Additional File 9. Yeast-two-hybrid table and MAPK sequences. Weak (+) and strong (+++) positive or negative (-) MPK-MKK and MKK-MKKK interactions are presented in the table (p. 2). Positive Y2H interactions for orthologous genes observed in Arabidopsis [1], rice [2, 3], brachypodium [4], maize [5] are also shown. MPK and MKK sequences used that do not match a nucleotide identifier from Additional File 3 are marked as clones or synthetic (syn), and the alignment for these sequences are provided at the end of this file (p. 6-18). TaMKKK sequences are provided (p. 4-5) along with phylogenetic analysis (p. 3) of MKKK sequences used here together with MKKK sequences identified in Wang et al. [6].

Reference:

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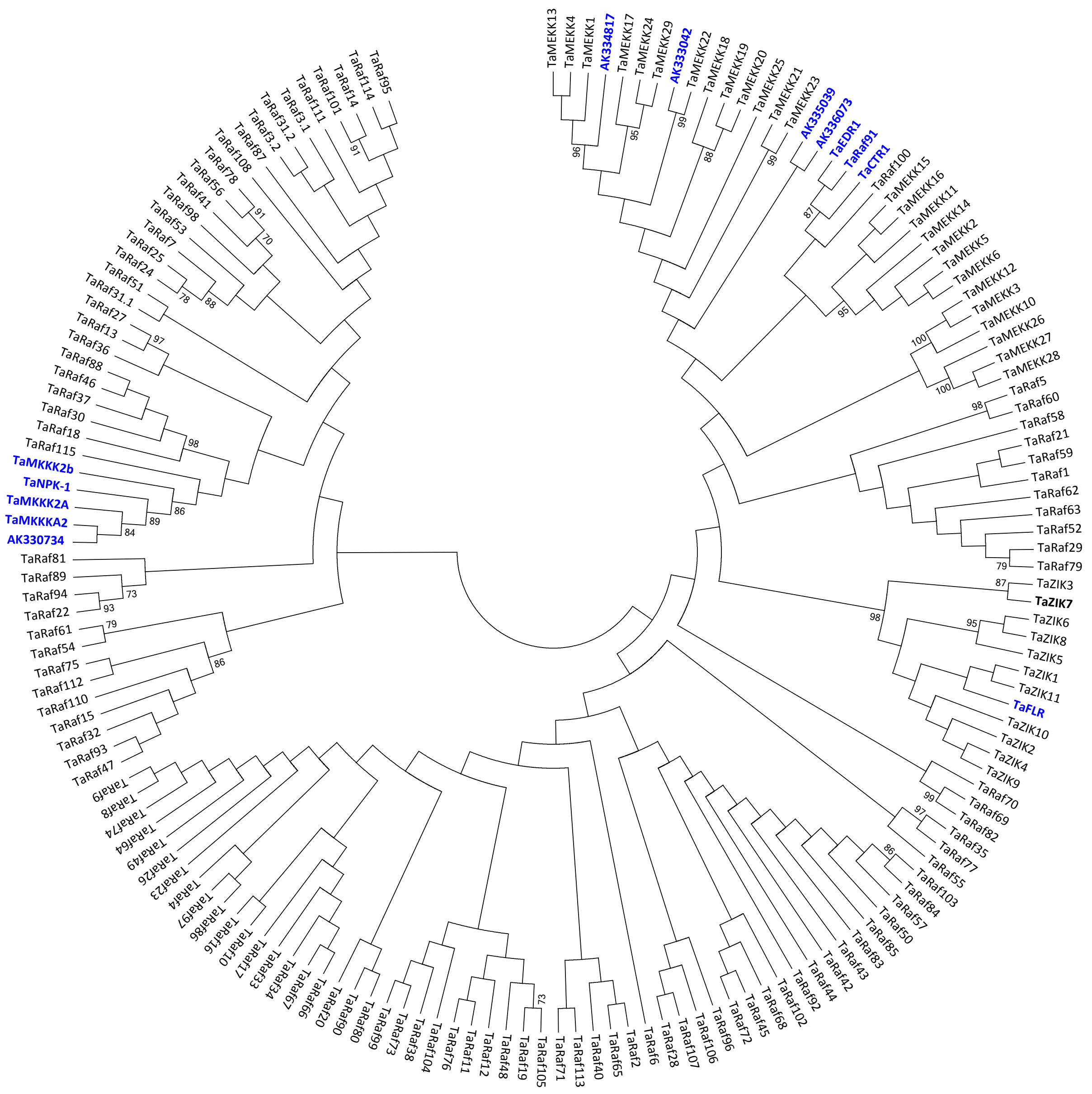
Table. Weak (+) and strong (+++) positive or negative (-) MPK-MKK and MKK-MKKK Y2H interactions. n.d. = no data. Positive interactions for orthologous genes were observed in [a]Arabidopsis [1], [b]rice [2, 3], [c]brachypodium [4], [d]maize [5]. It should be noted that Arabidopsis and rice have only one paralogue of MKK3, and Arabidopsis has only one MKK10. The reported MKK6-MPK16 in rice was observed for OsMPK16-1, whereas the OsMKK6-OsMPK16-2 was negative. Other notable interactions from previous reports include: OsMKK10-2 with OsMPK7 [3]; BdMKK3-1, but not BdMKK3-2, with BdMPK7-1/11 [4], and ZmMKK3-1 with ZmMPK6-2/7 [5].

TaNPK-1 (syn)	-	+	+	-	+	-	-	-	-	-	-
TaZIK7 (Traes_2BS_18264AA5C)	-	+++	-	-	-	-	-	-	-	-	-
TaMKKKA2 (syn)	-	-	-	-	-	n.d.	-	+	-	-	-
TaMKKK2b (syn)	-	-	-	-	-	-	-	-	-	-	-
TaMKKK2a (syn)	-	-	-	-	-	n.d.	-	+	-	-	-
TaFLR (AY173961)	-	-	-	-	-	-	-	-	-	-	-
EDR-1 (AY743662)	-	-	-	-	-	-	-	-	-	-	-
TaCTR1 (DQ211934)	-	-	-	-	-	-	-	-	-	-	-
AK336073	-	-	-	-	-	-	-	-	-	-	-
AK335039	-	-	-	-	-	-	-	+	-	-	-
TaMEKK1 (AK334817)	-	-	-	-	-	-	-	-	-	-	-
TaMEKK22 (AK333042)	-	-	-	-	-	-	-	-	-	-	-
AK330734	-	-	-	-	-	-	-	-	-	-	-
	TaMKK1-1 (syn)	**TaMKK3-2a** (KT187393)	**TaMKK3-2b** (clone)	**TaMKK3-3** (syn)	**TaMKK4** (syn)	**TaMKK5a** (syn)	**TaMKK5-2b** (syn)	**TaMKK6** (RFL_4066)	**TaMKK10-2** (syn)	**TaMKK10-1/3** (4AL)	**TaMKK10-4** (4DS)
TaMPK3 (4DL)	-	-	-	-	-[a,b]	-	-	-	-	-	-
TaMPK4 (clone)	+++[a,b,d]	-	-	-	-	-	-	+++[a,b]	-	+	-
TaMPK6 (7DS)	-[b]	-[b]	-[b]	-[b]	-[a,b]	+[a,b]	-[a,b]	+[a,b,c]	-[b,d]	+	-
TaMPK7 (7BL)	-	-[a,b]	-[a,b]	-[a,b]	-	n.d.	-	-	-[b]	-	-
TaMPK11 (7BL)	-[a]	-	-	-	-	n.d.	-	-[a]	-	-	-
TaMPK14 (6DS)	-	-[a,b]	-[a,b]	-[a,b]	-	-	-	+++	-	-	-
TaMPK16 (1BS)	n.d.	n.d.	n.d.	n.d.	n.d.	-	n.d.	-[b]	-	-	-
TaMPK17 (clone)	-	-	-	-	-	-	-	-	-[a]	-[a]	-[a]
TaMPK20-1 (3AL)	-	-	-	-	-	-	-	-[b]	-	-	-
TaMPK20-2 (clone)	-	-	-	-	-	-	-	-	-	-	-
TaMPK20-3 (KR422425)	-	-	-	-	-	-	-	-[b]	-	-	-
TaMPK20-4 (clone)	-	-	-	-	-	-	-	-[b]	-	-	-
TaMPK20-5 (KR422426)	-	-	-	-	-	-	-	-	-	-	-
TaMPK21-1 (KR422427)	-	-	-	-	-	-	-	-	-	-	-
TaMPK21-2 (clone)	-	-	-	-	-	-	-	-	-	-	-
TaMPK24 (clone)	-	-	-	-	-	-	-	-	-	-	-



Phylogenetic Tree. Previously reported TaMAPKKK protein sequences [6] were aligned with TaMAPKKK (blue font) sequences used for Y2H experiment presented in the Table above. TaMAPKKK sequences used for Y2H are presented below.

>TaFLR (AY173961)
MSSPRRPEMSPAARNSDNGYVETDPTGRYGRFDELLGKGAMKSVYRGFDEVRGVEVAWNQANLADVLRTPDALQRMYSEVHLLSTLRHDAIIAFHASWVSVSSPSPRGGCTGGTPRRTFNFITELFSSGTLRAYRLRYPRVSLRAVRGWARQILRGLAY
LHAHDPPVIHRDLKCDNVFVNGHQGTVKIGDLGLAAVLRGAQAAHSVIGTPEFMAPEMYDEDYDELVDVYSFGMCMLEMLTVEYPYAECSNPAQIYKKVTSGKLPDAFYRVDDADARRFIGRCLVPASHRPSAQELLLDRFLSTQDTTMTLSPPPLLPA
LPTSGDRKDNPEEAEPVAARTDMTITGKLNTDDDTIFLKVQIVDEAGHSRNIYFPFDIAGDTATEVAREMVKELDITDRDPSEIAAMIEQEITRLVPDWVGGGCDDQQEYYTYADNDDNEEQPPFYYLSSSPTSSNGSHCGTGPTTSGGGYAGWFQDYA
VSSDDDETSSTRSALHYSSEEAQPEEKPGVSKTGQVKATRFGPGDSGTAGHDVSSSRAGRPRHHRGSPDAGGDEGRPRRQQGRMTRNRSMVDVRSQLLHRTLVEELNKRMFFNTVGAVENIGFRRIPGYGGGPSSSSATVTSSRGGDQRGRRSGKDKHQ
FFMF

>TaNPK-1
MAIAVSGQWTRLRTLGCGASGAVVTLAADAASGELFAVKSVRAVDAAQLSREQGILSGLSSPHVVGCIGGGGDRDGSYHLFLEFAPGGSLADEAARNGGRLEERAIRAYAADVLRGLAYIHGKSLVHGDVKSRNVVIGADGRAMIADFGCARALGSAGP
IGGTPAFMAPEVARGEEQGPAADVWALGCTVVEMATGRAPWGEMDNVLAAVHRIGYTDAVSEVPTWLSAEAKSFLAMCFARNARDRCTAAQLLEHPFVALQAGEAKARWVSPKSTLDAAFWESETDEEEEEVSESPCERIKSLSCSVLPDWDSDEGWID
VLGEQCEEACDSPAATKGPADVSSRAPSKVLGSPAAPAEDAAVVGTLSSDELDAEDEPFGDDIILAADPLVDRQIQVCWSSR

