

Blast results by querying AtTT2 to cacao genome

Sequences producing significant alignments:	(bits)	Value
Tc00_g016740 GHMYB10	199	2e-51
Tc09_g007160 MybPA2	194	9e-50
Tc09_g005570 Putative GHMYB10	191	4e-49
Tc09_g005580 Putative Transcription factor MYB558	191	6e-49
Tc01_g029340 Putative uncharacterized protein	189	1e-48
Tc01_g004300 Putative MybPA2	189	3e-48
Tc02_g026610 Putative uncharacterized protein	188	3e-48
Tc01_g034240 TT2 like MYB transcriptoin factor	168	5e-42
Tc09_g005590 Putative uncharacterized protein	167	6e-42
Tc02_g027560 Transcription repressor MYB4	167	1e-41

>Tc00_t016740

MGRNPCCSKEGLNRGAWTAHEDKILTQYIKAHGEGSWRNLPKRAGLKRKCGKSCRLRWLNLYLRPDIKRGNISADEEELIIRLH
KLLGNRWSLIAGRLPGRTDNEIKNYWNTNLGKKVQHHQNPSSAAPGHNKSNRGRVTRKREQLATAAGTPSSHVVRTRAIRC
VFINPHQKIEPFDRNREAKPSIDGECRPMQTQSAPSPIKALSENEDQNVHNKPFDFMVDNMGFECLSELLNSDFSDLVGLN
YSNDSNAISPSSDQPLIFSEEILQDWTSSHHAQQNVASNPVSLASFLDYGEEWLAE

alignment with top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 202 bits (515), Expect = 2e-52, Method: Compositional matrix adjust.
Identities = 90/116 (77%), Positives = 104/116 (89%)
Frame = -1

Query: 1 MGRNPCCSKEGLNRGAWTAHEDKILTQYIKAHGEGSWRNLPKRAGLKRKCGKSCRLRWLNLY 60
MGR PCCSK GL+RG WT ED +L +YI+AHG+G WR+LPK+AGL RCGKSCRLRW+NY
Sbjct: 1167 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRS LPKKAGLLRCGKSCRLRWMNY 988

Query: 61 LRPDIKRGNISADEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLGKKV 116
LRPDIKRGNI+ DE++LIIRLH LLGNRWSLIAGRLPGRTDNEIKNYWNT+L K++
Sbjct: 987 LRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRTDNEIKNYWNTLHLSKRL 820

>Tc09_t007160

MGRKPCCAKVGLNRGAWSAKEDKILTNYIKIHGEGKWRDLRQAGLKRKCGKSCRLRWLNLYLRPDIKRGNISSEEEELIVRLH
KLLGNRWSLIAGRLPGRTDNEIKNYWNTNLSKRVQGNKNTPKGTQTSNMQLNKLKLGCIKSSOMEITTAEHKVIKAVK
CTKAVNVNPHLSDCQTAENNSVPKSESTTASESPSSSAINEDNSMDFLIDFDINELLVSDAPMSDLHQTQQVDENGENVVD
NWECRNGFNLNIDVELYSSVDELARPDNWRPSTDLFQTSETLDLLSLASYLNLEN

alignment with top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 211 bits (538), Expect = 4e-55, Method: Compositional matrix adjust.
Identities = 96/135 (71%), Positives = 112/135 (82%)
Frame = -1

Query: 1 MGRRPCCSKEGMNRGAWTLTEDKILTQYIKAHGEGKWRNIPKEAGLKRKCGKSCRLRWMNY 60
MGR PCCSK G++RG WT ED +L Y++ HG+G WR++PK+AGL RCGKSCRLRWMNY
Sbjct: 1167 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRS LPKKAGLLRCGKSCRLRWMNY 988

Query: 61 LRPDIKRGNISADEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTLHLSKRGQKE 120
LRPDIKRGNI+PDE+DLIIRLH LLGNRWSLIAGRLPGRTDNEIKNYWNTLHLSKR +
Sbjct: 987 LRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRTDNEIKNYWNTLHLSKRLLSQG 808

