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ORIGINAL ARTICLE

Identification of a potentially functional *MKS2/ALT* homolog gene in the genome of the cultivated potato *Solanum tuberosum*

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SUPPLEMENTARY MATERIAL

The authors are fully responsible for both the content and the formal aspects of the supplementary material. No editorial adjustments were made.

Supplementary File 1. Oligonucleotides used for the qRT-PCR analysis

Primer name	Primer sequence (5′-3′)	Brief description
StRPL19-qF	TTTGCAAGGAGGGAAGAAC	forward primer for *StRPL19*
StRPL19-qR	CTTCGACTTCTTAGATCCCTGA	reverse primer for *StRPL19*
StMKS2-3-qF	CTAGAAAGGATTGGTATAAGTGC	forward primer for *StMKS2-3*
StMKS2-3-qR	ACTACGAATCTATCTCCACTCC	reverse primer for *StMKS2-3*

Supplementary File 2. Four *StMKS2* gene models found in the genome of potato *Solanum tuberosum* (Exons are underlined)

>StMKS2-1

ACAACAGATTTCCCAATTCTCTTCTATCTCTGAAATTTTTCATCAA**ATG**TCTCATTCGTTTAGCATTGCACCCAACCTAGTGTTGCTGAATCATCATCGGTCACCACCGTCTACATTTCCGGTCATCCCTCACCGGCAACTCCCGCTCCCAAATTTACAGTTATCGGCCCGTAAATCGAGGAGTTTTGAAGCTCATAATGCATTCGATCTCAAAGCTACCCAAGGGTATGTATTATTCAGTGGCAGTACACAAAATTTTTCGTTACCTTTTGAAATAAGTACCAACTAATAAAACAACGTAACACAATATTAAAAAAAGAACAAAAACCTCTTATAATTTCATTTTTTTTTCTATTGGTATGAGTTTACATTTATCTGTGAACTTTGCAGAATGAGTGATCAGCTTTATCTCCATGAAGTTGAACTCAAAGTCAGGGACTATGAATTGGATCAGTTTGGTGTTGTAAACAACGCTACTTATGCAAGTTATTGTCAACATTGTAAGGTTTACTGTTTCGATAATCGATCGTACACATATGACAATATTTGAACTTAAGTAAGACTTATTTTTCAATAAATGAAACAGGCCGTCATGAGTTTCTAGAAAAGATTGGCGTAAGTGTTGATGAAGTAGCGCGAAATGGCGATGCATTAGCAGTAACAGAGCTCTCATTTAAGTTTCTAGCACCACTAAGGGTATGGCCAATTTCATCATGTATTTGGTAGTTTTGTCAATTGAATATAGTTTTTACCTTAGTCGAATTTGGAGTATTGCTTTGTTCAGAGTGGAGATAGATTCGTGGTGAAGGTGCGATTATCCCGCTCTACAGCAGCTCGATTATTTTTCGAGCATTTCATCTTCAAGCTTCCAGATCAAGAGGTCAGTTACCTCTATTATCATTCAATTACAAAGAGTCACTTTATACTCGTCAAATCTTACTGTATTTTCTTAAAATTTTCACAGCCTATATTGGAGGCAAGAGGAATAGCAGTGTGGCTTAATAGAAGTTACCGTCCTGTCCGAATTCCGTCAGAGTTCAGTTCAAAATTTGTTCAGTTCCTTCACCAGAAGAGTTGCGGTACACAACATCATCGTCTC**TAA**ACCTTACTTGTGGAATTACATTGTTATTATTTCTGAATTTAGTGCTTGTAATG