>TaMKKKA2
MDVAVAKQLRRIRTLGRGASGAVVWLASDEASGELLAVKSAGAGGAAQLEREGSVLTGLCSPHIIPCLGSRAAECGEYQLFLEFAPGGSLADEAARSGGCLPEPAIRAYAGDVARGLEYLHARSLVHGDVKARNVVIGGDGRARLTDFGCARAVDSLLP
MGGTPAFMAPEVARVEEQGPASDVWALGCTVVEMATGRAPWSDMNDLLAAVHRIGYTAAVPEVPGWLSAEAKDFLDGCFRRQPSDRSTAAQLLDHPFVASAAAAGDYKAAPAKQQYTSPKSTLQDALWDSDTDDEADEMSATPAERIGALACGNSALPD
WDSDDGWIDVCDEVHRVPDSPPADAGYDLVWPEESDAEREPFAVAADDSNDIPRNAVVTDSSIWQDSYVRPVHLGSCRNQFHPFQSDGDENLRFDRRCNKDRVTGDDPVAAAEVVPAPAKHHVPLEVLDLHPEHAPLVHRQPNHAREPLDDQPGVHHLH
ELARDDEHGEVLVVLDLLVEAQRLPGPLLVALPRRSSP

>TaMKKK2A
MSVSKQWTRVRTLGRGASGAEVFLAADDASGELFAVKSASAACAAALRREQRVMAGLSSPRVVSCIGGRGAPDGSYQLFLEFAPGGSLADQMATGLDELAVRGYAADVAAGLAYLHSAGMVHGDVKARNVVIGADGRAKLADFGCSRKAGADVPIIGGT
PAFMAPEVARGEEQSPAADVWALGCMVVEMATGRTPWSGMDGDALAALHRIGYTEAMPEVPEWLSADAKDFLARCLVRQASDRCTAAQLLEHPFLASAVVEAKAQAVESKWVSPKSTLDAAFWESDSDTEEAEHDSSAETRIRALACPASELPDWDSDE
GWIDVLSSPTGATGAVPVVVEEMTDLDEDATTDEEPSGAESRVLAITLDVEYNSVLNAVEACDDSFRRHQSLECLASHELSCTELLLCNRKTNAIDLVVAQALCFRTAALCFTAPHCDTFE

>TaMKKK2b
MGVGEWTRGPAIGRGSSATVSIAVDRRTGGVIAVKSVGADRAAELRREQGILRGLTSPYVVRCLEAEVSASVDGGLDMLMEYAPSGSLADEIRRCGGRCAEALVRSRARDILLGLAHVHAAGVAHCDVKGRNVLIASDGRALIADFGCARRTGGGIAGE
ERQRPTGGTPMFMAPEAARGEEQGPAADIWAVGCTVIEMATGAAPWQRFASPVATLHHVAFSGEAPEFPACLSDQGKDFLARCLRQDPRERWTAEQLLEHEFVAAAGTASSSNSAPGITEKATFVSPKSVLDQALWEDDDDDTAADTADPTDRVRALAA
GAPAVPDWTWDASWITVHAGPSGXADEEPAMPSEPEASTDTDSDDSPVGDGGSAGRAAAAEVGASSSHQASHANSDRYDGTGSCNVERSDDGNHVVSDDCSTVPITSNGFFSDTTSCFACPSRSQAGRTGPFTVLLYHISSPRCCSSCHLFLASPLLAG
VSGTRSPT

>TaEDR1 (AY743662)
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SIGDLGYEVIVVDYKFDNALQEMKEVAECCLLGCPDITVLVRRIAEVVADHMGGPVIDANEMITRWLSKSIEQRTSHQTSLLHIGSIEIGLSRHRALLFKILADIVGIPCKLVKGSHYTGVEDDAINIIKMDDKREFLVDVMAAPGTLIPADVFNSKGT
PFKFSQTLGQNQVVESASNIEDDPVALQSEHKRNQGHMFANNNRISDNLSSYENTVTAGSSASEPGTLDPRMQLGKTSTLASAPSKQKKNLQLIPDSHETEESRKLFAEFDPFNATKSGKSSLVFKGLNNRNNEFQRRRENVVPPSVRSQQPLVMKNWS
ACNDISNNKQYNVADGSVPRRNATDNASSSQLALSTAKHYNSNVRELNDRVYAAPARNYDNKIVGTSAMAKALTGECPDRSQVPPGLYYDKMLGTSSMNAASTSGIGKVAEKDPHNDPGKGPIYSRFDGELSKNAQGFTPERDEHKENCGSHDHKMLYP
DPRKSPLDRFMDRPRQSIECVFPSQVGSNKADMVLDEVSECEILWEDLVIDERIGIGSYGEVYHADWNGTEVAVKKFLDQEFYGDALEEFRCEVRIMRRLRHPNIVLFMGAVTRPPHLSIVSEYLPRGSLYKIIHRPNCQIDEKRRIKMALDVARGMNC
LHTSVPTIVHRDLKSPNLLVDDNWTVKVCDFGLSRLKHSTFLSSKSTAGTPEWMAPEVLRNEQSNEKCDIYSFGVILWELATLRKPWHGMNQMQVVGAVGFQDRRLDIPKEVDPIVASIIRDCWQKDPNLRPSFIQLTSYLKTLQRLVIPSHQETASNH
VPYEISLYR

>TaCTR1 (DQ211934)
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NGCLSWGDKIAHGFYNXMGIDPHXWAMCNADEGEGRRLPTLAALREVDASDQSSLEVVLVDKCGDSVLVDLERRALDLYRALGATLDLVRRLALLVSDHMGGALRSEDGDLYMRWKAGSKRLRKQQKSVVVPIGRLSIGFCRHRAILFKALADFIGLPC
RIAQGCKYCSAPHRSSCLVKIENDRRYSREYVVDLVVAPGSICSPDSSINGQLLXSVSSPFKTSCTASLENYAAPVAAWNRAIADDRCNSVFSDSQXSVAGDKNPVQADTKCGQVMQNDNCNNMSVFQVXRQFKAMEVGTEGVNKENIPGLTLPKHLLA
ESSFAMDWLEISWDELELKERIGAGSFGTVYRADWHGSDVAVKVLTDQGDGEAQLKEFLREISIMKRVRHPNVVLFMGAVTKCPHLSIVTEYLPRGSLFRLISXASSGEILDLRRRLRMALDVAKGINYLHCLNPPIVHWDLKTPNMLVDKNWSVKVGD
FGLSRFXATTFISSKSVAGTPEWMAPEFLRGEPSNEKCDVYSFGVILWELLTMQQPWGGLGPAQVVGAVAFQNRRLPIPKDTIPELAALVESCWSDDPRQRPSFSSIVDTLKKLLKSMQGSGS

>AK336073

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VSAKSYQRPWAESKAILVESERVETSTREVTAVSEPENAGEGKGNDKLAKVEISREERTREVVVEATREKATGALALVVAESNSCDIEHLVSPSPNRRFRRTITSWIKGGHIGSGSFGSVYEAISDDGFFFAVKEVSLIDQGINAKQRIVQLEHEVSLL
SRLEHDNIVQYYGTDKEDGKLYIFLELVTQGSLAALYQKYCLQDSQVSAYTRQILNGLNYLHQRNVLHRDIKCANILVDANGLVKLADFGLAKEMSILSQARSSKGTVFWMAPEVAKAKPHGPPADIWSLGCTVLEMLTGKVPYPDMEWTHALLKIGRG
IPPKIPNTLSEDARDFIAKCVQANQKDRPSAAQLLEHPFVKRPLQH
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>AK335039

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MGRPSQDTATSTSPSGSCRSSKRGPRLDRRNASKNIGYEYDPAKLFCSYPPSPSRASSASASAAPSVASSVDLSSFRIGGSGDGGGDVQLLCRNLGLSGPEDFAISLTDWEAHKAFRSSAFSSASSSPSARSQPDRPVRESPLRHEAVEEPTLPADADF
ELPAKETARDPPVEAPVRPAWLDPPEPARPDVKKPGCEGGIKGVRPPPVMLKPPPSMALPPASQAGSTWDILLSFAPEEQGQPQAIRSVPDFGDPDAEDEDAAEVLTLEDLRLGESSEEFTGTSSISTTNDDETTESMFYISPNGRFKRKIRSWSRGVL
LGSGSFGTVYEGISDEGVFFAVKEVSLHDQGSNAQQCIFQLEQEIALLSQFEHENIVHYFGTDKEDSKLYIFLELVTQGSLVSLYQKYRLRDTHVSAYTRQILNGLNYLHERNIVHRDIKCANILVHANGSVKLADFGLAKQTSKLNVLKSCKGTVYWM
APEVVNPKKTYGPAADIWSLGCTVLEMLTRQLPYPDLEWTQALYRIGKGEPPAIPSGLSKEARDFISQCVKPNPEDRPSASKLLDHPFVNRSMRSIRSMRTYTRPNSSTRGTSG
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>AK334817

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MPAWWKGKGRSKSKAAAPAGDAGTIPAGRDGEKDRKNKKASSFDEALIGREGRGKQLQQPAPAVGHPLPRPASMPSASAPASASASASSGGSSSLGSSAASDEPLDLGIYRISDANRTPAIDSRKQSLVLEEGRFVVNNLASENNRSCEPSVSPRKEFQ
PNILDLPSDRTTYCHGRKSTEIVFATRMPNSPPSSRGKHCPTSPVHSRAFGQCPGSPTAWQDDARNSSSPHPLPLPPGSPCTSSRSLHSQWKKGKLLGSGTFGQVYLGFNSEGGQMCAIKEVKVIADDSNSKECLRQLNQEMLLLNQLSHPNIVQYYGS
ELSSETLSVYLEFVSGGSIHKLLQEYGPFGETILRNYTAQILSGLAYLHGRNTVHRDIKGANILVDPNGDIKLADFGMAKHISAYTSIKSFKGSPYWMAPEVIMNTNGYSLSVDIWSLGCTILEMATARPPWSQYEGVAAIFKIGNSKDIPDIPDHLSS
EAKSFLKLCLQRDPAARPTAAQLIEHPWVKDQASVRSSRSGSGITRDMFSTSTDGSKATVKTSIELSSYRSLSPLRDTNLRMRNLVVPASSIPSISTHRASAISASNVRMNMSLPVSPCTSPLRQYRQSNRSCLPSPPHPAYSAGAANYSPINNVLYPT
RPSNYLTDPWLETPRQKTQTFDSPRRL
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>AK333042

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MAFSPRSPWSRSKKPDIYSTVVVHDDEDDARGGGAARAEDDDDDDPSALPPLLQRLPKDFGGASFDDDDDPYSSDLDDASLSATVVIKRGAPASTSSSSRSPFLDLRRSSPRAAEADPFSTFVVHGTARSGGASSPRESVSGTFIRHSGGPPSPRESVS
GTFIRHTRGSSSPHESFSGTFIHHTSSASSPRDSASGAGAGFGSSFITPSSGQAEEDRQPSLLMQQQQSRRKASMSSLPDSVTREDPSTKYELLHELGKGSYGAVYKARDLRTQELVAVKIISLTEGEEGYEDIRGEIEMLQQCSHPNVVRYFGSYQGE
EYLWIVMEYCGGGSVADLIGITEEPLDEPQIAYICRETLKGLAYLHTIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQESRYDGKVDVWALGVSAIEMAEGMPPRSTVHPMRVIFMISSEPAPMLEDKEKWSLLF
HDFIAKCLTKDARLRPPAIEMLKHKFIEKCNTGASKMLAKIKEAKIIRETAVQNQLPDSDDAMDATVRINEDYGETVPTNSQSTHETKNDGSGGDFGTMIVHPEDGDEAAESSIFPRAEFIPGLGSINSFTHDPKRAELISKFWAESTAESDASKERDL
YGLPDIQEPKTMPRSTGTVKHHKGVEGTVLRHDITASPGVASTMNKLSSSPSRKAFSVQDKLWSIYAAGNTVPIPFLKAIDISPLALVSDSVAGNGPAGSSTTDALEAVRELFSGDGQAKKGRKGQNEAPLPPGVHDRLTTSPTLMNLAQALAYHKTCY
EDMPLQDSQATEEQQTIQNLCDTLRTILRL
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>AK330734

