

Supplementary File 3: Alignment of GmMKS2-X1, GmMKS2-X2, and GmMKS2-X3 transcript sequences and of protein sequences encoded by these transcripts. (a) Alignment of three *GmMKS2* transcripts. The region of intron 3 inserted between exon 3 and exon 4 to generate *GmMKS2-X1* and *GmMKS2-X3* transcripts are boxed. Stop codons are in bold; (b) Alignment of three GmMKS2 isoforms. Identical residues are shaded in black, and similar residues are shaded in grey.

(a)		
GmMKS2-X2	ATGAGCTACAACCACACTTCCTCGATGTCATTGCCTTCCCCATTGTACCTGAATACTACG	60
GmMKS2-X1	ATGAGCTACAACCACACTTCCTCGATGTCATTGCCTTCCCCATTGTACCTGAATACTACG	60
GmMKS2-X3	ATGAGCTACAACCACACTTCCTCGATGTCATTGCCTTCCCCATTGTACCTGAATACTACG	60

GmMKS2-X2	TCGTTTCGCCTCACGCGCCAATCTCCTTTTCCCTTTTCCCCGCCGCGCTTCAATCCACCG	120
GmMKS2-X1	TCGTTTCGCCTCACGCGCCAATCTCCTTTTCCCTTTTCCCCGCCGCGCTTCAATCCACCG	120
GmMKS2-X3	TCGTTTCGCCTCACGCGCCAATCTCCTTTTCCCTTTTCCCCGCCGCGCTTCAATCCACCG	120

GmMKS2-X2	GCTTTCGATCAGTTTCGCCGTTGAGTTCCAGCCCCCTCTGCATCACTCTTCGATCTCAGA	180
GmMKS2-X1	GCTTTCGATCAGTTTCGCCGTTGAGTTCCAGCCCCCTCTGCATCACTCTTCGATCTCAGA	180
GmMKS2-X3	GCTTTCGATCAGTTTCGCCGTTGAGTTCCAGCCCCCTCTGCATCACTCTTCGATCTCAGA	180

GmMKS2-X2	GGGGGCAAAGGAATGAGTGGATTCCATGACGTTGAACTGAAGGTGCGCGACTATGAGTTG	240
GmMKS2-X1	GGGGGCAAAGGAATGAGTGGATTCCATGACGTTGAACTGAAGGTGCGCGACTATGAGTTG	240
GmMKS2-X3	GGGGGCAAAGGAATGAGTGGATTCCATGACGTTGAACTGAAGGTGCGCGACTATGAGTTG	240

GmMKS2-X2	GATCAGTACGGTGTGGTTAACAATGCAGTTTATGCTAGTTATTGCCAGCACGGTCGTCAT	300
GmMKS2-X1	GATCAGTACGGTGTGGTTAACAATGCAGTTTATGCTAGTTATTGCCAGCACGGTCGTCAT	300
GmMKS2-X3	GATCAGTACGGTGTGGTTAACAATGCAGTTTATGCTAGTTATTGCCAGCACGGTCGTCAT	300

GmMKS2-X2	GAACTCTTGCAAAACATTGGTATTAATTGCGATGCTGTGGCTCGCAGTGGTGATGCATTG	360
GmMKS2-X1	GAACTCTTGCAAAACATTGGTATTAATTGCGATGCTGTGGCTCGCAGTGGTGATGCATTG	360
GmMKS2-X3	GAACTCTTGCAAAACATTGGTATTAATTGCGATGCTGTGGCTCGCAGTGGTGATGCATTG	360

GmMKS2-X2	GCATTGTCTGAACTATCGCTCAAATTCCTTGACCTCTAAGA-----	402
GmMKS2-X1	GCATTGTCTGAACTATCGCTCAAATTCCTTGACCTCTAAGA-----	402
GmMKS2-X3	GCATTGTCTGAACTATCGCTCAAATTCCTTGACCTCTAAGA GTAAGCCTCTCCAATTTT	420