>StMKS2-2

AGACAACAGATTTCCCAATATTTGCAATTTCCTTCTCTTCTACCTCTGAAATTTTTCGTCAA**ATG**TCTCATTCCGTCTGCATTGCACCACCCAACCCACTGTTGCTGAATCATCGGCCACCACCGTCTACATTTCCGGTCATCCCTCACCGGCAACTCCCGCTCCCAAATTTACAGTTATCGGCCCATAAATCGAGGAGTTTTGAAGCTCATAATGCATTCGATCTCAAAGGTACCCAAGGGTATGTATGTTCAGTGGCAGTACACAGAATTTTTCGTTACCTTTTAAAATATGTACCAACAAATAAAACAATGTAACACAATATTAAAAAAAGAACAAAAACCTCTTATAATTTCATTTTTTTTTTTCCTATTGGTATGAGTTTACATTTATCTGTGAACTTTGCAGAATGGGTGATCAGCTCTATCAACATGAAGTTGAACTCAAAGTCAGGGACTATGAATTGGATCAGTTTGGTGTTGTAAACAATGCTACTTATGCAAGTTATTGTCAACATTGTAAGGTTTACTGTTTCGATAATCGATCGTACACATATGACAATATTTGAACTTAAAAGACTTATTTTTCAATAAATGAAACAGGCCGTCATGAGTTTCTTGAAAAGATTGGTGTAAGTGTTGATAAAATATGTCGCAATGGTGATGCATTAGCAACAACAGAGATTTCACTTAAGTTTCTAGCACCACTAAGGGTATGGCGAATTTCATCATGTATTTGGTAGTTTTGTCAATTGAATACAGTTTTTACCTTAGTCGAATTTGGAGCATTCAAAAAAATTGGAAATCCAACTATAAAAACACGGGCGACCTGATATAACATTGTTTTGTTCAGAGTGGAGATAGATTCGTGGTGAAGGTGCGAATATCCCGCTCTACAGCAGCTCGATTATTTTTCGAGCATTTAATCTTGAAGCTTCCAGATCAAGAGGTCAGTTACCTCAATTATCATTCAATTACAAAGAGTCACTTTATACTTGTCAAATTTTACTGTATTTTCTTAAAACTTTCACAGCCTATATTGGAGGCAAGAGGAATATCAGTGTGGCTTAATAGAAGTTACCGTCCTATCCGAATTCCGTCAGAGTTCAGTTCAAAATTTGTTCAGTTCCTTCACCAGAAGAGTTGCGGTACACAATACCGTCTC**TAG**ACCCTACTTGTGGAATTAGTGCTTGTAATATCTAACTACTTTT

>StMKS2-3

TCTAATCTCCGTCTATTCTACCTCTGCAAATTCTTCACCATTTCTGTTGGAGGGCACAA**ATG**TCTCAGTCCCTCGCTTCCCCTTTGATTCGCAGCATTGGATCCACTTCAGTCGGGAACTCACTGTTGCCGAATCATCGGCCACCGTTTACATTACCGGTCATTCCTCACCGGCAACTCCTGCTTCCAAATTTACAGTTATCCGTCAGTAAATTGAGGAGTTTTGAAGCTCATGCATTTGATCTCAAAGGTAGCCAAGGGTATGTATGTATATATCTCTTACTCCATCAGTCCCAATTTATCTAATAATGTTTGACTAGGCATGGAGTTTAAGAATTAAAAAGAAAGACCTTTGAAATTTGTGATCTTAATTAACCTATATATATGTGTATGTATGTATATATTGTATGGTTATAAATCATCTAATGAAATGGAAAATTTAAAGTCTAAAATGTTATTAAATATAGAAATGTGATAGGGTAAAGTGAGAAGTTTGAAGTCAAATTGTTACTGAATGTAGAAAGGTGTCTCAGGTGATCTTGTAAAATGGCAAGTTTGAAGTCAAATTGCTACTGAATATAGAAAGGTGTCTCAAGGTGATCTTGTTAAGTGGCAACTTTGAAGTCAAATTGTTAGTGAATGTAGAAAGGTGTCTGGGTGATCTCGTAAAATGGCAAGTTTGAAGTCAAATTTTTTACTGAATATAGAAAGGTGTCTTAGTGTGATCTCGTAAAATGGGAAGCTTGAAATCAAATTGTTACTGTATATAGAAAGGTGTCTCGGGTAGCAACTTATAGTTCCATTCAAATTCATCTGATGTGACAAAACATAGTCCCGATCATGCTTTGGATGAAGGATGGGGGTTGTCTAGGTTGATGATTAGGTGTAAATCAGTCTAATTATGATCAAATTCTCTGAATATTGGATTCATTGGCATGTGTCCACTTGACTTTGACTGAATAGGCAGAGCACTTATGTAGTTGGTTTTAACTAGTTTGAGCTTTAGATATAGTTGATTGATTGGTTTTACTGTAGCTTCTGTTAGGTTTGAACTTGATTAGAACCTATGTTTTCTCCATCTTAATGAAGGGTTTGTGCATTTTCAATTTCTACAATTGAGGGCAAATGATT-

