Supplementary Material

Table S1 Specific primer of 32 RcBBX members used in this study.

Table S2 Protein sequences of 32 RcBBX proteins.

Table S3 BBX protein sequences used to construct the phylogenetic tree.

Table S4 Domain organizations of BBX proteins in *R. chingii*.

Table S5 The 44 anthocyanin biosynthetic enzymes in *R. chingii*.

Table S6 Correlation between RcBBX26 and anthocyanin biosynthetic genes.

Figure S1 Semi-qRT-PCR analysis of MOCK and *RcBBX26* in transgenic *R. chingii* leaves.

Figure S2 Analysis the transcript level of anthocyanin biosynthetic genes in transgenic *R. chingii* leaves. Asterisks indicate significance between MOCK and *RcBBX26* based on the student's *t*-test at $p < 0.01$.

Table S1

Gene ID	Forward primer (5′ to 3′)	Reverse primer (5′ to 3′)
RcBBX1	CGCAAGTGCTTCCTCAAATG	GCTCCGCATCTATATCGTAAGG
RcBBX2	GATCGACGGTATGGGAAGAAAG	TAAACGACCAGCACTGTAACC
RcBBX3	AGGTGAGACCAGAAGAGTACAA	CATCATCACTGGCATCCGATAG
RcBBX4	GTCGGCAGTATGGTGATTCTAA	TCATCAGATCGCCTACCATTTC
RcBBX5	TACCTTCCCATCGTCTCCATAG	GAACACCACTTTGGCGTTATTG
RcBBX6	TACCAAGCACCCAACAACTC	CTTGGGTGTAACGGGTCTAATG
RcBBX7	GAAGCAGCGTGTCTGTGATTA	GACTTCTCGGTCGCAAGTAAAG
RcBBX8	ACGAGCACTGCTTCGAAAT	TCCAGTGACGATGAGGATACA
RcBBX9	TCAGCAGGACAGAGCAATTC	CAGAGGTAGCAGAGAGCTTAAC
RcBBX10	CCGAGTTCACCATGCCAATA	CATGCCTTTCCTGGCAGATA
RcBBX11	CGCAGGAAGAACGAGAAGAA	AACCTGAAGTAGAGGGTGAGA
RcBBX12	CAGAGCTTTGGCTACATGGATA	TGCACTCATAATCCTCCTGTTC
RcBBX13	GGAAGACGATGAGGATGAGAAC	CGCTTCACTATCCGAAGAACA
RcBBX14	CCACCAGGCTCAACTTCTTTA	CCTGCGCTTACATGGATATGA
RcBBX15	TCCACAGCCTTCTTCTCTATCT	GCCTCGATGATCTGCAGTAAA
RcBBX16	CTCCGAACGGTAGGAACAAA	CTTGCCTTCCTCGACTCATATC
RcBBX17	GGCATTGACCTCCACTTGTA	GGCATGTGATGTTGGCATTT
RcBBX18	GTGCCAAATGCGATGTTGAG	GTCGCATCTAGGGAGTTTGTT
RcBBX19	GTTCTATCTGCCACAGGAGTTT	CTGCTCCCATTTCCTCGTTAT
RcBBX20	TCAGCCGAGTCAATCGTTAAG	TGAGGTTCGGAATGAGGAAAG

RcBBX21	GCGGGTTTGTTACCGAATTAC	CATCAAGCCCTCTGCCTAATA
RcBBX22	CAACCCTGTCATTCTCTGTCTC	CCGAGTGTCCAACATCCATT
RcBBX23	CCGTGTGACGAGTTGGATAA	CAGTCCTCATCAAGTCCCTTAC
RcBBX24	GCAACTCACAACCAGCATTAG	GTGTTTGCCTCTTGTGTGATG
RcBBX25	CCAGGAGACTGTTGGTTACTTC	ACGAGTTCGCTGTGTGTATG
RcBBX26	CTGTGTCTCTAGCACCGAATC	AGCATCCCAAGCCTTTCC
RcBBX27	CAACAACAAGGAGGGAGGAA	CTTGTAGTTGAAGGAGGTGGAG
RcBBX28	GCCAAGTGTGCAACTCAAAG	AGCATTGGCCGAGTGAAT
RcBBX29	CTGCTGAATCCCGTGAAGAA	ACCTCCACTCCGAAGAAGAA
RcBBX30	GTCAACAATGGCGAGAGAGA	AAATCGTCCTGAGAGCGAAG
RcBBX31	GAACCTTGGGACTCTACTTTGG	CTGGCCTTTCTAGAGGCATATC
RcBBX32	AAGCCTGCAAGACCCTTATC	CAGCACACCGTCGTCTAAA

