

Table 1 Compilation of employed *AtSHM1* specific primers.

The oligonucleotide primers were designed according to the annotated genomic (Genbank Acc. No.) and cDNA (Genbank Acc. No. AJ271726) sequences of the At4g37930 (*AtSHM1*) locus. The annealing positions of the primers are given relative to the start-ATG of the gene and refer to the 5' end of the oligonucleotide.

Primer	Orientation	Sequence	Position in genomic DNA	Position in cDNA
prSHM1	forward	5' ATT CGA TCC ACT TCA TGT TAC 3'	64	64
prSHM2	reverse	5' GTA ACA TGA AGT GGA TCG AAT 3'	84	84
prSHM3	forward	5' GTG TCA GCA ATG GAA TCC TCT 3'	2723	1426
prSHM4	reverse	5' AGA GGA TTC CAT TGC TGA CAC 3'	2743	1446
prSHM5	forward	5' CCT TAT GCC AGA AGC GCG CTC TT 3'	843	368
prSHM6	reverse	5' GTC CAC GAA GTG ACT TGT GAG 3'	1674	871
prSHM7	forward	5' CCA TAA TTC TGT TAA TCT TAT TCC 3'	-442	-
prSHM8	reverse	5' GTT GTC CGG TTA CAG AAC CAT 3'	3208	-
prSHM9	forward	5' GGC CAT GGC TCT TCG AAG GCT 3'	9	9
prSHM10	forward	5' AGC ATG AGA AAG CTA GAC AAT GG 3'	476	200

prSHM11	reverse	5' CCT CCA TAG TAT CTG GCA CCA 3'	712	341
prSHM12	reverse	5' GGC CTG AAA AGA GTA GCA CTT 3'	1396	671
prSHM13	forward	5' ACA CAA CCA CAC TAT CAC AGG 3'	1886	996
prSHM14	reverse	5' CTC AGG ACT TGT TCT TGG TAT GCT 3'	2053	1082

Table 2. Information on the applied 23 CAPS markers (obtained from the TAIR database www.arabidopsis.org, unless indicated otherwise – see footnote).

Marker	Chr	Position	Primer 1 (5' → 3')	Primer 2 (5' → 3')	Restr. Enz.	Fragments Col-0 (bp)	Fragments Ler (bp)
T7A14-1	I	7.7 cM	ATGTGGGTGACGAATACCGTAC	AATGAAGCTCACCAATGAGGG	Sspl	1269; 231	1500
UFO ²	I	49.6 cM	AAGGCATCATGACTGTGGTTTTTC	GTGGCGTTTCAGACGGAGAGG	TaqI	983; 316	600; 383; 316
ADH ¹	I	117.5 cM	GCGTGACCATCAAGACTAAT	AAAAATGGCAACACTTTGAC	Xba I	1291	1097; 262
RGA	II	1.7 cM	TTCGATTCAGTTCGGTTTAG	GTTTAAGCAAGCGAGTATGC	RsaI	140;128	263
PhyB ²	II	34.5 cM	CAATCCTATGAAGAATGGCG	ATAAACCATTAGCCCACGTG	XhoI	1100	700; 400
ER	II	50.6 cM	GAGTTTATTCTGTGCCAAGTCCTG	CTAATGTAGTGATCTGCGAGGTAATC	DdeI	550	360; 140
VE017	II	69.1 cM	GAGCAATCCAGTAGAGGATA	CTTGAAGCTTAAATCTCAGC	PstI	214;143	357
ABI3 ²	III	38.1 cM	GGGCCTCCGGCTTTTGTCCGCTCGG	CCACGTCAGCAGGTGGTACCAGATC	HinfI	800; 700; 100	1500;100
GL1 ¹	III	48.5 cM	CCATGATCCGAAGAGACTAT	ATATTGAGTACTGCCTTTAG	TaqI	298; 100; 74; 47	372; 100; 47
LD	IV	17 cM	CTCATGTACTGGCTATTCCTTGG	TCGATCAGTCCAAGATGTCGTCG	PvuII	1400 (2x); 900; 500	2300; 1400; 500
DET1.1	IV	31.4 cM	GAGCATCAACAAGATGACC	CAAAATGTGAATGTCC	SacI	1100	600; 500
G4539	IV	57.6 cM	GGACGTAGAATCTGAGAGCTC	GGTCATCCGTTCCCAGGTAAAG	HindIII	600	480; 120
AG	IV	63.1 cM	CAAACACCATTTAATCTTGACA	CAACAGGTTTCTTCTTCTCTC	XbaI	1366	1073; 293
RPS2 ²	IV	75.7 cM	TTCGACGGATGGACTCTCGTG	CTCAGAGTCTGGACTTGTCG	Sau3A I	605; 180	354; 251; 180;
g8300a ³	IV	81.2 cM	TAAAAGCTTGGACTGGCGTGATTGACG	CCGAATCCCAGCGGCATTGCCAGGC	HindIII	700	500; 200
F20D10.1 ³	IV	95 cM	TTAGAGCTCGGTATGTCAGCG	AACACGTAACGGGATCTGAGC	EcoR V	1433	923; 510
F20D10.2 ³	IV	95 cM	AGAGAGTCACTGAGTGG	ATCGAACCTGTGATCCAATGC	EcoR I	735; 438	1193
F23K16	IV	103 cM	TGTACGTAATATGTCGCATGC	CTTGGTTATTGCATAGAAGCC	Xho I	837; 451	1288

ASA1 ¹	V	18.3 cM	CCTCTAGCCTGAATAACAGAAC	CTTACTCCTGTTCTTGCTTAC	BclI	1042; 686	686; 553; 489
PAT1 ²	V	26 cM	GTATGAGAACATAGTAACCCCATG	GTCGACGTGGTGCGGTGGGTTG	Ddel	1000; 600; 300	1000; 900
PhyC ²	V	71.1 cM	CTACAGAATCGTCCTCAACG	CCTAATGGAGAATCATTCCGG	PstI	1700; < 300	800; 700; <300
EG7F2 ²	V	117 cM	GCATAGAATTTGACGATAACGAGC	GATCTGTGTAGGACTACGAGAC	XbaI	1200	700; 500
MUB3-1	V	127 cM	CCACGCGAAACGGCTGACGTCG	AGCTTATTCAGGTACGTGAATG	AccI	1134	640; 494

¹ see Konieczny and Ausubel, 1993

² see Baumbusch et al., 2001

³ this paper