GATTCAATTTAATGTATTTTTGCTTTCAGATTTCTGGAAAAAGTTTATTTTGGGAAGAAAAATGGAAAATCTTTGATTCTTGTTGTGTCGAGTGTTATATAGGATTCACCTTTCTTGTAGTTTCATTTTAAGTTTCAGCAAAAATTGATGTTTTTAGTTTGCTCATTGACATAGGCTATTTTTTCCTATTTACATGAGCTTACCTTTTGCTCTTGCTTTGCAGAATGGCTGAGTTCCATGAAGTTGAACTCAAAGTCCGGGACTATGAATTGGATCAGTATGGTGTTGTAAACAATGCTACTTATGCAAGTTATTGCCAACATGGTAAGGTTTATGGTTTTGATCTGTACTTCAGTTTACAACTACCATATTATAGTGCTTTCATTCATAAAAAAAACTGCGCTTTTCCCTTTTGATGAAAAAAGATTTATTCAAGGGAGAAAAATTTTCTGGCAACTGTTACGAGTAGAAAACTAGAAATTACTGAAAAAGGATCTTCTGTATCTGTTCTATTTTACTTCTTTGTGACCCTATAGTTAGATCATCTGTTACCCTTGTTCACGGAATGTGTTTTCTCTCTCAATAACTTGAGATGATGTCATCCAAAATTTGGATAATGAATAGGATTTCCTTTGCTCTGCTTATTACTAGAACATATTGAATACCAAATTTGAAGGGAACTTATGTGGTCAATGACTGTTTGAATCTTGCGTTTACACATACTAAAGATAAAGCCAATATCCAATTTGTATGTGAACATAATTGATTGCCAAATAGTTGTTCTGCCAGAACTTTGCTCAGTTAGTAGCTCTCTTTCCGAATTAGAGATAATTTTAAGTTAATAATATGTCTATCCTTATCAAAAAAGAAGTTAATAATATGTCTATTCAAATGTTGTTAAGTAATTGTCATGGATCATTACCTGAATACCCGTGATACTGAACCAAGGATAATACAAATTCAAGTTTTTCCAATGTAATAAGGCCTGTTACGTTGTGCGTGACCTATGTATACAAATTGAGTTTCTTAATAATCAATATAAATTTCTGTTTAAAATTCTGTAAATTTATATCAGATCTTTCTAGCTCCTCCACTATTATTGATTACATCCTTGCTTTGTTCCACTAACCCTTTTCCTTCTCATGGGAAAAAAGAAATAGGAAAAAGGGAAAGCAGGAACTTAAATTTTAATTGAAGGGTACTGACAAGATCATTACTTTAAATGACTTAAAGCATTTGGCCAGCCAAAAATGAGAAAATTGAAAAATATTTTCCTTTCATACCAAACACCCAAGTAGTTATCAATATGAAGTTATTCTGGGATTGTTGCCCTAATCTCCTTCTGTAGAAGGACCTACCTCATTGTCTATTACATAATACTGGATATGATAGTCCATATCAAAGACTTTCAAATGATAATATATAACTTATCTTGTTCGTTATGACTTATTTTCAATAAATGAAACAGGTCGTCATGAGCTTCTAGAAAGGATTGGTATAAGTGCTGATGAAGTGGCACGCAGTGGTGATGCACTAGCACTAACAGAGCTGTCACTTAAGTATCTAGCACCTCTAAGGGTATGACCTCATCTAAACATCATTAAGAACCAATTAATATGCAACCAGAAACTTTAGACCTTGGTTAAATGTCCTATTCAATTTAAATTTCGTGGCACAAAACTTTGCTTTTGAATATGAATTATAGATCTTTGGAACATATTGAAATGAAGAAGGCTTAAAATGTTCAATTTCAAGTGTGAGAAGTTTGGATAAGCATAGTTAGAAGGTTAAGGTCAATGGATGATGGGTCGGCAAATGAAGCTTTTTACAGCTGATTATAATGTGACACTCCCTTCTTTCCAAATTACTTGGGACAATGTCTTTGTTTATCTCTAATTACTTGACCTTTCTCTTGAGTAAGAAACTTTTACTTTACCATGAATTGGAGTCAGTACAAACAAATAGGTATTAGTTTACACTCTGTTAATCGTTATTTGGCATGCTTTCAATTGATTATTCTACAATTTAAATTGAACTATTATGTTAGATATTTATCATCTGTCTCTAAGTTGACAATTTATTCAAACGAACCTTGTGTTCTGTACTATCAGACTCAGTCATTTACGTGGGGACGTGAGCTTCTTTTTTCTGAACCATTTTTGGTTGCCTGAGGGAGAATTTCTGTTGCTAAGTGATGCACAAATATTATTCATTAGACTAAGAAATTGTGCTTCCAGCTTACTTGATCAAATATCTGTGAACTCCTCTTTGTCATGTTGCATTAATTCCCAAGAGCCTTACACTTCTAACTTGCCTGAGGCGGCCTTGATTATCAAATATCTCAAAAGGCATAAAATACGACGTGTATTGAAAAGACTTCTGCAGCCAACAACTGCTTCTAGTATTTTTTTGAAACACACCATTGAACATTTGCAGCTGCGTACTTGGTGTTGCTACTCCAATTTATTTGACTTGCCTTTCTACTGGTCCCATTGGTTATCTTGACCTGGTATGATATTCTTTCGTCGAATTCAAATATTTTCTACCCTCACTCCAAATGTTACCACATAAGAATGATAAAGAATTGAGGATCGGAGGGGAGTGCTTTTGACATTTGGCATAGTGGTACTACATCTCAGTATTTACCTCGTCATGGACTGGAATTCTATCTGATCAGGAATTTTATCCTGTTAATGGTTCATGTATTTGTTAGTGTTGTCAACTGAATATAGTTTTTCAGATTAAAAATATTACCTTAGTAAACAGAACTGCTTGATCTCTTATAACTACAAACGTGAACAGAACTGCTTGAAATTTGTGTTATCCTGCCTGTTCTCATTGCTTTCATCATTGGTTCAGAGTGGAGATAGATTCGTCGTGAAAGCACGAATATCTGATTCTTCAGCTGCTCGGTTGTTTTTCGAACACTTCATCTTCAAGCTTCCAGATCAAGAGGTCAGTTACCACTATTACCGCCGGTTTTTTTTTGGGGAGCAAAACCACTTGCATATCTTAATGTATTCTGTTACTACTTTTTTCCAGCCCATCTTAGAGGCAAGAGGAATAGCAGTGTGGCTTAATAAAAGTTACCGTCCTGTCCGAATTCCATCAGAGTTCAGAGCAAAATTTGTTCAGTTCCTTCGCCAGGAGGCATCTAAC**TAA**TGTGCTCGTCAACAAAATCCAGAAGAGTTATTTTGATCAAAACATTTT