Table S2

Protein name	Amino acid sequences
RcBBX1	MGSRKEEERNEKIIRGLMKLPPNRRCINCNSLGPQYVCPNFWTFVCTTC SGIHREFTHRVKSVSMSKFTSQEVEALQNGGNQRAREIYLKDWDLQRQ RLPDSSKVDKIREFIRSVYVDRQYAGGRTSEKPPRDLQNHRIREDETRR ASSYHSYSQSPPYDYQYEDRRYGKKAAALTRKPGSDRGRYEGKLSSFG YSAGRLSDQMYEDRFENDGSGSIVSDYSVSSGGDASRSGVQSPNFQKD IGSSSPSFQPSQDTISEVRCQAKSTVLETNVNRDAEAKPFSQRTVSSGSF GSVDSYSMSVKSFNSGGLTDAVSEPDQYAGTLQAKPTSLSSLFGSSDRL DLFKAPVQQEISSAASSVDLFQLPAASSSLSIHSFQPSVLSSASSLNVHQP PQALTPSLELFADFPQHQSPAKQVQESVPKNEGWATFDTHQPSTSISGT ENIIPANIASNDGGSIGNFDLFSSSNPGMQWPSFENISNPWSDNLHDFTA PNTTESTQSWNAFEDSIGHFSLEGTKKSGESVGTDKLLSAGDQYMGVR ISEDSSKDGIQRAASEGEPHDPSLPLHILGPPYTPQVLPQMGEIKSDATN HRSNNPFDIPYDIDAEQTNMFFDISSLQASLPNAPLQSSFLSDISQPWFPQ NAATVMPYIPAAVEGGLTYLAGQAQSTQIPNVSTQGPVASIGGNPFA
RcBBX2	MGSRKEEERNEKIIRGLMKLPPNRRCINCNSLGPQYVCPNFWTFVCTTC SGIHEFTHRVKSVSMSKFTSQEVEALQNGGNQRAREIYLKDWDLQRQR LPDSSKVDKIREFIRSVYVDRQYAGGRTSEKPPRDLQNHRIREDETRRA SSYHSYSQSPPYDYQYEDRRYGKKAAALTRKPGSDRGRYEGKLSSFGY SAGRLSDQMYEDRFENDGSGSIVSDYSVSSGGDASRSGVQSPNFQKNI GSSSPSFQPSQDTISEVRCQAKSTVLETNVNRDAEAKPFSQRTVSSGSFG SVDSYSMSVKSFNSGGLTDAVSEPDQYAGTLQAKPTSLSSLFGSSDRLD LFKAPVQQEISSAASSVDLFQLPAASSSLSIHSFQPSVLSSASSLNVHQPP QALTPSLELFADFPQHQSPAKQVQESVPKNEGWATFDTHQPSTSISGTE NIIPANIASNDGGSIGNFDLFSSSNPGMQWPSFENISNPWSDNLHDFTAP NTTESTQSWNAFEDSIGHFSLEGTKKSSELVGTDKLLSAGDQYMGVRIS EDSSKDGIQRAASEGEPHDPSLPLHILGPPYIPQVLPQMGEIKSDATNHR SNNPFDIPYDIDAEQTNMFLDISSLQASLPNAPLQSSFLSDISQPWFPQN AATVMPYIPAAVEGGLTYLAGQAQSTQIPNVSTQGPVASIGGNPFA
RcBBX3	MRTLCDSCESAAAIVFCAADEAALCRACDEKVHLCNKLASRHVRVGL ATPSAVPRCDICENAPAFFYCEIDGSSLCLQCDMVVHVGGKRTHGRYL VLRQRVEFPGDKPGNIVEDPPSQPIDPGETRRVQHQQPRMTIGENHQNH RTSPIRLSDASDDGHVKMDNKLIDLNMKPNRMHGQASNKEDQ
RcBBX4	MNLTRTATVRELLHLQRIEEVRMANRVKEDEKNERIIRGLLKLPENRR CINCNSLGPQYVCTNFWTFVCTNCSGIHREFTHRVKSVSMAKFTSQEV KSLQEGGNQRAKELYLKELDPQRNSFPDSSNVERLRDFIKHVYVDRRY TGERNFDKPPRVKMGDKEDSYENRRLDYHGGSRSPPYDDERRYSERSS PGGRSYEEQRSPGYDQESRQYGDSKRSPSRPEIVNDWRREDRFGNGRR SDDRRISDGDSKLDAKSPERPRDINSSSPPMVRPVRDILGEKTIPLRIIEPP KANSVRATDGSVVTQRTASSSSLGSANGNPVEVKLETSGSLIDFDADIE PASAAAVPQAQQTSVTQSYSQPVNSDSDTNWASFDVAPQVKVSQAPA NANSLESLLSQLSVSAPVPSYVSGTAGNTGAFTAAGQMTAPFSGNSVIT PVGHTMLPTATGSHTIAPVTSLSTFPPVGAPVAAPGLAQIFPANAGNFP ATGSGQWPNMPHQQPSLFPSNGLQSASQQYIPSVGGASSNQPWNLAH APNAQVQPSNPATQAPQHVSRSIHNVSTIASQPSAGDVKSIGRSELPAD

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RcBBX6	MGNRIKEEEKIERIIRGLLKLPENKRCMNCNSMGPQYVCTTFLTFVCTN CSGVHREFTHRVKSVSMAKFTAEEVSSLQAGGNERARQIYFKEFDPQY HSFPDSSNINRLRDFIKHVYVDRKYTGERSVQKLPRLRLSEEPDESRKV GAYHGGSRSFHDEERKVGAYYGGSRSFRDEDWKVAVPYGGSRSFRDH EDRFEQNYSQGSSPSVRDQNKKSSILSRKFKKRRFQEKPLRFEVVDNRI RDDRKARSGFPTGESRSQSRTPENKKNMDSSSFPVARFVKGKPGENEL PPQVGEISIANDQKHADGSAHNQKMKSMSSHDGNAVELKSQPQQIPPL NNDSNWASFESSTKENASQVPKPDTLESLLFELSTPTSVPAITASEAPSN DDAPSTACTNNMSAGGVASDAPAEQMLSLFDTVCASTSSSISTSVPVQP SDAGHLQALPTSGGDTSVRVTDAQQLPSTQQDQYSISFASESGFTSQHT VTPVGASNGLSRTSSLAPNTQGSLSVSAETPSQSMLRTQSLPVETKSSE REELPVDLFAASYSSIPSQASGWHNGPPHGMGFHMQYYPNIEPIDILVS FTACSCISGSRKPTNPFDLNDNKSVVPSTHFPSMSSVEDALHNVSVPPSL MHTSSLGSYSSHLKPPQSPSHESMMPSHSLPSYASFSPSMGEQLHNNAQ FLRPHEIGGFSSNEAAVFGNLSTSQQPSIRYQAPNNSETFSPMGERGTTL YTNCIRPVTPKINIINPVVTPAAIISGIPKSGPFVNAEATNGLHGLDGHW DAVYGTTNNVVVPDENQCCTHVKVLS
RcBBX7	MDGSKEGGGGGGHQNMRAQKQRVCDYCGDSMALLYCRADSAKLCF TCDREVHSANQLFSKHTRSQLCDACDKAPASIFCSTESSVMCQNCDWE RHNLSSSSVHDRRPLEGFTGNPCLNELLAFVGFENLDKKALIFSEESGS GGDGDGLDGSLGLSDGFSDLLVWETPSVVSLDDLIVSNPAHKFQAMG VPPLPKNRNAACGRHKEEVLSQLRTLAKSEPDLMNENVDLNSFMSFQS LESEQNMQSAGFCTIFEQDAEPLAFPAYEAQEFESNDCGKSANQDFFPK TLQRSYLQDCSMVPDLNSNNDGTASHASDGYGGQMNSEASSAFPKVP SHECSLHRESALSRYKEKKKTRRYDKHIRYESRKVRAESRTRIKGRFAK MNN
RcBBX8	MASKLCDSCKSATATLFCRADSAFLCINCDTKIHAANKLASRHARVWL CEVCEQAPAHVKCKADDATLCVTCDREIHSANPLSRRHERVLVTPFYD SLNSDNSSPVKSGAAVNFLDDRYFSDVDGETTEVSREEAEAASWLLPN PKAMDSPDLNSCQYVFSDMDPYLDLDYGAVDPKIEAQEQNSCGTDGV VPVQSKSVQPQIVNEHCFEMDLPGSKPFIYGFNGHCLSQSVSSSSLDVS VVPDGNMLTDVSDPYPKSIGSMVDQLSHPTVQISSADREARVLRYREK RKNRKFEKTIRYASRKAYAETRPRIKGRFAKRTEVEIEAERLCRYGVVP SF
RcBBX9	MKIQCDVCNKDDASVFCTADEAALCEGCDHRVHHANKLASKHQRFSL IHPSSSKQSPLCDICQERKAFLFCQQDRAILCRECDVPIHSANEHTQKHS RFLFTGVKLSATSAVYTSSSDSATVTDLKSQINNKSIVSAASISNPPSIPKI