Query: 121 RGPKNHSHKVGKKPI 135

P + H K+ + P+

Sbjct: 807 TDPNT-HKKLSEPPV 766

>Tc09_t005570

MGRRPCCSKEGMNRGAWTLTEDKILTDYVKVHGEKWRNIPKEAGLKRCGKSCRLRWMNYLRPDIKRGNISPDEEDLIIRLH
KLLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRGQKGERGPKSNHSGVGGKPIITVKVDEDLVSSRVIRTKALRFKEVFITPD
AQQHRIENHHRNVAIPPSMDPNLVQNPAGSESSDRSLITLSSNEEYPVDFMVDISAGEISVPEIFASDFTSFSDHDLGASEM
DKVMRGDDADNYMSKIAPSQAFLPEEMEQNWSGSDYYIQANLDSDFGSLTAFLESAAEWLI

alignment with top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 211 bits (538), Expect = 4e-55, Method: Compositional matrix adjust.
Identities = 96/135 (71%), Positives = 112/135 (82%)
Frame = -1

Query: 1 MGRRPCCSKEGMNRGAWTLTEDKILTDYVKVHGEKWRNIPKEAGLKRCGKSCRLRWMNY 60
MGR PCCSK G++RG WT ED +L Y++ HG+G WR++PK+AGL RCGKSCRLRWMNY
Sbjct: 1167 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRS LPKAGLLRCGKSCRLRWMNY 988
Query: 61 LRPDIKRGNISPDEEDLIIRLHKLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRGQKKE 120
LRPDIKRGNI+PDE+DLIIRLH LLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKR +
Sbjct: 987 LRPDIKRGNITPDEEDLIIRLHSLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLLSQG 808
Query: 121 RGPKSNHSGVGGKPI 135
P + H K+ + P+
Sbjct: 807 TDPNT-HKKLSEPPV 766

>Tc09_t005580

MGRKPCCSKEGLNRGAWSAIEDQILIDYIKTNGEGKVGWGNIPKKAGLKRCGKSCRLRWLNLYLRPDIKRGNISQEEEDLIIRLH
KLLGNRWSLIAGRIPGRTDNEIKNYWNSTLGKVKKAEQAKQSKDDLKAKIQPLAETPOSTALRTKASKCSTCLVTQEAAYKA
EIIDADLVHDARLEPPKSEGTLTSTISEEAHSVNSALEFDIGELLASDISDSEFWNCCQVNNTSMEEAESSGVARNMWSLSE
QHLQFSEEMLTDWIRDDI

alignment with the top contig hit

>[CL2621Contig1](#)

Length = 1332

Score = 201 bits (511), Expect = 4e-52, Method: Compositional matrix adjust.
Identities = 98/185 (52%), Positives = 128/185 (69%), Gaps = 15/185 (8%)
Frame = -1

Query: 3 RKPCCSKEGLNRGAWSAIEDQILIDYIKTNGEGKVGWGNIPKKAGLKRCGKSCRLRWLNLYLR 62
RKPCCK+G N+GAWS EDQ LIDYI+T+GEG W ++PK AGL RCGKSCRLRW+NYLR
Sbjct: 1224 RKPCCDKQGTNKGAWSKQEDQKLIDYIRTHGEGCWRS LPKAAGLHRCGKSCRLRWLNLYLR 1045
Query: 63 PDIKRGNISQEEEDLIIRLHKLGNRWSLIAGRIPGRTDNEIKNYWNSTLGKVKKAEQAK 122
PDIKRGNI+Q+EEEDLII+LH LLGNRWSLIAGR+PGRTDNE+KNYWNST + +K+
Sbjct: 1044 PDIKRGNFAQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSTHIKRLIKLIGID 865
Query: 123 QSKDDLKAKIQP-----LAETP-QSTALRTKASKCSTCLVTQEAAYKAEII 167
+ L + ++P +A P +S+A + + S ++CL + + + +
Sbjct: 864 PNNHKLNYPLRPQPQHVSPSSPASLNVARKPRRSSAAKDRVSDAASCLEDERSGRVSKL 685
Query: 168 DADLV 172
D DL
Sbjct: 684 DLDLT 670