>StMKS2-4

AAAATAATTTTCCCAATATTTTGAATTTCCATCTGCAAATTCTTCACCAA**ATG**TCACAATCCCTATTTTCCCCTTTGATTGGCAGCAATTGCCTTAACTCACTGTTGCCGAATCATCGGTCACCGTAGACACATTTCCGGTCAGGCAACTCCCCCTTCCAAATTTACAATTATCAGCCAATAAATCGAGGAGTTTTGAAACTAATGCATTTGATCTCAATGGTACACAAAGGTATGTATATGTATCTATTAGACTTCCTCTGTTCCAATCCAATTTATAATGTGATCTCGTAATATGACAAGTTTGAAGTCAAATTGTTACTAAATATAGAAAGAGTTTCCTATTTGCTCGTTAACATAGTCGATTATTTATTTGTGAACTTTGCAGAATGGGTGATCAGCTCTATTTCCATGAAGTTGAACTCAAAGTCAGGGACTATGAATTGGATCAGTTTGGTGTTGTAAACAATGCTATTTATGCAAGTTATTGTCAACATTGTAAGGTTTTAGTAATACCATATGAAATAGTCCATATATCATAGACTTAATTCTACCATATGAAATAGTCCATATATCATAGACTTTTTCAAATGACAATATTTTTCAATAAATGAAACAGGCAGTCATGAATTCTTCGAAAGAATTGGCGTAGTTGTTGATGAAGTGGCTCGCAATGGTGATGCATTAGCAACAACAGAGCTTTCACTTAAGTATCTAGCACCTCTAAGGGTATGTATAACCCTCATCTAAACATCATTAACGACCAATCAATATGCATCTGTTATATATATAATACTTAGTACTTCAAGTCGAATTTGGAGCATTTAAAAAATTTGGAGATCCAACTTCAAAAACACAGGTAGTCTGATACAACATTGCTTTGGTATCTGACTATCTGTGACTTTAGTCATATGGGAAAACAGAACTCATGTTTAGTCTTTTATGACTACAAATGTGAACACAGCTGCTTAAAAGTTATCATTTCTTTTATCATTGGTTTAGAGTGGAGATAGATTCGTCGTGAAGGTGAGAGTATCCGGCTCTACAGCAGCTCGTTTGTATTTCGAACATTTCATCTTCAAGCTTCCAGATCAAGAGGTTAGTTACCTCTATTATCATTCAATTACAAAGAAATACTTTTTACTACTTGTGAAATCTTAATGTATTTTCTTGAATTTACATAGCCTATCTTGGAGGCAAGAAGAACATCAGTGTGGCTTAATAAAAGTTACCGTCCTGTCCGAATTCCGTCAGAGTTCAGATCAAAATTTGATCAGTTCATTCACCAGAAGGGATCTAAC**TAA**TGTGTTTGTGAACAAAATGCAGAAGAGTTCTTCTGATCAGGTGAAAATTTGGTTAATTTATTTAC

