

SUPPLEMENTARY MATERIAL

corresponding to:

**Identification of the maize Mediator CDK8 module,
and transposon-mediated mutagenesis of *ZmMed12a***

ANA L. ALONSO-NIEVES, TANIA NÚÑEZ-RÍOS, JULIO A. MASSANGE-SÁNCHEZ,
KEVIN R. AHERN, DANIEL LEPE-SOLTERO, MARCELINA GARCÍA-AGUILAR, THOMAS P. BRUTNELL,
RUAIRIDH J.H. SAWERS and C. STEWART GILLMOR

identical residues (*)
highly conserved residues (same color) (:)
semi-conserved residues (.)

Colors:

Red = Small and hydrophobic residues (AVFPMILW)

Blue = Acidic residues (DE)

Magenta = Basic residues (RK)

Green = Hydroxyl + Amine (STYHCNGQ)

Percent Identity Matrix - created by Clustal2.1

1: HsCDK8	100.00	39.59	43.39	43.73
2: AtCDK8	39.59	100.00	73.13	75.54
3: ZmCDK8_EU	43.39	73.13	100.00	90.64
4: ZmCDK8_BT	43.73	75.54	90.64	100.00

Alignment made with Clustal Omega <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Figure S2. CLUSTAL O (1.2.1) multiple sequence alignment of CycC proteins from *Homo sapiens* (Hs) (P24863), *Arabidosis thaliana* (At) (BX833973), and *Zea mays* (Zm) (alternate splice products BT040922 and BT036293). The black bar indicates the Cyclin domain (cd00043).

```

HsCycC          MAGNFWQSSHYLQWILDKQDLLKERQKDLKFLSEEEYWKLQIFFTNVIQALGHEHLKLRQQ 60
AtCycC1;1      MAANFWNSSHYKQLLDPEEVDVVDLKDKERGISIDDFKLIKFMNSNHMKLAQHIVRQR 60
ZmCycC_BT04    MAANFWTSSSHCKQLLDPEVDVLPAAADRERGITPEEFRLIKIHMSFHIWRLAQQVKVRQR 60
ZmCycC_BT03    -----MPYQY---KHLMISDIWRLLAQQVKVRQR 25
                :: : : * *.:*:*:

HsCycC          VIATATVYFKRFYARYSLKSIDPVLMAPTCVFLASKVEEFGVVSNTRLIAAATSVLKTRF 120
AtCycC1;1      VVATAITVMRRVYIRKSMVEFEPRLVALTCLYLASKAESIVQARNL-----VFYIKR 113
ZmCycC_BT04    VVATAIAYFRRVYTRKSMSDYDPRLVAPTCLYLASKVEESTVQARLL-----VFYIKK 113
ZmCycC_BT03    VVATAIAYFRRVYTRKSMSDYDPRLVAPTCLYLASKVEESTVQARLL-----VFYIKK 78
                *:* * .*:*: * * : . : * * * : * : * : * : * : * : * : * :

HsCycC          SYAFPKEFPYRMNHILECFYLLLEMDCCILIVYHPYRPLLQYVQDMGQEDM-LLPLAWRI 179
AtCycC1;1      LYP-DEYNKYELKDILGEMKVLALDYLLVVFHPYRSLSEFLQDAALNDVNMNQITWGI 172
ZmCycC_BT04    MCGSDDKYRFEIKDILEMEMKLEALDYLLVVFHPYRPLLQLLQDAGITD--LTQFAWGL 171
ZmCycC_BT03    MCGSDDKYRFEIKDILEMEMKLEALDYLLVVFHPYRPLLQLLQDAGITD--LTQFAWGL 136
                . :.:*: * : * : * : * : * : * : * : * : * : * :

HsCycC          VNDTYRTDLCLLYPPFMIALACLHVACVVQKDKARQWFAELSVDMEKILEII----- 231
AtCycC1;1      VNDTYKMDLILVHPPYRIALACIYIASVHREKDI TAWFEDLHEDMNLV----- 220
ZmCycC_BT04    VNDTYKMDLILYPPYMIALACIYIASVLKDKDT TAWFEELRVDMNIV----- 219
ZmCycC_BT03    VNDTYKMDLILYPPYMIALACIYIASVLKDKDT TAWFEELRVDMNIVSSSIIGFPAIYS 196
                *****: ** *.:*: * : * : * : * : * : * : * : * : * :

HsCycC          -----RVILKLYEQWKNFDERKE----MATILSKMPKPKPPNSEG 268
AtCycC1;1      -----KNIAEILDYENYRITTE----EKVNSAFSKLALKL----- 253
ZmCycC_BT04    -----KNISMEILDYDYKIDPQRGIPEDKISPVMNKLPKA----- 257
ZmCycC_BT03    VLFSSPNSVTCNSQVKNISMEILDYDYKIDPQRGIPEDKISPVMNKLPKA----- 249
                **.:*: :: : : : :.:*

HsCycC          EQGPNGSQNSSYSQS 283
AtCycC1;1      ----- 253
ZmCycC_BT04    ----- 257
ZmCycC_BT03    ----- 249

```

identical residues (*)
highly conserved residues (same color) (:)
semi-conserved residues (.)

Colors:
Red = Small and hydrophobic residues (AVFPMILW)
Blue = Acidic residues (DE)
Magenta = Basic residues (RK)
Green = Hydroxyl + Amine (STYHCNGQ)

Percent Identity Matrix - created by Clustal2.1

```

1: HsCycC          100.00  36.99  41.77  42.66
2: AtCycC1_1      36.99  100.00  66.93  63.89
3: ZmCycC_BT04   41.77  66.93  100.00  95.95
4: ZmCycC_BT03   42.66  63.89  95.95  100.00

```

Figure S3. CLUSTAL O (1.2.1) multiple sequence alignment of Med12 proteins from *Homo sapiens* (Hs) (NP_005111), *Arabidosis thaliana* (At) (AB690341), and *Zea mays* (Zm) (Med12a=KP455660 and Med12b=KP455661). Identical and conserved residues corresponding to the Med12 domain (pfam09497) are shaded in black and grey.