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RcBBX10	MKIRCDVCDKAEATVFCCADEAALCDVCDRRVHHANKLASKHKRFFL LQPTVKDSPQCDICQERHGFLFCQEDRAILCRECDHSIHKANEHTKKHN RFLLTGVKLSTDTTLLPTSSSSCSTFSDGGVINNSTDHARVTKSSTKRPR TGCNEQTLSSSSYKVEENCSISDNGLVISTNSISEYLMGDQTAEWRVED LLDVSFDFDGLYEVGRAPYI
RcBBX11	MVRHHQREVCSSSTCMEDEMNSMSKPAWLQGLMGETFFGGCGVHEN RRKNEKNVFCLHCCLSICPHCLQSHRSHPLLQVRRYVYHDVVRLGDLE KLIDCSYIQPYSNNGAKVIFLNQRPQSRPLSRTNGNKGFAANICFTCDRI LQEPFRFCSLSCKVDHLVLQEEDLSGILYRFDESDFTISQFEGLRMDGSE VIDDDGQMMPSSILEDHELQFRDSSCSNNSDSVMSRSTEAVVKKKNKG ILPGIMLSLGGRRKGAPQRAPLS
RcBBX12	MKIQCNVCEAAEANVLCCADEAALCWACDEKVHAANKLASKHQRVP LSASHMPKCDICQEAVGYFFCLEDRALLCRKCDVAIHTANSLVSGHRR FLLTGIKVGPEPNPPGSGGGVAGSSSSVKSHSGSLSKFDVNNQLAEECK VAPSSVDGMPFAGGSAAGSAPQWPMDEFLGFTDFDQSFGYMDNGSSK ADCGKLGESDSSFLRSSEEEQEDYECIGQVPETSWMVPQVPSPPTASGL CWPKSYQGPSDCAVFVPDVCYSEMQNSLHCQQNDISAGPLTSSLTI
RcBBX13	MKECELCGLRARMYCDADHASLCWDCDEKVHGANFLVAKHPRRLLC HVCHSPTPWTGSGPKLTPTVSVCENCVQSHRKIDLNQEQESEAENEED EEEEFDDEDDDVDDESEDEEDDEDENQVVPWSCCSYSQAQPPPAACSS DSEAEISGSKRVRENVDVDSSDDEVGFNGTALYGGSLRPLKRPRLNED QNHLQRSSDGDGGCEAEWRAKIIMSSMQRLEKEVIDGGDHPSAAVLRI WKLSRDEGSR
RcBBX14	MRKCELCDSVAKMYCESDQASLCWDCDIKVHGANFLVAKHSRTLLC HVCQSLTPWNASGPKFGPTVSVCLNCVNTSNKESRNEEEEEEEGDDSG GDDDDDDDEEENSIREDDDHEEENSIGEDDDHDGGGDNDADDNGGG GNDDDDDEENQVVPWSSSFSPPPGSTSLSDEEECCNESFSKSRSSYSYP CKRRRFNAH
RcBBX15	MEEEMLVPSWLESLLSTAFFSICPTHRDAPRSECNMYCLDCHNGAFCF YCRSSRHRDHQVIQIRRSSYHDVVRVNEIQKVLDIGGVQTYVINSARVL FLNERPQPKTAVKGSSHICEICGRSLLDPFRFCSLGCKLVGLKKNGDAS FIFSAKNGEDNEEGRREGLAIRLPSKEVDHQDPLRSEGTMQPKQEQDM YQSTPPPPPPQYSRSRRRKGIPHRAPLGQ
RcBBX16	MVSPKSGTGEGIPCDFCSEQPAVLYCKADSAKLCLFCDQHVHGANLLS RKHVRSQICDNCASEPVAFRCSTDNLVLCHECDWDSHGSLLRLRRPRS HPDRGLLRLPVASRARLLMGTRSPRHQQESGSGRPDPEPEQGLGLLLLL LDRNGGVYQNCGELIPAKRQSSGGILGKQKHGIQKQLVELLRRDFDGG GENLEAPIPNSNGWQRSDDAHANANANAEGFDVENGRVDGVNVGGA TVTSQPLLQEQAPFTSLLMMAEGIVDRQLLWDTNPHTHTTHNTQIWDF NLGKLRDHEETVPLDVAYGSSASGFMIKNFSELLKEASVTDTKMFGDV

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RcBBX29	MLKEESNDAAAGNSWPRICDTCRAAACTVYCRADSAYLCSGCDATIH AANRVASRHERVWVCEACERAPAAFLCKADAASLCTACDADIHSANP LARRHQRVPILPISGFHHSPPATDSGGQILVGSTLADTTEDGLDEAMDE EDEDEAASWLLLNPVKNGNGNGNNHNTNTNNNPSNNNNGFFFGVEV DDYLDLVEYNSSSCADQNQFSTTSATNDQHNQYAVPHKISYGGDSVV PVQYGDGKVTQMQMQQQHKHNFHQLGMEYESSKAAYSYDGSITHTV SVSSMDVGVVPDSTMSDMSVSHPRTPKGTIDLFNGPTIQMPTQLSPMD REARVLRYREKKKTRKFEKTIRYASRKAYAETRPRIKGRFAKRTDIEVE VDQMFSTSLMGETGYGIVPSF
RcBBX30	MKNCELCQLPARTYCESDQAILCWDCDFKVHGANFLVARHSRTLLCR ACHAQTPWKASGEKLGHTFTVCERCVARNENRGDDEESQGGNDDDID TDNDDLDEDHVSDDDDDADGDIDFDEDGENQVVPWAATPPPPAASSS GSEDEASLVNNGERDDSRSVAAVFLKRARDDASDLRSQDDFHRSTAR LRRQTACTGHSGRSGADGGAISIDSSKDRRVDLNGSGSRTSPAIESPRR NRQQNSRKLSEGSEAVDLDSSEPRIPQI
RcBBX31	MARLCLNCDGCVHSANALARRHPRWLLCDKCNVQPAIIRCLDENVSL CQSCEWNHSNGVTGMGHQSQAISCYTGCPSLSEISRIWSAVLDGGSAS GGFAASGWESLAGSGVPKNDTDCISNCLERRDSEGSSFGVVSAGKLNE VLAESNCTPKFEPWMAPSTIIPSNPNCIQPQCKDQAPFLPQESSQLPKEL QDSSNFKDLGIQDDHDICEGLNMDDVPLDVENGDQLFSCSEGPSRYPF EDGELDCLLMDQKNLSVTESNGPLSDNAIQQASPSRQQDCTVGFQSSC VSDSVMAPVMNASSSVNCSLLMNPNCTRNINLQGLINPTGQVHSSISLS LSSITRETTHPDYQDCGLSPVFLSAEPWDSTLETGSPRARDKAKMRYEE KKKTRTFGKQIRYASRKARADTRKRVKGRFVKSGEEYDYDPLVRSSF
RcBBX32	MFVPSNLLPSWLAVLLTEKFFNACIIHEEERKNEKNIYCLDCCISFCPHC FTPHQSHRLLKIRRYVYHDVIRLDDAARLIDCAFVQSYTSNSAKVVFLN QRPQTKNSRGSGNMCSTCDRSLQDPYLYCSISCKIDHLIRTEGGLSKYL RQCKFMALPDPGLDDGVLTPDSVLETACSVRTSSGSGGYAELGCLSLA CTATTEVVRKKRSSLSALRAACRPVFSPVSEISGGRRKGTPHRAPLH