Supplementary File 3. Nucleotide sequence alignment between the isolated *StMKS2-3* CDS and the predicted *StMKS2-3* CDS (Mismatches between two sequences are bold)

```
StMKS2-3-isolated          ATGTCTCAGTCCCTCGCTTCCCCTTTGATTCGCAGCATTGGATCCACTTCAGTCGGGAAC
StMKS2-3-predicted         ATGTCTCAGTCCCTCGCTTCCCCTTTGATTCGCAGCATTGGATCCACTTCAGTCGGGAAC
                           ************************************************************
StMKS2-3-isolated          TCACTGTTGCCGAATCATCGGCCACCGTTTACATTACCGGTCATTCCTCACCGGCAACTC
StMKS2-3-predicted         TCACTGTTGCCGAATCATCGGCCACCGTTTACATTACCGGTCATTCCTCACCGGCAACTC
                           ************************************************************
StMKS2-3-isolated          CTGCTTCCAAATTTACAGTTATCCGTCAGTAAATTGAGGAGTTTTGAAGCTCATGCATTT
StMKS2-3-predicted         CTGCTTCCAAATTTACAGTTATCCGTCAGTAAATTGAGGAGTTTTGAAGCTCATGCATTT
                           ************************************************************
StMKS2-3-isolated          GATCTCAAAGGTAGCCAAGGAATGGCTGAGTTCCATGAAGTTGAACTCAAAGTCCGGGAC
StMKS2-3-predicted         GATCTCAAAGGTAGCCAAGGAATGGCTGAGTTCCATGAAGTTGAACTCAAAGTCCGGGAC
                           ***********************************************************
StMKS2-3-isolated          TATGAATTGGATCAGTATGGTGTTGTAAACAATGCTACTTATGCAAATTATTGCCAACAT
StMKS2-3-predicted         TATGAATTGGATCAGTATGGTGTTGTAAACAATGCTACTTATGCAAGTTATTGCCAACAT
                           ********************************************** *************
StMKS2-3-isolated          GGTCGTCATGAGCTTCTAGAAAGGATTGGTATAAGTGCTGATGAAGTGGCACGCAGTGGT
StMKS2-3-predicted         GGTCGTCATGAGCTTCTAGAAAGGATTGGTATAAGTGCTGATGAAGTGGCACGCAGTGGT
