

Table S1: PCR-based markers used to genotype identified mutants, reference lines, and constructs

Mutant	Alias	Primer name (5' to 3' sequence)	Enzyme	Amplicon size (bp)	
				Wt	Mutant
<i>acx1-4</i>	R574	R574-1 (CCTCTTCCGAATATAACTGTTGGTGATCTC) R574-2 (CCGATGGAACATATTCTCCTTCTTGTG)	<i>Ava</i> I	184, 87, 27	211, 87
<i>acx2-2</i>	R223	R233-1 (GTATATATTTGCAGTCTCGG) R737-ACX2-R (CAGTCATGGCAAAGCAACC)	<i>Ava</i> I	102, 16	118
<i>acx2-3</i>	R737	ACX2-5 (TAAGATGGGCGTTCAATACAGG) R737-ACX2-R (CAGTCATGGCAAAGCAACC)	<i>Bsa</i> XI	162, 30, 74	266
<i>atg7-3</i>	SAIL_1 1_H07	ATG7-23 (GTTGCCATGTCTAATCCAGTCAGG) ATG7-Tsp45I (GTTGCCATGTCTAATCCAGTCAGG) LB1-SAIL (GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC) ATG7-24 (GTTGCCATGTCTAATCCAGTCAGG)	-	539	-
<i>chy1-1</i>		K14B20-20 (AGAAGTAATTGGCACCGAGTCTCCAGGTAC) K14B20-21 (ACCCTAGTGTGAAACTTGTCATCCTAAAGG)	<i>Kpn</i> I	228	258
<i>chy1-5</i>	R189	R189-1 (AGGTCTCGCTATAATTTCTTTTTG) R189-2 (GGAGGCGCCTACATCTGGA)	<i>Acc</i> I	185, 103	288
<i>chy1-6</i>	R499/ R506	R499-F (GGATGACAAATAGGTCGC) R499-ApoI-R (CAAGAAGTAGGAGGCGCCTAAAT)	<i>Apo</i> I	117	93, 24
<i>chy1-7</i>	R728	R728-1 (TTTCTTGTCTTTTTGTCCA) R728-2 (CGTTGAAGGCACAAAATGAGTTGC)	<i>Sty</i> I	106	88, 18
<i>drp3a-3</i>	SALK_ 066958	drp3a-3-1 (AACCGCACAGTCAAGGAAGC) drp3a-3-2 (TATCCGCGACTTCAAATCCG) drp3a-3-1 (AACCGCACAGTCAAGGAAGC) LB1-SALK (CAAACCAGCGTGGACCGCTTGCTGCAACTC)	-	544	-
<i>drp3a-4</i>	R224	drp3a-1-1 (TTCCCTTCCCTTGCTTTATTTG) drp3a-1-2 (GGGACGCCTATGGTGATG)	<i>Dra</i> I	533	333, 200
<i>drp3a-5</i>	R402	R402-1 (CGCCTTCTCCGTCTTCT) R402-2 (AATCTATTCTCAGCCTACAAA)	<i>Mlu</i> I	239, 219	458
<i>icl-3</i>	R291	R291-1 (AAGAAGGGAGATTCCAAGCC) R291-2 (ATGGCCACGTAGAGCCACCACG)	<i>Sty</i> I	116	97, 19
<i>icl-4</i>	R601	R601-1 (GTACGGCCTCTCGCACCTTA) R601-2 (TGTGTGAGTGGACGAGCACTGCC)	<i>Dde</i> I	93, 17	110
<i>icl-5</i>	R951	R951-1 (TTTCCGTATTATTTGTTAGTTCC) R951-2 (ATCAGGGCTTGCCGTTCCATCC)	<i>Dde</i> I	316	184, 132
<i>lon2-2</i>	SALK_ 043857	LON2-17 (TGATTCCTTACCATATGGGCCAACACAGTCC) LON2-16 (AGTCTTGTCTCGGTATTGCATTGGGGGTAG) LON2-17 (TGATTCCTTACCATATGGGCCAACACAGTCC) LB1-SALK (CAAACCAGCGTGGACCGCTTGCTGCAACTC)	-	350	-
<i>lon2-8</i>	R109	lon2-R109-F (GTGCTGGAAGTGATTCTGG) lon2-R109-R-Rsal (CTGGTGTGCCATTGAAGATCGT)	<i>Rsa</i> I	59, 47	47, 36, 23
<i>lon2-9</i>	R498	LON2-Hpall (TCAACCTATTCCACCTCCTTCTAGACC) LON2-24 (CCTCCTTCGGCCATTCTACCATTA)	<i>Hpa</i> II	258, 147, 28	286, 147
<i>lon2-10</i>	R973	R973-1 (TCAGCGTCACACTAGTGGAGCAAGAGCCAT) R973-2 (GGATTAATCATCGTCCCAATTGAAGAACCC)	<i>Nco</i> I	88, 27	115
<i>mdar4-4</i> (<i>sdp2-4</i>)	SALK_ 068667	sdp2-4-1 (GGGAATGCGTTGTTATCG) sdp2-4-2 (AGTGGCTCCCCTTTGA) LB1-SALK (CAAACCAGCGTGGACCGCTTGCTGCAACTC)	-	537	-
<i>mdar4-5</i>	R340/ R343	sdp2-4-2 (AGTGGCTCCCCTTTGA) R340-MDAR-4-F (ACTATAAGTTACAAATTTGATCATTGCAACGG) R340-MDAR-4-R (AGGCCACAACCTTTAGCAG)	<i>Fok</i> I	322	276, 46