Table S3

Plant name	BBX protein sequences
Arabidopsis thaliana	>AtBBX1 MLKQESNDIGSGENNRARPCDTCRSNACTVYCHADSAYLCMSCDAQVHS ANRVASRHKRVRVCESCERAPAAFLCEADDASLCTACDSEVHSANPLARR HQRVPILPISGNSFSSMTTTHHQSEKTMTDPEKRLVVDQEEGEEGDKDAKE VASWLFPNSDKNNNNQNNGLLFSDEYLNLVDYNSSMDYKFTGEYSQHQQ NCSVPQTSYGGDRVVPLKLEESRGHQCHNQQNFQFNIKYGSSGTHYNDNG SINHNAYISSMETGVVPESTACVTTASHPRTPKGTVEQQPDPASQMITVTQL SPMDREARVLRYREKRKTRKFEKTIRYASRKAYAEIRPRVNGRFAKREIEA EEQGFNTMLMYNTGYGIVPSF >AtBBX2 MLKVESNWAQACDTCRSAACTVYCRADSAYLCSSCDAQVHAANRLASRH ERVRVCQSCERAPAAFFCKADAASLCTTCDSEIHSANPLARRHQRVPILPIS EYSYSSTATNHSCETTVTDPENRLVLGQEEEDEDEAEAASWLLPNSGKNSG NNNGFSIGDEFLNLVDYSSSDKQFTDQSNQYQLDCNVPQRSYGEDGVVPL QIEVSKGMYQEQQNFQLSINCGSWGALRSSNGSLSHMVNVSSMDLGVVPE STTSDATVSNPRSPKAVTDQPPYPPAQMLSPRDREARVLRYREKKKMRKFE KTIRYASRKAYAEKRPRIKGRFAKKKDVDEEANQAFSTMITFDTGYGIVPSF >AtBBX3 MLKEESNESGTWARACDTCRSAACTVYCEADSAYLCTTCDARVHAANRV ASRHERVRVCQSCESAPAAFLCKADAASLCTACDAEIHSANPLARRHQRVP ILPLSANSCSSMAPSETDADNDEDDREVASWLLPNPGKNIGNQNNGFLFGV EYLDLVDYSSSMDNQFEDNQYTHYQRSFGGDGVVPLQVEESTSHLQQSQQ NFQLGINYGFSSGAHYNNNSLKDLNHSASVSSMDISVVPESTASDITVQHPR TTKETIDQLSGPPTQVVQQLTPMEREARVLRYREKKKTRKFDKTIRYASRK AYAEIRPRIKGRFAKRIETEAEAEEIFSTSLMSETGYGIVPSF >AtBBX4 MASSSRLCDSCKSTAATLFCRADAAFLCGDCDGKIHTANKLASRHERVWL CEVCEQAPAHVTCKADAAALCVTCDRDIHSANPLSRRHERVPITPFYDAVG PAKSASSSVNFVDEDGGDVTASWLLAKEGIEITNLFSDLDYPKIEVTSEENS SGNDGVVPVQNKLFLNEDYFNFDLSASKISQQGFNFINQTVSTRTIDVPLVP ESGGVTAEMTNTETPAVQLSPAEREARVLRYREKRKNRKFEKTIRYASRKA YAEMRPRIKGRFAKRTDSRENDGGDVGVYGGFGVVPSF >AtBBX5 MASKLCDSCKSATAALYCRPDAAFLCLSCDSKVHAANKLASRHARVWMC EVCEQAPAHVTCKADAAALCVTCDRDIHSANPLARRHERVPVTPFYDSVSS DGSVKHTAVNFLDDCYFSDIDGNGSREEEEEEAASWLLLPNPKTTTTATAG IVAVTSAEEVPGDSPEMNTGQQYLFSDPDPYLDLDYGNVDPKVESLEQNSS GTDGVVPVENRTVRIPTVNENCFEMDFTGGSKGFTYGGGYNCISHSVSSSS MEVGVVPDGGSVADVSYPYGGPATSGADPGTQRAVPLTSAEREARVMRY

REKRKNRKFEKTIRYASRKAYAEMRPRIKGRFAKRTDTNESNDVVGHGGIF
SGFGLVPTF

>AtBBX6

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VETFFDSAETAVAKISASSTFGILGSSTTVDLTAVPVMADDLGLCPWLLPND
FNEPAKIEIGTENMKGSSDFMFSDFDRLIDFEFPNSFNHHQNNAGGDSLVPV
QTKTEPLPLTNNDHCFDIDFCRSKLSAFTYPSQSVSHSVSTSSIEYGVVPDGN
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>AtBBX7

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CYSGCPSSSELASIWSFCLDLAGQSICEQELGMMNIDDDGPTDKKTCNEDK
KDVLVGSSSIPETSSVPQGKSSSAKDVGMCEDDFYGNLGMDEVDMALENY
EELFGTAFNPSEELFGHGGIDSLFHKHQTAPEGGNSVQPAGSNDSFMSSKTE
PIICFASKPAHSNISFSGVTGESSAGDFQECGASSSIQLSGEPPWYPPTLQDNN
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KAGEAYDYDPLTPTRSY

>AtBBX8

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SSAELSSIWSFCMDLNISSAEESACEQGMGLMTIDEDGTGEKSGVQKINVEQ
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FGSAFNSSRYLFEHGGIGSLFEKDEAHEGSMQQPALSNNASADSFMTCRTE
PIICYSSKPAHSNISFSGITGESNAGDFQDCGASSMKQLSREPQPWCHPTAQ
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VKSGEAYDYDPMSPTRSY

>AtBBX9

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GKIWSSTLEPSVTSLVSPFSDTLLQELDDWNGSSTSVVTQTQNLKDYSSFFP
MESNLPKVIEEECSGLDLCEGINLDDAPLNFNASNDIIGCSSLDNTKCYEYE
DSFKEENNIGLPSLLLPTLSGNVVPNMSLSMSNLTGESNATDYQDCGISPGF
LIGDSPWESNVEVSFNPKLRDEAKKRYKQKKSKRMFGKQIRYASRKARAD
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>AtBBX10

