Additional File 2

Figure S2. Maize BX2-BX5 alignment showing putative helices, P450 motifs, SRSs and sites under positive selection according to M8 results. In blue are sites potentially under positive selection according to M8 results from codeml analyses. Putative helices are indicated in dotted boxes, SRSs are in orange boxes and the five P450 motifs are in purple.

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                1                                                          53
BX4_Z_mays      MALE---AAYD-YLHVAVVQC--TPTQAAAVL-----GVLLLLAIRLAAAARSSSATSPK
BX3_Z_mays      MALG---AAYHHYLQLAGDHG---TATHALLL-----GVLIFLVIRLVSARRTGTTSANK
BX5_Z_mays      MALQ---AAYE-YLQQAVGHGAWSSTQTLTLL-----LIAVPTVLLLLASLAKSTSSSGR
BX2_Z_mays      MAAQLHHALYE-LLHEAA------AAQRALLLAIPFSLLLLPLLLRYLAASASASASATK

               54                                                         112
BX4_Z_mays      W---------KQH---RLPPTPPGKLPIIGHLHLIGSHPHVSFRDLHAKYGHNGLMLVQV
BX3_Z_mays      R---------KQQQRLPLPPSPPGKLPIIGHLHLIGAETHISIRDLDAKHGRNGLLLLRI
BX5_Z_mays      G---------KP----PLPPSPPGTLPIVGHLHHIGPQTHISLQELVAKYGHNGFLFLRA
BX2_Z_mays      NDGAAAVAASDPDKLLSLLPSPPMKLPIIGHLHLMGDIPYVSLAALATRYGPD-LMLLRL

              113                                                         172
BX4_Z_mays      GAVPTIVVSTPQAAEAVLRTHDHVLASRPRNPVADIIRYNSTDVAFAPYGEYWRTARKVV
BX3_Z_mays      GAVPTLFVSSPSAADAVLRTQDHIFASRPPSMAAEIIRYGPSDVAFVPYGEYWRQGRKLL
BX5_Z_mays      GAVPTLIVSSPSAAEAVMRTHDHIFASRPWSMASHILRYNTCDVAFSPLGEYWQQTRKLM
BX2_Z_mays      GAVPTVVVSSPRVAEAVLRTYDHVFSSRPRSLVSDIIMYGATDSCFAPYGDHFRKARKLV

              173                                                         230
BX4_Z_mays      NTHLLSAKMVFSKRREREEEVRLVVARIRDAAEASPGTALDMTELLGGYASDFVCRAVLG
BX3_Z_mays      TTHMLSTKKVQSFRHGRQEEVRLVMDKIRAAATAAPPAAVDLSDLLSGYTNDVVCRAVLG
BX5_Z_mays      NTHLLSNKKVYSFRHGREEEVCLVVDNLREAAAKSPSTAVDMSEVLAAYTNDVVSRSVLG
BX2_Z_mays      TVHLLNASKVRSQRPAREEEVRGALDRVRRAAAAR--EALDMSELLHSFVNNLVCRAVSG

              231                                                         289
BX4_Z_mays      ESHRKQGRNKLFRELTETSAALLGGFNVEDYF-PKLADVDLFLRIICAKAKGVSKRWDSL
BX3_Z_mays      ASHRNQGRNRLFSELTEINVSLLGGFNLEDYFPPNMAMADVLLRLVSVKARRLNQRWNDV
BX5_Z_mays      STHRKKGRNTLFREMTMTNVDLLVGFNLEYYI-PRWPLTDLLFRLVCWKVTRHLKRWDAL
BX2_Z_mays      KFSMEEGRNRLFRELTDINAGLLGGFHIQDYF-PSLGRIELVRKVACAKTRRVRKRWDDL

              290                                                         348
BX4_Z_mays      FNELLSEYALSGGKQGD--HNSEDFVHLLLSLQKDYGLTTDNIKGILVNMFEAAIETSFL
BX3_Z_mays      FDELIQEHVQSR-PSGESEESEADFIHVLLSIQQEYGLTTDNLKAILVDMFEAGIETSYL
BX5_Z_mays      LEEVIHEHVEMRKLSGDKEKESDDFIDIFLSRYEEYGFTMDNVKSLLMNVFEAAIETSYL
BX2_Z_mays      LDKLIDDHA-ARMATHQDEDDDKDFIYVLLSLQKEYGLTRDHIKAILIDMFEAGTDTSYM

              349                                                         404
BX4_Z_mays      VLEYSMSELMNNRHVLAKLQKEVRTA--TPDGR---MVMEEDLSRMPYLKATIKESMRIH
BX3_Z_mays      TLEYGMAELINNRHVMEKLQTEVRTTMRSPDGKKLDMLAEEDLGSMPYLKATIKETLRLH
BX5_Z_mays      VLESAMAELMNHRRVMKKLQAEVRA---YGAEKKLDMIREDDLSSLPYLKASMKEALRLH
BX2_Z_mays      TLEFAMTELIRKPHLMKKLQEEVRRN--VPAGQ--EMVTEDNLPGMTYLKAVIKETLRLH

              405                                                         464
BX4_Z_mays      PPAPFLLPHFSTHDCEINGYTIPAGTRVIVNAWALARDPTCWDKAEEFFPERFLEQGRDA
BX3_Z_mays      PPAPFLLPHYSTADSEIDGYFVPAGTRVLVNAWALGRDRTTWEKPEEFMPERFVQEPGAV
BX5_Z_mays      PPGPLLLPHYSTADCQIDGYHIPANTRVLVNGWAIGRDPAVWEKPEEFMPERFMRDGWDK
BX2_Z_mays      PPVPLLLPHYSLDACEVAGYTIPANTRVVVNAWALGRHSGYWERENEFVPERFLSGDVAG

              465                                                         523
BX4_Z_mays      EVDMYGKDIRFVPFGAGRRICAGATFAIATVEIMLANLIYHFDWEMPAEMERTGAKVDMS
BX3_Z_mays      DVHMKGKDLRFIPFGSGRRICPGMNFGFATMEIMLANLMYHFDWEVPG----SAAGVSMD
BX5_Z_mays      SNSYSGQDFRYLPFGSGRRICPGANFALATMEIMLANLMYHFDWEVPNEKEDGGGKVSMD
BX2_Z_mays      GVDLKPNEFQFLAFGSGRRMCPGVHSASATIEAMLSNLMYRFDWQLPAGM--KAEDVDMT

              524               542
BX4_Z_mays      DQFGMTLRRTQKLYLVPRIPK
BX3_Z_mays      ESFGLTLRRKEKLLLVPRIAS
BX5_Z_mays      ETFGLMLRRNEPLYLVPRAV-
BX2_Z_mays      EVFGITVSRKEKLLLVPQAA-
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Figure S2