

Supplementary Materials

	*	20	*	40	*	60	*	80	*	
CsMPK3-3	:	-----				-MAYKSNSYQHRLT-----			DAG :	15
CsMPK3-4	:	-----				-MRPI-----			CSPLTG :	24
CsMPK3-5	:	--MLWSMGCSASPNTGCDPVYPVSTPLQGPTTPLNRSRNGIAGUHTLQIHSQWFSRRLN-GDPIAATQSTQSPPRCDRRTGTCM-TG								90
CsMPK3-2	:	--MTDVNHNVSG-HLFETAKYPPIMPLGRGAYGIVCS-MLSETNEHIAKKIS-DADNYTDAKTIREIKLLR-HLSHEN-TG								81
CsMPK3-1	:	--MADSNNHIFG-NLFETAKYSPIMPIGRGAYGIVCS-VMSETNEHVAIKKIA-N-ADNFIDAKTIREIKLLRHMDHENVI-AA								81
CsMPK6	:	QPYDTVMSEAAYNIFG-NIFEVTAKYKPPIMPIGKGAYGIVCS-ALSETNEHVAIKKIA-N-ADNKIDAKTIREIKLLCHMDHEN-VIK								89
CsMPK4-4	:	MTLFLSLPSFKC-----LFEHRFDIMILTYCC-ATNSETEKEVAIKR--IANADNRIDAKTIREIKLLCHMDHEN-VIK								71
CsMPK4-2	:	MTPFFFS-----ESNFSA-AVNSETHEELAIKK--IGNADNQIDAKTIREIKLLCHMDHEN-ELA								58
CsMPK4-1	:	MTAKVULSGPKRNAITGGNATPATNELCLQIIPCPQLQSVKSWT-KINESTKDAAVIAQADKFICDD-DNNEQAQQQIDFRKAYLLHYDWRYNLIA								92
CsMPK4-3	:	MSECGNIAC---FEVSRKYIAPP-----IRPVGRGAYGIVCA-AVNSETREEVAIKK--IGNAIDNRIDAKTIREIKLLHHHD----VIA								75
CsMPK7	:	--MATLVEPPNYYTSMWQILFEIDTKYVP-IKPILGRGAYGVVCS-SINRETNEKVAIKKIN-NVIGCNRIDALPTERELLLRHIREHN--VIA								85
CsMPK1-2	:	RQMQPQVNPYTSMWQILFEIDTKYVP-IKPILGRGAYGIVCS-SINRETNEKVAIKKIH-NVIGCNRIDALPTERELKLRLPHLRHEN--VIA								87
CsMPK1-1	:	--MATLPVEPPNYYTSMWQTLFEIDTKYVP-IKPILGRGAYGIVCS-SINRETNEKVAIKKIH-NVIGCNRIDALPTERELKLRLPHRHEN--VIA								85
CsMPK20	:	LKGRLILVECMRSTEMLDFSEYCGDANRYKIQEVIGKGGSYGVVCS-AIDTHTGVKAIIKKH-DIEEHISDAAPILREIKLLRLLRHPD--IVE								88
CsMPK19-1	:	--MDFFTTEYCDNSRNYKILIEIIGKGGSYGVVCS-AIDTHTGEKVAIIKKH-DIEEHISDAAPILREVKLLRLLRHPD--IVE								74
CsMPK19-2	:	--PKEMDFFTTEYCDANRYKILKIIKGKTYGCVVCS-AIDTHTGEKVAIIKKH-DIEENTSDAPILREVKLLRLLRHPD--IVE								77
CsMPK16-2	:	--MQPDQRSTVDFFTEYCEGGYRRIEVEIGKGGSYGVVCS-AYDSHLGKVAIIKKH-DIEHVSDATPILREIKLLRLLRHPD--IVE								83
CsMPK16-1	:	PTPGCVKSDQRAADVEFFTEYCEGNRYRIEVEIGKGGSYGVVCS-AYDTHLGKVAIIKKH-DIEHVSDATPILREIKLLRLLRHPD--IVE								88
CsMPK9-1	:	--MLDKEFFTEYGEASQYEIQEFVGKGGSYGVVAA-AVDTHTGERVAIIKKH-NVIEHVSDATPILREIKLLRLLRHPD--IVE								77
CsMPK15	:	CVRRWFQRRPSTDTEFFTEYCEASRYQVQEVVGKGGSYGVVCS-AIDTHTGERVAIIKKH-DVIEHVSDATPILREIKLLRLLRHPD--IVE								88
CsMPK9-2	:	TVIDYFLTS-STLDTEFFTEYGEASRYQIQEUVKGGSYGVVCS-AIDTHTGERVAIIKKH-DVIEHVSDATPILREIKLLRLLRHPD--IVE								87

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	*	100	*	120	*	140	*	160	*	180
CsMPK3-3	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-Y-LYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								105
CsMPK3-4	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								115
CsMPK3-5	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								181
CsMPK3-2	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								172
CsMPK3-1	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								172
CsMPK6	:	IRDVUPPLQRELSDVYIATELM-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								180
CsMPK4-4	:	IKDIIRPPPERDEMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								162
CsMPK4-2	:	IKDIIRPPPKQVMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								149
CsMPK4-1	:	IKDIIRPPPKRENMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								184
CsMPK4-3	:	IKDIIRPPPKENMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARPITS								166
CsMPK7	:	LKDVMMPSDMSEDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARTSR								176
CsMPK1-2	:	LKDVMMPHIERTMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARTSS								178
CsMPK1-1	:	LKDVMMPHIERTMDVYIAYELMD-----TDLHQIIIPSKQSLSEEHQC-YFLYQI-LFCLKYIHSANVHEDLKFPSNLVNANCDLKICDFCLARTSS								177
CsMPK20	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVAF								179
CsMPK19-1	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVAF								165
CsMPK19-2	:	IKSIIHLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-MLRANKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVAF								168
CsMPK16-2	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVAF								174
CsMPK16-1	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVAF								172
CsMPK9-1	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVSF								168
CsMPK15	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVSF								179
CsMPK9-2	:	IKHIMLPPSPRDIDYVVFELMESDLHQVIRANDDLTREHYQ-FFLYQ-LLPAKYIHTANVHEDLKFPSNLVNANCDKLKICDFCLARVSF								178