HsMed12	-----MAAFGI-----LSYEHRLPK	15
AtMed12	MQRYHAANCTSAVNNNAIGGASARDSGRADSSSIGNYSLNSRRPPPLTPYKLLKCEKDG-L	59
ZmMed12a	----MQRYAGF---SGSRDGA-RLEASPFSSSSSSGYPVSSRRQQQLTPYKLLKCDKDP-L	51
ZmMed12b	MHRYSSNSAGF---SGGRDGA-RLEASPFSSS-SSGYPVSSRRQQQLVPYKLLKCDKDP-L	54
	. : :	*. : :
HsMed12	RPRLGPPDVYPQDPKQKEDELTAALNVKQGFNNQPAVSGDEHGSAKNVS----FNPAKISS	71
AtMed12	NSRLGPPDFHPPTSNSPEENLTKEYVQFGYKQTV--DGLKESEEIILSQVHTFSKP-VVH	116
ZmMed12a	NNKLGPPDFYPQTLNCPPEETLTKDYVQYGYKQTV--EGIEEAREIVISQIPYFCKPDVVI	109
ZmMed12b	NNKLGPPDFYPQTPNCPPEETLTKEYAQAGYKQTV--EGIEEAREIVLSQIPYFCKPDAVI	112
	. : *****. : * : * : * : * : * : * : * : *	
HsMed12	NFSSIIAEKLRCNTLPDTGRRK-PQVN-----QKDNFVLVTARSQSAINTWFTDE	120
AtMed12	KCKEAVRKCRLAINESRALKRKAGQVYGVPLSGSLLC KPG-FPEQRSCGEETKKRWIESE	175
ZmMed12a	KCKEALKKRLRAINESRAQKRKAGQVYGVPLSGSLLIKPGVYPEQRPCNEDTRRWVEAL	169
ZmMed12b	KCKEALKKRLRAINESRAQKRKAGQVYGVPLSGSLLIKPGVYPEQRPCNEDARRKWIEAL	172
	: . . : : ** . . : : ** ** : : : : : : : : : : : : *	
HsMed12	AG-TKPLTQLAKKVPIFSKKEEVFGYLAQYTVPMVRAAWLIKMTCAYYAAIS----ETK	174
AtMed12	SQQHKRRLSLADNIP-GYRRKTLFEVLIKNNVPLLRAFWFIKVTYLNQVRPSPAAISSGT	234
ZmMed12a	AQPNKRLRSLSSEHVPHGYRRKSLFEGLIKYNVPLLRAFWFIKVTYLNQA--RPAPNSTSV	227
ZmMed12b	AQPNKRLRSLSSEHVPHGYRRKSLFEGLIKYNVPLLRAFWFIKVTYLNQLQTRQTPNSISV	232
	: * * * . * : . : * : : : * : * : * : * : * : * : * : *	
HsMed12	VKKRHVDPFMEWTQIITKYLWEQLQKMAEY----YR-----PGPA-GSGGCGSTIGP	221
AtMed12	PDKTQASRCEQWTKDVI EYLQYLLDELLSRNSSFPAQQTRDRSPQMLYTGSMQKNS---P	291
ZmMed12a	-VASDNQRSNQWTKDVVEYLQOILDEVCSKEGAIVPPSFKEQSSPGLAAGTNQIKMKTES	286
ZmMed12b	-AGSDNQRSNQWTKDVVEYLQHILDEFCSKEGAFVHPSFREQSSPGPTAGTNQIKMKTEA	291
	. . : ** : : ** * : . . : *	
HsMed12	L----PHDVEVAIRQWDYTEKLAMFMFQDGLDRHEFLTWVLECFEKIRPGEDELLKLLL	277
AtMed12	ASTSLYGEETSLHFKWWYMVRLQWHHAEGLLFPNLIVDWVLLKLLQEK--EIFEILQLLL	349
ZmMed12a	SP-AGDSEELVHFKWRVMVRLIQWHLTEELLVPSVLI EWLSNQLQER--DSDDVLELLL	343
ZmMed12b	SPAAGDIEELVHFKWRVMVRLIQWHLTEELLVPSVLI EWLSNQLQER--DSVDVLELLL	349
	: : * * * : * : : * : : * : : : : : : : * : * : *	
HsMed12	PLLLRYSGEFVQSAYLSRRLAYFCTRRLLALQLDGVSSSHSHVISAQSTSTLPTTPAPQPP	337
AtMed12	PIVYGVLESIVLSQTYVQSLVAIAVRFIQEPAPGGSDLVDN-----	390
ZmMed12a	PIILGLVDTITLSQTYVRMFVLELLVRRLN-----VDR-----	375
ZmMed12b	PIMLGLVDTITLSQTYVRMFVLELLVRRLNDA-----SVVDS-----	385
	* : : : . * : : . : * : :	
HsMed12	TSSTPSTPFSDLLMCPQHRPLVFLGSLCILQTIILLCCPSALVWHYSLTDSRIKGTGSPLDHL	397
AtMed12	----SRRAYT-----LSALIEMVRYLVLAAAPDTFV-----ASDFF	421
ZmMed12a	----PKRFSV-----SSVIAELLRYMVLAVPDTFV-----SLDCF	406
ZmMed12b	----PKGPSV-----SSVIAELLRYMVLAVPDTFI-----SLDCF	416
	: : : : * . * : : : *	* :
HsMed12	PIAPSNLPMPEGNSAFTQQ-----VRAKLREIEQQIKERGQAVEVRSFDFKQ-----	445
AtMed12	PLPPSVAACGPNVSYTSKAYENLEKLRSNSAEISAQFQGRGV--LSRFEFLSFDYTIIST	479
ZmMed12a	PFPSFVVPDVY-----GRG---ALLKITSG-----GGILCSKR--RDAYRYLSCGYAVSS	451
ZmMed12b	PLPSFVVPDVY-----GRG---ALLKITSS-----GGISSSKR--CDAYRYLSCGYAVCS	461
	* : : : : : : : : : : .	
HsMed12	-----EATAGFTIGRV--LHTLEVLDSSHFSRSDFSNSLDSL CNRIFGLG----	488
AtMed12	IQRSADDLAKIASAGYPQHNVAKAVQALDKALSDGDIRAAYSYLFDL CNGAVDEAWITD	539
ZmMed12a	IQKRAHDLAAVANPSLQARGAAKVVALDKALVTGNLSVAYFSLFNDLS DALMEERWIKE	511
ZmMed12b	IQKRAYDLATVANPNLQARGAAKVVALDIALVTGNLSVAYSSLFNDLS DTLMEERWIKE	521
	* . . : : * : . : : * : . : : * : . : .	