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DFNRMWSSILEPPVSGLLSPFVGSFPLNDLNNTMFDTAYSMVPHNISYTQNF
SDNLSFFSTESKGYPDMVLKLEEGEEDLCEGLNLDDAPLNFDVGDDIIGCSS
EVHIEPDHTVPNCLLIDKTNTSSFTGSNFTVDKALEASPPGQQMNINTGLQL
PLSPVLFGQIHPSLNITGENNAADYQDCGMSPGFIMSEAPWETNFEVSCPQA

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DPSSPTTNN

>AtBBX11

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CPSVPELLAIVGLDDLTLDSGLLWESPEIVSLNDLIVSGGSGTHNFRATDVPP
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>AtBBX12

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VPYDVSCKKQSFSFGRSKQVVFEQLELLKRGFVEGEGEIMVPEGINGGGSIS
QPSPTTSFTSLLMSQSLCGNGMQWNATNHSTGQNTQIWDFNLGQSRNPDE
PSPVETKGSTFTFNNVTHLKNDTRTTNMNAFKESYQQEDSVHSTSTKGQET
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>AtBBX13

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DCDREGACDGDGDGEAGEGLMVPEMSERLKWSRDVEEINGGGGGGVNQ
QWNATTTNPSGGQSSQIWDFNLGQSRGPEDTSRVEAAYVGKGAASSFTIN
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>AtBBX14

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FPMMPLSFKSSDEEDDDNAESCLNGLFPTDMELAQFTADVETLLGGGDREF
HSIEELGLGEMLKIEKEEVEEEGVVTREVHDQDEGDETSPFEISFDYEYTHK
TTFDEGEEDEKEDVMKNVMEMGVNEMSGGIKEEKKEKALMLRLDYESVI
STWGGQGIPWTARVPSEIDLDMVCFPTHTMGESGAEAHHHNHFRGLGLHL
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SSIGVAH

>AtBBX15

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SFDYESSHKTSEEEVMKNVESSGECVVKVKEEEHKNVLMLRLNYDSVIST

WGGQGPPWSSGEPPERDMDISGWPAFSMVENGGESTHQKQYVGGCLPSSG
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LAAAASPLGVNY

>AtBBX16

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KCENGGSKDSDREASNDKDRKTSLFLRLDYGAVISAWDNHGSPWKTGIKP
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>AtBBX17

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RSRYEKKPQQKIDDERRREDPRVPEIGGEVMFFIPEANDDDMTSLVPEFEGF
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QYLMSCKKDYDNVITVSEKTEEIEDCYENNARHRLNYENVIAAWDKQESP
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>AtBBX18

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GSHNQEEGIDVNNANNHEHE

>AtBBX19

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>AtBBX20

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SNCYYGIEENYHHVSDSGSGSGCTGSISEYLMETLPGWRVEDLLEHPSCVS
YEDNIITNNNNSESYRVYDGSSQFHHQGFWDHKPFS

>AtBBX21

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GDDDGVLPYMEPEDDNNTKRNNNNNNNNNNNTVSLPSKNLGIWVPQIPQT

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>AtBBX22

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QQEGVIPGTKVNDQTSTKLPLVSSGSTTGSIPQWQIEEIFGLTDFDQSYEYM
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>AtBBX23

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>AtBBX24

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>AtBBX25

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>AtBBX26

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>AtBBX27

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>CmBBX4

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>CmBBX5

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>CmBBX6

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>CmBBX7

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>CmBBX8

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>CmBBX9

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VKNGELEMEETKIVKNKKKISLSLDSEAVIIAWGSRGTPWTSGDRPNLDLDY
YWPDYMGTYESDCYYQPYGEFGSGIGRHAVTGVEGEREARVSRYREKRRT
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S

>CmBBX10

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>CmBBX11

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>CmBBX12

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>CmBBX13

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>CmBBX14

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>CmBBX15

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>CmBBX16

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>CmBBX17

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>CmBBX18

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>CmBBX19

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>CmBBX20

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>CmBBX21

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>CmBBX22

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>CmBBX23

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>CmBBX24

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>CmBBX25

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Cucumis sativus

>CsBBX1

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>CsBBX2

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>CsBBX4

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>CsBBX5

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>CsBBX6

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>CsBBX7

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>CsBBX8

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>CsBBX9

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>CsBBX10

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>CsBBX12

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>CsBBX13

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>CsBBX14

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>CsBBX15

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>CsBBX16

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>CsBBX17

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>CsBBX18

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>CsBBX19

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>CsBBX20

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>CsBBX21

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>CsBBX22

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>CsBBX23

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>SlBBX5

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>SlBBX6

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>SlBBX7

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>SlBBX8

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>SlBBX9

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>SlBBX10

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DF

>SlBBX11

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>SlBBX12

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>SlBBX13

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>SlBBX14

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>SlBBX15

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>SlBBX16

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>SlBBX17

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>SlBBX19

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>SlBBX22

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>SlBBX24

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>SlBBX25

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>SlBBX27

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>SlBBX28

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>SlBBX29

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Zea mays >ZmBBX1

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LPEPDNSHEDSAAADSFFAEPDAYLGVDLDFARCVDGVKAIGVPVTPAPLEL
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>ZmBBX12

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ASSFPYW

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FWCF

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QRFLLTGVQVGLDPADPVPPIAEKHVNASGGSVKQSVRHLPRRSPGVQFSVE
GSASVPSKNVSNGDYSRQNSVPTARAEVVDWTKNNTTIQSVESPPKYMSEES
PTLLQSSQTTTVFSNQINGNSDGTYHLSFSSGNVTDSLPDWPVDEFFSNSEYV
PNLGFSEHGSSKGDNAKLESAGGSLQCRLAEGSIAEELLGQVPGLITDDYMS
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VPSSFKRRRREY

>ZmBBX21

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KRVGGAALGFDKAPASVVVVPTQGCVTERTWNSDSDVFAVPELPQPPPAKK
ARPAPAPTFWCF

>ZmBBX22

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FGRKARTPRGGHAKSVGQVALSRRLVVPHAAGGDSDSPDERNGGEEEQLLY
RVPILDPALAEFCSPPPLEDAAGLALDASVCNEDGAIEDPAKPDPAAPLAQFC
PVSGHFNFGPTDAELREFAADMEALLGHGLDDGNEEDSSFYMETLGLLDPM
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DTATDERAASSDTGADAQFLQTSLSLTLNYEAIIQSWGSSPWTGGGERPHVK
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QGNIDSKMIDLNMRPVRTHGQESNSQVCHAHCD