Table S1 continued

Mutant	Alias	Primer name (5' to 3' sequence)	Enzyme	Amplicon size (bp)	
				Wt	Mutant
<i>mdar4-6</i>	R541/ R577	R541-1 (CTGGTGGAGGAACTGAAGAAAAC) R541-2 (GGACCAAACAACAACGATGAT)	<i>Ddel</i>	361	181, 180
<i>mdar4-7</i>	R923	R923-JP1 (TGCTGCCAGAAGGTAAG) R923-JP2 (TCAGAAAAGAATCCCGTAG)	<i>PstI</i>	157, 137	294
<i>mfp2-6</i>	R281	MFP2-30 (ATGACATTCTCCAGTAGTAAACGAGGCG) MFP2-31 (GATCCCCTCTCAGCCAAAAAAGC)	<i>MbolI</i>	292, 44	227, 64, 44
<i>mfp2-7</i>	R778	R778-1 (AAGTAGCGGCATGATATGAG) R778-2 (CTCAGGATCGAATTGTTGGAGC)	<i>AluI</i>	148, 20	168
<i>mfp2-8</i>	R794/ R809	R794-JP1 (TCTGGCTTTTTCTTTTTCTTTAC) R794-JP2 (TGCCAATTCCAGCCTCCAG)	<i>BsmAI</i>	242	131, 111
<i>mfp2-9</i>	R1009	R794-JP1 (TCTGGCTTTTTCTTTTTCTTTAC) R1009-1 (CAGGAATTTTCATTTACCG)	<i>AcI</i>	141, 65, 33	141, 85
<i>mls-3</i>	SALK_ 002289	mls-3-1 (AATTTTGTGTTGGGGTTTGAA) mls-3-2 (AGGGTCTCGATAAGCACAGTTG) mls-3-1 (AATTTTGTGTTGGGGTTTGAA)	-	520	-
<i>mls-4</i>	R332	LB1-SALK (CAAACCAGCGTGGACCGCTTGCTGCAACTC) R332-MLS-F (TTGTTCCGGTGGTATGATCG) R332-MLS-R (ATGCAGATTGGGATGAGTC)	<i>TaqI</i>	163	143, 20
<i>ped1-96</i>		PED196-1 (CAATGGCATGGGAAGGTCAGTCAA) PED196-Rsal (CCCATAGGAAGAAGACAATTGT)	<i>RsaI</i>	156	130, 26
<i>ped1-4</i>	R814	R814-1 (TGAGGGTCTGCTATCTTTTCT) R814-2 (AGTTCTGACAGCCACGGTTTCT)	<i>HinfI</i>	218, 105	163, 105, 55
<i>ped1-5</i>	R883	R123-PED1-F (GCTGCGTTCTATGCTGGTTTC) R123-PED1-R (GCTGCGTTCTATGCTGGTTTC)	<i>AluI</i>	265, 90	157, 108, 90
<i>pmdh1-2</i>	R92	PMDH1-7 (TGTTTTAGGTTCTGATTTCTC) PMDH1-2 (ATCATCCCTCGTCATCCCTGGTTTCCTC)	<i>AcI</i>	86, 30	116
<i>pme31-1</i>	R79	R79-PME31-1 (TTATAATTGTCGATTCTCA) R79-M14-R (GTATCCTGCATTTACATTTTG)	<i>Ddel</i>	158, 17	175
<i>pme31-2</i>	R363	pme31-1-1 (GGCAACGACTCGAATGGTTAGGG) pme31-1-2 (TTCTCAAAAGTAATGTTCTCTGC)	<i>HinfI</i>	141, 99, 84, 74, 9	215, 99, 84, 9
<i>pme31-3</i>	R922	R922-1 (CTGTTACATCGAGGGAAGTGTGG) R922-2 (CGTTTCCCCAGTTATGCCAACCC)	<i>BsrI</i>	219, 6	219, 133, 6
<i>pxa1-1</i>		T5J17-24 (ATGGGAGTCACTTTTCATAACCTCATCTCAA) T5J17-25 (CCATCAATCAGCCTTAGCTCCAAGGAATGG)	<i>SmlI</i>	150, 30	180
<i>pxa1-4</i>	R751	R751-1 (GCTGGGACGGCGATAAGAAA) R751-2 (GCAACTGTGGCCCAAGATACT)	<i>MnII</i>	269	143, 126
<i>pxn-3</i>	SAIL_ 636F12	PXN-1 (CTAATGCAGAAGCTCTGGTTGCTGT) PXN-2 (ATTGCATTGACGGATTACTTAC) LB1-SAIL (GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC) PXN-1 (CTAATGCAGAAGCTCTGGTTGCTGT)	-	~400	-
<i>pxn-4</i>	R109	R109-1 (CGGAGCTGTGGCGAACTCGG) R109-Avall (AATCATTTTCAGAATCGCGTCCAATGGTC)	<i>Avall</i>	196, 29	225
<i>pxn-5</i>	R162	R109-1 (CGGAGCTGTGGCGAACTCGG) PMP38-1 (GCCCCGAGTCACCTTCTTC)	<i>NruI</i>	152, 61	213
<i>pxn-6</i>	R986	R986-1 (CCCCGAGTCACCTTCTCTAATG) R986-2 (AGGCACGCTTTTTCTTCAG)	<i>ApoI</i>	449	235, 214
<i>pxn-7</i>	R987/ 995	R995-F (GCTACAGTCACAACCTACCC) R995-HindIII-R (TTCATGATAAGAGGGAAAGC)	<i>HindIII</i>	111	90, 21
<i>sdp1-6</i>	R330	R330-SDP1-F1 (TAATGACACAAGGGGCTCTACACG) R330-SDP1-R1 (TCACTGCGCTCCATATAACCACAT)	<i>StyI</i>	201	147, 54