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IGGTPAFMAPEVARGEEQGLAADVWALGCTVIEMATGRAPWGDMDDVFAAVHRIGYTDAVPELPASLSPQAKDFLCKCLARNPRHRSTAAQLLEHPFLASAFRDVDAEPAKQDWMSPKSTLNAEFWESDEESETEDMLTSAAERIASLASPCSALPDWE
SDDGWIDVHGERPEASETTSATAIAGTDFGPWSREEGLEAELGVRFADADAGRWYDLVRNVDGAHYFGWYERDFSVSVATDRPLCLIVSHGRKIVKFGCHCDRERTMHFDFAQIFRSLELPSHAVCILSSTEWGYCRFLAFSFYN
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TaMKK1-1(7AS)      MKKPGKLALPSQDSTIGKFLTQSGTFKDGDLLVNKDGLRIVPQSEEGEAPPIKPLDNNHQ LSIDDLDSIKVIGKGNSGTVQLVRHKWTGQFFALKVIQLNIQESIRKQMAQELKISLFTQ
TaMKK1-1(4AL)      MKKPGKLALPSQDSTIGKFLTQSGTFKDGDLLVNKDGLRIVPQSEEGEAPRIKPLDNNHQ LSIDDLDSIKVIGKGNSGTVQLVRHKWTGQFFALKVIQLNIQESIRKQMAQELKISLFTQ
TaMKK1-1(7DS)      MKKPGKLALPSQDSTIGKFLTQSGTFKDGDLLVNKDGLRIVPQSEEGEAPPIKPLDNNHQ LSIDDLDSIKVIGKGNSGTVQLVRHKWTGQFFALKVIQLNIQESIRKQMAQELKISLFTQ
TaMKK1-1(syn)      MKKPGKLALPSQDSTIGKFLTQSGTFKDGDLLVNKDGLRIVPQSEEGEAPPIKPLDNNHQ LSIDDLDSIKVIGKGNSGTVQLVRHKWTGQFFALKVIQLNIQESIRKQMAQELKISLFTQ
                   ************************************************** ********* ************************************************************

TaMKK1-1(7AS)      CQYVVTCYQCFYVNGVISIALEYMDGGSLADFLKAVRTVPEAYLAAICKQVLKGLMYLHH EKRVIHRDLKPSNILINHRGEVKISDFGVSAIISSSSAQRDTFTGTFNYMAPERISGQKH
TaMKK1-1(4AL)      CQYVVTCYQCFYVNGVISIALEYMDGGSLADFLKAVRTVPEAYLAAICKQVLKGLMYLHH EKRVIHRDLKPSNILINHRGEVKISDFGVSAIISSSSAQRDTFTGTFNYMAPERISGQKH
TaMKK1-1(7DS)      CQYVVTCYQCFYVNGVISIALEYMDGGSLADFLKAVRTVPEAYLAAICKQVLKGLMYLHH EKRVIHRDLKPSNILINHRGEVKISDFGVSAIISSSSAQRDTFTGTFNYMAPERISGQKH
TaMKK1-1(syn)      CQYVVTCYQCFYVNGVISIALEYMDGGSLADFLKAVRTVPEAYLAAICKQVLKGLMYLHH EKRVIHRDLKPSNILINHRGEVKISDFGVSAIISSSSAQRDTFTGTFNYMAPERISGQKH
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TaMKK1-1(7AS)      GYMSDIWSLGLVMLECATGNFPYPPRESFYELLEAVVDQPSPSAPSDQFSPEFCSFISAC IQKNAADRSSAQTLSAHPFLSMYDDLNIDLSDYFTTAGSPLATFKQIAL
TaMKK1-1(4AL)      GHLSDIWSLGLVMLECATGNFPYPPRESFYELLEAVVDQPSPSAPSDQFSPEFCSFISAC IQKNAADRSSAQTLSAHPFLSMYDDLNIDLSDYFTTAGSPLATFKQIAL
TaMKK1-1(7DS)      GHLSDIWSLGLVMLECATGNFPYPPRESFYELLEAVVDQPSPSAPSDQFSPEFCSFISAC IQKNAADRSSAQTLSVHPFLSMYDDLNIDLSDYFRTAGSPLATFKQIAL
TaMKK1-1(syn)      GHLSDIWSLGLVMLECATGNFPYPPRESFYELLEAVVDQPSPSAPSDQFSPEFCSFISAC IQKNAADRSSAQTLSVHPFLSMYDDLNIDLSDYFTTAGSPLATFKQIAL
                   *::********************************************************* ***************.******************* *************

1: TaMKK1-1_7AS_  100.00   99.14   98.85   99.14
2: TaMKK1-1_4AL_   99.14  100.00   99.14   99.43
3: TaMKK1-1_7DS_   98.85   99.14  100.00   99.71
4: TaMKK1-1_syn_   99.14   99.43   99.71  100.00
```

TaMKK1-1(syn) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK1-1 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

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TaMKK3-2(clone)     MAGLEELKKKLQPLLFDDSDKGGVSTRVPFPEDTCDSYVVSDGGTINLLSRSFGEYNINE HGFHKRSTGPEEPDTGEKAYRCASEDMHIFGPIGSGASSVVQRAIFIPVHRILALKKINI
TaMKK3-2(5BL)       MAGLEELKKKLQPLLFDDSDKGGVSTRVPFPEDTCDSYVVSDGGTINLLSRSFGEYNINE HGFHKRSTGPEEPDTGEKAYRCASEDMHIFGPIGSGASSVVQRAIFIPVHRILALKKINI
TaMKK3-2(5DL)       MSGLEELKKKLQPLLFDDSDKGGVSTRVPFPEDTCDSYVVSDGGTINLLSRSFGEYNINE HGFHKRSTGPEEPDTGEKAYRCASEDMHIFGPIGNGASSVVQRAIFIPVHRILALKKINI
                    *:********************************************************** **********************************.*************************

TaMKK3-2(clone)     FEKEKRQQILNEMRTLCEASCYPGLVEFQGAFYMPDSGQISIALEYMDGGSLADVIRVKK SIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANLLVKLKGEAKITDFGVSAGLDNTM
TaMKK3-2(5BL)       FEKEKRQQILNEMRTLCEASCYPGLVEFQGAFYMPDSGQISIALEYMDGGSLADVIRVKK SIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGVSAGLDNTM
TaMKK3-2(5DL)       FEKEKRQQILNEMRTLCEASCYPGLVEFQGAFYMPDSGQISIALEYMDGGSLADVIRVKK SIPEPVLAHMLLKVLLGLKYLHEVRHLVHRDLKPANILVNLKGEAKITDFGVSAGLDNTM
                    ************************************************************ ************************************:**:********************

TaMKK3-2(clone)     AMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYNVNEGPANLMLQIL DDPSPTPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHAFIKRYEQTGVDLATYVRGV
TaMKK3-2(5BL)       AMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYNVNEGPANLMLQIL DDPSPAPPEDAYTPEFCSFINDCLRKDADARPTCEQLLSHPFIKRYEQTGVDLAAYVRGV
TaMKK3-2(5DL)       AMCATFVGTVTYMSPERIRNENYSYAADIWSLGLTILECATGKFPYNVNEGPANLMLQIL DDPSPAPPEDAYTPEFCSFINDCLRKYADARPTCEQLLSHPFIKRYEQTGVDLAAYVRGV
                    ************************************************************ *****:******************** ************* *************:*****

TaMKK3-2(clone)     VNPTERLKQIAEMLAVHYYLLFNGSEGPWNYMKTFYKEESSFSFSGNVYVGQSAIFDTLS NIRKKLKGDRPREKIVHVVEKLHCRANGETEIAIRVSGSFITGNQFLIFGEGLQAEGMPS
TaMKK3-2(5BL)       VNPTERLKQIAEMLAVHYYLLFNGSEGPWNHMKTFYREESSFSFSGNVYVGQSAIFDTLS NIRKKLKGDRPREKIVHVVEKLHCRANGETEIAIRVSGSFITGNQFLIFGEGLQAEGMPS
TaMKK3-2(5DL)       VNPTERLKQIAEMLAVHYYLLFNGSEGPWDHMKTFYREESSFSFSGNVYVGQSAIFDTLS NIRKKLKGDRPREKIVHVVEKLHCRANGETEIAIRVSGSFITGNQFLISGEGLQAEGMPS
                    *****************************::*****:*********************** ************************************************ ***********

TaMKK3-2(clone)     LEEIDIDIPSKRVGQFREQFTVHPGTSMGCYYIARQDLYIIQA
TaMKK3-2(5BL)       LDGIDIDIPSKRVGQFREQFTVHPGTSMGCYYIAKQDLYIVQS
TaMKK3-2(5DL)       LDEINIDIPSKRVGQFREQFTVLPGTSMGCYYIAKQDLYIVQS
                    *: *:***************** ***********:*****:*:
```

```
1: TaMKK3-2_clone_  100.00   97.71   96.56
2: TaMKK3-2_5BL_     97.71  100.00   98.47
3: TaMKK3-2_5DL_     96.56   98.47  100.00
```

TaMKK3-2(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK3-2 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMKK3-3(5AL)      MAGLEDLKRRLQPIFFDADGNVVPPPAADGTSDDSSSDDCEVLDSGTVNLLSRSSDEYNI SKLGFHKRTTRPDGDYATDKAYRCSCHDMHIFDSVGIGASSVVHRAIYVPVHRVLALKKI
TaMKK3-3(5BL)      MAGLEDLKRRLQPIFFDADGNVVPPPAADGTSDDSSSDDCEVLDGGTVNLLSRSSDEYNI SKLGFHKRTTRPDGDYATDKAYRCSCHDMHIFDSVGNGASSVVYRAIYVPVHRVLALKKI
TaMKK3-3(syn)      MAGLEDLKRRLQPIFFDADGNVVPPPAADGTSDDSSSDDCEVLDGGTVNLLSRSSDEYNI SKLGFHKRTTRPDGDYATDKAYRCCCHDMHIFDSVGNGASSVVHRAIYVPVHRVLALKKI
TaMKK3-3(5DL)      MAGLEELKRRLQPIFFDADGNVVPPPAADGTSDDSSSDDCEVLDGGTVNLLSRSSDEYNI SKLGFHKRTTRPDGDYATDKAYRCCCHDMHIFDSVGNGASSVVHRAIYVPVHRVLALKKI
                   *****:**************************************.*************** ************************.*********** ******:****************

TaMKK3-3(5AL)      SIFDKEKRQQILNEITTLSAASCYPGLVEFQGIFYTPDSGEIYFALEYMDGGSLADIIRV KKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKRDTKITDFGVTSGLHD
TaMKK3-3(5BL)      NIFDKERRQQILNEIRTLSAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIIRV KKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVTSGLHD
TaMKK3-3(syn)      NIFDKERRQQILNEIRTLSAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIIRV KKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVSSGLHD
TaMKK3-3(5DL)      NIFDKEKRQQILNEIRTLSAASCYPGLVEFQGVFYTPDSGEIYFALEYMDGGSLADIIRV KKFITEPVLSHMLQKVLLALRYLHEVRRLVHRDIKPANLLLNLKGDTKITDFGVSSGLHD
                   .*****:******** ****************:*************************** ******************************************** *********:*****

TaMKK3-3(5AL)      SVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQ ILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCNELLSHSFIKKYEGPGVDLAEYNK
TaMKK3-3(5BL)      SVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQ ILEDPSPTPPQHMHSEEFCLFIDACLQKDADARPTCDELLSHSFIKKYEGPGVDLAEYNR
TaMKK3-3(syn)      SVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQ ILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDQ--------KYEGPGVDLAEYNK
TaMKK3-3(5DL)      SVTMCATFLGSVTYMSPERIRNENYSYAADIWSLGLTALECATGRYPYDVNGGEADLMLQ ILEDPSPTPPQHMHSEEFCSFIDACLQKDADARPTCDQLLSHSFIKKYEGPGVDLAEYNK
                   ************************************************************ ******************* ****************::        *************:

TaMKK3-3(5AL)      SVHDPAERLSQIAHMLAVHYYLIF--------HMKSFYGQDSTFSFSGETHVGKSDIFDT LSRIREMLKGNSRCEKIGRVMEKVYCRAHWEEGMSVRVSGSFIMGNEFLVCADGFCAEGM
TaMKK3-3(5BL)      SVHDPAERLSQIAHMLAVHYYLIFDGGDDQWHHMKSFYGQDSTFSFSGETHVGKSDIFDT LSRIREMLKGNSRCEKIGRVMEKVY-RAHGEEGTSVRVSGSFIMGNEFLVCADGFCAEGM
TaMKK3-3(syn)      SVHDPAERLSQIAHMLAVHYYLIFDGGDDQWRHMKSFYGQDSTFSFSGETHVGKSDIFDT LSRIREMLKGNSRCEKIGRVMEKVYCRAHGEEGMSVRVSGSFIMGNEFLVCADGFCAEGM
TaMKK3-3(5DL)      SVHDPAERLSQIAHMLAVHYYLIFDGGDDQWRHMKSFYGQDSTFSFSGETHVGKSDIFDT LSRIREMLKGNSRCEKIGRVMEKVYCRAHGEEGMSVRVSGSFIMGNEFLVCADGFCAEGM
                   ************************        **************************** ************************* *** *** **************************

TaMKK3-3(5AL)      LSMVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISKQELHIGVS
TaMKK3-3(5BL)      LSIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHIGVS
TaMKK3-3(syn)      LSIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHIGVS
TaMKK3-3(5DL)      LSIVELSPDILSKQAGHFQEDFFMEPGTAMGCYVISRQELHIGVS
                   **:*********************************:********

1: TaMKK3-3_5AL_  100.00   97.09   97.25   97.29
2: TaMKK3-3_5BL_   97.09  100.00   98.45   98.09
3: TaMKK3-3_syn_   97.25   98.45  100.00   99.61
4: TaMKK3-3_5DL_   97.29   98.09   99.61  100.00
```

TaMKK3-3(syn) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK3-3 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMKK4(6DL)      MRPGGPPNARPGLQQQQPGTPGRARRRPDLTLPLPQRDLTSLAVPLPLPPPPSSAPSSTSSS----GSGGASSMPMPMSMTPPNSAGSTPPAPPPLGELERVRRVGSGAGGTVWLVRHAP
TaMKK4(syn)      MRPGGPPNARPGLQQQQPGTPGRARRRPDLTLPLPQRDLTSLAVPLPLPPPPSSAPSSTSSSGSGSGSGGASSMPMPMSMTPPNSAGSAPPAPPPLGELERVRRVGSGAGGTVWLVRHAP
TaMKK4(6AL)      MRPGGPPNARPGLQQQQPGTPGRARRRPDLTLPLPQRDLTSLAVPLPLPPPPSSAPSSTSSSGSGSGSGGASSMPMPMSMTPPNSAGSAPPAPPPLGELERVRRVGSGAGGTVWLVRHAP
TaMKK4(6BL)      MRPGGPPNARPGLQQQQPGTPGRARRRPDLTLPLPQRDLTSLAVPLPLPPPPSSAPSSTSSSGSGSGSGGASSMPMPMSMTPPNSAGSAPPAPPPLGELERVRRVGSGAGGTVWLVRHAP
                 **************************************************************    **********************:*******************************

TaMKK4(6DL)      TGRAYALKVLYGHHDEAVRRQITREIAILRTAEHPSIVRCHGMYEQAGELQILLEYMDGGSLDGRRIASESFLADVARQVLSGIAYLHRRHIVHRDIKPSNLLIDCARRVKIADFGVGRI
TaMKK4(syn)      TGRAYALKVLYGHHDEAVRRQITREIAILRTAEHPSIVRCHGMYEQAGELQILLEYMDGGSLDGRRIASESFLADVARQVLSGIAYLHRCHIVHRDIKPSNLLIDCGRRVKIADFGVGRI
TaMKK4(6AL)      TGRAYALKVLYGHHDEAVRRQITREIAILRTAEHPSIVRCHGMYEQAGELQILLEYMDGGSLDGRRIASESFLADVARQVLSGIAYLHRCHIVHRDIKPSNLLIDCGRRVKIADFGVGRI
TaMKK4(6BL)      TGRAYALKVLYGHHDEAVRRQITREIAILRTAEHPSIVRCHGMYEQAGELQILLEYMDGGSLDGRRIASEAFLADVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSGRRVKIADFGVGRI
                 **********************************************************************:****************** ***************..*************

TaMKK4(6DL)      LNQTMDPCNSSVGTIAYMSPERINTDLNDGNYNGYAGDIWSFGLSILEFYLGRFPLGENLKQGDWAALMCAICYSESPAAPPTASPELRSFISCCLQKNPAKRPSAAQLLQHRFIASPP
TaMKK4(syn)      LNQTMDPCNSSVGTIAYMSPERINTDLNDGNYNGYAGDIWSFGLSILEFYLGRFPLGENLGKQGDWAALMCAICYSESPAAPPTASPELRSFISCCLQKEPAKAPSAAQLLQHRFIASPP
TaMKK4(6AL)      LNQTMDPCNSSVGTIAYMSPERINTDLNDGNYNGYAGDIWSFGLSILEFYLGRFPLGENLGKQGDWAALMCAICYSESPAAPPTASPELRSFISCCLQKNPAKRPSAAQLLQHRFIASPP
TaMKK4(6BL)      LNQTMDPCNSSVGTIAYMSPERINTDLNDGNYNGYAGDIWSFGLSILEFYLGRFPLGENLGKQGDWAALMCAICYSESPAAPPTASPELRSFISCCLQKNPAKRPSAAQLLQHRFIASPP
                 ***************************************************************************************************:*** ****************

TaMKK4(6DL)      QQQPQALAAPPC
TaMKK4(syn)      QQQPQVLAAPPC
TaMKK4(6AL)      PQQPQALAAPPC
TaMKK4(6BL)      QQQPQVLAAPPC
                  ****.******

1: TaMKK4_6DL_  100.00   98.37   98.91   98.64
2: TaMKK4_syn_   98.37  100.00   98.92   98.66
3: TaMKK4_6AL_   98.91   98.92  100.00   98.66
4: TaMKK4_6BL_   98.64   98.66   98.66  100.00
```

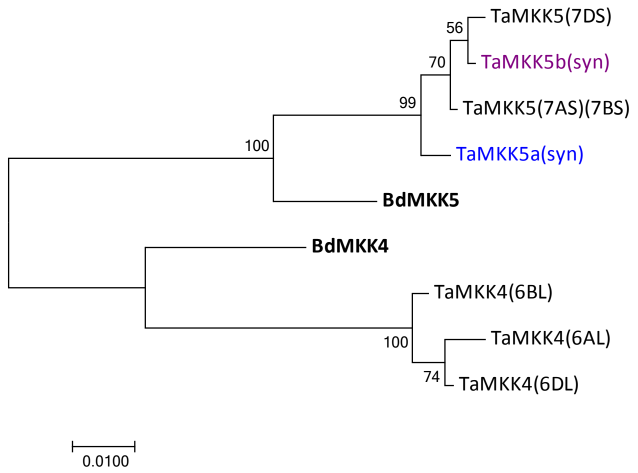
TaMKK4(syn) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK4 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMKK5b(syn)      MRPAGGS--LPA--QPGTPGRPRRRPDLTLPMPQRPDVSSSLAVPLPAPSPDRRSPRRR----PRPAARGPARAPPPLHELERVRRVGSGAGGTVWMVRHRATGRCYALKVLYGNHDDTV
TaMKK5(7DS)       MRPAGGGSSLPAQPGPGTPGRPRRRPDLTLPMPQRPDVSSSLAVPLPLPPPTAAPPGA-GPAQPLVAPP---APPPPLHELERVRRVGSGAGGTVWMVRHRATGRCYALKVLYGNHDDTV
TaMKK5a(syn)      MRPAGAG--LPA--QPGTPGRPRRRPDLTLPMPQRPDVSSSLAVPLPLPPPTAAPPGRRPA---ARGPARGDPAPPPLHELERVRRVGSGAGGTVWMVRHAPTGRCYALKVLYGNHDDAV
TaMKK5(7AS)       MRPAGGS--LPA--QPGTPGRPRRRPDLTLPMPQRPDVSSSLAVPLPLPPPTAAPPTGAGPAQPLVAPPAAAPPPPPLHELERVRRVGSGAGGTVWMVRHRATGRCYALKVLYGNHDDAV
TaMKK5(7BS)       MRPAGIS--LPA--QPGTPGRPRRRPDLTLPMPQRPDVSSSLAVPLPLPPPTAAPP---GAAQPLVAPPAATPPPPPLHELERVRRVGSGAGGTVWMVRHRATGRCYALKVLYGNHDDAV
                  ***** .  ***   ******************************** * *    *          .       **************************  ****************:*

TaMKK5b(syn)      RRQIAREIAILRTAEHPAVVRCHGMYERGGELQILLEYMDGGSLDGRRIADEPFLAHVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSARRVKIADFGVGRILNQTMDPCNSSVGTIAYM
TaMKK5(7DS)       RRQIAREIAILRTAEHPAVVRCHGMYERGGELQILLEYMDGGSLDGRRIADEPFLAHVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSSRRVKIADFGVGRILNQTMDPCNSSVGTIAYM
TaMKK5a(syn)      RRQIAREIAILRTAEHPAVVRCHGMYERGGELQILLEYMDGGSLDGRRIADEPFLAHVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSSRRVKIADFGVGRILNQTMDPCNSSVGTIAYM
TaMKK5(7AS)       RRQIAREIAILRTAEHPAVVRCHGMYERGGELQILLEYMDGGSLDGRRIADEPFLAHVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSARRVKIADFGVGRILNQTMDPCNSSVGTIAYM
TaMKK5(7BS)       RRQIAREIAILRTAEHPAVVRCHGMYERGGELQILLEYMDGGSLDGRRIADEPFLAHVARQVLSGIAYLHRRHIVHRDIKPSNLLIDSARRVKIADFGVGRILNQTMDPCNSSVGTIAYM
                  ****************************************************************************************:*******************************

TaMKK5b(syn)      SPERINTDINDGAYDGYAGDIWSFGLSILEFYLGRFPFGENLGRQGDWAALMVAICYSDPPEPSPATASPEFRGFIACCLQKNPANRLSAAQLLQHPFVALPQPQPLAAPPS-
TaMKK5(7DS)       SPERINTDINDGAYDGYAGDIWSFGLSILEFYLGRFPFGENLGRQGDWAALMVAICYSDPPEPSPATASPEFRGFIACCLQKNPANRLSAAQLLQHPFVALPQPQPLAAPPSS
TaMKK5a(syn)      SPERINTDINDGAYDGYAGDIWSFGLSILEFYLGRFPFGENLGRQGDWAALMVAICYSDPPEPSPATASPEFRGFIACCLQKNPANRLSAAQLLQHPFVALPQPQPLAAPPSS
TaMKK5(7AS)       SPERINTDINDGAYDGYAGDIWSFGLSILEFYLGRFPFGENLGRQGDWAALMVAICYSDPPEPSPATASPEFRGFIACCLQKNPANRLSAAQLLQHPFVALPQPQPLAAPPSS
TaMKK5(7BS)       SPERINTDINDGAYDGYAGDIWSFGLSILEFYLGRFPFGENLGRQGDWAALMVAICYSDPPEPSPATASPEFRGFIACCLQKNPANRLSAAQLLQHPFVALPQPQPLAAPPS-
                  ****************************************************************************************************************
```

```
1: TaMKK5b_syn_  100.00   95.00   93.59   94.77   95.01
2: TaMKK5_7DS_    95.00  100.00   95.91   97.97   97.95
3: TaMKK5a_syn_   93.59   95.91  100.00   94.80   95.91
4: TaMKK5_7AS_    94.77   97.97   94.80  100.00   99.13
5: TaMKK5_7BS_    95.01   97.95   95.91   99.13  100.00
```



TaMKK5a(syn) and TaMKK5b(syn) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK5 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided. Since percent identity is low for synthetic TaMKK5s compared with variability with genomic copies, the phylogenetic analysis (Clade C MKK branch shown above) shows relationship between TaMKK5a and 5b with MKK5.