                           ************************************************************
StMKS2-3-isolated          GATGCACTAGCACTAACAGAGCTGTCACTTAAGTATCTAGCACCTCTAAGGAGTGGAGAT
StMKS2-3-predicted         GATGCACTAGCACTAACAGAGCTGTCACTTAAGTATCTAGCACCTCTAAGGAGTGGAGAT
                           ************************************************************
StMKS2-3-isolated          AGATTCGTAGTGAAGGCACGAATATCTGATTCTTCAGCTGCTCGTTTGTTTTTCGAACAC
StMKS2-3-predicted         AGATTCGTCGTGAAAGCACGAATATCTGATTCTTCAGCTGCTCGGTTGTTTTTCGAACAC
                           ******** ***** ***************************** ***************
StMKS2-3-isolated          TTCATCTTCAAGCTTCCAGATCAAGAGCCCATCTTAGAGGCAAGAGGAATAGCAGTGTGG
StMKS2-3-predicted         TTCATCTTCAAGCTTCCAGATCAAGAGCCCATCTTAGAGGCAAGAGGAATAGCAGTGTGG
                           ************************************************************
StMKS2-3-isolated          CTTAATAAAAGTTACCGTCCTGTCCGAATTCCATCAGAGTTCAGAGCAAAATTTGTTCAG
StMKS2-3-predicted         CTTAATAAAAGTTACCGTCCTGTCCGAATTCCATCAGAGTTCAGAGCAAAATTTGTTCAG
                           ************************************************************
StMKS2-3-isolated          TTCCTTCGCCAGGAGGCATCTAACTAA
StMKS2-3-predicted         TTCCTTCGCCAGGAGGCATCTAACTAA
                           ***************************
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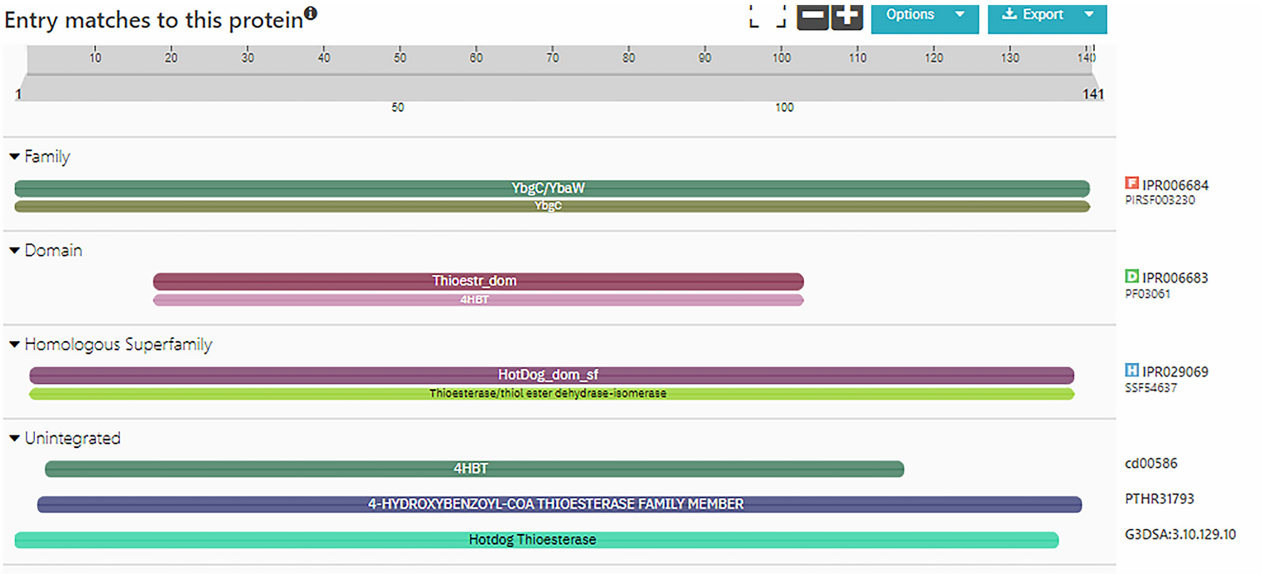
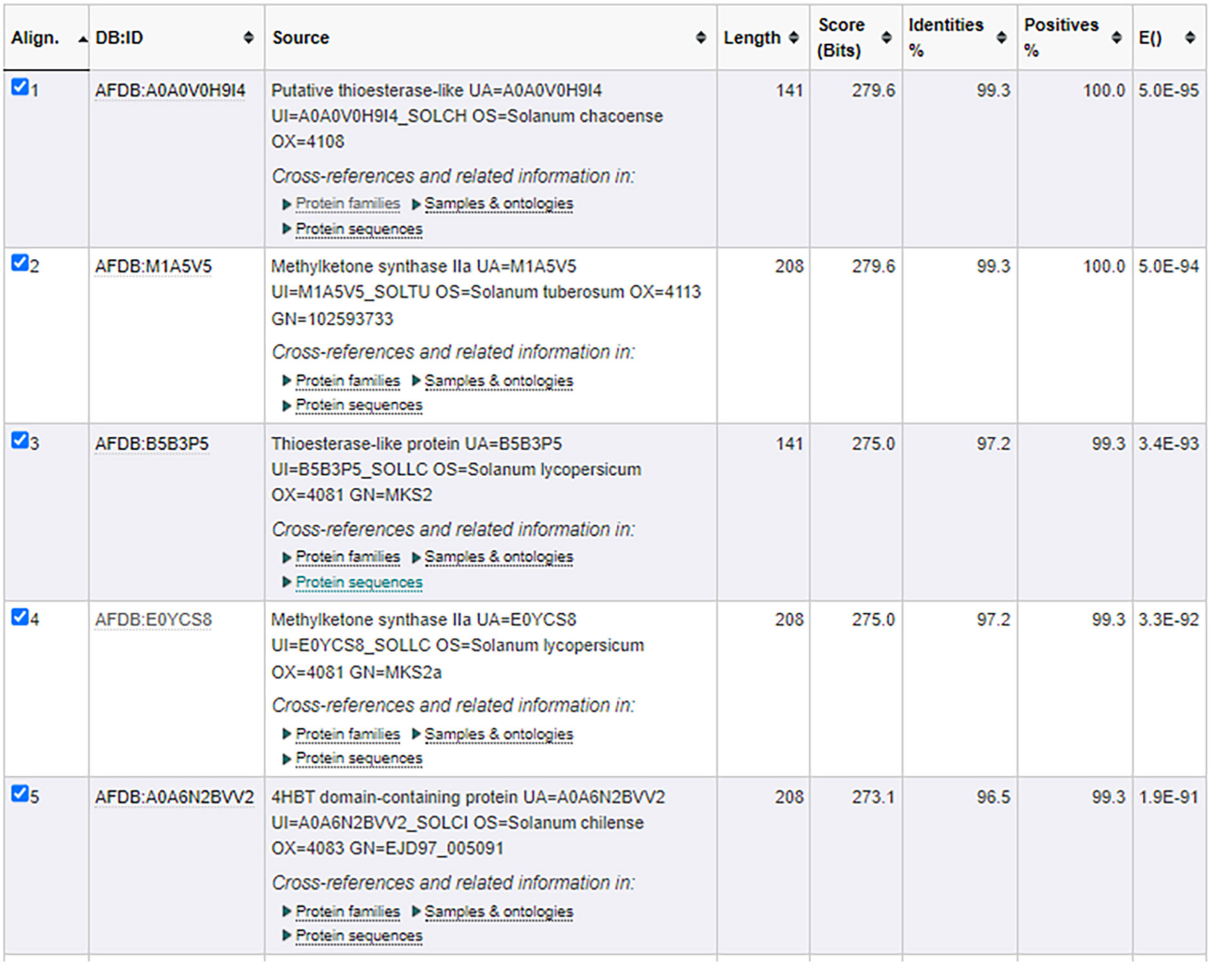
Supplementary File 4. Amino acid sequence alignment between the protein encoded by the isolated *StMKS2-3* CDS and the one encoded by the predicted *StMKS2-3* CDS (Mismatches between two sequences are bold)

