```
GmDREBP         ----------------------------------------------------------    0
OsDREBP2A       -----------------------------------ME---------------------    2
TaDREBP1       ------------------------------------MET--------------------    3
DREBP1A         ----------------------------------------------------------    0
CRT/DREBP       ----------------------------------------------------------    0
OsDREB1F        -----------------------------------MDT--------------------    3
CbCBF           --------------------------MNSSFSAFSEMF---------------------   12
BnCBF           --------------------------MNSVSTFSELL---------------------   11
CaCBF1B         --------------------------MNIFRSYYSDPLTE------------------   14
PaDREB1F        --------------------------MDMFFSQLSDSVDQ------------------   14
GhDBP           MAAAMDF---ISIGVDQSDLYGGELMEALEPFMKSVSSSSPSPSPSPSPSSLPSTSYLSF  57
GmDREBP_NP      MGTAIDMYNSSNIVADFLDPYSEELMKALKPFMKSDYFSASSSSSL-------------  46
ZmDBF1          ----------------------------------------------------------    0
TINY2           --------------------------------MAEEYYSL------------------    8
ERF034          --------------------------------MVEPLS------PT------------    8
ZmDBF2          --------------------------------MAQELHETSSCSAT------------   14
ERF038          --------------------------------MAMAKELQETSSSSS-----------   15
GhDREBP1        ----------------------------------------------------------    0
ERF_QDB64575.1  --------------------------------MVD---TPRSS----------------   8
ERF_QCF46602.1  --------------------------------MVDKQRLHTSS---------------   11
ERF             --------------------------------MVEK--IAVSS---------------    9
PpDBF1          --------------------------------MVEK--VVVSS---------------    9
DsDBF1          --------------------------------MVEK--TAPSS---------------    9
DREBP5          --------------------------------MVEK--AVSST---------------    9
ERF039-like     ----------------------MGESIGVVAEQQPTT---------------------   15
OsRAP           ----------------------------------------------------------    0
ERF_TINY-like   --------------------------------MVQK----------------------    4
GmDREBP3        ----------------------------------------------------------    0
ERF016          ----------------------------------------------------------    0
ERF016_XP       ----------------------------------------------------------    0

GmDREBP         -------------------------------MHMLVK-NHNKGDGSKSLADTLAKW------   24
OsDREBP2A       -----RGEGRRGD-----------CSVQVRKKR-TRRKSDGPDSIAETIKWN------   37
TaDREBP1        -----GGSKREGD-----------CPGQERKKK-VRRRSTGPDSVAETIKKW------   38
DREBP1A         -----------------------------------------------------------    0
CRT/DREBP       -----------------------------------------------------------    0
OsDREB1F        -----------------------------------------------------------    3
CbCBF           -----------------------------------------------------------   12
BnCBF           -----------------------------------------------------------   11
CaCBF1B         -----------------------------------------------------------   14
PaDREB1F        -----------------------------------------------------------   14
GhDBP           SSSETQPNFYPDSCCYPYPTPMDSVSCPQQPQTGSTIGLNSLTQAQIHQIQLQFHLHNNQ  117
GmDREBP_NP      ---ESQ------PCSF------SSNSLPTSYPSSNQIKLNQLTPDQIVQIQAQIHIQQQQ   91
ZmDBF1          ------------------------------------MQFIQAQLHLQRNP           14
TINY2           ------------------------------RS---------------------------   10
ERF034          -----SSSACSSSCLPTS-----------------------------------------   21
ZmDBF2          -----TTSSCTTSCCSSTVT--DSSSSPPSPAAANAAPA--------------------   46