```
TaMKK10-2(syn)      MALVRQRRQLPHLTLPLDHFALRAPPPPP-PAVAP---CEGLARLSDYERISQLGQGNGG TVFKARHRRTAQQVALKLFA----DPSAAREAEILMLASGAPHVVRLHAVIPSPAAEQPA
TaMKK10-2(4AS)      MALVRQRRQLPHLTLPLDHFALRAPPPPLPPAVAPCAPAEGLARLSDYERISQLGQGNGG TVFKARHRRTAQHFALKLFAAGDGDPSAAREAEILMLASGAPHVVRLHAVIPSPAAEQPA
TaMKK10-2(4BL)      MALVRQRRQLPHLTLPLDHFALRAPPP-PPPAVAPC---EGLARLSDYERISQLGQGNGG TVFKARHRRTAQQVALKLFAAGDGDPSAAREAEILMLASGAPHVVRLHAVIPSPAAEQPA
TaMKK10-2(4DL)      MALVRQRRQLPHLTLPLDHFALRAPPPPPPPAVAPC---EGLARLSDYERISQLGQGNGG TVFKARHRRTAQQVALKLFAAGDGDPSAAREAEILMLASGAPHVVRLHAVIPSPAAEQPA
                    ***************************   *****    ********************* ************:.******    ************************************

TaMKK10-2(syn)      ALASSSVSGGSLAGLLRRLGRPMGERPIAAVARQALLGLAALHALRVVHRDLKPANLLVG AGGEVKIADFGAGKVLRRRLDPCASYVGTAAYMSPERFDPEAYSGDYDPYAADVWSLGMA
TaMKK10-2(4AS)      ALALELVSGGSLAGLLRALGRPMGERPIAAVARQALLGLAALHALRVVHRDLKPANLLVG AGGEVKIADFGAGKVLRRRLDPCASYVGTAAYMSPERFDPEAYSGDYDPYAADVWSLGMA
TaMKK10-2(4BL)      ALALELVSGGSLAGLLRALGRPMGERPIAAVARQALLGLAALHALRVVHRDLKPANLLVG AGGEVKIADFGAGKVLRRRLDPCASYVGTAAYMSPERFDPETYSGDYDPYAADVWSLGMA
TaMKK10-2(4DL)      ALALELVSGGSLAGLLRALGRPMGERPIAAVARQALLGLAALHALRVVHRDLKPANLLVG AGGEVKIADFGAGKVLRRRLDPCASYVGTAAYMSPERFDPEAYSGDYDPYAADVWSLGMA
                    *** . *********** ****************************************** *****************************************:******************

TaMKK10-2(syn)      ILELYLGHFPLLPAGQRPDWAALMCAICFGEAPEAPAAASDEFRDFVARCLEKKAGRRAS VAELLQHPFIAERDAEEAQRCLAALVAEAAELGDQ
TaMKK10-2(4AS)      ILELYLGHFPLLPAGQRPDWAALMCAICFGEAPEAPAAASDEFRDFVARCLEKKAGRRAS VAELLQHPFIAERDAEEAQRCLAALVAEAAELGDQ
TaMKK10-2(4BL)      ILELYLGHFPLLPAGQRPDWAALMCAICFGEAPEAPAAASDEFRDFVARCLEKKAGRRAS VAELLGHPFIAERDAEEAQRCLAALVAEAAELGDQ
TaMKK10-2(4DL)      ILELYLGHFPLLPAGQRPDWAALMCAICFGEAPEAPAAASDEFRDFVARCLEKKAGRRAS VAELLQHPFIAERDAEEAQRCLAALVAEAAELGDQ
                    ************************************************************ ***** *****************************
```

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1: TaMKK10-2_syn_  100.00   97.55   98.15   98.77
2: TaMKK10-2_4AS_   97.55  100.00   98.49   99.10
3: TaMKK10-2_4BL_   98.15   98.49  100.00   99.40
4: TaMKK10-2_4DL_   98.77   99.10   99.40  100.00
```

TaMKK10-2(syn) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMKK10-2 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK4(clone)      MDTS-GGGTAAGGAAQIQGMATHGGRYVLYNVYGNLFEVASKYAPPIRPIGRGAYGIVCA AVSSDTGEEVAIKKIGNAFDNHIDAKRTLREIKLLRHMDHENILAIKDLIRPPRRDDFKD
TaMPK4(1AL)        MDTSGGGGGAAGGAAQIQGMATHGGRYVLYNVYGNLFEVASKYAPPIRPIGRGAYGIVCA AVSSDTGEEVAIKKIGNAFDNHIDAKRTLREIKLLRHMDHENILAIKDLIRPPRRDDFKD
TaMPK4(1BL)        MDTS-GGGTAAGGAAQIQGMATHGGRYVLYNVYGNLFEVASKYAPPIRPIGRGAYGIVCA AVSSDTGEEVAIKKIGNAFDNHIDAKRTLREIKLLRHMDHENILAIKDLIRPPRRDDFKD
TaMPK4(1DL)        MDTS-GGGAAAGGAAQIQGMATHGGRYVLYNVYGNLFEVASKYAPPIRPIGRGAYGIVCA AVSSDTGEEVAIKKIGNAFDNHIDAKRTLREIKLLRHMDHENILAIKDLIRPPRRDDFKD
                   **** ***  ************************************************** ************************************************************

TaMPK4(clone)      VYIVTELMDTDLHQIIRSNQSLTDDHCQYFLYQLLRGLKYVHSANVLHRDLKPSNLFLNA NCDLKIADFGLARTTSETDLMTEYVVTRWYRAPELLLNCSQYTAAIDVWSVGCILGEIIT
TaMPK4(1AL)        VYIVTELMDTDLHQIIRSNQSLTDDHCQYFLYQLLRGLKYVHSANVLHRDLKPSNLFLNA NCDLKIADFGLARTTSETDLMTEYVVTRWYRAPELLLNCSQYTAAIDVWSVGCILGEIIT
TaMPK4(1BL)        VYIVTELMDTDLHQIIRSNQSLTDDHCQYFLYQLLRGLKYVHSANVLHRDLKPSNLFLNA NCDLKIADFGLARTTSETDLMTEYVVTRWYRAPELLLNCSQYTAAIDVWSVGCILGEIIT
TaMPK4(1DL)        VYIVTELMDTDLHQIIRSNQSLTDDHCQYFLYQLLRGLKYVHSANVLHRDLKPSNLFLNA NCDLKIADFGLARTTSETDLMTEYVVTRWYRAPELLLNCSQYTAAIDVWSVGCILGEIIT
                   ************************************************************ ************************************************************

TaMPK4(clone)      RQPLFPGRDYIQQLKLITELIGSPDDSSLGLLRSDNARRYMKQLPQYPRQDFRLRFRNMS DGAVDLLERMLVFDPSRRITVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEEHM
TaMPK4(1AL)        RQPLFPGRDYIQQLKLITELIGSPDDSSLGFLRSDNARRYMKQLPQYPRQDFRLRFRNMS DGAVDLLERMLVFDPSRRITVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEEHM
TaMPK4(1BL)        RQPLFPGRDYIQQLKLITELIGSPDDSSLGFLRSDNARRYMKQLPQYPRQDFRLRFRNMS DGAVDLLERMLVFDPSRRITVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEEHM
TaMPK4(1DL)        RQPLFPGRDYIQQLKLITELIGSPDDSSLGFLRSDNARRYMKQLPQYPRQDFRLRFRNMS DGAVDLLERMLVFDPSRRITVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEEHM
                   ******************************:***************************** ************************************************************

TaMPK4(clone)      KELIWRETLAFNPEILPT
TaMPK4(1AL)        KELIWRETLAFNPDPPY-
TaMPK4(1BL)        KELIWRETLAFNPDPPY-
TaMPK4(1DL)        KELIWRETLAFNPDPPY-
                   *************:

1: TaMPK4_clone_  100.00   98.40   98.67   98.40
2: TaMPK4_1AL_     98.40  100.00   99.73   99.73
3: TaMPK4_1BL_     98.67   99.73  100.00   99.73
4: TaMPK4_1DL_     98.40   99.73   99.73  100.00
```

TaMPK4(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK4 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK17(clone)      MGGGNGIVDGFRRSFHRRTPSGSVLGSSNQSSAGEDSSDVEAAEGLDLVGLRSIRVPKRK MPLPVESHKKNIMEKEFFTEYGEASQYQIQEVVGKGSYGVVAAAIDTRTGERVAIKKIND
TaMPK17(7DL)        MGGGNGIVDGFRRLFHRRTPSGSVLGSSNQSSAGEDSSDVEAAEGLDLVGLRSIRVPKRK MPLPVESHKKNIMEKEFFTEYGEASQYQIQEVVGKGSYGVVAAAIDTRTGERVAIKKIND
TaMPK17(7AL)        MGGGNGIVDGFRRLFHRRTPSGSVLGSSNQSSAGEDSSDAEAAEDLDLVGLRPIRVPKRK MPLPVESHKKNIMEKEFFTEYGEASQYQIQEVVGKGSYGVVAAAIDTRTGERVAIKKIND
TaMPK17(U)          MGGGNGIVDGFRRLFHRRTPSGSVLGSSNQSSAGEDSSDVEAVEDLDLVGLRPIRVPKRK MPLPVESHKKNIMEKEFFTEYGEASQYQIQEVVGKGSYGVVAAAIDTRTGERVAIKKIND
                    ************* *************************.**.*.******* ******* ************************************************************

TaMPK17(clone)      VFEHVSDATRILREVKLLRLLRHPDVVEIKHIMLPPSRREFQDIYVVFELMESDLHQVIR ANDDLTAEHYQFFLYQLLRALKYIHGANVFHRDLKPKNILANADCKLKICDFGLARVSFN
TaMPK17(7DL)        VFEHVSDATRILREVKLLRLLRHPDVVEIKHIMLPPSRREFQDIYVVFELMESDLHQVIR ANDDLTAEHYQFFLYQLLRALKYIHGANVFHRDLKPKNILANADCKLKICDFGLARVSFN
TaMPK17(7AL)        VFEHVSDATRILREVKLLRLLRHPDVVEIKHIMLPPSRREFQDIYVVFELMESDLHQVIR ANDDLTAEHYQFFLYQLLRALKYIHGANVFHRDLKPKNILANADCKLKICDFGLARVSFN
TaMPK17(U)          VFEHVSDATRILREVKLLRLLRHPDVVEIKHIMLPPSRREFQDIYVVFELMESDLHQVIR ANDDLTAEHYQFFLYQLLRALKYIHGANVFHRDLKPKNILANADCKLKICDFGLARVSFN
                    ************************************************************ ************************************************************

TaMPK17(clone)      DAPSAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAELLTGRPLFPGKNVVH QLDIITDLLGTPSSETLSRVRNEKARRYLSCMRKKHPVPLTQKFPNADPLAVRLLGRLLA
TaMPK17(7DL)        DAPSAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAELLTGRPLFPGKNVVH QLDIITDLLGTPSSETLSRIRNEKARRYLSCMRKKHPVPLTQKFPNADPLAVRLLGRLLA
TaMPK17(7AL)        DAPSAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAELLTGRPLFPGKNVVH QLDIITDLLGTPSSETLSRIRNEKARRYLSCMRKKHPVPLTQKFPNADPLAVRLLGRLLA
TaMPK17(U)          DAPSAIFWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAELLTGRPLFPGKNVVH QLDIITDLLGTPSSETLSRIRNEKARRYLSCMRKKHPVPLTQKFPNADPLAVRLLGRLLA
                    ************************************************************ *******************:****************************************

TaMPK17(clone)      FDPKDRPSAEEALADPYFASLANVEREPSRHPISKLEFEFERRKVTKDDVRELIYREILE YHPQMLEEYMKGGDQISFLYPSGVDRFKRQFAHLEEHYSKGERGSPLQRKHASLPRQRVG
TaMPK17(7DL)        FDPKDRPSAEEALADPYFASLANVEREPSRHPISKLEFEFERRKVTKDDVRELIYREILE YHPQMLEEYMKGGDQISFLYPSGVDRFKRQFAHLEEHYSKGERGSPLQRKHASLPRQRVG
TaMPK17(7AL)        FDPKDRPSAEEALADPYFASLANVEREPSRHPISKLEFEFERRKVTKDDVRELIYREILE YHPQMLEEYMKGGDQISFLYPSGVDRFKRQFAHLEEHYSKGERGSPLQRKHASLPRQRVG
TaMPK17(U)          FDPKDRPSAEEALADPYFASLANVEREPSRHPISKLEFEFERRKVTKDDVRELIYREILE YHPQMLEEYMKGGDQISFLYPSGVDRFKRQFAHLEEHYSKGERGSPLQRKHASLPRQRVG
                    ************************************************************ ************************************************************

TaMPK17(clone)      ASNDGNNEQHISDQEMSAEPDAHGAVSPQKSQDAPGVGQNGLSPTSLSSRTYLKSASISA SKCVVVNPNKQPEYDDAISEETEGAVDGLSEKVSKMHA
TaMPK17(7DL)        ASNDGNNEQHISDQEMSAEPDAHGTVSPQKSQDAAGVGQNGLSPTSLSSRTYLKSASISA SKCVVVNPNKQPEYDDAISEETEGAVDGLSEKVSKMHA
TaMPK17(7AL)        ASNDGNNEQHISDQEMSAEPDAHGAVSPQKSQDAPGVGQNGLSPTSLSSRTYLKSASISA SKCVVVNPNKQPEYDDAISEETEGAVDGLSEKVSKMHA
TaMPK17(U)          ASNDGNNEQHISDQEMSAEPDAHGAVSPQKSQDAPSVGPNGLSPTSLSSRTYLKSASISA SKCVVVNPNKQPEYDDAISEETEGAVDGLSEKVSKMHA
                    ************************:********* .** ********************* **************************************
```

```
1: TaMPK17_clone  100.00   99.31   99.13   98.79
2: TaMPK17_7DL     99.31  100.00   99.13   98.79
3: TaMPK17_7AL     99.13   99.13  100.00   99.31
4: TaMPK17_U       98.79   98.79   99.31  100.00
```

TaMPK7(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK7 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK20-2(clone)      MQQAQRSKGSAEADFFTEYGDANRYKIQEVIGKGSYGVVCSALDLQTRQKVAIKKIHNIF EHTSDAARILREIKLLRLLRHPDVVEIKHIMLPPSRKDFKDIYVVFELMESDLHQVIKAN
TaMPK20-2(1AL)        MQQAQRTKSSAEVDFFTEYGDANRYKIQEVIGKGSYGVVCSALDLQTRQKVAIKKIHNIF EHTSDAARILREIKLLRLLRHPDVVEIKHIMLPPSRKDFKDIYVVFELMESDLHQVIKAN
TaMPK20-2(1BL)        MQQAQRSKGSAEADFFTEYGDANRYKIQEVIGKGSYGVVCSALDLQTRQKVAIKKIHNIF EHTSDAARILREIKLLRLLRHPDVVEIKHIMLPPSRKDFKDIYVVFELMESDLHQVIKAN
TaMPK20-2(1DL)        MQQAQRSKSSAEVDFFTEYGDANRYKIQEVIGKGSYGVVCSALDLQTRQKVAIKKIHNIF EHTSDAARILREIKLLRLLRHPDVVEIKHIMLPPSRKDFKDIYVVFELMESDLHQVIKAN
                      ******:*.***.********************************************** ************************************************************

TaMPK20-2(clone)      DDLTKEHYQFFLYQLLRALKYIHTASVYHRDLKPKNILANSNCKLKICDFGLARVAFNDT PTTVFWTDYVATRWYRAPELCGSFFTKYTPAIDIWSIGCIFAEVLTGKPLFPGKNAVHQL
TaMPK20-2(1AL)        DDLTKEHYQFFLYQLLRALKYIHTASVYHRDLKPKNILANSNCKLKICDFGLARVAFNDT PTTVFWTDYVATRWYRAPELCGSFFTKYTPAIDIWSIGCIFAEVLTGKPLFPGKNVVHQL
TaMPK20-2(1BL)        DDLTKEHYQFFLYQLLRALKYIHTASVYHRDLKPKNILANSNCKLKICDFGLARVAFNDT PTTVFWTDYVATRWYRAPELCGSFFTKYTPAIDIWSIGCIFAEVLTGKPLFPGKNVVHQL
TaMPK20-2(1DL)        DDLTKEHYQFFLYQLLRALKYIHTASVYHRDLKPKNILANSNCKLKICDFGLARVAFNDT PTTVFWTDYVATRWYRAPELCGSFFTKYTPAIDIWSIGCIFAEVLTGKPLFPGKNVVHQL
                      ************************************************************ *******************************************************.****

TaMPK20-2(clone)      DLMTDLLGTPSMDTISRVRNEKARRYLSSMRKKDPVPFSQKFPNADPLGVKLLEKLLAFD PKDRPTAEEALTDPYFRGLSKPEREPSCQPIRKMEFDFEHSRASKDDIRELIFQEILEYH
TaMPK20-2(1AL)        DLMTDLLGTPSMDTISRVRNEKARRYLSSMRKKDPVPFSQKFPNADPLGVKLLEKLLAFD PKDRPTAEEALTDPYFRGLSKPEREPSCQPIRKMEFDFEHSRVSKDDIRELIFQEILEYH
TaMPK20-2(1BL)        DLMTDLLGTPSMDTISRVRNEKARRYLSSMRKKDPVPFSQKFPNADPLGVKLLEKLLAFD PKDRPTAEEALTDPYFRGLSKPEREPSCQPIRKMEFDFEHSRVSKDDIRELIFQEILEYH
TaMPK20-2(1DL)        DLMTDLLGTPSMDTISRVRNEKARRYLSSMRKKDPVPFSQKFPNADPLGVKLLEKLLAFD PKDRPTAEEALTDPYFRGLSKPEREPSCQPIRKMEFDFEHSRVSKDDIRELIFQEILEYH
                      ************************************************************ ******************************************.*****************

TaMPK20-2(clone)      PQLLKSYVDGTERTTFLYPSAVDHFKKQFSHLEESDGSGPVVPADRKHASLPRSTIVHSA PISAKDTRPLFGKPCSKTSSETGRYAGNGRGASQASHAAQAVVSRRAAGSALPYDAASRP
TaMPK20-2(1AL)        PQLLKSYVDGTERTTFLYPSAVDHFKKQFSHLEESDGSGPVVPADRKHASLPRSTIVHSA PISAKDTRPLFGKPCSKTSSETGRYAGNGRGASQASHAAQAVVSRRAAGSALPYDAASRP
TaMPK20-2(1BL)        PQLLKSYTDGTERTTFLYPSAVDHFKKQFSHLEESDGSGPVVPADRKHASLPRSTIVHST PIPAKDTRPLFGKPCNKTSSETGRYAGNGHGASQASHAAQAVISRRAAGSALPYDAASRP
TaMPK20-2(1DL)        PQLLKSYIDGTERTTFLYPSAVDHFKKQFSHLEESDGSGPVVPADRKHASLPRSTIVHST PIPAKDTRPLFGKPCNKTSSETGRYAGNGHSASQASHAAQAVVSRRAAGSALPYDAASRP
                      ******* ***************************************************: ** ************.*************:.***********:*****************

TaMPK20-2(clone)      TISPGCPPQQQIPQMYGQYQHQAPA----GAGIPQAMGGYACGGYTKGTAPNAA-AAPAM RAPPYRHLPAGQKNGPLDRLAVETTDIYTRSLNGIVAAAAASAGTASAHRKVGAVPFGMPTTY
TaMPK20-2(1AL)        TISPGCPPQQQIPQMYGQYQHQAPA----GAGIPQAMGGYACGGYTKGTAPNAA-AAPAM RAPPYRHLPAGQKNGPLDRLAVETTDIYTRSLNGIVAAAAASAGTASAHRKVGAVPFGMPTTY
TaMPK20-2(1BL)        TISPGCPPQQQIPQMYGQYQHQAPPGAGAGAGIPQAMGGYACGGYTKGTAPNAAAAAPAM RAPPYRHLPTGQKNGPLDRLAVETTDIYTRSLNGIVAAAAASAGATGAHRKVGAVPFGMPTTY
TaMPK20-2(1DL)        TISPGCP-QQQIPQMYGQYQHQAAPGA--GAGIPQTMGGYACGGYTKGTAPNAA-AAPAM RAPPYRHLPAGQKNGPLDRLAVETTDIYTRSLNGIVAAAAASAGATSAHRKVGAVPFGMPTTY
                      ******* ***************      ******:****************** ***** *********:**********************************::.****************
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1: TaMPK20-2_clone  100.00   99.16   97.83   97.49
2: TaMPK20-2_1AL     99.16  100.00   97.66   97.99
3: TaMPK20-2_1BL     97.83   97.66  100.00   98.50
4: TaMPK20-2_1DL     97.49   97.99   98.50  100.00
```

TaMPK20-2(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK20-2 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK20-3(7DL)      MQNNDLRKKSAAEIDFFTEYGDTNRYKVLEVIGKGSYGLVCSANDTQTGEKVAIKKIHNI FEHISDAARILREIKLLRLLRHPDVVEIKHILLPPSKKDFKDIYVVFELMESDLHQVIKA
TaMPK20-3(clone)    MQNNDLRKKSAAEIDFFTEYGDTNRYKVLEVIGKGSYGLVCSANDTQTGEKVAIKKIHNI FEHISDAARILREIKLLRLLRHPDVVEIKHILLPPSKKDFKDIYVVFELMESDLHQVIKA
TaMPK20-3(7AL)      MQNGDLRKKSAAEIDFFTEYGDTNRYKVLEVIGKGSYGLVCSANDTQTGEKVAIKKIHNI FEHISDAARILREIKLLRLLRHPDVVEIKHILLPPSKKDFKDIYVVFELMESDLHQVIKA
TaMPK20-3(7BL)      MQNSDLRKKSAAEIDFFTEYGDTNRYKVLEVIGKGSYGLVCSANDTQTGEKVAIKKIHNI FEHISDAARILREIKLLRLLRHPDVVEIKHILLPPSKKDFKDIYVVFELMESDLHQVIKA
                    ***.******************************************************** ************************************************************

TaMPK20-3(7DL)      NDDLTREHYQFFLYQMLRALKYMHTANVYHRDLKPKNVLANANCKLKICDFGLARVAFND APTTVFWTDYVATRWYRAPELCGSFYSKYTPAIDIWSIGCIFAEVLIGKPLFPGKNVVHQ
TaMPK20-3(clone)    NDDLTREHYQFFLYQMLRALKYMHTANVYHRDLKPKNVLANANCKLKICDFGLARVAFND APTTVFWTDYVATRWYRAPELCGSFYSKYTPAIDIWSIGCIFAEVLIGKPLFPGKNVVHQ
TaMPK20-3(7AL)      NDDLTREHYQFFLYQMLRALKYMHTANVYHRDLKPKNVLANANCKLKICDFGLARVAFND APTTVFWTDYVATRWYRAPELCGSFYSKYTPAIDIWSIGCIFAEVLIGKPLFPGKNVVHQ
TaMPK20-3(7BL)      NDDLTREHYQFFLYQMLRALKYMHTANVYHRDLKPKNVLANANCKLKICDFGLARVAFND APTTVFWTDYVATRWYRAPELCGSFYSKYTPAIDIWSIGCIFAEVLIGKPLFPGKNVVHQ
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TaMPK20-3(7DL)      LDLITDVLGTPSLDAISQVRNDKARKYLTCMRKKQPASFSQKFPKADPLALRLLRRLLAF DPKDRPSAEEALADPYFNGLAKVEREPSCQPIPKLEFEFEGRRVTKEDIKELIFEEILEY
TaMPK20-3(clone)    LDLITDVLGTPSLDAISQVRNDKARKYLTCMRKKQPASFSQKFPKADPLALRLLRRLLAF DPKDRPSAEEALADPYFNGLAKVEREPSCQPIPKLEFEFEGRRVTKEDIKELIFEEILEY
TaMPK20-3(7AL)      LDLITDVLGTPSLDAISQVRNDKARKYLTCMRKKQPASFSQKFPKADPLALRLLRRLLAF DPKDRPSAEEALADPYFNGLAKVEREPSCQPIPKIEFEFEGRRVTKEDIKELIFEEILEY
TaMPK20-3(7BL)      LDLITDVLGTPSLDAISQVRNDKARKYLTCMRKKQPASFSQKFPKADPLALRLLRRLLAF DPKDRPSAEEALADPYFNGLAKVEREPSCQPIPKIEFEFEGRRVTKEDIKELIFEEILEY
                    ************************************************************ **********************************:*************************

TaMPK20-3(7DL)      HPQLLKEHISGTDRRNFVHLSAVDQFKKRFAELEENGGENGSAVSTQRKHSSLPRQSFNPR
TaMPK20-3(clone)    HPQLLKEHISGTDRRNFVHLSAVDQFKKRFAELEENGGENGSAVSSQRKHSSLPRQSFNPR
TaMPK20-3(7AL)      HPQLLKEHISGTDRRNFVHLSAVDQFKKRFAELEENGGENGSAVSSQRKHSSLPRQSFNPH
TaMPK20-3(7BL)      HPQLLKEHISGTDRRNFVHLSAVDQFKKRFAELEENGGENGSAVSSQRKHSSLPRQSFNPE
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```
1: TaMPK20-3_7DL     100.00   99.76   99.05   99.29
2: TaMPK20-3_clone    99.76  100.00   99.29   99.52
3: TaMPK20-3_7AL      99.05   99.29  100.00   99.52
4: TaMPK20-3_7BL      99.29   99.52   99.52  100.00
```