HsMed12	--PSKDG-----HEISSDDDAVVSLLCEWAVSCKRSGRHRAMV-----VA	526
AtMed12	VSPCLRSSLRWIGAISTSFVCSVFFLI EWATCDFRDFRAGVPKDIKFSGRKDCSQVYLV	599
ZmMed12a	VNPLQSSLMWIGTVELSLICSIFFLCEWATCDYRDCRASPSQNVKFTGRRDLSQIHMAV	571
ZmMed12b	VSPSLQSSLMWIGTVELSLICSIFFLCEWATCDYRDCRASPSRNKVFTRRDLSQIHMAV	581
	* . . : . . : : * * * . . * . *	
HsMed12	KLLEKRQAEIEA-----ERCGESEAADEKGSIASG-----	556
AtMed12	QLLKQKILGGFTARKG-----KNCRNNFLGVS KPS	630
ZmMed12a	SILKNKMDENNNLSRPKSSSTRITLNKVAKG--SLNDACLTAAAVDDSSGLRSNAKNVDEKK	630
ZmMed12b	SILKNKMDENNNLSRSKSSTRVTLNNITKGSLLTDACLTAAAVDDTSGLQSNAKNVDEKK	641
	. : * : : : :	
HsMed12	-SLS-APSAPIFQDVLQFLDTQAPMLTDPRESERVEFFNLVLLFCELIRHDFVSHNMY	614
AtMed12	GSMDAFESPGPLHDIIVCWLDQH-----EVHK--GGAKRLQLLVFELIRSGIFNPIAY	681
ZmMed12a	DTNDFIFESPGPLHDIIVCWLDQH-----EVSNAVGFTRVDVLI AE LIRNGIFFPQVY	682
ZmMed12b	DTNDFIFESPGPLHDIIVCWLDQH-----EVSNAVGFTRVDVLI V E LIRNGIFFPQAY	693
	: . * : : * : : : : * : . . : : * . * * * : * *	
HsMed12	TCTLISRGDLAFGAPGRPPSPFDDPADDPEHKEAEGSSSSK-----L-----ED	659
AtMed12	VRQLIVSGMIDVIQPA-----VDPERRMRHHRILKQLPGCFVHETLEEAQLFGG	730
ZmMed12a	VRQLIISGITDKNDTM-----LDVERKRRHHR TLKQLPGSSLFDVLEETR TAE E	731
ZmMed12b	VRQLIISGITDKNDTM-----LDVERKRRHHR TLKQLPGSSLFDILEETR TVE E	742
	. ** * * * * : . . : :	
HsMed12	PGLSESMIDPSSSV-LFEDME-----K-PDFSLFSPTMPCGKGS PS	700
AtMed12	DKLSEAVRTYSNERLLLRELLVEKGYWNNLVLS DQKSKKISTSLSSVIFPRACNAKSN	790
ZmMed12a	QQLYEMMSTYSSERRLVSELSCGHSFYASGRGEYTS-----SSCI-RKQS-DLPV	780
ZmMed12b	QQLYEMMSTYSSERRLVSELSCDHSFYASGRGEYTA-----SSCI-RKQS-DLPL	791
	* * : . . : : :	
HsMed12	PEKPDVEK---EVKPPPKKEKIEGLGVLYDQPRHV-----QYATHF-----	738
AtMed12	SKGPRKHTKSSVDIRELKERISALLQFPG--MSCGVE TPVRDEFQNSV KRSSGSVYSKMD	848
ZmMed12a	ASEGDKHGRVLEQVEDVKALLSSLLGFTYPPVSKLC---EIKTSFQESVTSTLTQVE	836
ZmMed12b	ASGGDKHGRVPEQVEDVKALLSSLLGFTYPSVSEPR---EIKTSFQESATSTLSQVE	847
	. . * : . . : . . :	
HsMed12	---PIPQEESCSHECNQRLVV---LFGVGK--QRDDARHAIKKITKDILKVLNR----	784
AtMed12	QPEATPGCEDCRRAKRPKMNDKSSCYQNSPIASDEEDNWWIKKGSKTVESSLVDPQI	908
ZmMed12a	TGEAKSGCEDCMRSKQGKLDSD--ATPFQGFPLIQSGEEDIWVVKKGT KLQ--ESFNIEPVQ	894
ZmMed12b	TGEAKSGCEVCMRSKQGKLDSD--ATPFQGFSLIQSDEEDIWVVRKGT KLQ--ESFNIEPVQ	905
	* * : : : * . : : : * * : . : :	
HsMed12	-----KGT---AETDQLAPIVPLNPGLTFLGGEDGQKRR-----RNPEAFP TAE	827
AtMed12	EITKQVPRGRQMARKTQSLAQL---QA---ARIEGSGASTSHVCDNKVSCPHHGPVE	962
ZmMed12a	KSVKQTSRGRKAVVRKTQSLAQL---AA---ARIEGSGASTSHVCE SKMSPHPNND	948
ZmMed12b	KSVKQTSRGRKAVVRKTQSLAQL---AA---ARIEGSGTSTSHVCE SKMSPHHPNID	959
	: * : * . * * : : : * . * . * : :	
HsMed12	----DIFAKFQ-----HLSHYDQHQTAVQS---RNVLEQ-----	855
AtMed12	GENQKVVDFRTSTPVDMVS VGNLSKQLQFVDKRSIAVWLT TAVRQLVEEPQKSSVRVQG	1022
ZmMed12a	GDNVKDFDH---TRAANVTAIGKSLKRLRLLERRSVSSWLLKSIRQLVDGNGMTASKATN	1005
ZmMed12b	GDNVKDFDH---TRVANLTEIGKSLKRLRLLERRSVSSWLLKTVRQLIEGNETTAAKATN	1016
	. . : * : : : : : * : : :	
HsMed12	-----ITSFALGMSYHLPLVQHVFIFDLMEYSLSISGLIDFAIQLLNELSV	902
AtMed12	FN--RGAPVEEKN TIRWKLGADELY---SILFL---LDISLDLVS AVKFLWLLPKANS	1073
ZmMed12a	SISILPLQPD DK T ASKWR LGDEELL---SVLYV---LDTCCDSVSGVKFLIWL LKIR-	1057
ZmMed12b	SISILSLQSDDKTTSKWR LGDEELL---SVLYL---LDTCCDLVSCARFLVWLLAKIRG	1069
	: * * . : : : : . . * : * * :	
HsMed12	VEAELLKSSD---LVGSYTTSLCLC---IVAVLRHYHACLILNQDMAQVFEGLCGVV	955
AtMed12	TPSFAVQGGRNLVTVPRNVENNMCEIGEAILVSSLRRYENIL--LSADLVPEAMTALMNR A	1132
ZmMed12a	GVGSSGQPGRTYM-LMRNRDHQVCQVNEALVFSLLRYENIL-LATDILPDVLSALVNRN	1115
ZmMed12b	GMGSSGQPGRSSM-HTRNRDHQVCQVSEALVFSLLRYENIL-LAADILPDVLSALVNRN	1127
	. . . : * : : * : * * * : : : . *	