>ZmBBX25

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PRGGRAKSDVRTLSRRLVVPHAAGGDSPDGRNDEGEFEAEEPEEEVLYRVP
VFDPALAEFCSPQPLEDAAALASSCNEDGAVEDPAKTDRETPAAAPLVQFFP
DGGHANFGPTDAELREFAADMEALLGYGLDDGNEESSSFCMETLGLLEPVE
VGEDASRVKVETDAGSACEASGTLACALELLDPDASDEMLDIDFNYGSPQD
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NHINSNTKQYGMQEQQLLLHKEFGDKEGSEYVVPSQVGQQQSGYHRVIGTE
QAASMTPGISFSSSMEVGIVPDNMATTDMPSSGILLTPAGAISLFSSGPPLQMP

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DIGTCDKLLVGSSSGAGVNLLPLATGQTETAGSVDSTPDKDSCMQVPYTPDK
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KEGATTEVFFADSDPYLDLDFARSMDDIKTIGVQGGPPELDLAGAKLFYSDD
SMNHSVSSSEAAVVPDAVAGAAPEVAVVCRGLEREARLMRYREKRKSRRF
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W

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WARRTGLTAADARRRAAAAARALRAHAHGLASARVAPRVAMAAALWRE
VAGRGGTGGGGHGHGEALRRLEACAHVPAGLVVAVAKSMARARGRGDEA
DTDAAAEGWDECAWAGPKSSPPRP

Table S4

Type	Domain organization (N-terminus to C-terminus)	Number
I	B-box1 + B-box2 + CCT	3
II	B-box1 + B-box2 + CCT	6
III	B-box1 + CCT	2
IV	B-box1 + B-box2	7
V	B-box1 only	14

Table S5

Name	Amino acid sequences
RcPAL1	MESITQNGHHHQNGIQNGSLDDGLCIKTESIKTGYSVSDPLNWGAAAE SMTGSHLDEVKRMVTEYRKSVVKLGGETLTISQVAAIANHDSGVKVE LAESARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGAA LQKELIRFLNAGVFGNGTESAHTLPHSATRAAMLVRINTLLQGYSGIRF EILEAISKFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAIGPK GETLTAAEAFAQVGISSGFFELQPKEGLALVNGTAVGSGLASMVLFET NILALLSEILSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILD GSSYVKAAKKLHEQDPLQKPKQDRYALRTSPQWLGPQIEVIRFSTKSIE REINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMF AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFL ANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTFLVALC QAIDLRHLEENLKSTVKNTVSQLAKRVLTTGVNGELHPSRFCEKDLLM VVEREYLFTYIDDPCSATYPLMQRLRQVLVEHALTNGENEKNANTSIF QKITAFEEELKTILPKEVESTRAAYESGNAAIPNRIVECRSYPLYKFVRE ELGGEFLTGEKVRSPGEECDKVFTAMCQGNIIDPILDCLSGWNGEPLPI C
RcPAL2	MESFKNCNAAVESFCEGHDPLNWNMAAESLKGSHVDELKRMVSDYR KPVVKLGGETLTIGQVAAIASHDGGVRVELAEEKRAGVKASSDWVMD SMGKGTDSYGVTTGFGATSHRRTKNGGALQRELIRFLNAGIFGSSLDST HILPHTATRAAMLVRINTLLQGYSGIRFEILEAITKFLNGNITPCLPLRGT ITASGDLVPLSYIAGLLIGRPNSKSVGPKGETLSPAEAFKLAGIEGGFFEL QPKEGLALVNGTAVGSGMASMVLFDVNTLAVLSEIMSAIFAEVMQGK PEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKEAKKVHEMDPLQK PKQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKA LHGGNFQGTPIGVAMDNTRLAIASIGKLMFAQFSELVNDYYNNGLPSN LSGGSNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDV NSLGLISSRKTSEAVDILKLMSSTFLVALCQAIDLRHLEENLKIVVKTTV SNVAKRTLTVSPNGELHPSRFSEKDLLTVVDREYLFSYIDDPCLATYPL MQKLRAELVEHALKNGERERSANTSIFHKISAFEEELKTILPKEVDNARI EIENGKSEIPNRIKECRSYPLYRFVREELGTSLLTGEKIKSPGEECDKLFN AICAGKLIDPLLECLKEWNGAPLPIS
RcC4H	MDFLLLEKTLLGLFVAVVVAITVSKLRGKKFKLPPGPIPVPVFGNWLQ VGDDLNHRNLTDMAKKFGDVFMLRMGQRNLVVVSSPELAKEVLHTQ GVEFGSRTRNVVFDIFTGKGQDMVFTVYGEHWRKMRRIMTVPFFTNK VVQQYRYGWESEAAAVVEDVKKHPEAATNGMVLRRRLQLMMYNN MYRIMFDRRFERSERRESRLAQSFEYNYGDFIPVLRPFLRSYLKICKEV KEKRIQLFKDYFVDERKKLASTQATTNEGLKCAIDHILDAQQKGEINED NVLYIVENINVAAIETTLWSIEWGIAELVNHPEIQKKLRVELDTVLGRG VQITEPEIQKLPYLQAVVKETLRLRMAIPLLVPHMNLNEAKLGGFDIPA ESKILVNAWWLANNPAHWKKPEEFRPERFLEEESKVEANGNDFRYLPF GVGRRSCPGIILALPILGITLGRLVQNFELLPPPGQTQLDTTEKGGQFSL HILKHSTIVMKPRT
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QVAEEPQTFLCTVPMFHIYGLATFATGFLTSGSTIVVLSKFEMHDMLSA
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IEGFLEKYPTVGISQGYGLTESTGLGASTDTLEESRRYGTAGMLSPNME
AKIVDPDTGRALTVNQTGELWLKGPTIMKGYFCNEEASASTVDSQGW
LRTGDLCYIDDDGFIFVVDRLKELIKYKAFQVPPAELEALLLTHPQIAD
AAVIPFPDEKVGQFPMAYVVRKAGSNLSETAVMDFVAKQVAPYKRIR
KVAFIASVPKNPSGKILRKDLIQLATTSTSKL

Rc4CL2 MEKSGYGRDGIFRSLRPPLVLPRDPNLTMVSFLFRNSSSYPHKPALIDD
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AIGAIATTSNPLYTVSELSKQVKDSNPKLVITVPELWEKVKGFNLPAVIL
GQKTSSSQTESSSRIVGFHDLVESSGPVSDFPSVNVKQTDTAALLYSSG
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CAIVSVENTLVGPRHSGSAGSLASGVESQIVSVDTLKPLPPKQLGEIWV
RGPNMMIGYFNNPEATKLTLDKNGWIHTGDLGYFDESGQLFVVDRIKE
LIKYKGFQVAPAELEGLLVSHPEILDAVVIPFPDAEAGEVPVAYVVRSP
NSSLTEEDIKSFIASQVASFKRLRRVTFINTVPKSASGKILRRELIEKVRS
KI