TaMPK20-3(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK20-3 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK20-4(clone)      -MPEANAGARGGGEQRSKVQSSDVMSFFSEYGDASRYKIEEIIGKGSYGVVCSAIDRQTG DRVAIKKVSNIFEHITDAARMLREIKFLRLLRHPDIVQIKHIMLPPSRRDYKDIFVVFEL
TaMPK20-4(3AL)        ----M-----QPDQNQQRRKGSSEMDFFSEYGDANRYKIQEVIGKGSYGVVCSAIDQHTG DKVAIKKIHNIFEHLSDAARILREIKLLCLLRHPDIVEIRHIMLPPSRRDFKDIYVVFEL
TaMPK20-4(3DL)        MQPD-------QHQQQQRRKGSSEMDFFSEYGDANRYKIQEVIGKGSYGVVCSAIDQHTG DKVAIKKIHNIFEHLSDAARILREIKLLRLLRHPDIVEIRHIMLPPSRRDFKDIYVVFEL
AK333309.1            MQPDQ-----QQHQHQQRRKGSSEMDFFSEYGDANRYKIQEVIGKGSYGVVCSAIDQHTG DKVAIKKIHNIFEHLSDAARILREIKLLRLLRHPDIVEIRHIMLPPSRRDFKDIYVVFEL
TaMPK20-4(3B)         MQPDQ-----QQHQHQQRRKGSSEMDFFSEYGDANRYKIQEVIGKGSYGVVCSAIDQHTG DKVAIKKIHNIFEHLSDAARILREIKLLRLLRHPDIVEIRHIMLPPSRRDFKDIYVVFEL
                                   :::.: :.*. *.********.****:*:**************::** *:*****: *****::****:*****:* ********:*:**********:***:*****

TaMPK20-4(clone)      MDTDLHQVIKANDDLTKEHYQFFLYQMLRALKYIHTANVYHRDLKPKNILANANCKLKIC DFGLARVAFNDTPTTVFWTDYVATRWYRAPELCGSFFTKYSPAIDTWSIGCIFAEILTGK
TaMPK20-4(3AL)        MDTDLHQVIKANDDLTKEHHQFFLYQMLRALKYIHTANVYHRDLKPKNILANANCKLKIC DFGLARVAFNDTPTTVFWTDYVATRWYRAPELCGSFFTKYSPAIDIWSIGCIFAEILTGK
TaMPK20-4(3DL)        MDTDLHQVIKANDDLTKEHHQFFLYQMLRALKYIHTANVYHRDLKPKNILANANCKLKIC DFGLARVAFNDTPTTVFWTDYVATRWYRAPELCGSFFTKYSPAIDIWSIGCIFAEILTGK
AK333309.1            MDTDLHQVIKANDDLTKEHHQFFLYQMLRALKYIHTANVYHRDLKPKNILANANCKLKIC DFGLARVAFNDTPTTVFWTDYVATRWYRAPELCGSFFTKYSPAIDIWSIGCIFAEILTGK
TaMPK20-4(3B)         MDTDLHQVIKANDDLTKEHHQFFLYQMLRALKYIHTANVYHRDLKPKNILANANCKLKIC DFGLARVAFNDTPTTVFWTDYVATRWYRAPELCGSFFTKYSPAIDIWSIGCIFAEILTGK
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TaMPK20-4(clone)      PLFPGKNVVQQLDMMTDFLGSPSPEIISRIRNEKARRYLSSMRKKLPVPFSEKFPKADPA AVKLLQKLLAFDPKDRPTAEEALADPYFNGLAKVEREPSCQPISKMEFEFERRKFTREDV
TaMPK20-4(3AL)        PLFPGKNVVHQLDLMTDLLGTPSLDTVSRIRNEKARRYLSSMRKKQPVCFSERFPKADPA ALKLMQRLLAFDPKDRPTAEEALADPYFKGLGKVEREPSCQPISKFEFEFERKKVTKEDV
TaMPK20-4(3DL)        PLFPGKNVVHQLDLMTDLLGTPSLDTVSRIRNEKARRYLSSMRKKQPVCFSERFPKADPA ALKLMQRLLAFDPKDRPTAEEALADPYFKGLGKVEREPSCQPISKFEFEFERKKVTKEDV
AK333309.1            PLFPGKNVVHQLDLMTDLLGTPSLDTVS-------------------------------- ------------------------------------------------------------
TaMPK20-4(3B)         PLFPGKNVVHQLDLMTDLLGTPSLDTVSRIRNEKARRYLSSMRKKQPVCFSERFPKADPA AFKLMQRLLAFDPKDRPTAEEALADPYFKGLGKVEREPSCQPISKFEFEFERKKVTKEDV
                      *********:***:***:**:** : :*

TaMPK20-4(clone)      KELIFREILEYHPQLLKDYSNGSEKTNFLYPSAVDNFRRQFANLEEDGGKGGA---AERK HVSLPRTTTVHSTPVPTTNCPASQAPQRIPAARPGRVIASATPTENAAFTDRQMGRRMAR
TaMPK20-4(3AL)        KELIFREILEYHPQLLKDYMNGTEKTNFLYPSAVDNFRRQFANLEENGGKGGAIVPSDRK HVSLPRTTTVHSTPIPPKDQKSSQVPQRIPTGRPGRVVGPVIPFENSCAMDPYSQRRVAR
TaMPK20-4(3DL)        KELIFREILEYHPQLLKDYMNGTEKTNFLYPSAVDNFRRQFANLEENGGKGGAIVPSDRK HVSLPRTTTVHSTPIPPKDQKSSQVPQRIPTGRPGRVVGPVIPFENSCAMDPYSQRRVAR
AK333309.1            ------------------------------------------------------------ ------------------------------------------------------------
TaMPK20-4(3B)         KELIFREILEYHPQLLKDYMNGTEKTNFLYPSAVDNFRRQFANLEENGGKGGAIVPSDRK HVSLPRTTTVHSTPIPPKDQKSSQVPQRIPTGRPGRVVGPVIPFENSCAMDPYSQRRVAR