HsMed12	K---HGMNRS DGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFC SKVKN TIYCNVPESE	1012
AtMed12	ASLMSSNGKISGSAA-LVYTRYILKRYGSLPSV-VEWHNNFKATSEKK---LLSELDHTR	1187
ZmMed12a	S---MSATTRHPGSTA-FAYVRYFLKRYRDVASV-AKWEKNFRITTCQDR---LLAELDNGR	1168
ZmMed12b	S---VSAIVRHPGSTA-FAYVRYFLKRYRDVAGV-AKWEKSFRTTCQDR---LLAELDNGR	1180
	. : **:* * : . * . : : : * .. : . : : .	
HsMed12	SNMRWAEF MIDTLENPAAHTFTYTGLGKSLSEN PANRYSFVCNALMHVCVGHHPDRVN	1072
AtMed12	S---GNGEYGNPLGVPAG-----VDNDDY--LRK---KISIGGARPSRVG	1225
ZmMed12a	S---IDGLVSSSGILAG-----EEIDEQ--VRQ--KL--NGRSSRLV	1202
ZmMed12b	S---IDGELISSSGVSAG-----EEIDEQ--VRQ--KL--NGRSSRLV	1214
	* . * . : : : : : : : : : *	
HsMed12	D--IAILC---AELTGYCK S-----LSAEWLGVLKALCCSSNNGT	1107
AtMed12	LSMRDVLQRHVEEATHYLK--KLIGTGTMKASLAEKND DGYVAQQIVVGLMDCIRQTGG	1283
ZmMed12a	QNMKEIVQRQADGIQRSLKEKKVLAGAAPRNPLTFEKEDSYQIAHDI VGLVE CIRQNGG	1262
ZmMed12b	QNMKEIVQRQADEIQRSLKEKKVLA--TPRNPPTFEKEDSYQIAHDI VSGLVE CIRQNGG	1272
	: : * . * : * : * : *	
HsMed12	CGFN-DLL-----CNVD-----VSDL-----SFHDS---LATFVAILIAR	1138
AtMed12	AAQEGDPSLVSSAVSAIINSVGLS VARI TDFSLGNIYQNHPSGV DSSNIARYILRIHITC	1343
ZmMed12a	ANPDGDLIVASAVSAIVNAGHMIAKHLD FAGGN-YQGVNSVATSLNFVRHTLLIHINS	1321
ZmMed12b	ANPDGDLSTVASAVSAIVNAGHVI AKHLD FAGGN-YQGVNSVSNLNFVRHTLRHINS	1331
	. : * . . * : * * : : : *	
HsMed12	QCLLLEDLIRCAAIPSL LNAACSEQDSEPGARLTCRILLHLFKTPQL-----NPC--Q	1189
AtMed12	LCLLKEALGERQSRV--FEIALA---TES-----STAL TG VFAPVKGSRGQHQLSPESYD	1393
ZmMed12a	LCLLKETLGD RFSRA--FEIALA---VET-----SAAVTAAFAPPKMHRNQFQPSPEAHD	1371
ZmMed12b	LCLLKETLGD RFSRA--FEIALA---VET-----SGAVTAAFASPKMHRNQFQPSPEAHD	1381
	*** * * : : * : * . : * : : * : *	
HsMed12	SDGNKPTV GIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKG--SGFTVTGGTE	1247
AtMed12	SNANNSTIDMSNGTGK MALS--RATKI TAAVSALVIGSITHGVITLERIVGLLRLKDYLD	1451
ZmMed12a	AYGNHTSEL--SNSGKGFVG--RTAKVSAISALVVGAVVHGAVSLERMVATLKI KDGLD	1427
ZmMed12b	AYGNHTSDL--SNSGKGFVG--RTAKVSAAVSALVVGAVVHGAVSLERMVAALKI KDGLD	1437
	: *. : . : : : : * : * : : . . * * : . : : .	
HsMed12	ELPEEE---GGGSGRRQGGRNISVETASLDVYAKYV--LRSICQEQEWGERCLKSLCE	1302
AtMed12	FVQFVRRTKSSSNGSARSMGASKVE---SPIEVYVHWFRLLVGNCKTVSEG--LVLELVG	1506
ZmMed12a	IMQLLRGLKSN TNGVSHPTGGFIE--NSTEVSVHWFRI LLGNCR TVYDG--LIADILG	1482
ZmMed12b	ILQLLRGLKSSSNGVSRPTGTFRIE--HSTDVLVHWFRI LLGNCR TVYDG--LIADILG	1492
	: : * . . : * * . * : * : . :	
HsMed12	DSNDLQDPVLSSAQQR LMQ L-ICYPH-----RLLDNEDGENPQRQRIKRILQN	1350
AtMed12	ESS-----VVAISRMRMLPLKLVFP PAYSIIAFVLWRPFVSN SNSNSSVHEDTHRLYQS	1561
ZmMed12a	DPY-----I IALSRLQRLPLTVIFPPAYSIFAMVLWRRYIFNC-----EDPQLYQS	1529
ZmMed12b	DSY-----I IALSRLQQLPLSVIFPPAYSIFAMVLWRRYIFNR-----EDPQLYQS	1539
	: : : : : * : : * : * : *	
HsMed12	LDQWTMRQSSLELQ LMIKQTPNNEMNSLLENIAKATIEVFQQAETGSSSGSTASNMPSS	1410
AtMed12	LT-----MAFHDIKHL PFRDVC-----FRDTQGLYEL-----	1589
ZmMed12a	FS-----NAINDITRHQPFREIY-----FRNTHRLYNL-----	1557
ZmMed12b	LS-----NAISDITRHQPFREIC-----FRNTHRLYNL-----	1567
	: : : : * . . : * : : :	
HsMed12	SKTKPVLSSLERSGVWLVA PLIAKLPTS VQGHVLKAAGEELEKQHLGSSSSKERDRQKQ	1470
AtMed12	-----IVADSTDAEFASFVESHGL-----DMHLKS	1614
ZmMed12a	-----LASDVGDSKFAAMLESHSP-----DRNSKI	1582
ZmMed12b	-----LASDVGDEFAAMLETHSP-----DRNSKI	1592
	: . : . : : . : * .	
HsMed12	KSMSLLSQPFSLVLTCLKGDEQREGLLTSLYSQVHQIVNNWRDDQYLD DCKPKQLMH	1530
AtMed12	VAFAPLRARLFLNSLIDCKVPSSGY-----SHEGVSEAKNRHQGN--	1654
ZmMed12a	LPFIPLRARLFLDAI IDCNTPTIQG-----DGASEP-CDPKDN--	1619
ZmMed12b	LPFIPLRARLFLDAL IDCNTPTIQG-----DGASEP-CDPKDN--	1629
	: * : ** . : * : : :	


```

HsMed12      QGLQQTQQQQQ-----TAAQLVRQLQQQLSNTQPQPS---TNIFG----- 2175
AtMed12      SGTAAAQGKLKPTMLAPHQQQEADNTDVVDPW-TLLEDGTSSGLSSNA-----SNSSDM 2205
ZmMed12a     PT--NVSVRSK-----AALPSHDPETEVDPW-SLLEDGTNCPPSTASGSNGSSGVTGDH 2163
ZmMed12b     PT--NVSGRSK-----AALPSHDPEMEVDPW-NLLEDGTSCPS-TASGSHGASGVTGDH 2172
              .. : : * * : .

```

```

HsMed12      -----RY----- 2177
AtMed12      ANLRATCWLKGAVRVRRTDLTYVGSVDDDDS 2235
ZmMed12a     ANLKASSWLKGAVRVRRTELTYIGSVDDDDS 2193
ZmMed12b     ANLKACSWLKGAVRVRRTELTYIGSLDDDDT 2202

```

identical residues (*)
 highly conserved residues (same color) (:)
 semi-conserved residues (.)

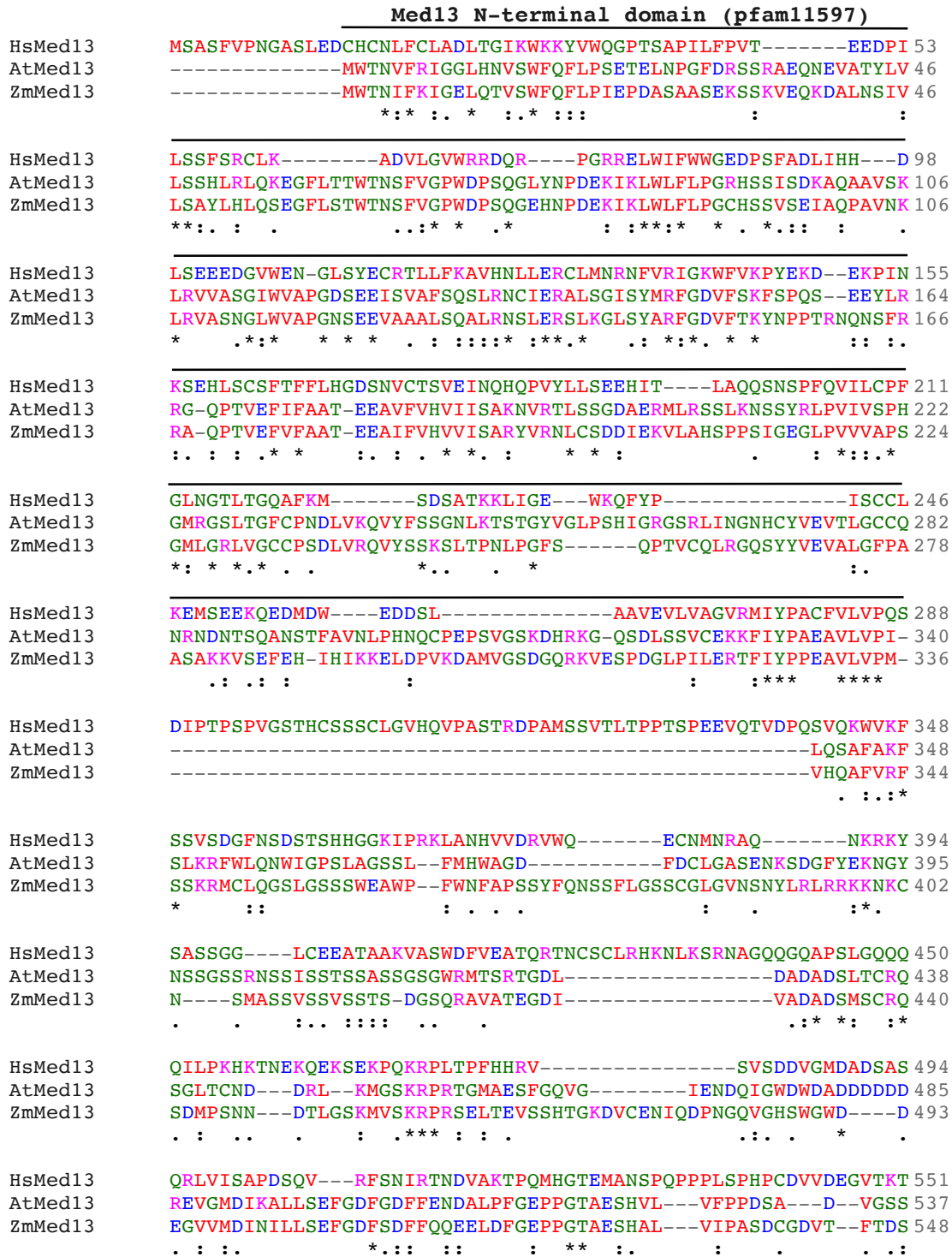
Colors:
 Red = Small and hydrophobic residues (AVFPMILW)
 Blue = Acidic residues (DE)
 Magenta = Basic residues (RK)
 Green = Hydroxyl + Amine (STYHCNGQ)

