

**Table S2.** List of PCR-based marker and oligonucleotide sequences.

## Fine mapping

Marker	SNP(s) position on chr. 3 (bp)	Forward primer	Reverse primer
CAPS1	15965927-15966730	CGCTATTATGCCAAGTAAAGTGA	CCCATTTGACGAAGTCCGTTGA
F1P2TGF	17541237-17541435	TTTGTCTGAAGATGTGGAGAGAGAG	CAAAACCCCACTCTTCATTATTGTT
MS004	18432036-18432238	GCTTATGGCAAACAGAAGTGA	CTCATAACAGTCGTATGCCAT
R30025	18938781-18937861	GGTCAAAGCAACATTACATTGTA	TTGGATGAGATTGCAAGCCTTCA
MS007	19714028-19714287	CCACTCACGAACACTCCTCA	TTCCGGGTCAGGATGTGGTA
MSAT3.28	20456770-20456979	TACAAGTCATAATAGAGGC	GGGTTTAGCATTTAGC
MSAT002	20619908-20620142	GGAGCAGGATTTTCCACTGA	CCTGACAGTCTGGATGATGT
MSAT005	20762734-20763171	GGAGGCTTTAGCAGAAGAAGA	CCATCGCCACCATAGCTTCT
P10bisFterR	21323125- 21324699	GGTGAGGTTGTCTCAGTT	CATCCAGCTCTTTCCTCAGA
CAPS5	21621166-21621946	GGGAGAGTAGCACTGATCTT	CCATACGTTACGTAATGCTA
MSAT015	21718159-21718629	CTTCCCTTCTCATTCTGCT	CAGGCAGCTAATGCTAAGGAGTT
CAPS8	21916695-21917086	GGACTAAGTTCCTTGAGACA	CGACCTAAGCCAGTACCAGAT
nga6	23031050- 23031192	ATGGAGAAGCTTACACTGATC	TGGATTTCTTCTCTCTTCCAC
nga112	23168570-23168372	CTCTCCACCTCCTCCAGTACC	TAATCACGTGTATGCAGCTGC
MS005	23377782-23378078	GCTCTACGTTACTTAAGCGA	CCAGACGATTTCGTCGAGA
3-57670	21371957-21372687	CTGTGAAGTCTGAGACTGA	CATGTCCCACATATGCA
TK280-281	21375355-21376613	CATACAGTAATTGGAGGGAT	CTCCTTCAGATCAGCCTTGGAA
1_57700	21384814-21386191	GTGACCTCGTTGACTTGA	GAGTAGGCATCACAAGA
c13-c14	21386759-21388774	GTCACCGCATTAGCAATCTCT	CATCTCTCAGCTCGCAGCA
QF-1R57730	21390902-21391774	TGCCTTTGAGTTTGAGTTGA	CTCTCCCACGAAAGAAGGT
IK01-02	21393979-21395425	CAGTAGTTGACTATCACAAAT	CTATCTATTTGGCTTATCCAC
c9-c10	21396684-21398587	GGTCATTGATCCCGACTACA	CCTGATCTGAATCCAACACA
c19-c20	21408735-21410203	CATTGGGTGTGTGTGTGTGT	GTGTGCCAAAGTAGCCAGT
3-57810	21416364-21416859	CATGTTCTAGGAATGCTATCAG	GGACACTTACCAATGATAGAGT
Indel1bis	21417631-21418039	GGATGCCAATCACAGTGT	CCTGATATCACACTGACCA
c21-c22	21428169-21430091	GTGTCATCACTTGTAGACGA	GTGGTCGTTTAGCTGAAGAGA
c25-c26	21440178-21442273	GTCATGGAATCTCTGTGCA	CTGCGCTCATGGATATCTCT
c1-c2	21447091-21449665	GGAGGGAAGAGCAATATCCGA	CCTGGTCACGAGACTTGTCA
c29-c30	21460205-21461470	CACAGTCACACACAAGACA	GTCTACTGTCTACAGACTCT
c5-c6	21477423-21478533	GCAGAGGTCCAGAAACCGAA	CCAAGCATGTCACCGTTAGA
MSAT012bis	21509784-21510124	GACACGTGTTGGTGAAGA	GTCCGAGGCTTCGAAGCA
QF-QR_710	21387173-21387109	ACGGTAAATCCATTCTATTTCG	GAAATTGTTGGTGGCTTTCAA
QF-QR_720	21388622-21388696	AACATATTGCTAGCTACGTGAAAGG	CCATCACCTTAGGATCTATTACTCA

## Sequencing primers Col-0 and Kas-1

Marker	Forward primer	Reverse primer
RKS1-1	CATAAGTTGTTGACTTAGAC	TCAAGCAGATTGAAGCATCA
RKS1-2	CTAATGCACCTTGAACAGG	GAGGTGGTTCTTGGATAACGGA
RKS1-3	ACCTCTTTAACTCTATGTCG	ATACATAAAACCCCTCTGCGG
RKS1-4	CTGAGATCTGGATCGTTAGA	CCAAGTCTGCATCTTGAACAC
RKS1-5	ATCCACTAGCTCTGATGGGG	CACATCTACTTCCAGCTGAGT