64 66 Pp f D6Y EL6 3DLh 6I L H 5f6 Q LR h AN6 HDLKP N61 NA1C LK1cDFCLAR

	*	200	*	220	*	240	*	260	*	28
CsMPK3-3	:	ET-----QELTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMNRRPLACKDHQHOLDLILIELLGPTESDGFERSIDAPSYICQ								192
CsMPK3-4	:	ET-----QELTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMNRRPLACKDHQHOLDLILIELLGPTESDGFERSIDAPSYICQ								202
CsMPK3-5	:	ET-----QELTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMNRRPLACKDHQHOLDLILIELLGPTESDGFERSIDAPSYICQ								254
CsMPK3-2	:	ET-----QELTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMNRRPLACKDHQHOLDLILIELLGPTESDGFERSIDAPSYICQ								259
CsMPK3-1	:	EN-----EGHTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMNRRPLFFNDHQLHOLDLILIELLGPTESDLEFERSIDARRYRQ								259
CsMPK6	:	ET-----DFTTEYYVTRMYRAPELLLNSSDY-TAAIDVUSVGCFMELMDRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								266
CsMPK4-4	:	ET-----DFTTEYYVTRMYRAPELLLNCSSEY-TAAIDIISVGCFMELKLRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								249
CsMPK4-2	:	ET-----DFTTEYYVTRMYRAPELLLNCSSEY-TAAIDIISVGCFMELKLRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								236
CsMPK4-1	:	ET-----DFTTEYYVTRMYRAPELLLNCSSEY-TAAIDIISVGCFMELKLRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								271
CsMPK4-3	:	ET-----DFTTEYYVTRMYRAPELLLNCSSEY-TAAIDIISVGCFMELKLRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								253
CsMPK7	:	DNC-----QELTEYYVTRMYRAPELLLCDDNT-GTSIDVUSVGCFIAELLCGRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								264
CsMPK1-2	:	GHD-----QELTEYYVTRMYRAPELLLCDDNT-GTSIDVUSVGCFIAELLCGRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								266
CsMPK1-1	:	GRG-----QELTEYYVTRMYRAPELLLCDDNT-GTSIDVUSVGCFIAELLCGRPLFFCRDHAKHOLDLILIELLGPTESDGFERSIDARRYRQ								265
CsMPK20	:	SDPTTIFDYYAIRMYRAPELCCGSFFFSK-TG-----VSSSF-----WAFG								221
CsMPK19-1	:	NDTPITIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFAEVLTCRPLFFCKSVHOLDLITDLLCTPSSTDTSGRNEKARRYLIG								257
CsMPK19-2	:	KDTPTAIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFAEVLTCRPLFFCKSVHOLDLITDLLCTPSSTDTSGRNEKARRYLIG								260
CsMPK16-2	:	NDTPTAIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFAEVLTCRPLFFCKSVHOLDLITDLLCTPSSTDTSGRNEKARRYLIG								266
CsMPK16-1	:	NDTPTAIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFSELITCGRPLFFCKSVHOLDLITDULLCTPSPECIARGRNEKARRYLIG								264
CsMPK9-1	:	SDAPSTIFDYYAIRMYRAPELCCGSFFFSKLYTPAVDIWSIGCIFAEHLTCRPLFFCKSVHOLDLITDULLCTPSSESARGRNEKARRYLIG								261
CsMPK15	:	NEAPSAIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFAEHLTCRPLFFCKSVHOLDLITDULLCTPSPESTARGRNEKARRYLIG								271
CsMPK9-2	:	NDAPSAIFDYYAIRMYRAPELCCGSFFFSK-YTPAIDIWSIGCIFAEHLTCRPLFFCKSVHOLDLITDULLCTPSPESTARGRNEKARRYLIG								270

f T Y V TRMYRAPEL t a d w s g c f e p g q g q g a 5

	0	*	300	*	320	*	340	*	360	*
	p	p a L	6 FdP	r	al p	l	ep	p	f fe	e
CsMPK3-3	:	FPQHPRQQQLAKVFPHVHPALADLVDKHLTFDPKAGITVEE--	ALAHDYLARHDAADEFVCLDFS---	FDFE-QA GEEQIRDILYQDIALAL	:	279				
CsMPK3-4	:	LPQHPRKQLAKVFPHVHPALADLVDKHLTFDPKAGITVEE--	ALAHDYLARHDAADEFVCLDFS---	FDFE-QA GEEQIRDILYQDIALAL	:	289				
CsMPK3-5	:	TPTSS-AAVSKGFPACHPLALDLVDKHLTFDPKAGITVEE--	ALAHDYLARSHDAADEFVCLDFS---	FDFE-QA GEEQIRDILYQDIALAL	:	340				
CsMPK3-2	:	FPQHPRQQQLAKVFPHVHPALADLVDKHLTFDPKAGITVEE--	ALAHDYLARHDAADEFVCLDFS---	FDFE-QA GEEQIRDILYQDIALAL	:	346				
CsMPK3-1	:	FPQHPRQQQLAKVFPHVHPALADLVDKHLTFDPKAGITVEQ--	ALAHDYLARHDIADEFVCTESFS---	FDFE-QA GEEQIRDILYQDIALAL	:	346				
CsMPK6	:	PPPFHRQSLTEIGFPHVHPAADLVLBKLMLTFDPKAGITVEG--	ALAHDYLTSHDISDEFTICLTDFS---	FDFENHAASEQQAKELIYRQDIALAF	:	354				
CsMPK4-4	:	LPCVPKKPFSHKCPDASPLAIDLAEPRLVFDPSKRITVEE--	ALNHDPFLSCHEINEEITCPSDIFI---	FDFEQQSSLSEEDIKELIWRPSLNF	:	337				
CsMPK4-2	:	LPRYVKQQFSARPNNMSPLAIDLLEKHLVDPPTKDIITVDE--	ALCHDYLSSLHDINDETICPSDFS---	FDFEQPAFPNEEKIKDOLIMMDSIKF	:	324				
CsMPK4-1	:	LPQYPRQQFSARPNNMSPGAAIDLLEKHLVDPPTKDIITVEG--	ALCHDYLAPLHDINNEEIVCPDFSF---	FDFEQPSFTTEENIKELIWRPSVRF	:	359				
CsMPK4-3	:	LPQYSRQQFSARPNNMSPAADVLDLEKHLVDPPTKDIITVDC--	ALSHDYLAPLHDINNEEIVCPDFN---	FDFEQPSFTTEENIKELIWRPSVRF	:	341				
CsMPK7	:	LPYARGVQLSSLYPHADPLADLQLQRHLVFDPSKRITVTE--	ALHHDPYMSLWYDPSRNIPAQVHID---	LDID-ENI CEGHICRQLMLRQHMH	:	351				
CsMPK1-2	:	LPCSPGTPFSCLYPNAHPLAIDLQLQRHLVFDPSKRITVTE--	ALQHDPYMSLWYDQSSDIPAQVHID---	LDID-EDI CEGEMIREHHNPMHH	:	353				
CsMPK1-1	:	LPYSPGTPFSRLYPNAYPLAIDLQLQRHLVFDPSKRITVTE--	ALQHDPYMSLWYDSNCIDIPAQVHID---	LDID-EDI CEGEMIREHHNQDHMH	:	352				
CsMPK20	:	MS-----LILLLHHHP-KDN-----								237
CsMPK19-1	:	MRKKQPVLFSKEIPNADPLAIDLQLRLLAEPDKDPEPAAEE--	ALADDPYFKCIAKAEPEPSC-QISKLEFEFERRRTKEDIRELIFRILEY							347
CsMPK19-2	:	MRKKQPVPFSKEIPNADPLAIDLQLRLLAEPDKDPEPAAEE--	ALADDPYFKCIAKVEREPSC-QISKLEFEFERRRTKEEIRKLFIRILEY							350
CsMPK16-2	:	MRRKRPPIPFCQKCPNADPLAICLLEKHLAEPDKDPEPSAEE--	ALADDPYFKMALARVERESSA-QVTKMEEDFERRRTKEDVPL--WKYLAK							353
CsMPK16-1	:	PKGGKPIPFTQKCPNADPLAIPLLERPHLAEPDKDPEPSAEE--	ALADDPYFKMALARVERESA-QVTKMEFEFERRRTKEDVPL--IYRILEY							354
CsMPK9-1	:	MRRKPPVPFSQKCPNADPLAISLLERLLAEPDKDPEPSAEE--	ALADDPYFSSMANVEDPSA-QISKLEFEFERRRTKDD-----ILEY							343
CsMPK15	:	MRRKSPVPFSQKCPNADPLAIPLLERPLIAEPDKDPEPSAED--	ALTDPPYFTGLANADREPASAQISKLEFEFERRRTKDDVRELIYRILEY							362
CsMPK9-2	:	MRRKPPVPFTHQCPSVTPLAICLLEKHLAEPDKDPEPSAEEVLLADDPYFHGLANUDREPAT-QISKLEFEFERRRTKDDVRELIYRILEY								362