Percent Identity Matrix - created by Clustal 2.1

HsMed12	100.00	20.01	19.42	19.86
AtMed12	20.01	100.00	46.02	46.04
ZmMed12a	19.42	46.02	100.00	91.14
ZmMed12b	19.86	46.04	91.14	100.00

Alignment made with Clustal Omega <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Figure S4. CLUSTAL O (1.2.1) multiple sequence alignment of Med13 proteins from *Homo sapiens* (Hs) (NP_005121), *Arabidopsis thaliana* (At) (At1g55325.2), and *Zea mays* (Zm) (KP455662). The positions of the Med13 N- and C-terminal domains are indicated with black lines.



HsMed13 PSTPQSQH FYQMPTPDPLVPSKPMEDRIDSLSQSFPPQYQEA VEPTVYVGTAVNLEEDEA 611
AtMed13 PVD----- 540
ZmMed13 PST----- 551
*

HsMed13 NIAWKYYKFPKKKDVEFLPPQLPSDKFKDDPVGPFQESVTSVTELMVQCKKPLKVSDLE 671
AtMed13 -----MMDVSDQIVLPVGFSSFFESFN----- 561
ZmMed13 -----AMDIPEQR LSPVGF T TLD AFD----- 572
. . : : * . * : . : .

HsMed13 VQQYQIKNQCLSAIASDA---EQEPKIDPYAFVEGDEEFLFPDKKDRQNSE REAGKKHK 727
AtMed13 -PVPPIIDECLIKSQEVLHSSITVPSNQMSISSTGEFDHLLKAE-----AMMTFA 611
ZmMed13 -HQIMAPAQDVVAKVQEPHNDTATPAQSHSQVLSGRFDYLTKAE-----AKLTFA 622
: : . . * : . * : * . .

HsMed13 VEDGTSSVTVLSHEEDAMSLFSPSIKQDAPRPTSHAR--PPSTSLIYDSLAVSYTDLDN 785
AtMed13 PE--YGAVEAPMSE- ISSTFFKSPY----LPKSHKVESSNSPTS NYVYGATPPTTDSG 663
ZmMed13 PE--YAAVEILIAE-APTPLFTNPY----FPRSKKPGSSSF SARVYSYDVAQSSQ-IES 673
* . : * * : * : : :

HsMed13 LFNSEDELT P GSKKSANGSD-----DKASC KESKTGNLDPL-SCI STADLHKMYPT 836
AtMed13 ----AGDMILFGSKSCIGNNAGRTLYHSREHYTQVEGRKGRHDKLPTVISDN-----SST 714
ZmMed13 ----TGDKPKDKTSKLISGNHL--HDISSSNLYTLVQGGNKGSDKILKSTD T-----QPS 721
* ** : : : . * : . . :

HsMed13 PPSLEQHIMGFSPMNMNKEYGSM D T PGGTVLEGNSSS IGAQFKIEVDEGF CSPKPEI 896
AtMed13 KEGVSQSIHSHK-----SAANAVKVVQ GK---KTDGI 743
ZmMed13 KGELSPPI SGV-----TSFNFSLV SQK---KSGNM 748
: . * . : . . : * :

HsMed13 KDFSYVY--KPENCQILVGC SMFAPLKTLP SQYL PPIKLP EECIYRQSWTVGKLELLSSG 954
AtMed13 SAVVSTLLSSK TLLATDVGVSVMFQAFMCRMRHIITSSKHSSPVSLTRL SGNFFLNQLSNE 803
ZmMed13 FNAGYFLLSMKTALATEIECITFQAAMCRIRHTLLSLRSKASAEFNSATSSFIQT N VSNK 808
: . * : : : : : * .

HsMed13 PSMFPIKEGDGNSMDQEYGTAYTPQTHTSF GMPSSAPP SNSGAGILPSPSTPRFP TPRT 1014
AtMed13 PSTL---TDNISARNEIYK KDI-----PTR--IAGDFDGGMLDSHMSAPVGVWRT 848
ZmMed13 -----SDLTPRSLMDNVGVWRP 825
. : . . *

HsMed13 PRTPRTPRGAGGPASAQGSVKYENS DLYSPASTPSTCRPLNSVEPATVPSIPEAHSLYVN 1074
AtMed13 VSVPKTAKPASSPNIEAGSSL-----PHSSFSEDSLLSYGQRQPLQDLLDGIALLVQ 900
ZmMed13 VVTPKGPKSL ELSL-----ANTLTGAS PSLSIQRQPVDLLCAMTLLVQ 869
.* : : . : : : : . : * * :

HsMed13 LILSESVMNLFKDCNFDSCCICVCNMNIK GADVGVIYIPDPTQEAQYRCTCGFSAVMNRKF 1134
AtMed13 Q-----ATSFVDLALDSDCG-----DGPYGLWALEELWRR--ELSCGPSAG----- 939
ZmMed13 Q-----STSFVMSLDMDDG-----DGSFFWLSLDEQKRR--GFSCDPSMV----- 908
. * * : * . : . * *

HsMed13 GNNSGLFLEDELDIIGRNTDCGKEAEKRFEALRATS AEHVNGGLKESE-----KLSDDLI 1189
AtMed13 -----HAGCGGT LA-----SCHSLDIAGVKLVDP LSAEVFPSSVI 974
ZmMed13 -----HAGCGLLG-----TCHSKDCAGVDLVDPLSAEVSEPSMI 943
. : ** : . . . * . : :

HsMed13 LLLQ-DQCTNLFSPFGAADQDFPKSGVISNWVRVEERDCCNDCYLAL EHG RQFMDNMSG 1248
AtMed13 TLLQSDIKTALKSAFGQSDG-P---LSVTDWCKGRNQSGDG-----GSI SEGFTAE--- 1021
ZmMed13 SLLQSDIRVALKAAFANMDG-P---LSVIDWCRGRGNAES-----AGTGDAYSFYQYSS 993
*** * . * : * . * * : : * : . . : :

HsMed13 GKVDEALVKSSCLHPWSKRNDVSMQCSQDILRMLLSLQPV LQDAIQKR TVRPWGVQGPL 1308
AtMed13 -S-----ALSEVSNAI-----DGGKGD ETAQ----- 1041
ZmMed13 GD-----ILEPSSLS-----IGGDSMSPPQPTSSNRGI 1022
. * * . . :

