Supplemental Figure S1.

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BpCBF2       1 -GAMHLSDEEIQLASRNPKKRAGRTKFKETRHPVYRGVRRRNSGKWVCEVREPNKQSRIW
BpCBF4       1 -GAMNLSDEEIQLASRNPKKRAGRKKFKETRHPVYRGVRRKNSGKWVCEVREPNKQSRIW
BpCBF1       1 -GAMHLSDEEIRLASRNPKKRAGRKKFKETRHPVYRGVRRRNSGKWVCEVREPNKQSRIW
PtCBF1       1 QPGAIFSDEEVILASRNPKKRAGRKKFRETRHPVYRGVRRRNSGKWVCEVREPNKKSRIW
PtCBF2       1 -----------MLASRNPKKRAGRKKFRETRHPVYRGVRRRNSGKWVCEVREPNKKSRIW
AtCBF1       1 ----QGGDYCPTLATSCPKKPAGRKKFRETRHPIYRGVRQRNSGKWVSEVREPNKKTRIW
AtCBF2       1 --VSSGGDYSPKLATSCPKKPAGRKKFRETRHPIYRGVRQRNSGKWVCELREPNKKTRIW
AtCBF3       1 --VSSGGDYIPTLASSCPKKPAGRKKFRETRHPIYRGVRRRNSGKWVCEVREPNKKTRIW
PtCBF3       1 --DSPSSNEKVLLATSRPKKRAGRRIFKETRHPIFRGVRKRNGDKWVCELREPNKKSRIW
PtCBF4       1 --RVVHSDEEVLLATSFPKKRAGRRIFRETRHPVFRGVRKRNGNKWVCEMREPNKKSRIW
BpCBF3       1 --AVDNYDEEVLLASSMPKRRAGRKKFKETRHPVYRGVRRRNKNKWVCEMRKPNEKTRIW
consensus    1       ..... **.. **..***..*.*****..****..*..***.*.*.**...***

BpCBF2      60 LGTFPTAEMAARAHDVAAIALRGNSACLNFADSAWRLPLPASGTAKDIQRTAVEAAEAFR
BpCBF4      60 LGTFPTAEMAARAHDVAAIALRGNSACLNFADSALRLPVPASVTAKDIQRTAAEAAEAFR
BpCBF1      60 LGTFPTAEMAARAHDVAAIALRGNSACLNFADSAWRLPVPASGTAKDIQRTAAEAAEEFR
PtCBF1      61 LGTFPTADMAARAHDVAALALRGRSACLNFADSAWRLPTPASSDAKDIQKAAAEAAEAFR
PtCBF2      50 LGTFPTAEMAARAHDVAALALRGRSACLNFADSAWRLPVPASSEAKDIQKAAAEAAGGFR
AtCBF1      57 LGTFQTAEMAARAHDVAALALRGRSACLNFADSAWRLRIPESTCAKDIQKAAAEAALAFQ
AtCBF2      59 LGTFQTAEMAARAHDVAAIALRGRSACLNFADSAWRLRIPESTCAKEIQKAAAEAALNFQ
AtCBF3      59 LGTFQTAEMAARAHDVAALALRGRSACLNFADSAWRLRIPESTCAKDIQKAAAEAALAFQ
PtCBF3      59 LGTYPTPEMAARAHDVAALAFRGKSACLNFADSAWRLPVPISNEAKDIRRAASEAAELFR
PtCBF4      59 LGTYPTPEMAARAHDVAALALRGKSACLNFADSAWRLPVPVSKDSKDITRAANEAAELFR
BpCBF3      59 LGTYPSAEMAARAHDVAALALRGSSACLNFADSAWSLPVPASTDAGEIQRAAAAAAEGFQ
consensus   61 ***.....**********.*.**.**********..*..*.*. ...*...*..**..*.

BpCBF2     120 PTETKAVE----ERQPSEG----------------VFFMDEEAVFGMPGLLVNMAEGMLL
BpCBF4     120 PAETKAAE----ERQPSEG----------------VFFMDEEAVFGMPGLLVNMAEGMLL
BpCBF1     120 PAESKAVE----DRQPSES----------------LFFMDEEAVFGMPGLMINMAEGMLL
PtCBF1     121 PEGSLGVE----LTRTGDEVEKVAGTAAGD-----VFYMDDDADFGMPGLLANIAEGMLL
PtCBF2     110 PEGCVGGE----LMRTGDEGEKAAETTAEAG--EEVFYMDDEAVFGMPGLLANMAEGMLL
AtCBF1     117 DETCDTTT----TDHGLDMEETMVEAIYTPEQSEGAFYMDEETMFGMPTLLDNMAEGMLL
AtCBF2     119 DEMCHMTT----DAHGLDMEETLVEAIYTPEQSQDAFYMDEEAMLGMSSLLDNMAEGMLL
AtCBF3     119 DEMCDATT----DHG-FDMEETLVEAIYTAEQSENAFYMHDEAMFEMPSLLANMAEGMLL
PtCBF3     119 TSDLGGQVMEDFRREDRGEVCSSTNDDIRDLPSENVGYIDEEAEFNMPGLLASMAEGLLL
PtCBF4     119 PQEFG-------------ENDVFFKEAVFAMPGEND-VFFEEAVFDMPGLLVDMAEGLLL
BpCBF3     119 PSEFG-EDCEEVLERCTERVDDHQEAEVRGVEESGVLYMDEEAVFDMPGLLANMAEGLLL
consensus  121 . .  . .         .  .              ...........*..*. ..***.**

BpCBF2     160 PPPYCVGDDDVYGGDDVEAH-ADVSLWSYSI
BpCBF4     160 PPPYCVGDDDGYGGDDVEAH-ADVSLWS---
BpCBF1     160 PPPYCVGDDDGYGGDVMEAH-AEVSLWSYSI
PtCBF1     172 PPPNCCGYSGGDSLDNMENNDTDMSLWSFSV
PtCBF2     164 PPPHCG--GGGDGWDNMENIDADMPLWSFSI
AtCBF1     173 PPPSVQWNHNYD----GEGDGD-VSLWSY--
AtCBF2     175 PSPSVQWNYNFD----VEGDDD-VSLWSY--
AtCBF3     174 PLPSVQWNHNHE----VDGDDDDVSLWSY--
PtCBF3     179 SPPHYTG-----DWNDGE-IDADWSLWSS--
PtCBF4     165 SPPRYVR-NDCNDLDHME-NGSDLSLWSY--
BpCBF3     178 SPP---------QWDDMESIISEVSLWSFSI
consensus  181 ..*          . ...   ...***.
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Supplemental Figure S1. Sequence alignment of C-REPEAT BINDING FACTOR/DROUGHT RESPONSIVE ELEMENT BINDING (CBF/DREB1) protein family members of Arabidopsis, poplar and birch.