Figure S1: Protein sequence multi-alignment of CsMPKs. Alignment was performed using the ClustalW program. The TXY phosphorylation sites are indicated by red box. Conservative sequences are highlighted by gray or black shading.

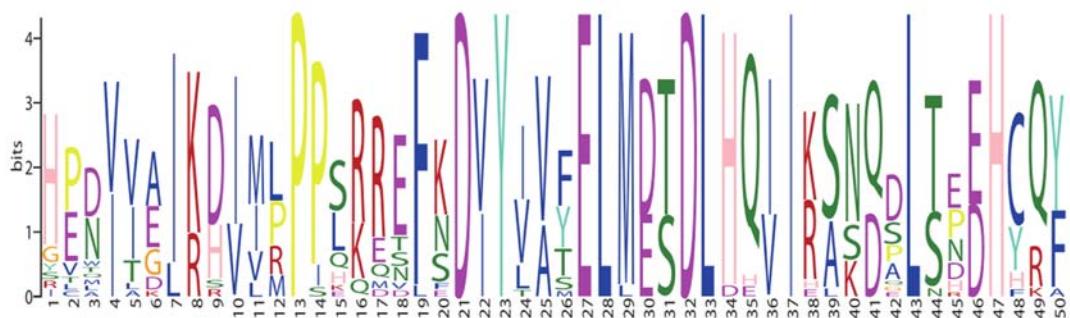
Motif 1



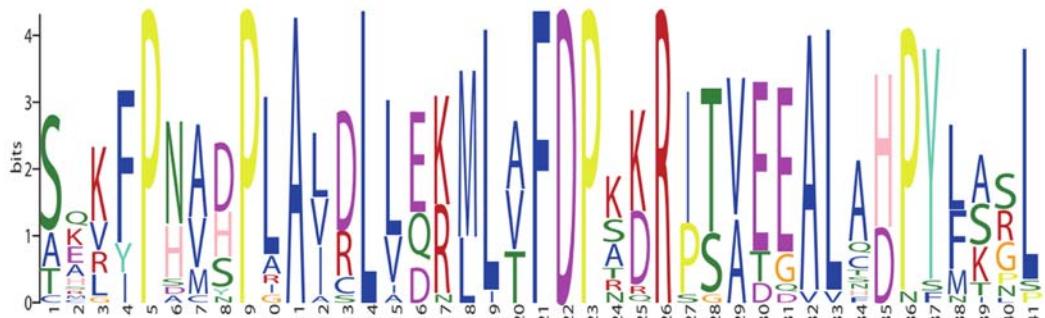
Motif 2



Motif 3



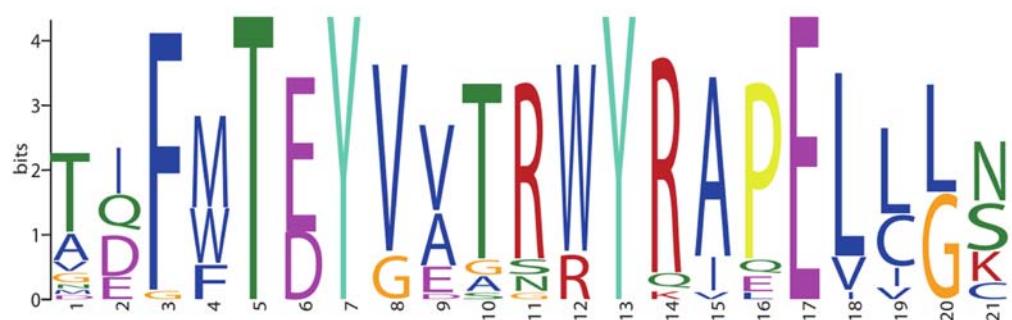
Motif 4



Motif 5



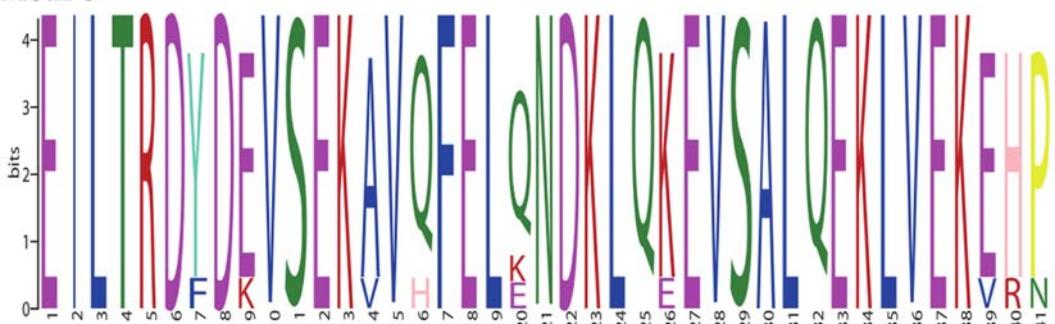
Motif 6



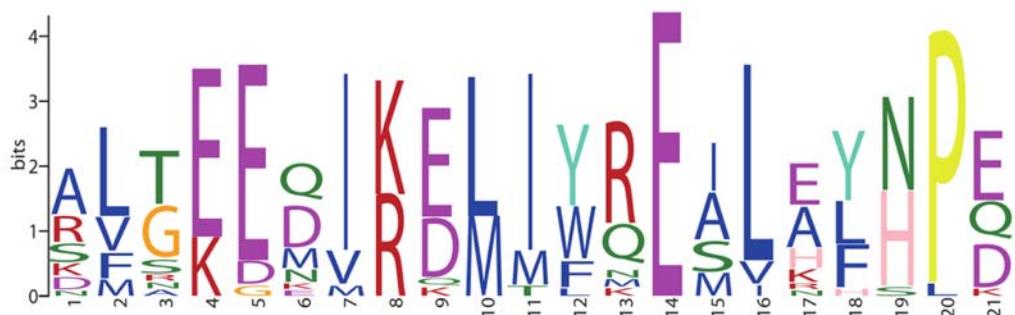
Motif 7



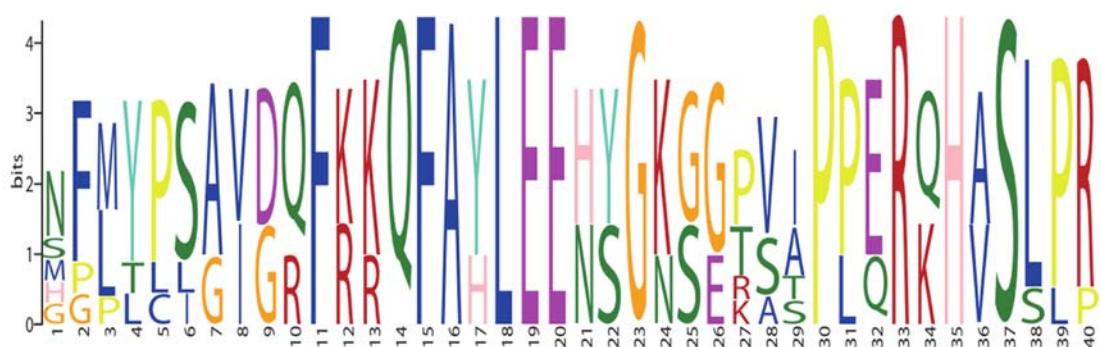
Motif 8



Motif 9



Motif 10



Motif 11



Figure S2: The sequence information of 11 conserved motifs of CsMPKs in tea plant detected by the online tool MEME. (Color figure online).

Table S1: The protein sequences of CsMPKs in tea plant

>CsMPK3-3

MAYKSNYQHRLTIAGIRDVPPPLQRELSDVYIATELMDTDLHQIIRSKQSLSEEHQCQL
YQILRGLKYIHSANVIHRDLKPSNLLVNANCNCDLKICDFGLARPSETQFMTEYVVTRWYR
APELLNNSSDYTAIDVWSVGCIFMELMNRKPLLAGKDHVHQLRLIELLGRTESDIGF
IRSIDARSYICQLPQHPRQQLAKVFPHVHPLAVDLVDKMLTFDPAKRITVEEALAHPYLA
RLHDAADEPVCLEPFSFDSEQALGEEQIKDMIYQEALALNPEYA

>CsMPK3-4

MRRIGSVRSVLADRYIRCSPPLVTGIRDVPPPLKREFSDVYIATELMDTDLHQIIRSKQS
LSEEHQCQFLYQILRGLKYIHSANVIHRDLKPSNLLVNANCNCDLKICDFGLARPSETQFM
TEYVVTRWYRAPELLNSSDYTAIDVWSVGCIFMELMNRKPLLAGKDHVHQLRLIELL
GTPTESDIGFIRSKDARSYICQLPQHPRQQLAKVFPHVHPLAVDLVDKMLTFDPAKRITV
EEALAHPYLARLHDAADEPVCLEPFSFDSEQALGEEQIKDMIYQEALALNPDSVTLASQG
WVNNLIVFLIGQFNVKSINATQIFNVINGCVMFPILGAIVADSFLGSFFVIWSSLISV