>Tc01_t029340

MWMRRVAGGNHRMFLIFGWQTGSKTSMCLCSSFRTSIKTGNSDPIHWETTANFRLGVCTFSYIQTPAONTGRDTIEQQQMGRK
PCCSKEEGLNRGAWTATEDKILTLDYIKARGEKGRSIPKAAGLKRCEKSCRLRWLNLYLRPGIKRGNITRDEEDLIIRLHKLL
GNRWSLIAGRLPGRTDNEIKNYWNTVLSKRAQVKKFDHTNKDETKQRFISWSKKAPTSSGVIQAKAGRCTKVFTTPQQQVIG
RGENNNIARTAPSTDAKFVHETAVESGFSDGSFTLLSSKEENPSISKFAMDFDIGDINISEALASDFAQLGDFELRDINSVI
YEYGTNDCGQALLSAEGMVGNWSGNDVCVEANLDSDFGLAAFLGSAEL

alignment with the top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 196 bits (498), Expect = 2e-50, Method: Compositional matrix adjust.
Identities = 95/151 (62%), Positives = 111/151 (73%)
Frame = -1

Query: 74 IEQQQMGRKPCCSKEEGLNRGAWTATEDKILTLDYIKARGEKGRSIPKAAGLKRCEKSCR 133
+ ++ MGR PCCSK GL+RG WT ED +L YI+A G+G WRS+PK AGL RC KSCR
Sbjct: 1182 LRERGMGRAPCCSKV-GLHRGPWTPREDTLLVKYIQAHGDGHWRS LPKKAGLLRCGKSCR 1006

Query: 134 LRWLNLYLRPGIKRGNITRDEEDLIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTVLSK 193
LRW+NYLRP IKRGNIT DE+DLIIRLH LLGNRWSLIAGRLPGRTDNEIKNYWNT LSK
Sbjct: 1005 LRWMNYLRPDIKRNITPDEDDLIIRLHSLGNRWSLIAGRLPGRTDNEIKNYWNT HLSK 826

Query: 194 RAQVKKFDHTNKDETKQRFISWSKKAPTSSG 224
R + D + + + +K +S G
Sbjct: 825 RLLSQGTDPNTHKKLSEPPVQQVEKRKSSRG 733

>Tc01_t004300

MGRKPCCLKEGVNKGAWSAQEDKILTNYIELHGEKGNWNTLPQKAGIRLNRCGKSCRLRWNYLRPGIKRGNISPDEEDLIIR
LHRLGNRWSLIAGRLPGRTDNEIKNYWNSVLSKKNLGDASKPPNRQCECEGKESVEKYRSGSTPNVIAPKARRCTGTLLISL
VKG NHLPNPCLASSTPADDEL TLESQKDDVQMPNVEDEALIDSELYMPNTLDYLD FSQTRIEDMFENGMHSEELAPMLEM
ELENLTSLGLLEDEWRELDVEND

alignment with the top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 191 bits (486), Expect = 4e-49, Method: Compositional matrix adjust.
Identities = 88/125 (70%), Positives = 103/125 (82%)
Frame = -1

Query: 1 MGRKPCCLKEGVNKGAWSAQEDKILTNYIELHGEKGNWNTLPQKAGIRLNRCGKSCRLRWM 60
MGR PCC K G+++G W+ +ED +L YI+ HG+G W +LP+KAG L RCGKSCRLRWM
Sbjct: 1167 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRS LPKKAG--LLRCGKSCRLRWM 994