HsMed13 TWQQFHKMGARGSYGTDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLLEPYGSQRD 1368
 AtMed13 --SQDI----YSSELLRPTLFVLPSPAILVGYQDDWLKISTNSLTHWEKAPFEPYALPKS 1095
 ZmMed13 SELEFQ----KGYHRVPRPTIAVLPSPSMLVGYQDDWLKASVNSLKTWEKAPFEPYALPKP 1078
 : . : ** *:*:*:*:* * : * ** : :***. :

HsMed13 IAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLTLDGIMRV 1418
 AtMed13 INYAVVCPDIDPLTCAATDFQQLGTVYETCRLLGTHLPQSLGNQMEKDVGRLLLLSSSGFVLL 1155
 ZmMed13 VTYIALCPDIDMLTSAVADFFMQLGTVYEVCKLGTHTSPQNNGGQMEKLSPKYLPVSGLVLV 1138
 : * .:***: : * .. .** : * :*:** * * * . .***: :

HsMed13 GSTASKKLEKLVAEWFSQAADGNNEAFSKLKYA--QVCRYDLGPYLASL-----PL 1469
 AtMed13 DCPQSMKIE-----SNNTSLLGSLSDYFLSLNNGWVNSYKLSLKALKGLKL 1203
 ZmMed13 DCPEQLKKVR-----CGHLGPISSTSDCLQAFSKHWSVKSFVTSISRILKDIKL 1187
 . . * . :. . :. : : * : *

HsMed13 DSSLLSQPN-----LVAPTS-----QSLITPPQMT-----NT 1496
 AtMed13 GSGLYTNQKEGSGSPCVVYIVCPFPDPSAVLRTIVESSIALGSVIQSDRDRSILNSQV 1263
 ZmMed13 TSNISTNQKESSSGPCTVIYVVCFFPEPCAILQTLVECSVALGYVISSPERERKLLYSQV 1247
 * : : : : :*.* : * . :. :

HsMed13 GNANTPSATLASAASMTVTVTSGVAISTSVATANSTLTASTSSSSSSNLNSGVSSNKLP 1556
 AtMed13 ARAFSSSTAVDEASISHIPVLSGFSVPKLVQVVSVDSE-----IFRITSP 1308
 ZmMed13 AKALNSSASVDEASASNVVLSGFSIPKLVQIVTIET-----VLRMDKP 1292
 ..* . *::: .*: * : : **::: . * : : : *

HsMed13 SFPPFGSMNSNAAGSMSTQANTVQSQGLGGQQTALQTAGISGESS---SLPTQPHPDVS 1613
 AtMed13 SFNELVILKDTAF-SVYNKARRISRGMP---NDAFFSSSL-PSRSS-SALTPMNSISGI- 1361
 ZmMed13 N-KELAVLKDI AF-TVYNKARRIPRAVS---TSDMFQSPTYLGRSQSTMHVTSAPATL- 1346
 . : :. * : :.*. : . :. :. :. : :

Med13 C-terminal domain (pfam06333)

HsMed13 ESTMDRDKVGIPTDGDHAVTYPPAIVVYIIDPFTYENTDESTNSSVWTLG---LLRCF 1670
 AtMed13 ---WKC CGSRMTGSTHPRDG-----EIDVSLRTSGWDTSTSWQIPRSGGLSCD 1407
 ZmMed13 ---WKECLVPRMSGPTLSRET-----DFDASMRSATWDN--SWQPARSGGL-LD 1389
 : : * : : . :. * *

HsMed13 LEMVQTLPPHIKSTVSVQIIPCOYLLQPV-----KHEDREIYPQHLKSLAFSAFTQCRR 1724
 AtMed13 PNRN---G-----DFYL-NDEIFYLFEPLFILSEPGSVERGVSPFTFS-----LGSESSK 1453
 ZmMed13 PSKL---P-----DLCA-QDDRYAFEPFLILADPGSADLNALMEPSK-----SGADA-- 1433
 . . * :*: : . . :. :

HsMed13 PLPTSTNVKTLTGFGPGLAMETALRSPDRPEICIRLYAPPFILAPVKDKQTELG-ETFGEA 1783
 AtMed13 PIPED---GGGSGPGMNSMEGITSGSS-----SQG---DVSQLE 1487
 ZmMed13 -----SG---SRVYGSISGSN-----SDSGVSPLLDVSE 1459
 * . * . :. :

HsMed13 GQKYNVLFVGYCLSHDQRWILASCTDLYGELLETCIINIDVPNRARRKSSARKFGLQKL 1843
 AtMed13 GKAIPLSHCCYGWTEWRWLVS IWT DARGELL DTHIFPFGGISSRQDTKGL-QCLFVQVL 1546
 ZmMed13 SDSAASLHCCYGWTEWRWLVC IWT DARGELLDSLIFPFGGISSRQDTKVL-QSLFIQIL 1518
 .. * . * :.* **::. ** *****: * : . : . * : : : * *

HsMed13 WEWCL-----GLVQMSSLPWRVVIGRLGRIGHGELKD-----WSCLLSR 1882
 AtMed13 QQCQILQACSSPDNGSFKPRDFVITRIGNFFELEYQEWQKAIYSAGGPEIKKWPIQLRR 1606
 ZmMed13 QQCQIMS--SSPEASNMRPRDVIITRIGGFLELEIQEWQKAIYSYGGNEVKKWVQLRR 1576
 : * . . * .:* *:* : . * : : * *

HsMed13 RNLQSLSKRLK-----DMCRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGVS 1935
 AtMed13 SAPSGIATNSNGSSLQQQ---DLSLIQERAS--STSTLYSSHKQSTFVKGS---MGQS 1657
 ZmMed13 SIPEGIPPSNGPTLQQQQQQDMALIQRNMPSSPNPLYSPHP-KSSFMKGA----LGQS 1631
 .: : : . * . :. : * : *

```

HsMed13      FGRSTLLNQTSQLNTPQDT--SCTHILVFPPTSASVQVASATYTTENLDLAFNPN---NDG 1991
AtMed13      AGRKQIMGGQ-TISGTPRGLFQVHHSISFA---SISLDHSLHFVLPALVLSAGG---GQS 1710
ZmMed13      GNKKQILVEQ-SGMDTSRGSLLHLVRSISLV---AVSQDHSLLHLTCQADLLSRPASAGEGS 1687
              :. : * : * : . : : : : : : : : : *
              -----
HsMed13      ADGMGIFDLLDTGDDLDPIINILPASPTGSPVHSPGSHYPHGGDAGKGQSTDRLSTE- 2050
AtMed13      STGMSSVNYIEGFTPVK--SLGST--AFSYMMIPSPNMRFLHPSPLQL---PTCLTAESP 1763
ZmMed13      QGSSGPWSYLEGFTPVK--SIGSMSASHSYLLVPSPSMRYLSPATLQL---PTCLTSESP 1742
              . . . : : : : : : * : : . * : .
              -----
HsMed13      --PHEEVPNILQQPLALGYFVSTAKAGPLPWFWSACPQAQYQCPLFLKASLHLHVP-- 2106
AtMed13      PLAHLHLSKGYAIPSTGFVSVKAVPSMRKDSR----INVKEEWPSVLSVSLIDYGGYD 1819
ZmMed13      PLAHLHLSKGTAIPLAMGYVSVKAVPPVRRDSA----QLTKDEQPSVLSVSIIDHYGSS 1798
              * : ** : * . * . * * : : * . * . * : : .
              -----
HsMed13      VQSDELLHS-----KHSHP-----DSNQTSDVLRVLEQYNALSWLTCDPATQ 2150
AtMed13      NAHDKILQGIKQGGGKE-----TRDFEVESHLLIESIAAELHALSWMTVPAYL 1870
ZmMed13      GTVQEKMSR--GGGGGSKQARNLSQETTGRECEMEMHSVLEAVAAELHLSWLTVPVYT 1856
              : : : * . . : : * . : : . : * * : * . *
              -----
HsMed13      DRRSCLPIHFVVLNQLYNI--MNML----- 2174
AtMed13      DRRRTALPFHCDMVLRLRRLRHAFADKEVSRIPDKTGLKVLTTDSGSQSLMSLPRDHLGI 1930
ZmMed13      ERRRTALPFHCDMVLRMRRLLHYADKYLSEPKGETTH----- 1892
              : * : * : * : : : : : : : : :
              -----
HsMed13      ----- 2174
AtMed13      CFQHTDCNFLRCCSPFLSGHIRRDGEQVNGQIKTAAIYYGVSLFPGKIDNLNAMVWSHSC 1990
ZmMed13      ----- 1892

HsMed13      ----- 2174
AtMed13      CRPLSSMHHMA 2001
ZmMed13      ----- 1892

```

identical residues (*)
 highly conserved residues (same color) (:)
 semi-conserved residues (.)