LGIILLISATLDSLRRPPCGNGSNLCITPSKLQFAVLYLGITLATIGAAGTRFTLGMG
ADQFDNPKHQGSYFNWFIFTLYMASIISSTAIYVEDSVSFGLGFGLCAAANIGLVIFV
LGKRFYRHVKPQGPFTSLARVFVAIRKRKILLSQRSEDYYNKIHGVTMMAVTPTKT
FNFLNRAALKTEGDIRADGSIAKLWNLCVQQVEDLKALIKIAPLWSSGIFLSTPLAIQY
SLATLQALTMDRHLGPHFKIPPGMSAVFIMIATCITIVLLDRFLYAAWQKLTSPFTPLQ
RVGVGHVLCVLSMALSAIVESKRLKIARSHNLQDQSVLIVPMASFVLPQLALAGIGEAF
HFPGNTALFYQEFPMSLKSTAMVAMFVGIAVVSTALVSGVQRTTGWLPPNNIHGRMD
NMYWLLFVIGVVFNFYFVVCAWLYKYQGVAKVVDENPSSDDK

>CsMPK3-5

MLWSMGSASTGPGTGTGMVLVRTAIERRPNTGGDPVPVSTPLQGPTTPLNSRDNGIAGW
SALFVGKHTLIQHSQWFLSERRNLNGDPIPAATQSTQSPRRCRKDRRTGTTGTMVTGIRDV
VPPPLQREFSDVYIATELMDTDLHQIIRSKQSLSEEHQCQFLYQILRGLKYIHSANVIHR
DLKPSNLLVNANCNCDLKICDFGLARPSETQFMTEYVVTRWYRAPELLNSSDYTAIDVW
SVGCFMELMNRKPLLAGKDHVHQLRLIEQRCKKLYLSTTPSSAAVSKGFPACHPLAV
DLVDKMLTFDPAKRITVEEALAHPYLARSHDAADEPVCLEPFSFDSEQALGEEQIKDMTY
QEALALNLEYA

>CsMPK3-2

MTDVNSAGGELVHGGQFIRHNVSGLFEITAKYRPPIMPLRGAYGIVCSMLNSETNEMI
AMKKISDAFDNYTDKRTLREIKLLRHLSENVTGIRDIVPPPLKREFFDVYIATELMDT
DLHQIIRSKQSLSEEHQCQFLYQILRGLKYIHSANVIHRDLKPSNLLVNANCNCDLKICDFG
LARPSETQFMTEYVVTRWYRAPELLNSSDYTAIDVWSVGCIFMELMNRKPLLAGKD
VHQLRLIELLGTPTESDIGFIRSKDARSYICQLPQHPRQQLAKVFPHVHPLAVDLVDKM
LTFDPAKRITVEEALAHPYLARLHDAADEPVCLEPFSFDSEQALGEEQIKDMIYQEALAL
NPEYA

>CsMPK3-1

MADSNNTVAGQFPEFPAIPTHGGQFIQHNIFGNLFITAKYRSPIMPIGRGAYGIVCSVMN
SETNEMVAIKKIANAFDNFMDAKRTLREIKLLRHLHENVIARDVIPPLRQEFDVYI
AMELMMDTDLHQIIRSNQGLSEEHQCQFLYQILRGLKYIHSANVIHRDLKPSNLLNANC
LKIIDFLARPTSENEMGTEYVVTRWYRAPELLNSSEYTAIDVWSVGCIFMELMNRKP