Query: 61 NYLRPGIKRGNISPDEEDLIIRLHRLGNRWSLIAGRLPGRTDNEIKNYWNSVLSKKNLNG 120
NYLRP IKRGNIT+PDE+DLIIRLH LLGNRWSLIAGRLPGRTDNEIKNYWN+ LSK+L
Sbjct: 993 NYLRPDIKRNITPDEDDLIIRLHSLGNRWSLIAGRLPGRTDNEIKNYWNT HLSKRLLS 814

Query: 121 DASKP 125
+ P
Sbjct: 813 QGTDP 799

>Tc02_t026610

MGRKPCCSQEEGLNRGTWTATEDKILTEYIKAHGEGKWSIPKAAGLKRCGKSCRLRWLNYPDIKRGNITRDEEDLIIRL
HKLLGNRWSLIAGRLPGRDNEIKNYWNSVLSKRAQVKEFDHTNKDEKKQRFISCSRKAPTSSGVIHAKAGRCTKVSFSPQQ
KVTGEDDNTIVRTAPSMDVELVHDTAVVSGSSDGSFTLLSSKEENPSISRFAAMDFDIGESSIPEALASDFSQLSDFDFCDI
NTVIYEYGTGDNGQALVSLGEMVGNWSGNGLVDANLDSDFGFLAGFLES DGDLTI

alignment with the top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 202 bits (513), Expect = 3e-52, Method: Compositional matrix adjust.
Identities = 92/116 (79%), Positives = 102/116 (87%)
Frame = -1

Query: 1 MGRKPCCSQEEGLNRGTWTATEDKILTEYIKAHGEGKWSIPKAAGLKRCGKSCRLRWLN 60
MGR PCCS+ GL+RG WT ED +L +YI+AHG+G WRS+PK AGL RCGKSCRLRW+N
Sbjct: 1167 MGRAPCCSKV-GLHRGPWTPREDTLLVKYIQAHGDGHWRSLPKKAGLLRCGKSCRLRWLN 991

Query: 61 YLRPDIKRGNITRDEEDLIIRLHKLLGNRWSLIAGRLPGRDNEIKNYWNSVLSKR 116
YLRPDIKRGNIT DE+DLIIRLH LLGNRWSLIAGRLPGRDNEIKNYWN+ LSKR
Sbjct: 990 YLRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRDNEIKNYWNTHLSKR 823

>Tc01_t034240

MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRSLPKKAGLLRCGKSCRLRWLNYPDIKRGNITPDEDDLIIRLH
SLLGNRWSLIAGRLPGRDNEIKNYWNTHLSKRLLSQGTDPNTHKKLSEPAVQQVKKRKS SRGNSNKKQNSKKGKAKVEPE
KPKVHLPKPVVTSFSLPRNDSFDQCNTFSTVSSSQGEGGLGTEVVQGPWSDNVNDDENGTFGLAAYDDHGFVNGSDFECQ
SHVPASDDDNSLEKLYEEYLQLLKTNDQVQLDSFAESLLI

alignment with the top EST contig hit

>[CL1309Contig1](#)

Length = 1392

Score = 514 bits (1325), Expect = e-146, Method: Compositional matrix adjust.
Identities = 252/287 (87%), Positives = 252/287 (87%)
Frame = -1

Query: 1 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRSLPKKAGLLRCGKSCRLRWLN 60
MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRSLPKKAGLLRCGKSCRLRWLN
Sbjct: 1167 MGRAPCCSKVGLHRGPWTPREDTLLVKYIQAHGDGHWRSLPKKAGLLRCGKSCRLRWLN 988