Colors:
 Red = Small and hydrophobic residues (AVFPMILW)
 Blue = Acidic residues (DE)
 Magenta = Basic residues (RK)
 Green = Hydroxyl + Amine (STYHCNGQ)

Percent Identity Matrix - created by Clustal 2.1

HsMed13	100.00	22.49	20.33
AtMed13	22.49	100.00	49.37
ZmMed13	20.33	49.37	100.00

Alignment made with Clustal Omega <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Figure S5. CLUSTAL O (1.2.1) multiple sequence alignment of *Zea mays* (Zm) *ZmMed12a* (KP455660), *ZmMed12b* (KP455661), and *Sorghum bicolor* (Sb) *SbMed12* (XP_002466024) (Sb01g050280).

CLUSTAL O(1.2.1) multiple sequence alignment

ZmMed12a	---MQRYAGFSGSRD GARLEASPFSSSSSSSGYPVSSRRQQQLTPYK LKCDKDPLNNKLG	56
ZmMed12b	MHRYSSNSAGFSGGRD GARLEASPFSSS-SSGYPVSSRRQQQLVPYK LKCDKDPLNNKLG	59
SbMed12	MQRYAGNSAGFSSGRDAARSESSPFSSS-SSGYPVSSRRQQQLAPYK LKCDKEALNNKLG	59
	. ****. . * . * * * :***** *****.*****: *****	
ZmMed12a	PPDFYQP TLNCP EETLT KDYVQYGYKETVEGIEEAREIVISQIPYFC KPDVVIKCKEALK	116
ZmMed12b	PPDFYQP TPNCP EETLT KEYAQAGYKETVEGIEEAREIVLSQIPYFC KPDVVIKCKEALK	119
SbMed12	PPDFYQP TPNCP EETLT KEYAQAGYKETVEGIEEAREIVLSQIPYFC KPDVVIKCKEALK	119
	***** *****: * . * *****:*****:*****:*****	
ZmMed12a	KRLRAINESRAQKRKAGQVYGVPLSGSLLIKPGVYPEQRPCNEDTRRKWVEALAQPNKRL	176
ZmMed12b	KRLRAINESRAQKRKAGQVYGVPLSGSLLIKPGVYPEQRPCNEDARRKWIEALAQPNKRL	179
SbMed12	KRLRAINESRAQKRKAGQVYGVPLSGSLLIKPGVYPEQRPCNEDARRKWAEALAQPNKRL	179
	*****.*****:***** ***** *****	
ZmMed12a	RSLSEHVP HGYRRKSLF EGLIRYNVPLLRATWFIKVTYLNQA--RPAPNSTSVVASDNQR	234
ZmMed12b	RSLSEHVP HGYRRKSLF EGLIRYNVPLLRATWFIKVTYLNQLQTRQTPNSISVAGSDNQR	239
SbMed12	RSLSEHVP HGYRRKSLF EGLIRYNVPLLRATWFIKVTYLNQLQTRQTPNSISVAASDNQR	239
	***** ***** * :*** ** .*****	
ZmMed12a	SNQWTKD VVEYLQQLILDEVC SKEGAVPPSFK EQSSPGLAAGTNQIKMKT EESSP-AGDSE	293
ZmMed12b	SNQWTKD VVEYLQHILDEFCS KEGAVVHPSFREQSSPGPTAGTNQIKMKT EASPAAGDIE	299
SbMed12	SNQWTKD VVEYLQQLILDEFCS KEGAVVPPSFK EQSSPGLAAGTNQIKIKT EASPAAGDSE	299
	*****:*****:***** * ** :***** :*****:*****:*** ** *	
ZmMed12a	EPLVHFKWR YMVRLIQWHLTEELLVPSV LIEWLSNQLQERDSDDVLELLLP IILGLVDTI	353
ZmMed12b	EPLVHFKWR YMVRLIQWHLTEELLVPSV LIEWLSNQLQERDSVDVLELLLP IMLGLVDTI	359
SbMed12	EPLVHFKWR YMVRLIQWHLTEELLVPSV LIEWLSNQLQERDSVDVLELLLP IMLGLVDTI	359
	***** ***** ** :*****:*****	
ZmMed12a	TLSQTYVRMFV ELLVRRLN---VDRPKRF SVSSVIAELLRYMVLAVPDTFVSLDCFPPF	409
ZmMed12b	TLSQTYVRMFV ELLVRRLNDASVVDSPK GPSVSSVIAELLRYMVLAVPDTFISLDCFPLP	419
SbMed12	TLSQTYVRMFV ELLVRRLNDASVADSPK RPSVSSVIAELLRYMVLAVPDTFVSLDCFPLP	419
	***** ***** . * ** *****:*****:*****:*	
ZmMed12a	SFVVPDVYGR GALLKITSGGGILCSKRRDAYRYLSCGYAVSSI QKRAHDLAAVANPSLQA	469
ZmMed12b	SFVVPDVYGR GALLKITSGGISSKRC DAYRYLSCGYAVCSI QKRAYDLATVANPNLQA	479
SbMed12	SFVVPDVYGR GALLKITSGGGISSKRRDAYRYLSCGYAVCSI QKRAYDLATVANPNLQA	479
	***** ***** . *** .*** *****.*****:***:****.***	
ZmMed12a	RGAQVQALDKALVTGNLSVAYFSLFN DLSDALMEERWIK EVNPCLQSSLMWIGTVELS	529
ZmMed12b	RGAQVQALDIALVTGNLSVAYSSLFN DLSDTLMEERWIK EVSPSLQSSLMWIGTVELS	539
SbMed12	RGAQVQALDKALVTGNLSVAYSSLFN DLSDALMEERWIK EVSPCLQSSLMWIGTVELS	539
	***** ***** *****:***** ***** . * *****	
ZmMed12a	LICSIFFLCEWATCDYRDCRASPSQNVKFTGRRDLSQIHMAVSILKNKMD EMMNLSRPSKS	589
ZmMed12b	LICSIFFLCEWATCDYRDCRASPSRNKFTGRRDLSQIHMAVSILKNKMD EMMNLSRSKS	599
SbMed12	LICSIFFLCEWATCDYRDCRASPSQNVKFTGRRDLSQIHIAVSILKNKMD EMMNLSRSKS	599
	***** *****:***** *****:***** ***** *	
ZmMed12a	STRITLNVK VAKG-SLNDA CLTAAAVDDSSGLRSNAKNVDEK KDTNDIFESPGLHDIIVC	648
ZmMed12b	STRVTLNNTK GSSLTDA CLTAAAVDDTSGLQSNAKNVDEK KDTNDIFESPGLHDIIVC	659
SbMed12	STRVTLNNTK GSSLTDA CLTAATADDSSGLRSKAKNVDDK KDTNDIFESPGLHDIIVC	659
	: . : * * * .*****: * * :***: * :*****:***** *****	