```
StMKS2-3-isolated      MSQSLASPLIRSIGSTSVGNSLLPNHRPPFTLPVIPHRQLLLPNLQLSVSKLRSFEAHAF
StMKS2-3-predicted     MSQSLASPLIRSIGSTSVGNSLLPNHRPPFTLPVIPHRQLLLPNLQLSVSKLRSFEAHAF
                       ************************************************************
StMKS2-3-isolated      DLKGSQGMAEFHEVELKVRDYELDQYGVVNNATYANYCQHGRHELLERIGISADEVARSG
StMKS2-3-predicted     DLKGSQGMAEFHEVELKVRDYELDQYGVVNNATYASYCQHGRHELLERIGISADEVARSG
                       ***********************************.************************
StMKS2-3-isolated      DALALTELSLKYLAPLRSGDRFVVKARISDSSAARLFFEHFIFKLPDQEPILEARGIAVW
StMKS2-3-predicted     DALALTELSLKYLAPLRSGDRFVVKARISDSSAARLFFEHFIFKLPDQEPILEARGIAVW
                       ************************************************************
StMKS2-3-isolated      LNKSYRPVRIPSEFRAKFVQFLRQEASN-
StMKS2-3-predicted     LNKSYRPVRIPSEFRAKFVQFLRQEASN-
                       ****************************
```

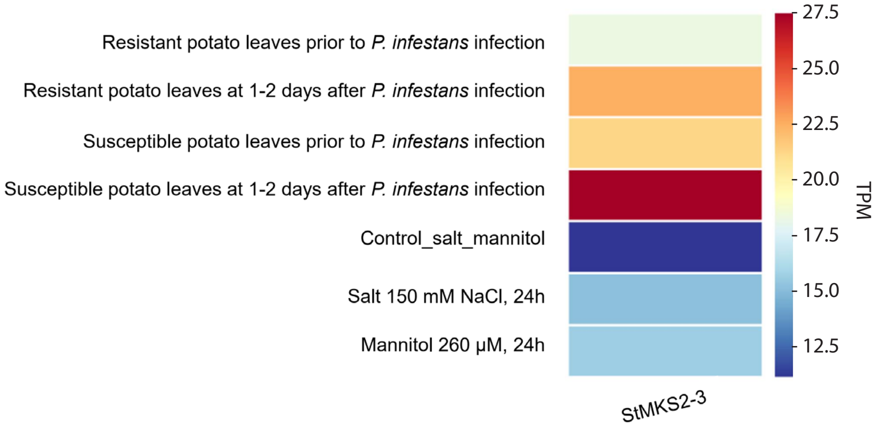


Supplementary File 5. Domain prediction of *StMKS2-3* using Interpro



Align.	DB:ID	Source	Length	Score (Bits)	Identities %	Positives %	E()
☑1	AFDB:A0A0V0H9I4	Putative thioesterase-like UA=A0A0V0H9I4 UI=A0A0V0H9I4_SOLCH OS=Solanum chacoense OX=4108 *Cross-references and related information in:* ▶ Protein families ▶ Samples & ontologies ▶ Protein sequences	141	279.6	99.3	100.0	5.0E-95
☑2	AFDB:M1A5V5	Methylketone synthase IIa UA=M1A5V5 UI=M1A5V5_SOLTU OS=Solanum tuberosum OX=4113 GN=102593733 *Cross-references and related information in:* ▶ Protein families ▶ Samples & ontologies ▶ Protein sequences	208	279.6	99.3	100.0	5.0E-94
☑3	AFDB:B5B3P5	Thioesterase-like protein UA=B5B3P5 UI=B5B3P5_SOLLC OS=Solanum lycopersicum OX=4081 GN=MKS2 *Cross-references and related information in:* ▶ Protein families ▶ Samples & ontologies ▶ Protein sequences	141	275.0	97.2	99.3	3.4E-93
☑4	AFDB:E0YCS8	Methylketone synthase IIa UA=E0YCS8 UI=E0YCS8_SOLLC OS=Solanum lycopersicum OX=4081 GN=MKS2a *Cross-references and related information in:* ▶ Protein families ▶ Samples & ontologies ▶ Protein sequences	208	275.0	97.2	99.3	3.3E-92
☑5	AFDB:A0A6N2BVV2	4HBT domain-containing protein UA=A0A6N2BVV2 UI=A0A6N2BVV2_SOLCI OS=Solanum chilense OX=4083 GN=EJD97_005091 *Cross-references and related information in:* ▶ Protein families ▶ Samples & ontologies ▶ Protein sequences	208	273.1	96.5	99.3	1.9E-91

Supplementary File 6. Search results for proteins with predicted structures similar to *StMKS2-3* in the Protein Structure Sequences, AlphaFold DB, and UniprotKB PDB databases



Supplementary File 7. Heatmap of RNA-seq based expression data of the *StMKS2-3* gene in response to salinity (150 mM NaCl), drought (260 µM mannitol), and *Phytophthora infestans* infection