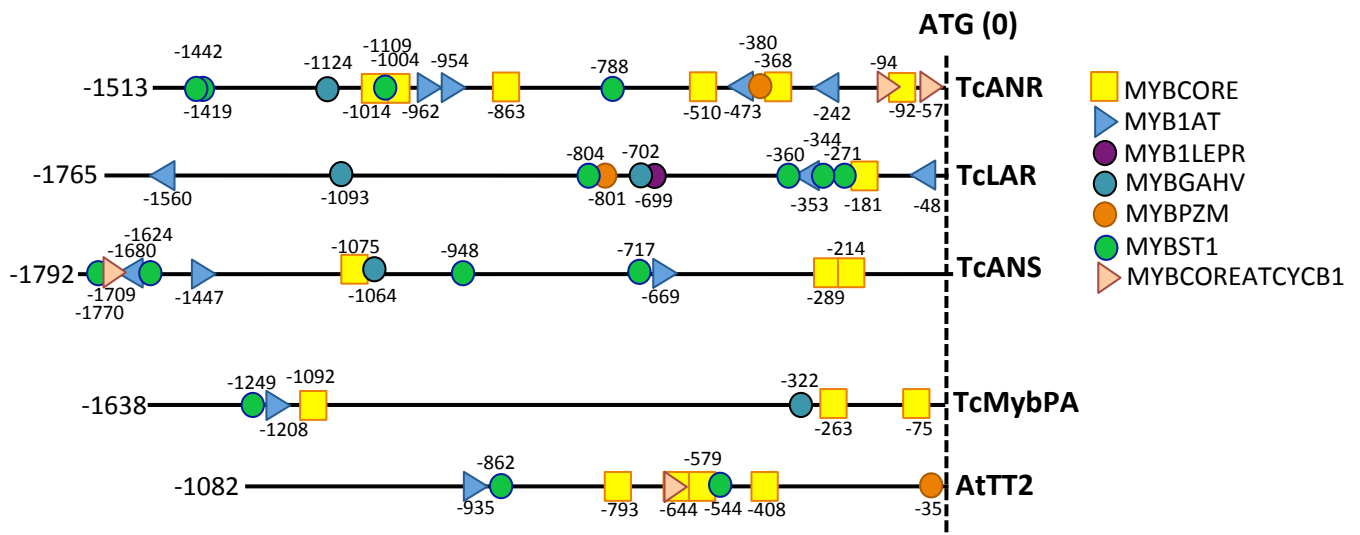
Query: 61 LRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRDNEIKNYWNTHLSKRLLSQG 120
LRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRDNEIKNYWNTHLSKRLLSQG
Sbjct: 987 LRPDIKRGNITPDEDDLIIRLHSLGNRWSLIAGRLPGRDNEIKNYWNTHLSKRLLSQG 808

Query: 121 TDPNTHKKLSEPAVQQVXXXXXXXXXXXXXXXXXXXXXXXXAKVEPEKPKVHLPKPVVTSFS 180
TDPNTHKKLSEP VQQV AKVEPEKPKVHLPKPVVTSFS
Sbjct: 807 TDPNTHKKLSEPPVQQVEKRRKSSRGNSNKKQNSKKGKAKVEPEKPKVHLPKPVVTSFS 628

Query: 181 LPRNDSFDQCNTFSTVSSSQGEGGLGTEVVQGPWSDNVNDDENGTFGLAAYDDHGFVNG 240
LPRNDSFDQCNTFSTVSSSQGEGGLGTEVVQGPWSDNVNDDENGTFGLAAYDDHGFVNG
Sbjct: 627 LPRNDSFDQCNTFSTVSSSQGEGGLGTEVVQGPWSDNVNDDENGTFGLAAYDDHGFVNG 448

Query: 241 SDFECQSHVPASDDDNSXXXXXXXXXXXXXXXXTNDQVQLDSFAESLLI 287
SDFECQSHVPASDDDNS TNDQVQLDSFAESLLI
Sbjct: 447 SDFECQSHVPASDDDNSLEKLYEEYLQLLKTNDQVQLDSFAESLLI 307

Supplemental Figure S1. Sequence analysis of other putative cacao TT2 like genes



Supplemental Figure S2. MYB-binding motifs in the promoters of cacao PA synthesis genes, *TcANR*, *TcLAR*, *TcANS*, transcription factor *TcMybPA* and Arabidopsis *AtTT2* detected using the PLACE database (<http://www.dna.affrc.go.jp/PLACE/signalup.html>).