ZmMed12a	IMQLLRGLKSNVTNGVSHPTGGFRIENSTEVSVHWFRIILLGNCRTVYDGLIADILGDPYII	1487
ZmMed12b	ILQLLRGLKSSSNGVSRPTGTFRIEHSSTDVLVHWFRIILLGNCRTVYDGLIADILGDSYIL	1497
SbMed12	ILQLLRGLKSSSNGVSRPTGTFRIENSTEVSVHWFRIILLGNCRTVYDGLIADILGDSYIL *:	1497
ZmMed12a	ALSRLQRMPLPTVIFPPAYSIFAMVLWRRYIFNCEDPQLYQSFNSAINDI TRHQPFREIY	1547
ZmMed12b	ALSRLQQMLPLSVIFPPAYSIFAMVLWRRYIFNREDPQLYQSLNSAISDI TRHQPFREIC	1557
SbMed12	ALSRLQQMLPLSVIFPPAYSIFAMVLWRRYIFNREDPQLYQSLNSAISDI TRHQPFREIC *****:	1557
ZmMed12a	FRNTHRLYNLLASDVGDSEFAAMLESHSPDRNSKILPFIPLRARFLDAIDCNPPTIQG	1607
ZmMed12b	FRNTHRLYNLLASDVGDSEFAAMLETHSPDRNSKILPFIPLRARFLDALIDCNPPTIQG	1617
SbMed12	FRNTHRLYNLLASDVGDSEFAAMLESHSPDRNSKILPFIPLRARFLDALIDCNPPTIQG *****:	1617
ZmMed12a	DGASEPCDPKDNEKLSERLMQLLDTLQPAKFHWQVEMRLLLDQALMEKVAAGKTILE	1667
ZmMed12b	DGASEPCDPKDNEKLSERLMQLLDTLQPAKFHWQVEMRLLLDQALMEKVAAGKTALE	1677
SbMed12	DGASEPCDPKDNEKLSERLMQLLDTLQPAKFHWQVEMRLLLDQALMEKVAAGKTALE *****:	1677
ZmMed12a	SLRSLSPKAEFGFALSDEKGFTEVILSRLLARPDAAPLYSELVHLLGKLQESLVM DVKWI	1727
ZmMed12b	SLRSLSPKAEFGFTLSDEKGFTEVILSRLLARPDAAPLYSEAVRLLGKLQESLVM DVKWI	1737
SbMed12	SLRSLSPNAEFGFALSDEKGFTEVILSRLLARPDAAPLYSEVVHLLGKLQESLVM DVKWI *****:	1737
ZmMed12a	LQGQDAILGRRSTRQQLVHIAQRKGLSTKAQVWKPWGSSLLSDAIPNKTAKRKLEVTSI	1787
ZmMed12b	LQGQDAILGRRSTRQQLVHIAQRKGLSTKAQVWKPWGSSLLSDVIPNKTAKRKLEVTSI	1797
SbMed12	LQGQDAILGRRSTRQQLVHIAQRKGLSTKAQVWKPWGSSLLSDVIANKAAKRKLEVTSI *****:	1797
ZmMed12a	EEGEVDDTVDAKRRTKTPPHSVDRSFEGRSINKYLTEKALAEVLVPCIDRSSADIRGI	1847
ZmMed12b	EEGEVDDTVDAKRPSKTPPHSVDRSFEAIRSINKYLTEKALAEVLVPCIDRSSADIRGI	1857
SbMed12	EEGEVDDTVDAKRPSKTPPHNVDRSFDAIRSINKYLTEKALAEVLVPCIDRSSADIRGI *****:	1857
ZmMed12a	LSVDLTKQMGAISEHIKAIARNGAKQAGSVSSGNEVPSNKS SGRGIRGGSPNIGRRAPV	1907
ZmMed12b	LSVDLIKQMGTISEHIKAIARNGAKQAGSVPSGNEVPSNKS SGRKIRGGSPNIGRRAPV	1917
SbMed12	LSVDLIKQMGAISEHIKAIARNGAKQAGSVPLGNEVPSNKS SGRKIRGGSPNIGRRAPV *****:	1917
ZmMed12a	GNDPSPPSASALRAALWLRQLFII RLLPVIMADRS MRHTLASAILGLLATRMIYEDADLP	1967
ZmMed12b	GNDPSPPSASALRAALWLRQLFII RLLPVIMADRS MRQTLASAILGLLATRMIYEDADLP	1977
SbMed12	GNDPSPPSASALRAALWLRQLFII RLLPVIMADRS MRQTLASAILGLLATRMIYEDADLP *****:	1977
ZmMed12a	LPPTNATALRRDVDSLLEPPLDVLLDRPGE SLFERLLCVLHALLGSYKPSWLKRSASRS	2027
ZmMed12b	LPPTNATALRREVDSLLEPPLDVLLDRPGE SLFERLLCVLHALLGSYKPSWLKRSASRS	2037
SbMed12	LPPTNANALRREMDLLEPPLDVLLDRPGE SLFERLLCVLHALLGSYKPSWLKRSASRS *****:	2037
ZmMed12a	SIKSQRDFS AFDNEAAEGLQSALDHMELPETIRRRIQ AAMPLPPSR RHPMOCQPPQLSL	2087
ZmMed12b	TIRIQRDFS AFDNEAAEGLQSALDHMELPETIRRRIQ AAMPLPPSR RHPSLQCQPPQLSL	2097
SbMed12	TNRTQRDFS AFDNEAAEGLQSALDHMELPETIRRRIQ AAMPLPPSR RHPMOCQPPQLSL : : *****:	2097
ZmMed12a	AALSPLQSSTSGVGPQQKSSCVSWVPTNVSVRSKAALPSHDPETEVD PWSLLEDGTNCPP	2147
ZmMed12b	AALTPLQSSTSGVGPQQKSSCASWVPTNVSGRSKAALPSHDPEMEVD PWNLLEDGTSCPS	2157
SbMed12	AALTPLQSSTSGAGPQQKS-SVSWVPTNVSSRSKAALPSHDPEMEVD PWNLLEDGTSCPS ***:	2157
ZmMed12a	STASGNSGSSGVTGDHANLKASSWLKGA VRVRTELTYIGSVDDDS	2193
ZmMed12b	-TASGSHGASGVTGDHANLKACSWLKGAVRVRTELTYIGSLDDDT	2202
SbMed12	-TTSGNSGASGVTGDHANLKACSWLKGAVRVRTELTYIGSLDDDS *:	2201

identical residues (*)
highly conserved residues (same color) (:)
semi-conserved residues (.)

Colors:

Red = Small and hydrophobic residues (AVFPMILW)

Blue = Acidic residues (DE)

Magenta = Basic residues (RK)

Green = Hydroxyl + Amine (STYHCNGQ)

Percent Identity Matrix - created by Clustal 2.1

ZmMed12a	100.00	91.14	91.73
ZmMed12b	91.14	100.00	95.23
SbMed12	91.73	95.23	100.00

Alignment made with Clustal Omega <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Figure S6. Scatterplot of tissue-specific expression in log₂-FPKM+1 for pairwise combinations of the different members of the CDK8 module. The red dashed lines represent the linear regressions, and *r* the corresponding Pearson correlation coefficients for each pair of genes (p value for each *r* in parentheses). The solid black lines represent the one-to-one expression ratio for any given gene pair. Tissue samples are the same as shown in Figure 3.