**Gene expression, constructions and transformant selection**

	Gene	Name	Primer (5' - 3')	
<b>Gene expression by Q-RT-PCR</b>	At3g57710	QF5_710	GCCCCAAAAGAAGAGGTATCAG	
		QR5_710	CGACTTGAAACAGGTCTATCTA	
		QR_710	GAAATTGTTGGTGGCTTTCAA	
		QRbis_710	TCCGTTATCCAAGAACCACCTC	
	At3g57720	QF3_720	CGTTGTACTIONTGCCTTGGAG	
		QR3_720	AGCTATATGTACAAATCTGAGTTC	
	At2g28390	TK322	AACTCTATGCAGCATTGATCCACT	
		TK323	TGATTGCATATCTTTATCGCCATC	
<b>RKS1 constructions</b>	At3g57700	QFbis_57700	GAGCGAGGTTTTGTTGACTGA	
		attB1-QFbis_57700	CCTTCAGTCGACCCCGGGGAGCGAGGTTTTGTTGACTGA	
		1R_at3g57700	GAGTAGGCATCACAAGA	
	At3g57710	attB1F-710	GGGGACAAGTTTTGTACAAAAAGCAGGCTTAATGAAGAAGCAGTATCTGAA	
		attB1F-710	GGGGACCACCTTTGTACAAGAAAGCTGGGTCGCTAGAATTTTTCAATGATGC	
		C15	GTCCCAGATCCAGATTTTCCAGA	
		Sqce_57710F	CTGCTTGAGTTCTTTAGCTACT	
		Sqce_57710R	GTGATAGATCCGAGGTTGATG	
	At3g57720	1R-at3g57720	CACATAGCCAGTAATACCTCT	
		QRter_57720	CCTCTGCTACTCTGTATTGAG	
		attB2-QRter_57720	CCGAGTGCGGCCGCCAGCAGCCTCTGCTACTCTGTATTGAG	
	<b>5' RACE</b>	At3g57710	710RACE-298R	TATGTCGTTTTCTGTAATCTCATCC
			710RACE-356R	TTACTGTGATTACTCATCCGAGCAG
710RACE-370R			AAAGTTGAAGAAAGTTACTGTGATTACT	
710RACE-686R			AGAACCATTACAGCTTCTATTCTCG	
710RACE-908R			TCTTTCATCAACCTCGGATCTATCAC	
710RACE-959R			AAAGCCAGCACACACATGCTTC	
710RACE-1026R			CTGCTTGAGTTCTTTAGCTACTTG	
<b>3'RACE</b>	At3g57710	710race-1F	ATGAAGAAGCAGTATCTGAAATCTGG	
		710race-47F	AGGACAAGGCGAAGAGGTGTTCTT	
		710race-213F	CTATAAATGGTATAGAGGTGAAATTGAA	
		710race-273F	GGATGAGATTACAGGAAAACGACATAG	
<b>amiRNA construction</b>	RKS1 amiRNA	57710-I-miR01-s	GATTATAGTATACATCTTGCGGGTCTCTCTTTTGTATTCC	
		57710-II-miR01-a	GACCCGCAAGATGTATACTATAATCAAAGAGAATCAATGA	
		57710-III-miR01*s	GACCAGCAAGATGTAAACTATATTCACAGGTCGTGATATG	
		57710-IV-miR01*a	GAATATAGTTTACATCTTGCTGGTCTACATATATATTCCCT	
	At3g57720 amiRNA	57720-I-miR01-s	GATAATTGGTCAGCATTGCGCTCTCTCTTTTGTATTCC	
		57720-II-miR01-a	GAGAGCGCAATGCTGACCAATTATCAAAGAGAATCAATGA	
		57720-III-miR01*s	GAGAACGCAATGCTGTCCAATTTTACAGGTCGTGATATG	
		57720-IV-miR01*a	GAAAATTGGACAGCATTGCGTTCTCTACATATATATTCCCT	
	RKS1+At3g57720 amiRNA	710/720-I-miR01-s	GATTTACCGTTACAATCAGGTACTIONTCTCTTTTGTATTCC	
		710/720-II-miR01-a	GAGTACCTGATTGTAACGGTAAATCAAAGAGAATCAATGA	
		710/720-III-miR01*s	GAGTCCCTGATTGTATCGGTAATTCACAGGTCGTGATATG	
		710/720-IV-miR01*a	GAATTACCGATACAATCAGGGACTCTACATATATATTCCCT	
	common	miR-A	CTGCAAGGCGATTAAGTTGGGTAAC	
		miR-B	GCGGATAACAATTTACACAGGAAACAG	
		attB1-miR	GGGGACAAGTTTTGTACAAAAAGCAGGCTCCCCTCGAGGTCGACGGTAT	
		attB2-miR	GGGGACCACCTTTGTACAAGAAAGCTGGGTCGCCAAGCTCGGAATTAACC	