TaMPK20-4(clone)      DPAGAPAAA----AGHHLRPDC--SDRQHEVEKDRAHYRPSHHFRDARVAPEAEARPSAY Y-----------------------IPPFNGIAAVGAAGRM-----------Y
TaMPK20-4(3AL)        NPVLPAAATNVSAYAYHRKSDSSERELQQELEKDRMQYQPMQRFMDAKMVSPD-LRSTSY YMPKGAPKADVAERTGLQPNMMQGIAPFNGIAAVGGSYNKASAVQYGVSRMY
TaMPK20-4(3DL)        NPVLPAAATNVSAYAYHRKSDSSERELQQELEKDRMQYQPMQRFMDAKMVSPD-LRSTSY YMPKGVPKADVAERTGLQPNMMQGIAPFNGIAAVGGSYNKASAVQYGVSRMY
AK333309.1            ------------------------------------------------------------ ----------------------------------------------------
TaMPK20-4(3B)         NPVLPAAATNVSAYAYHRKSDSSERELQQELEKDRMQYQPMQRFMDAKMVSPD-LRSTSY YMPKGVPKADVAERTGLQPNMMQGIAPFNGIAAVGGSYNKASAVQYGVSRMY
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```
1: TaMPK20-4_clone  100.00   76.81   77.22   76.75   83.59
2: TaMPK20-4_3AL     76.81  100.00   99.14   98.80   98.07
3: TaMPK20-4_3DL     77.22   99.14  100.00   99.66   99.62
4: TaMPK20-4_3B      76.75   98.80   99.66  100.00  100.00
5: AK333309.1        83.59   98.07   99.62  100.00  100.00
```

TaMPK20-4(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK20-4 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK21-2(3AL)      MAKKGSDKAGFFTEYGEATRYEIGEVVGKGSYGVVAAAVDTHTGERVAIKKIDDVFEHVA DATRILREIKLLRLLRHPDIVEIKHIMLPPSRREFRDIYIIFELMESDLHQVIKANDDLS
TaMPK21-2(3B)       MAKKGSDKGGFFTEYGEATRYQVGEVVGKGSYGVVASAVDTHTGESVAIKKIDDVFEHVA DATRILREIKLLRLLRHPDIVQIKHIMLPPSRREFRDIYIIFELMESDLHQVIKANDDLS
AK330685.1          MAKKGSDKGGFFTEYGEATRYQVGEVVGKGSYGVVASAVDTHTGESVAIKKIDDVFEHVA DATRILREIKLLRLLRHPDIVQIKHIMLPPSRREFRDIYIIFELMESDLHQVIKANDDLS
TaMPK21-2(clone)    MAKKGSDKGAFFTEYGEATRYQVGEVVGKGSYGVVASAVDTHTGEPVAIKKIDDVFEHVA HATRILREIKLLRLLRHPDIVQIKHIMLPPSRREFRDIYIIFELMESDLHQVIKANDDLS
TaMPK21-2(3DL)      MAKKGTDKGAFFTEYGEATRYQVGEVVGKGSYGVVASAVDTHTGEPVAIKKIDDVFEHVA DATRILREIKLLRLLRHPDIVQIKHIMLPPSRREFRDIYIIFELMESDLHQVIKANDDLS
                    *****:**..***********::*************:******** ************** .********************:**************************************

TaMPK21-2(3AL)      PEHFQFFFYQLLRGMKYMHAANVFHRDLKPKNILANADCKLKICDFGLSRVSFNDTPSAI FWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAEMLTGRPLFPGKNVVHQLDLMT
TaMPK21-2(3B)       PEHHQFFFYQLLRGMKYIHAANVFHRDLKPKNILANADCKLKICDFGLARVSFNDTPSAI FWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAEMLTGRPLFPGKNVVHQLDLMT
AK330685.1          PEHHQFFFYQLLRGMKYIHAANVFHRDLKPKNILANADCKLKICDFGLARVSFNDTPSAI FWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAEMLTGRPLFPGKNVVHQLDLMT
TaMPK21-2(clone)    PENHQFFFYQLLRGMKYIHAANVFHRDLKPKNILANADCKLKICDFGLARVSFNDTPSAI FWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAEMLTGRPLFPGKNVVHQLDLMT
TaMPK21-2(3DL)      PENHQFFFYQLLRGMKYIHAANVFHRDLKPKNILANADCKLKICDFGLARVSFNDTPSAI FWTDYVATRWYRAPELCGSFFSKYTPAIDIWSIGCIFAEMLTGRPLFPGKNVVHQLDLMT
                    **:.*************:******************************:*********** ************************************************************

TaMPK21-2(3AL)      DLLGTPSEESISRVRNEKARRYLGNMKKKHPIPFSQKFPGVDPMALHLLERLLAFDPADR PTAAEALADPYFTGLANSELEPTAQPISKLEFEFERRKLAREDLRELIYREILEYHPQML
TaMPK21-2(3B)       DLLGTPSAESISRIRNEKARRYLGNMKKKHPIPFSQKFPGVDPMALHLLERLLAFDPADR PTAAEALADPYFTGLANSELEPTTQPISRLEFEFERRKLGREDVRELIYREILEYHPQML
AK330685.1          DLLGTPSAESISRIRNEKARRYLGNMKKKHPIPFSQKFPGVDPMALHLLERLLAFDPADR PTAAEALADPYFTGLANSELEPTTQPISRLEFEFERRKLGREDVRELIYREILEYHPQML
TaMPK21-2(clone)    DLLGTPSAESISRIRNEKARRYLGNMKKKHPIPFSQKFPGVDPMALHLLERLLAFDPTDR PTAAEALADPYFTGLANSELEPTTQPISRLEFEFERRKLAREDVRELIYREILEYHPQML
TaMPK21-2(3DL)      DLLGTPSAESISRIRNEKARRYLGNMKKKHPIPFSQKFPGVDPMALHLLERLLAFDPTDR PTAAEALADPYFTGLANSELEPTTQPISRLEFEFERRKLAREDVRELIYREILEYHPQML
                    ******* *****:*******************************************:** ***********************:****:**********.***:****************

TaMPK21-2(3AL)      HDYLRGGDQANFLYPSGVDRFKSQFVHLEEIGAKGEKTSPQLRQHASLPRERVIGSSDEP EKPNADYCIKLHVDELPGHTSVTDGLNKPLLNTRNFLKSESIGASKCIVVKEKQEKDEES
TaMPK21-2(3B)       HEYLRGGDQANFLYPSGVDRFKRQFVHLEEIGAKGEKTSPQLRQHASLPRERVIGSSDEP EKPNADYCIKLHVGEVPGYTSVTDGLNKPLLNTRNFLKSESIGASKCIVVKEKREKDEES
AK330685.1          HEYLRGGDQANFLYPSGVDRFKRQFVHLEEIGAKGEKTSPQLRQHASLPRERVIGSSDEP EKPNADYCIKLHVGEVPGYTSVTDGLNKPLLNTRNFLKSESIGASKCIVVKEKREKDEES
TaMPK21-2(clone)    HEYLRGGDQANFLYPSGVDRFKRQFVHLEEIGAKGEKTSPQLRQHASLPRERVIGSSDEP EKPNADYCIKLHVGEVPGYTSVTDGLNKPLLNTRNFLKSESIGASKCIVVKEKREKDEES
TaMPK21-2(3DL)      HEYLRGGDQANFLYPSGVDRFKRQFVHLEEIGAKGEKTSPQLRQHASLPRERVIGSSDEP EKPNADYCIKLHVGEVPGHTSVTDGLNKPLLNTRNFLKSESIGASKCIVVKEKREKDEES
                    *:******************** ************************************* *************.*:**:**********************************:******

TaMPK21-2(3AL)      MSEYMHEASD
TaMPK21-2(3B)       MSEYMHEASD
AK330685.1          MSEYMHEASD
TaMPK21-2(clone)    MSEYMHEASD
TaMPK21-2(3DL)      MSDYMHEA--
                    **:*****
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```
1: TaMPK21-2_3AL      100.00   95.71   95.71   95.10   95.08
2: TaMPK21-2_3B       95.71  100.00  100.00   98.78   98.36
3: AK330685.1         95.71  100.00  100.00   98.78   98.36
4: TaMPK21-2_clone    95.10   98.78   98.78  100.00   99.18
5: TaMPK21-2_3DL      95.08   98.36   98.36   99.18  100.00
```

TaMPK21-2(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK21-2 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.

```
TaMPK24(6BS)        MEFFTEYGEASQYQIEEIIGQGSFGVVAAAVDTQTGERVAIKKIHDMFEHAPDGTRILRE IKLLRLLRHPNIVGVKHILLPPARREFRDIYVVFELMESDLQKVIQVNENLTAGHHRYFL
TaMPK24(U)          MEFFTEYGEASQYQIEEIIGKGSFGVVAAAVDTQTGERVAIKKIHDMFEHASNGTRILRE IKLLRLLRHPNIVETKHILLPPARREFRDIYVVFELMESDLQKVIQANENLTAGHHRFFL
TaMPK24(6DS)        MEFFTEYGEASQYQIEEIIGRGSFGVVAAAVDTQTGERVAIKKIHDMFEHASDGTRILWE IKLLRLLRHPNIVEIKHILLPPARREFRDIYVVFELMESDLQKVMQVNENLTAGHHRYFL
TaMPK24(clone)      MEFFTEYGEASQYQIEEIIGKGSFGVVAAAVDTQTGERVAIKKIHDMFEHASNGTRILRE IKLLRLLRHPNIVETKHILLPPARREFRDIYVVFELMESDLQKVIQANENLTAGHHRFFL
                    ********************:****************************** :***** * *************  *****************************:*.**********:**

TaMPK24(6BS)        YQLLHALKYIHAANVFHRDLKPSNILANSNCKLKICDFGLARALRDDAPLAIFWTDYVAT RWYRAPELCGSFFSKYTPAIDIWSIGCIFAEVLTGKPLFPGMNVTHQLDLITNVLGTPSY
TaMPK24(U)          YQLLHALKYIHAANVFHRDLKPSNILVNSNCKLKICDFGLARASRDDPPLAIFWTDYVAT RWYRAPELCGSFFSKXXXXXXXXXXXXXXXXXXXXXXXXXXXXVKHQLDLITDVLGTPSY
TaMPK24(6DS)        YQLLHALKYIHAANVFHRDLKPSNILVNSNCKLKICDFGLARASRDDPPLAIFWTDYVAT RWYRAPELCGSFFSKYTPAIDIWSIGCIFAEVLTRKPLFPGTNVKHQLDLITDVLGTPSH
TaMPK24(clone)      YQLLHALKYIHAANVFHRDLKPSNILVNSNCKLKICDFGLARASRDDPPLAIFWTDYVAT RWYRAPELCGSFFSKYTPAIDIWSIGCIFAEVLTRKPLFPGTNVKHQLDLITDVLGTPSY
                    **************************.**************** *** ************ ***************                            *.*******:******:

TaMPK24(6BS)        ETLSQIRNEKARRYLTGMKRKHPIPFPSIFCNADPQAVRLLERLLAFDPKDRPTAEEALA DPYFEGFPNLEHEPSPHPFSKLEFEFERWKLTKDGVRDLIYREILEYHPQMLQDYIRAGG
TaMPK24(U)          ETLSQIRNEKARIYLTGMKRKHPIPFPSMFCNADPQAVRLLERLLAFDPKDRPTAEEALA DPYFEGFPNLEHEPSPHPFSKLEFEFERWKLTKDGIRDLIYREILEYHPQMLQDYIGAGG
TaMPK24(6DS)        ETLSQIRNEKARRYLTGMKRKHPIPFPSMFCNADPQAVRLLERLLAFDPKDRPTAEEALA DPYFEGFPNLEHEPSPHPFSKLEFEFERWKLTKDGIRDLIYREILEYHPQMLQDYIRAGG
TaMPK24(clone)      ETLSQIRNEKARRYLTGMKRKHPTPFPSMFCNADPQAVRLLERLLAFDPKDRPTAEEALA DPYFEGFPNLEHEPSPHPFSKLEFEFERWKLTKDGIRDLIYREILEYHPQMLQDYIGAGG
                    ************ ********** ****:******************************* ***********************************:******************** ***

TaMPK24(6BS)        QTSFVYPSGVDGMRLQFVHLEENHLRGERGTPLRRRHASLPRERVCAPMGIDNQDCNNER R-TASSAAQITIRSQQEGLTHAYVYQNGTGIPDFCSGYYLQNGSTSASSCVIEENEGPKE
TaMPK24(U)          QTSFVYPSGVDGMRLQFVHLEENHLRGERGTPLRRRHASLPRERVCAPKGSDNQDCNNER RRTASSAAQTTIRSQQEGLTHAYVYQNGTSIPNFCSGYYLQNGSTSASSCVIDEHEGLEE
TaMPK24(6DS)        QTSFVYPSGVDDMRLQFVHLEENHLRGERGTPLRRRHASLPRERVCAPKGSDNQDCNNER RRTASSAAQTTIRSQQEGLTHAYVYQNGTSIPNFCSGYYLQNGSTSASSCVIDDHEGLKE
TaMPK24(clone)      QTSFVYPSGVDGMRLQFVHLEENHLRGERGTPLRRRHASLPRERVCAPKGSDNQDCNNER RRTASSAAQTTIRSQQEGLTHAYVYQNGTSIPNFCSGYYLQNGSTSASSCVIDEHEGLEE
                    ***********.************************************ * ********* * ******* *******************.**:*******************:::** :*


TaMPK24(6BS)        NGVSA-EKVAYELSERLARI
TaMPK24(U)          NGVSEEEKVAYELSQCFARI
TaMPK24(6DS)        NGVSEEEKVAYELSQCFARI
TaMPK24(clone)      NGLPGS--------------
                    **:

1: TaMPK24_6BS   100.00   88.55   93.98   93.80
2: TaMPK24_U      88.55  100.00   91.80   93.00
3: TaMPK24_6DS    93.98   91.80  100.00   96.50
4: TaMPK24_clone  93.80   93.00   96.50  100.00
```

TaMPK24(clone) protein sequences used for Y2H interactions (blue font) did not match a nucleotide identifier from Additional File 3. Sequence was aligned with Ensembl sequences encoding TaMPK24 using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). Percent identity of aligned sequences are also provided.