Rc4CL3 MADHTGSSCIDPYSGFCSKTKTFHSLRPKAPLPPETTPLSITHFIFSQLQA
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SPNSLHLPILFFSLFSLGVTVSPSNPASTNPEISRQIHLSKPVVAFATSATA
HKIPNSLRYGTVLLDSAEFESMMTCPGRTPDLPRARVYQSDTAAILYSS
GTTGMVKGVALTHRNWISMLAAAFAVRPSSPPAVWLCTVPFFHVYGF
GVCMRVLAFGETLVSISGRFDLRSTLSAIEEFRITHAAWAPPVVVALVK
LGSELDGYDLSSLQVIASGGAPLAKSVIDKLKKRLPNVQLAQGFGLTET
SGRVFGTVGPNETRVEGAVGKLMSNFEAKIIDPETGIALPPLMPGELWL
TGPFLMKGYIGDEDATASTMDSQGWFKTGDLCYIDEQGYLFFVDRIKE
LIKYKGYQVAPAELEHLLLSHPDIVDAAVVPYPDEEVGQVPMAFVVRC
VGSALDESQIKDFIAKQVAPYKKIRRVTFINEVPKSAQGKVMRKELIKL
ASSKL

Rc4CL4 MENKRQDNHEFIFRSKLPDIYIPNHLPLHTYCFENLSQFHDRPCLINGNT
GETFTYAEVELTSRRVAAGLDKLGIQQNDVVMLLLQNCPEFAFAFLGA
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AAILLMQKFEINKLLELVEKEKVTIAPFVPPIVLSIAKCPDLHRYDLSSIR
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KEPYEIKSGACGTVVRNAEMKIIDPDTNESLPRNQSGEICIRGSQIMKGY
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KDEAAGEVPVAFVVRSNGSKISEDDIKQYISKQVVFYKRISRVFFTDKIP
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Rc4CL6	MENKRQDNHEFIFRSKLPDIYIPNHLPLHTYCFENLSQFHDRPCLINGNT GETFTYAEVELTSRRVAAGLDKLGIQQNDVVMLLLQNCPEFAFAFLGA SYIGAMSTTANPFYTPAEVAKQAKASNAKLIITQSPYVDKVKDFAKLN DVKVMCVDETLSEDVLHF
Rc4CL7	MARTSSYNFNSQIPETPNIEKHKSLATQQHPWWFSPDTGIYHSKQPSIN LPTDPFLDVVSFVFSHKHNGVSALVDSSSGFSISYSKLYSLVKSMASGL HRMGISQGDVVLLLLPNSIYYPIVFFGVLYVGAVVTTMNPLSSVVELK KQIADCNACLAFTGSENVDKLQALGVPAIGVPENVVSDSTKEFFSVFHE LVYGKFSLAPRPVIKLQDTAAILYSSGTTGVSKGVLVTHGNFIATVELF VRFEASQYEYSSLNNVYLAVLPLFHIYGLSLFVVGLLSLGSRIVVMKKF DVNEMVKAIDRYKVTHFPVVPPILTALTKIAKDVGAHSLQSLKQVSCG AAPLSMKSIEDFVQTLPYVDFIQGYGMTETTAVGTRGFNTEKVRKYSSI GLLAPNMQAKVVDWNTGSFLPPARIGELWLRGPSIMRGYLNNARETM STIDDDGWLHTGDIVYFDEDGYLNICDRIKEIIKYKGFQIAPADLEAVLI SHPEILDVAVTGATDEECGEIPVAFVVRKHSSELSQQDVMDYVARQVS PTRRSERWCLQTQYQDLQQGRSSEGSSGFSWLLDCAWDFASYCFSRD RSCNRNFLAASFVAAAIL
Rc4CL8	MAEHTDNPSRWIDPKSGFCPRTKTFHNFRPPVPLPPLSQPLSLAQYTLSL LQSSTTAPTTPVLIDATSGRHVSYGQFLAQFHSLTRSLRSLISKGQVAFI LSPPSLHVPVLYFSLLALGVVVSPANPIGSESEVAYQVRLCKPAVAFAT SATAHKLPKGLTTILLDSPEFLSLIDGSRPGTRPDYPVEVNQTDSAAILY SSGTTGRVKGVISTHRNFIALIAGMHANRLEPDPNEPVVQAVSMFTLPL FHVFGFFMLIRAVSMGETMVLMERFNFEAMLRAVERFKVTYMPVSPP VIVALANSELAQKYDLSSLRLLGCGGAPLGKEVAERFNRKFPNVEIVQ GYGLTETGGGATRMIDPEEAKNYASVGRLAENMEAKIVDPETGEALPP GQRGELWLRGPTVMKGYVGDDKATAETLDKDGWLKTGDLCYFDDE GFIYIVDRLKELIKYKAYQVPPAELEQILLSHPDIADAAVIPYPDEEAGQI PMAYVVRRPGNNITEAIVMDFVAKQVAPYKKIRRVSFINSIPKSPAGKI LRRELVTLALSSGSSKL
Rc4CL9	MAAQTPQHDIVYRSKLPDIHIPNHLPLHSYIFQNKSHLSSKPCIINGTTG DIHSYADVELTSRKVASGFNKLGIKQGDVIMLLLPNTPEFVFAFLGASF CGAMTTAANPFFTPAEIAKQAKASKAKLIITLACYYDKVKDLSCDEVK LMCIDSPPPDSSCLHFSELTQSDENDVPDVDISPNDVVALPYSSGTTGLP KGVMLTHKGLVTSVSQQVDGENPNLYYSSDDVVLCVLPLFHIYSLNSV LLCGLRAGAAILVMQKFEIVSLLELMQKHRVSVAPIVPPIVLAIAKFPDL DKYDLGSIRVLKSGGAPLGKELEDTVRAKFPNVTLGQGYGMTEAGPV LTMSLAFAKEPFEVKPGGVGLSSETQS
Rc4CL10	MKGYLNDPEATRTTIDKQGWLHTGDIGFVDDDEELFIVDRLKELIKYK GFQVAPAELEALLVTHPNISDAAVVPMKDDAAGEVPVAFVVRSKGSQI TEDEIKQFISKQVVFYKRINRVFFIEAIPKSPSGKILRKELRTKLAAGFAN