(Continued)

Table S1: *Continued*

LFPGNNDHMHQMRLLIELLGPTESDLEFIRSEDARRYLRQFPQHPRQQQLAMVFPHVNPLA
 IDLIENMLTFDPSKRITVEQALAHPYLARLHDIADEPVCTESFSFDFEQAMGEEQIKDMI
 YQEAIALNPEFA
 >CsMPK6
 MDASAQPYDTVMSEAAPPPQSDPPPQPPAAGIEHIPATLSHGRFIQYNIFGNIFEVT
 AKYKPPIMPIGKGAYGIVCSALNSETNEHVAIKKIANAFDNKIDAKRTLREIKLLRHMDH
 ENVINFSSFPKMTLNVSFTQCERRSEVQAVRLKGPKARLQPHSITTYIIPNQNQST
 QIPNLSKKSVCSSPLGLSSSISITSISIEVSSPPPPPPPLLCWSLVAGCWVAIRDIP
 PPQRESFNDVYIAYELMDTLHQIIRSNQALSEEHCQYFLYQILRGLKYIHSANVLHRDL
 KPSNLLNANCNCDLKICDFGLARVTSETDFMTEYVVTRWYRAPELLNNSDYTAIDVWSV
 GCIFMELMDRKPLFPGRDHAQLRLLMELIGTPSEAEFGFLNENAKRYIRQLPPFHRQSL
 TEKFPHVHPAAIDLVEKMLTFDPRQRITVEGALAHPYLTSLHDISDEPICLTPFSFDFEN
 HALSEEQMKEIYREALAFNPEYQQJM
 >CsMPK4-4
 MTLFSLPSFKCLFEMRFDIMLTYYCCATNSETKEEVAIKRIANAFDNRIDAKRTLREIKLL
 CHMDHENNTIVQVIKIKDIIRPPEKDEFNDVYIAYELMDTLHQIHSQELDDHCQYF
 LYQLLRGLKYIHSANVLHRDLKPSNLLNANCNCDLKICDFGLARTTSETDFMTEYVVTRWY
 RAPELLNCSEYTAIDIWSVGICLMEILKREPLFPGKDYVQQLLITELLGSPEESDLG
 FLRSENARKYVKQLPCVKPKFHKFPDASPIAIDLAERMLVFDPDKRITVEEALNHPL
 SGLHEINEEPTCPSPFIFDFEQSSLSEEDIKEIWIRESLFNFPDEFFNVLTGCWEAVVVG
 IIILGLCFILSSRVCPMMNLYAKKKSDLKIQGAKKKAMRFSQIFVKASSSSHSRNRAS
 ASSLLLSTASRSFSHLRSPSQRPSFGIAFDIDGVILRGNTPIGGSPQALGRLYHDSFGTL
 KVPYVFLTNGEPFVSSCYTRPYTFQTAGKERSYFMGTKEVLLVDVAYVVRFENDLIAVG
 KGEPATVMSEYGFKNAFSIDEYASCFDNIDPLAQFKWTTGHVNQNNTIRSTACTQRVHA
 AFIVSDSVWSRDIQVLCIDLRTGGFPGREIAHQPSLYFANDLEYQAVFPSERLGMGAF
 RIALESIFNSIHPNALEYTSFGKPNPSVRNAETVLMETVPSYQSANHVTGGNHFRNL
 YMIGDNPSVDIKGAKQAGHPWFSILTRTVFKGKKNHAEPADLVGELTLYICNSNSFKF
 HFSLETIILLSTFASQT
 >CsMPK4-2
 MTPFFFSFSNFSAAVNSETHEEIAIKKIGNAFDNQIDAKRTLREIKLLCHMDHENILA
 DIIRPPKKQVFNDVYIVSELMDTLHQIIRSNQPLTDHCQYFMYQLLRGLKYVHSANVL
 HRDLKPSNLFNANCNCDLKICDFGLARTTSETDFMTEYVVTRWYRAPELLNCSEYTAID
 VWSVGICLGEIATREPLFPGRDYAEQLRLITELLGPNDTCGLFLRSNDNARRYVKQLPRY
 PKQQFSARFPNMSPLAIDLLEKMLVFDPTKRITVDEALCHPYLSSLHDINDEPICPSPFS
 FDFEQPAFNEEKIKDLIWMESLKFNPDPHT
 >CsMPK4-1
 MMLHIRRQMKMEMKVVEGGKSAEEDDEDVAKSVEGSINGNHTVEGLSDDVGGQSLERQ
 QQPYPYLADDALGELKVAYEALKEHNISSEAANIEVILYEFIKQHVCDIEAKKGELLGL
 YEAVRQHSTILGAENSELVKKLDYQPRISVLDRLDEMHSSEMASSISNQVEVLHKE
 VAERASILEQEWNSTVAQVVTVEKLDALIRSLFSTASVDAATKVIDNLQEKEASGKD
 TAMCSSYKDMIEKFNDLHRKNELAIGVLHGVBGNLQRLVNDSCQHVEQSQIINQNENLID

(Continued)

