	3	3
D5	+	-	+	+	+	-	0	0	4	3	0	0	0	0

[illegible]

Table 3 Suppl. The homologous analysis of cloned fragments differentially methylated using *BLAST*-searching (Z - Zheng58, C - Chang7-2).

No.	Primer comb.	Size[bp]	Patterns	Hybrids	Homology and putative protein	E value
Function of known proteins (13)						
1	E6/H3	321	B12	embryo (ZC)	AF466646: transposase (Z195D10.1) gene (<i>Zea mays</i>)	4e-52
2	E6/H7	279	B3	embryo (ZC)	AY728476: chalcone synthase C2-ldf-II gene (<i>Zea mays</i>)	4e-13
3	E6/H7	144	C4	embryo (ZC/CZ)	AY574035: rust resistance protein rp3-1 gene (<i>Zea mays</i>)	2e-24
4	E6/H8	188	B2	embryo (ZC)	AY574035: rust resistance protein rp3-1 gene (<i>Zea mays</i>)	3e-16
5	E7/H1	128	C5	embryo (ZC/CZ)	NM-001154659: transport inhibitor response protein (<i>Zea mays</i>)	3e-54
6	E7/H5	262	B2	embryo (CZ)	AY530951: growth-regulating factor (<i>Zea mays</i>)	2e-67
7	E7/H6	339	C2	embryo (ZC/CZ)	AY574035: rust resistance protein rp3-1 gene (<i>Zea mays</i>)	1e-83
8	E7/H6	176	B12	embryo (ZC)	FJ968747: hsp organizing protein (<i>Dactylis glomerata</i>)	4e-29
9	E7/H8	298	C7	embryo (ZC)	AB557931: cadmium selective transporter for low entry to shoot from Nipponbare (<i>Oryza sativa</i>)	2e-24
10	E6/H4	143	B12	root (CZ)	EU959517: histone H2A variant 3 mRNA (<i>Zea mays</i>)	2e-32
11	E7/H4	91	C5	root (ZC/CZ)	NM_001154086: ATP synthase delta chain mRNA (<i>Zea mays</i>)	1e-32
12	E6/H5	259	B12	leaf (CZ)	NM_001111894: G-box binding factor1 (GBF1) (<i>Zea mays</i>)	1e-67
13	E7/H2	114	B12	leaf (ZC)	FJ909711: transposon insertion Mu1007362 flanking (<i>Zea mays</i>)	3e-28
Function of unknown proteins (10)						
14	E1/H2	103	B12	embryo (ZC)	BT086813.1:cDNA clone ZM_BFb0367P05 (<i>Zea mays</i>)	1e-50
15	E7/H5	201	C3	embryo (ZC)	AC231933: Clone OM_Ba0189I19 (<i>Oryza minuta</i>)	4e-04
16	E3/H7	344	C3	embryo (ZC)	AC165178: Clone ZMMBBb-272P17 (<i>Zea mays</i>)	8e-04
17	E7/H8	308	B2	embryo (CZ)	AC118674.3: clone OSJNBb0093J20 (<i>Oryza sativa</i>)	2e-23
18	E5/H2	342	B12	embryo	NM_001195927.1: hypothetical protein LOC100501112 (<i>Zea</i>)	2e-49

				(ZC)	<i>mays</i>)	
19	E7/H2	302	C3	embryo (CZ)	AC209386.4: Clone CH201-98J13 (<i>Zea mays</i>)	2e-62
20	E3/H2	249	B5	embryo (ZC)	EU942430.1: clone 1497999 (<i>Zea mays</i>)	5e-106
21	E6/H3	104	D7	endosperm (ZC)	NM_001149799.1: hypothetical protein LOC100275801 (<i>Zea mays</i>)	1e-45
22	E5/H2	209	B2	endosperm (CZ)	BT038149.1: cDNA clone ZM_BFb0214G21 (<i>Zea mays</i>)	5e-92
23	E6/H8	208	B5	root (CZ)	EU951532.1: clone 706468 mRNA sequence (<i>Zea mays</i>)	6e-100
No significant similarity (27)						
24	E6/H4	206	B3	embryo (CZ)	No hit	
25	E3/H5	223	B6	embryo (ZC/CZ)	No hit	
26	E6/H2	223	B12	embryo (ZC)	No hit	
27	E5/H8	220	C3	embryo (ZC)	No hit	
28	E6/H7	382	B2	embryo (ZC)	No hit	
29	E1/H4	235	C6	embryo (ZC/CZ)	No hit	
30	E5/H8	190	B3	embryo (ZC)	No hit	
31	E6/H3	236	C3	embryo (CZ)	No hit	
32	E5/H2	181	C6	endosperm (ZC/CZ)	No hit	
33	E6/H8	169	C2	endosperm (ZC/CZ)	No hit	
34	E6/H8	421	B12	endosperm (ZC)	No hit	
35	E4/H2	211	C4	endosperm (ZC/CZ)	No hit	
36	E6/H5	220	C5	endosperm (ZC/CZ)	No hit	
37	E6/H3	119	C3	root (ZC)	No hit	
38	E7/H8	242	C3	root (ZC)	No hit	

39	E6/H4	242	C3	root (CZ)	No hit
40	E6/H6	242	B3	root (ZC)	No hit
41	E7/H8	160	B3	root (ZC)	No hit
42	E7/H8	173	C6	root (ZC/CZ)	No hit
43	E3/H4	258	C3	root (CZ)	No hit
44	E6/H4	258	C3	root (ZC)	No hit
45	E3/H5	114	C3	root (ZC)	No hit
46	E2/H8	135	B12	root (ZC)	No hit
47	E6/H5	171	C3	leaf (ZC)	No hit
48	E6/H5	158	C3	leaf (ZC)	No hit
49	E5/H3	251	C3	leaf (ZC)	No hit
50	E6/H7	176	C3	leaf (ZC)	No hit