GmMKS2-X2	-----	402
GmMKS2-X1	-----	402
GmMKS2-X3	GCTTGTCAATTTCTGTTTGTAGGATATAGTGCAACTGTGCAAATAACCTCCTTATACATT	480

GmMKS2-X2	-----	402
GmMKS2-X1	----- TTCTGTTTCCAATATTGTTT	424
GmMKS2-X3	TTAGTACACTAAAGATATGTTTTTCTGTATAAGTTAGTTCTGTTTCCAATATTGTTT	540

GmMKS2-X2	-----AGTGAGACAAATTTGTTGTAAGAGTTAGGATTCTG	439
GmMKS2-X1	TCATAATAAGAACATGCAACCAG AGTGAGACAAATTTGTTGTAAGAGTTAGGATTCTG	484
GmMKS2-X3	TCATAATAAGAACATGCAACCAG AGTGAGACAAATTTGTTGTAAGAGTTAGGATTCTG	600

GmMKS2-X2	GCTCTTCAGCTGCTCGTTTATACTTTGATCACTTCATCTATAAGCTGCCAAACCAAGAGC	499
GmMKS2-X1	GCTCTTCAGCTGCTCGTTTATACTTTGATCACTTCATCTATAAGCTGCCAAACCAAGAGC	544
GmMKS2-X3	GCTCTTCAGCTGCTCGTTTATACTTTGATCACTTCATCTATAAGCTGCCAAACCAAGAGC	660

GmMKS2-X2	CTATTTTGAAGCCAAGGCCATAGCGGTGTGGCTTGACAAAACTATCGTCCTATACGAA	559
GmMKS2-X1	CTATTTTGAAGCCAAGGCCATAGCGGTGTGGCTTGACAAAACTATCGTCCTATACGAA	604
GmMKS2-X3	CTATTTTGAAGCCAAGGCCATAGCGGTGTGGCTTGACAAAACTATCGTCCTATACGAA	720

GmMKS2-X2	TTCCAGCAGAGATGAAGTCTAAATTTGTAAAGTTTATTCGAATTGAGGACTCT TAA	615
GmMKS2-X1	TTCCAGCAGAGATGAAGTCTAAATTTGTAAAGTTTATTCGAATTGAGGACTCT TAA	660
GmMKS2-X3	TTCCAGCAGAGATGAAGTCTAAATTTGTAAAGTTTATTCGAATTGAGGACTCT TAA	776

(b)

GmMKS2-X2	1	MSYNHTSSMSLPSPLYLNTTSFRLTRQSPFPFPRRRFNPPAFRSVSPLSSSPSASLFDLR
GmMKS2-X1	1	MSYNHTSSMSLPSPLYLNTTSFRLTRQSPFPFPRRRFNPPAFRSVSPLSSSPSASLFDLR
GmMKS2-X3	1	MSYNHTSSMSLPSPLYLNTTSFRLTRQSPFPFPRRRFNPPAFRSVSPLSSSPSASLFDLR

GmMKS2-X2	61	GGKMSGFHDVELKVRDYELDQYGVVNNAVYASYCQHGRHELLQNIGINCDAVARSGDAL
GmMKS2-X1	61	GGKMSGFHDVELKVRDYELDQYGVVNNAVYASYCQHGRHELLQNIGINCDAVARSGDAL
GmMKS2-X3	61	GGKMSGFHDVELKVRDYELDQYGVVNNAVYASYCQHGRHELLQNIGINCDAVARSGDAL

GmMKS2-X2	121	ALSELSLKFLAPLR-----SGDKFVVRVRISGSSAARLYFDHFIYKLPNQ
GmMKS2-X1	121	ALSELSLKFLAPLRFCFPIFVLIIRTCNQSGDKFVVRVRISGSSAARLYFDHFIYKLPNQ
GmMKS2-X3	121	ALSELSLKFLAPLRV-----SLSNFACHFCILGYSAT-----

GmMKS2-X2	166	EPILEAKAIAVWLDKNYRPIRIPAEMKSKFVKFIRIEDS
GmMKS2-X1	181	EPILEAKAIAVWLDKNYRPIRIPAEMKSKFVKFIRIEDS
GmMKS2-X3	153	---VQITSLYILVH-----