Table S1: *Continued*

PLHLDNYDTLMEQLAVLLGERLQFKSMNDKLNLLEIDMAKEMEKLKKTGLSDSTILKLVE
 DVEGAVKLNGTGDSEKLESRLQRLLSISFLSDSLEILTRDYDEVSEKAVQFELQNDKLQKE
 VSALQEKLVEKEHPSDSLEILTRDYDEVSEKAVHFEKLQKEVSALQEKLVEKEHPS
 DSLEILTRDYDEVSEKAVQFELQNDKLQKEVSALQEKLVEKEHPSDSLEILTRDYDEVSE
 KAVQFELQNDKLQKEVSALQEKLVEKEHPSDSLEILTRDYDEVSEKAVQFELQNDKLQKE
 VSALQEKLVEKEHPSDSLEILTRDYDEVSEKAVQFELQNDKLQKEVSALQEKLVEKEHPS
 DSLEILTRDYDEVSEKAVQFELQNDKLQKEVSALQEKLVEKEHPSDSLEILTRDFDKVSE
 KVVFQLENDKLQEEVSALQEKLVEKVRNQEHIIEGEIRRLEDLVHDLLKDSVTEDVVSAG
 SSTKCLEQLKKLSEKYTALALEKPILVDSAEEKNTKTRPRPMTAKVLSGRKRSTRVRG
 RTLKGKVQKRIARKKGEGKLHVYVNRVLNAITGGNATPATNEGLQIRRLCPLQSVKSWT
 INESTKDQADKFVIGDDFDNEQAQQILDRAKAYLLYKDWRYNLKQEFLEEKGVDD
 PYSHPPSGVSLDDWRYLIDVAWKDESHLKKEEGCTFKPEWAAYEALKEHNISSEAANIE
 VVIIYEFIGHQHVC DIEAKKGELLGLYEA VRQH STILGAEN SELVKK LGD YQPRISV LDRQ
 LDEMHS S DEMASSISN QVE VLH KEVAERASILEQEWNSTVGQVVQTVEKLDALIRSFFL
 AWTYVAVIAIKDIIRPPLKENFNDVYIVYELDTDLHQIIRSNQPLNDDHC RALYTASGN
 ELFVKGYVSFFIHQGDVRNLTSNMQSVCNMITSVRADCIVHLIDSSILLMQYFLYQILRG
 LKYVHSANVLHDLKPSNLLNANC DLKIGDFGLARTTSETDFMTEYVTRWYRAPELL
 NCSEYTAIDIWSVG CILGEIMTRQPLFPGKD YVHQLRLITELIGSPDDASLGFLRSDNA
 RRYVRQLPQYPRQQFSARFPNMSPGAA DLKMLVFD PKNRITVEGALCHPYLA PLHDIN
 EEPVCPRPFSFD FEQPSF TEENIKELI WRES VRFNPD PPI SH
 >CsMPK4-3
 MSEGNIAGIPHTGGGRYVQYNVYGTLFEVSRKYIPPIRPVGRGAYGIVCAVNSETREEVA
 IKKIGNAFDNRIDAKRTLREIKLLLHMDHENVIAIKDIIRPPQKENFNDVYTVSELMDTD
 LHQIIRSNQQLSNDHCRYFLYQLRGLKYVHSANVLHDLKPSNLLNANC DLKIADFG
 ARTTSETDFMTEYVTRWYRAPELLNCSEYTAIDIWSVGCVFGEIMTRQPLFPGRDYV
 HQLRLITELIGSPDDASLGFLRSDNARRYVRQLPQYSRQQFSARFPNMSPAAVDLLEKML
 VFDPNRRITVDGALSHPYLA PLHDINEEPVCPRPFNFDFEQPSF TEENIKELI WRES VKF
 NPD PPI H
 >CsMPK7
 MATLVEPPNGVKPLGKHYYSMWQILFEIDTKVPIKPIGRGAYGVV CSSINRETNEKVAI
 KKINNVFGNRIDALRTLRELRLRH REN VIALKDVMMP SQRMS FEDVYLYELMDTL
 HHIIKSSQPLSNDHCKYFIFQLLRLRYLHSANILHDLKPGNLLVNANCELKICDFGLA
 RTSRDNGQFMTEYVTRWYRAPELLCCNDY GTSIDVWSIGC IFAEILGRKPI FPGSECL
 NQLKLIINVLGSQCEADLEFIDGQKARRFIKSLPYARGVQLSSLYPHADPLAVD LQRML
 VFDP SKRITVTEALHHPYMSSLYDPSRNPPAQVEINLDIDENMGEGMIRQLMLREMLHYH
 PEAACANT
 >CsMPK1-2
 MLKDLKNVIARQM ATQVEPPNGIKSVGKHYFSMWQTLFEIDTKVPIKPIGRGAYGIVCS
 SINRETNEKVAIKKIHNVFDN RIDALRTLRELKL RL REN VIALKDVMMP IHRRTFKD
 VYLVYELMDTLHQIJKSSQALTN DHCQYFLQ LRL KYLHSANILHDLKPGNLLINA
 NCDLKICDFGLARTSSGKDQFMTEYVTRWYRAPELLCCNDY GTSIDVWSVGCIFAELL

(Continued)

Table S1: *Continued*

GRKPVPGTECLNQLKLIINILGSQREDDIEFIDNPKARKYIKSLPCSPGTPFSCLYPNA
HPLAIDLLQKMLVFDPDKRIGVTEALQHPYMSSLYDQSSDPPAQVPIDLDIDEDLREEMI
REMMWNEMLHHHPEAAPANMEVNQ
>CsMPK1-1
MATPVEPPNGINSPGKHYYSMWQTLFEIDTKYVPIKPIGRGAYGIVCSSINRETNEKVAI
KKIHNAFENCVDALRTLRELKLLRHLRHENVIALKDVMMPHIERRTFKDVLVYELMDTDL
HQIIKSSQALTNDHCQYFLFQEDSVVLKLMKDSVNGQTFFGLDLCRDSGALGQNMEVTT
IGKSNGNFPSEQLLRGLKYLHSANILHRDLKPGNLLNANCNLKICDFGLARTSSGRGQFM
TEVVVTRWYRAPELLLCCNYGTSIDVWSVGCIFAELLGRKPIFPGTECLNQLKLIINIL
GSQREDDLEFIDNPKARKFIKSLPYSPTPSRLYPNAYPLAIDLQKMLVFDPSKRISV
TEALQHPYMSSLYDSNCDDPPAQVPIDLDIDEDLGEEEMIREMMWKEMLHYHPEAAATANVDV
S
>CsMPK20
MIVGGGEVLKGRILVECMRDLIRPCFVKNSKVRWDCSFVIRSRVLNKQTMQDHGKKN
STEMDFSEYGDANRYKIQEVGKGSYGVVCSAIDHTGVKAIIKIHIFEHISDAARI
LREIKLLRLRHPDIVEIKHIMLPPSRDFKDIYVFELMESDLHQVIKANDDLTREHYQ
FFLYQLLRAKYIHTANVYHRDLKPKNILANANCKLKICDFGLARVAFSDPTTIFWTDY
VATRWYRAPELCGSFFSKTGVISSFSWAFGMSLILLHHHLHFPKN
>CsMPK19-1
MDFFFTEYGDSNRYKILEIIGKGSYGVVCSAIDTHTGEKVAIKKINDIFEHISDAIRILRE
VKLLRLLRHPDIVDIKRIMLPPSRREFKDIYVFELMESDLHQVIKANDDLTHDHHRF
YQMLRAMKYMHTANVYHRDLKPKNILANANCKLKICDFGLARVAFNDPTTIFWTDYVAT
RWYRAPELCGSFFSKYTPAIDIWSIGCIFAEVLTGKPLFPGKSVVHQLDLITLLGTPSS
DTISGVRNEKARRYLTGMRKKQPVLFSEKIPNADPLRLLQRLLAQDPKDRPTAEAL
DPYFKGLAKAEREPECPQCPIKLEFEFERRVTKEDIRELIFREILEYHPQLLKDYLAGNE
GPNFLYPSAIGQFRKQFAYLEENSGKSGVIPPERKHVSLPRSTVNSSTVPPRTNQNLAS
CGSRQVTEESNSIRVTAISGGNFVKPSRPPPVPAAKPGRVVGPVLPYENGRRNINDVY
DARAFLRNGVVPQGISPYAARTNTVNHAKSSTEIDRNAQARQLPAQCNGVTQSPQIA
IDINANTYYQPQVKSSQLNDQIAINAKLLQESQLGAIGAAA
AVAARREVGAVALQLGS
>CsMPK19-2
MQRDQRKKSPKEMDFFTEYGDANRYKILKIIKGTYGVVCAAIDTHTGEKVSICKINDIF
ENTSDAIRVLREVKLLRLRHPDIVDIKSIMLPPSRREFKDIYVFELMESDLHQVIELN
DDLTHDHRRFLYQMLRAMKYMHTANVYHRDLKPKNILANADCKLKICDFGLARVAFKD
PTAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSVGCVFAEVLTGKPLFPGKNIVHQL
DLITDLLGTPSSDTISVVQNEKSRRYLTSMRKQPVFSEKIPNADPLRLLQRLLAQDPKDR
PKDRPTAEALADPYFKGLAKVEREPECPQCPIKLEFEFERRVTEEEIRKLIFREILEYH
PQLKYYLAGNEGANGFLYPSAVGQFRKQFAYLEENSGKSGVIPPERKHVSLPRAVGQFR
KQFAYLEENSGKSGVIPPERKHVYTPAIDIWSIGCIFAEVLTGKPLFPGKSVVHQLDLIT
DLLGTPSSDTISGVRNEKARRYLTGMRKKQPVLFSEKIPNADPLRLLQRLLAQDPKDR
PTAEEALADPYFKGLAKAEREPECPQCPIKLEFEFERRVTKEDIRELIFREILEYHPQLL
KDYLAGNEGPNFLYPSAIGQFRKQFAYLEENSGKSGVIPPERKHVSLPRSTVNSSTVPP