Rc4CL11 MHKVGYTLEILDILMKRGDCMLWIDLKSSSSVMVIRFPDVKAGEVPIA
CVVLAPNSLLTEQDILKFVEKQVAPLHHAKDYGA

Rc4CL12 MISIASNNNHNNNNNRVVVETPTKPEISPNIISDVISTSQTQPEQEQQPPT
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	EAHALHSLSDGKTPPVYPVGPILNITGNENLEDYSDLAKQKTDSTLKW LDDQPPLSVVFLCFGSMGTFEEGQVKEIACALEQSGLRFLWSLREPPAK GKIAYPSDYAGYRGVLPEGFLDRTSGIGKVIGWAPQVAVLAHPAIGGF VSHCGWNSMLESLWYGVPVGTLPMYAEQHLNAFEMARELGLAVEVS MDYRKNSDFVNAEEIQRGIRQVMDHDSDTRKRVKKMSEMSKKALMD GGSSYSSLGRFIEQIFLTS
RcUFGT11	MIFLKVHRQMKKPAELVFIYLRCRCRSFLNSRRSRSPSSSYLETTTSSSP SHRKESILIIKDHQHVFLKVIENEETRRARVHPLRRCRPPHIDGRDRQAP RISRPYVESIEAASQKRIKFINLPEPNLDFTNMTRNEFRIAFMETHKPYV RDAVTELAESTESAPRLAGFVIDMFCTTMIDVANEFGVPTYVFFTSNAG FLGLMFHLQTIHDKHDMDVTELKSLETELVLPSFVNPVPHKALPSTLM DKEGATTFLDYARRFRETKGILVNTFSELESHALRSLSSYGEIPPVYPVG PVLKLKTEDDAHEGSDQATQKTDIIEWLDDQLPSSVVFLCFGSMGSFG EDQVKEIACALEQSGHRFLWSLRRPPPKGKITRPSDYTDPAGVLPDGFL ERTARIGKVIGWAPQVAVLAHPAVGGFVSHCGWNSTLESLWFGVPIAT WPMYAEQQMNAFEMVKELGLAVKISVEYDTAEENKMLLSAEEIERGI RELMEPGSDIRKRVKQMSEMSKTTLLDGGSSYSSLGRFIDQIFL
RcUFGT12	MKKATELVFIPAPGIGHIVSAVEMAKLLVARDDQLFITVLIMKLPLDSK PKGTDDTYSRSERIKFINLPGINIDTQGISPFNFFKLFVESHKPHIKDAVS KLSQSQSQSNPRLAGFVIDMFCTSMIDVANELGVPTYVFFASNAGFLGL VFHLQTLSDEHNKDFTDFKDSDDELVLPGFVNPLPARALPSVFLDKDN TATFVNIGRRFRETKGILVNTFMELEAHALHSLSDGKTPPVYPVGPILNI TTNENHEDYSDLAKQKADSTLKWLDDQPPLSVVFLCFGSMGTFDEDQ VKEIACALEQSGLRFLWSLREPPAEGKIAYPSDYTDYRGVLPEGFLDRT SGIGKVIGWAPQVAVLAHPAIGGFVSHCGWNSMLESLWYGVPVGTLP MYAEQHLNAFEMARELGLAVEVSMDYRKNSDFVNAEEIQRGIRQVM DHDSDTRKRVKEMSELSKKALMDGGSSYSSLGRFIEQIFLTS

Table S6 Correlation between RcBBX26 and anthocyanin biosynthetic genes.

	Correlation coefficient
RcPAL1	-0.4742
RcPAL2	-0.9505
RcC4H	-0.4139
Rc4CL1	-0.4176
Rc4CL2	-0.5314
Rc4CL3	-0.6679
Rc4CL4	0.5479
Rc4CL5	0.6036
Rc4CL6	0.9157
Rc4CL7	0.4187
Rc4CL8	0.5126
Rc4CL9	-0.3761
Rc4CL10	-0.3591
Rc4CL12	0.8950
RcCHS1	-0.5107
RcCHS2	-0.5095
RcCHI1	0.6627
RcCHI2	-0.4134
RcCHI3	-0.5394
RcFLS1	0.7244
RcFLS2	-0.4750
RcFLS3	0.1724
RcFLS4	0.1497
RcF3H1	0.9083
RcF3H2	0.1497
RcF3′H1	-0.0484
RcF3′H2	-0.5130
RcF3′H3	0.8366
RcDFR1	-0.5634
RcDFR2	-0.5070
RcANS	0.8449
RcUFGT1	-0.2783
RcUFGT2	-0.3360
RcUFGT3	-0.3190
RcUFGT4	-0.4387
RcUFGT5	-0.4761
RcUFGT6	-0.4060
RcUFGT7	-0.4188
RcUFGT8	0.6242
RcUFGT9	0.7021
RcUFGT10	-0.3505
RcUFGT11	0.8840
RcUFGT12	-0.4615

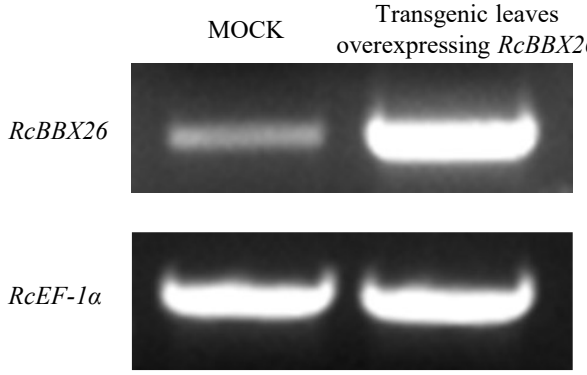
MOCK
Transgenic leaves overexpressing *RcBBX26*
RcBBX26
RcEF-1α

Figure S1

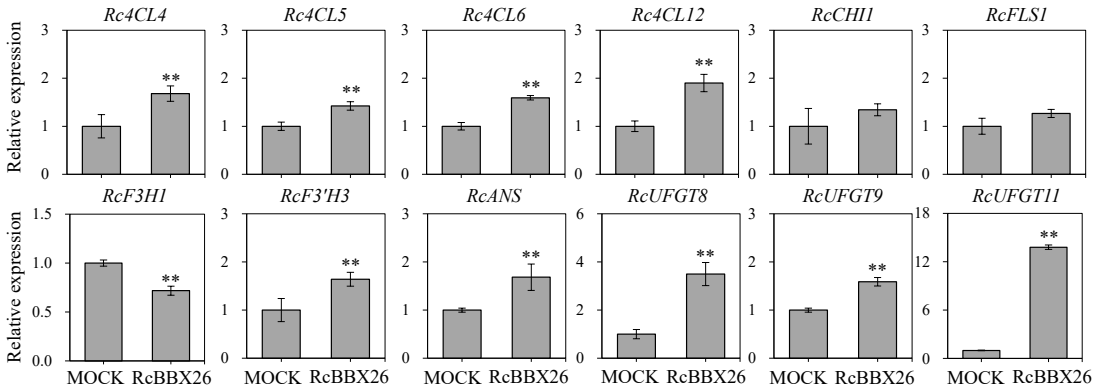
Rc4CL4
Rc4CL5
Rc4CL6
Rc4CL12
RcCHI1
RcFLS1
RcF3H1
RcF3'H3
RcANS
RcUFGT8
RcUFGT9
RcUFGT11
Relative expression
Relative expression
**
MOCK
RcBBX26

Figure S2