(Continued)

Table S1: *Continued*

RTNQNLASCGRQVTEESCNSIRVTDAISGGNFVKPSRPPPVPAGMVDLVKTHELKGLI
 LKETELGPEKRQVGRVLVESIGFILGWINTVLLCRPLRNALT/SNGDLKRHEVPARADPV
 VRVVSNPNSFSP
 >CsMPK16-2
 MQPDQRKKVVSSSMPMFSSNLGPSKGYVLHGSVDVDFTEYGEGRYRIEEVIGKGSYG
 VVCSDSHLGEKVAIKKINDIFEHSVSDATRILREIKLRLRHPDIVEIKHILLPPSRR
 EFKDIYVFELMESDLHQVIKANDDLTPEHYQFFLYQLLRLKVIHTANVFHRDLKPKNI
 LANADCKLKICDFGLARVAFNDPTAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSI
 GCIFAELLTGKPLPGKNVHVQLDLMTDLLGIPSPESIARIRNEKARRYLSSMRRKRP
 FCQKFPNADPRALCLLEKMLAFDPKDRPSAEEALADPYFKNLARVERESSAQPVTKMEFD
 FERRRTKEDVRWKYLLAKCLAVAFLVFQEDSMGMTCIAVDQFKKFAYLEEHYNGNGT
 VAPPERQHASLPRPCVLYSSDNSMQSSAEVTNDLKCCIKEVEKPHVDRISGIPKTRLPL
 QVPPTGVNFFYDHRSQAAAARPGKVVGSVLRYNNGCAEALEHRRMVRNPAPVPTQYAVS
 TSRRNPGSKNERREDGVEGSSVLQPKPPQYVSRKVAAQGGSGSHWH
 >CsMPK16-1
 MGLLRTFLPTPGCVKSDQRASISDLWISDDSVFRKHGCHRRLMSDSARTLLGFAVR
 NLSLKMEIASPTERENRRRRRGNEIIIAKPNYKELETQFKTSRNPNLEQKWKVVWIER
 KGIGMSEVAADVEFFTEYGEGRYRIEEVIGKGSYGVVC SAYDTHLGEKVAIKKINDIFE
 HVSDATRILREIKLRLRHPDIVEIKHILLPPSRREFKDIYVFELMESDLHQVIKAND
 DLTPEHYQFFLYQLLRLANVFRDLKPKNILANADCKLKICDFGLARVAFNDPTAIFWTD
 YVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFSELLTGKPLPGKNVHVQLDLMTDLLG
 TPSPEGIARIRNEKARRYLSSMRKKPIPFTQKFPNADPLRLERMLAFDPKDRPSAE
 EALADPYFKNLARVEREPSAQPVTKMEFEFERRVTKEDVRELIYREILEYHPKMLKEYL
 EGEEPTGFMYPSAVDQFKKFAYLEEHYNGNGTAAPPERQHASSLPRACVLYSDNSAQNS
 TEVTNDLSKCCIKEVERPHMDRTSGIPMTRMPPQVPPSIQAGGAARPGKVSSVLRNN
 GAAAAAAETVEQRRMVRNPVPTQYAVSSSSYARRNSACKNERGGEDGVEGSNGLQPKPQ
 YMPCRVAQQGGSGSQWLCTSLSRDLNLRCPQKFTNPLSVFHSKPQFLNRNCFKSPFQ
 SSISATHRLISSIYRMGDSRRPPTVPIPDVEIADKSELYRALEASLGSSFSNPLAPNPN
 PLIIVSGPSVGKDAVKGLREVREGIHFWVTATSRAKRPGEVEGKDYFFVSKEEFLSM
 VERDELLEYALVYGDYKGIPKQQIREFMAGHDIVLRVDIQGAATLRRILGNSAVFIFLV
 AESESALVKRLIGRKETKETLLRVATAAREEVKHLRFDYVVNAEGKLESAVKLVESI
 IDAEKAKVWQRTAVI
 >CsMPK9-1
 MLDKEFFTEYGEASQYEIQEFVGKGSYGVVAAVDTHTGERVAIKMNNVFEHVSDAIRI
 LREIKLRLRHPDIVEIKHIMLPPSRREFKDIYVFELMESDLDEVIKANDDLTPEHFQ
 FFLHQLLRLALKYIHTANVFHRDLKPKNILANADCKLKICDFGLARVSFSdapstifwtdy
 VATRWYRAPELCGSFFSKVTQSGFNNLSHCIKVCSNPVSCSGWLSEPHSEQPIQLEHVLN
 LYTPAVDIWSIGCIFAEMLTGKPLPGKNVHVQLDIITDLLGTPSSESIARIRNEKARRY
 LNSMRKKPPVFSQKFPNADPLASLLERLLAFPRDRSSAEEALADPYFSSLANVEDEP
 SAQPISKLEFERRLKTDILEYHPQMLQEYLDGVDRTSFMYPRSVLCGLRFSFDPRI
 YAVFEKVNPPAVRFAPTSLDLIRGKKVLTGFPNHSKKGIRLLMQLLPLMLLSQR
 ILPMECNREPEIRCEQSVEGAELRAFTFYIKAHSI

(Continued)

Table S1: *Continued*

>CsMPK15
MGSGTFVDGVRRWFQRRPSSPQNNTQLNNNSQLVSGFQGEDHNVVEDFDSLKI
VPKRINFHTSMDPKKTTLDTEFFTEYGEASRYQVQEVGKGSYGIVGSATDTHTGERV
AIKKINDVFDHVSDATRILREIKLLRLRHPDIVEIKHIMLPPSRREFKDIYVFELMES
DLHQVIKANDDLTPEHYQFFLYQLLRGLKFIHTANVFHRDLKPKNILANADCKLKICDFG
LARVSFNEAPSAIFWTDYVATRWYRAPELCGSFFSKYTPAIDVWSIGCIFAEMLTGKPLF
PGKNNVHQQLDLMTDFLGTAPESIARIRNEKARRYLSSMRKKSPVFSQKFPNADPLALR
LLERLIAFDPKDRPSAEDALTDPYFTGLANADREPASAQPISKEFERRKLTKDDVRE
LIYREILEYHPQMLQEYLRGGDQTSFMYPNGIDRFKRQFAHLEEHYGKGEKSTPLQRQHA
SLPRERVCGQKDETISQNDLEKRTAASVATTIQSSPKESEESENANTNAQSGLNKPNYS
ARTLLKSASISGSKCVVVAQAKDSKEEPIAEHEEVDELTQKLAAINS
>CsMPK9-2
MTQTVIDYFLTSSAPCPGLDCLSYPSTGYTLDTEFFTEYGEASRYQJQEVGKGSYGVVG
SAIDTHTGERVAIKKINDVFEHVSDATRILREIKLLRLRHPDIVEIKHIMLPPSRREFK
DIYVFELMESDLHQVIKANDDLTPEHYQFFLYQLLRGLKYIHTANVFHRDLKPKNILAN
ADCKLKICDFGLARVSFNDAPSIAFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCI
FAEMLTGKPLFPGKNNVHQQLDLMTDLLGTPSPESTARINQKARRYLSSMRRKPPVFT
KFPSVDPLALCLLERLLAFDPKDRPSAEVVFHNSNILPLADPYFHGLANVDREPATQ
PISKLEFEFERRKLAKDDVREIYREILEYHPQMHQEYLCGGDQTSFMYPRPDLPPLLCA
SAILAFVLAVHPPLLGVDRFKRQFAHLEEHYGKGERSSPLQRQHASLPRERVCPKDEA
TSQNDFEVRTTASVATTLSPPSENANTDAQNGPSKPNYSARSLLKSASISASKCIGAK
GRKDSEGEIIAEQNEEVDAASSQKVAALCA

Table S2: The primer sequences of the CsMPK genes in tea plant for quantitative RT-PCR

Name	Forward primers (5' to 3')	Reverse primers (5' to 3')
<i>CsMPK4-2</i>	TTCCAATTCAGTGCTGCTG	TGAAGATCGGTGCCATCAA
<i>CsMPK3-1</i>	ACCCACTGAATCGGATCTG	GACCGGTTCGTCAGCTATGT
<i>CsMPK19-1</i>	CGAAATGAGAAGGCAAGGAG	GTCGCCTCTGAACTCAAAC
<i>CsMPK4-1</i>	TTCCACAATAACCACGACAA	TCAGTGAATGATGGCTGCTC
<i>CsMPK9-1</i>	CCACAGATGCTGCAGGAGTA	GTTCGGAAACCCAGTGAGAA
<i>CsMPK6</i>	CTTCAGCTCAGCCCTACGAC	GAATTCAAAGCCGAGCAGAC
<i>CsMPK15</i>	ACAGTTGCCATCTGAGG	TGATTCCCTCGGATTCTTGG
<i>CsMPK19-2</i>	GCAGGAATGGTTGATCTGGT	GAGGCCGACATAAAGGACA
<i>CsMPK16-2</i>	GTGGAACTGTTGCTCACCT	AGCACCTGAGAACGATGAT
<i>CsMPK7</i>	ATCTCAACCGTTCCAATG	TAGCCGAAGTCGCATATCT
<i>CsMPK3-3</i>	CTTGCGGGTAAAGACCATGT	GATGGACATGTGGGAAACCC
<i>CsMPK3-2</i>	CTTGCGGGTAAAGACCATGT	GATGGACATGTGGGAAACCC
<i>CsMPK20</i>	GTGGAGTGATGAGGGATCT	TCAATGGCTGAGCAAACAC
<i>CsMPK4-3</i>	TATACGCCCTCACAAAAGG	CAATTGCATTGAGGAGCAA
<i>CsMPK1-2</i>	CCTGGAACCTCTCATCAA	AAAGATGCATCCGACAGACC
<i>CsMPK9-2</i>	ATCAGCTTCTCGTGGCTA	AGCACGATACCATCGGGTAG
<i>CsMPK4-4</i>	GAGTCTGCCCATGATGAAT	AGCGAAGGTGTGAGAAGGAA
<i>CsMPK16-1</i>	GTCAGCTCAGTGTGCGGTA	TTGGATCCTCGACTCCATC
<i>CsMPK1-1</i>	CCAGAGCTCCTCTGTGTTG	CCTGCTTCCGGTTATCAA
<i>CsMPK3-4</i>	CTTGCGGGTAAAGACCATGT	GATGGACATGTGGGAAACCC
<i>CsMPK3-5</i>	CTTGCGGGTAAAGACCATGT	AGCTCGTCATGTGATCTG
<i>Actin</i>	GCCATTTGATTGGAATGG	GGTGCCACAACCTGATCTT

Table S3: The number and composition of promoter elements of each CsMPK gene

	ABRE	TGACG-motif	CGTCA-motif	TCA-element	ERE	GARE-motif	P-box	LTR	MBS	MYB	MYC	ARE
<i>CsMPK1-1</i>		3	3					1		1	1	1
<i>CsMPK1-2</i>	1				1		1	1	1	4	2	
<i>CsMPK3-1</i>	2					2				4	2	
<i>CsMPK3-2</i>				1	2			1	1	3	1	2
<i>CsMPK3-3</i>	1					2					2	3
<i>CsMPK3-4</i>	6	1	1		1	1				3	4	2
<i>CsMPK3-5</i>	1	1	1	1				1	1	6	2	1
<i>CsMPK4-1</i>	2	2	2	1		1			1	4	3	1
<i>CsMPK4-2</i>		1	1	1						2	3	6
<i>CsMPK4-3</i>	2	2	2			5		1	1	2	5	2
<i>CsMPK4-4</i>									1	1	2	1
<i>CsMPK6</i>						3		1	1	4	7	1
<i>CsMPK7</i>						3				1	4	
<i>CsMPK9-1</i>				1				1	2	6	3	4
<i>CsMPK9-2</i>	1	1	1							3	2	6
<i>CsMPK15</i>				2	1		1			6	1	4
<i>CsMPK16-1</i>		1	1			2				4	5	1
<i>CsMPK16-2</i>	2	1	1		1					4	3	1
<i>CsMPK19-1</i>				2			1			4	2	3
<i>CsMPK19-2</i>		2	2	1				2	1	1	3	
<i>CsMPK20</i>					4		1			3	2	5