ERF038          ------SSAASTSSCSSAVT--DAWSSPARPNAVAGGK---------------------   45
GhDREBP1        ------------------------------M----------------------------    1
ERF_QDB64575.1  ------------------------------PVS--------------------------   11
ERF_QCF46602.1  ------------------------------PSR--------------------------   14
ERF             ------------------------------LHA--------------------------   12
PpDBF1          ------------------------------LRR--------------------------   12
DsDBF1          ------------------------------ISA--------------------------   12
DREBP5          ------------------------------LRG--------------------------   12
ERF039-like     ------------------------------IWD--------------------------   18
OsRAP           -----------------------------------------------------------    0
ERF_TINY-like   ------------------------------DWS--------------------------    7
GmDREBP3        -----------------------------------------------------------    0
ERF016          -----------------------------------------------------------    0
ERF016_XP       -----------------------------------------------------------    0
```

```
GmDREBP          ----------------KEYNAWLESNNE---------AEKPVRKVPAKGSKKGCMKGKG    58
OsDREBP2A        ----------------KEQNQKLQEE------------NSSRKAPAKGSKKGCMAGKG    67
TaDREBP1         ----------------KEENQKLQQE------------NGSRKAPAKGSKKGCMAGKG    68
DREBP1A          ---MCGIKQEM-----------SGESSGSPCS-SAS-AERQH-QTVWTAPPKRPAGRTK   42
CRT/DREBP        ----------M-------------DT------AA-AGS-PREGH-RTVCSEPPKRPAGRTK  29
OsDREB1F         ----------------EDTSSASSSSVSPPSSPGGGH---HHRLPPKR----RAGRKK   38
CbCBF            --------------------GSEYESPVSSGGGDYCPTLATSCPKK----PAGRKK    44
BnCBF            -------------------RSENESPVNTEGGDYI--LAASCPKK----PAGRKK    41
CaCBF1B          ------------------SSSSFSDSSIYSPNRAIFSDEEVILASNNPKK----PAGRKK   52
PaDREB1F         ------------------PQSSLLSDASVTTRGASCSDGDVILASSRPKK----RAGRRV   52
GhDBP            PSYLCQSPQPNTISANSNPMVSFLCPK-----------------------PVPMKHVG   152
GmDREBP_NP       QHV-------------AQTQTHLGPK-----------------------RVPMKHAG   112
ZmDBF1           G--------------------LGPR-----------------AQPM-KPAVPVPPAP   33
TINY2            ----------------ERVTQLLVPNSESD----------SVS-DKSKAEQSEKKTKRG   42
ERF034           ------------------------------------KSEEKETNAVCG---SRAVKKQII   42
ZmDBF2           ------------------TRKRQALEAEAEAEA---GGEEEEEEEEGCAGNKAAPAKKRPR  86
ERF038           ------------------RKKEVVGEADEAAGGGAGEEEEEEEAEAAAAGKSSAATKKRKR  87
GhDREBP1         ----------------ELGDCCLTS--------------------SPASGEKRKLH   21
ERF_QDB64575.1   ------------------RRGSGFLKP-----------KKKRKSKKGCKGVMSE--GGGD   40
ERF_QCF46602.1   ------------------RRGSKFLKS-----------SRKKKKQKEEAGSSAE--KE-S   42
ERF              ------------------KRGGNLLAS-----------LKLNA-YSIAKKSSSKLVKPVS   42
PpDBF1           ------------------KRGGNLLAP-----------LKRNV-SSIAKKSSTPK---SG   39
DsDBF1           ------------------KRGGKLLAP-----------LK-THSGAIAKKSSAPEKLSIS   42
DREBP5           ------------------KRGGSLLAP-----------TLRARSGVIGKKLSSH-----V   38
ERF039-like      ------------------RRRSKR-------------------RVVE---SSDEYPPTSP   38
OsRAP            ------------------------------------MS-----------SSSPVVA    9
ERF_TINY-like    ------------------SRGTLDIGT-----------DTLHCQGLG---RDKQQHAMMK   35
GmDREBP3         ------------------------------------MAKPSSE---------KP--    9
ERF016           ------------------------------------MVRPSGG---------RE--    9
ERF016_XP        ------------------------------------MVRPGRG---------RDNG   11

GmDREBP          GPENLRCNYRGVRQRTW-GKWVAEIREPNR-GSRLWLGTFPTAISAALAYDEAAMAMYG-  115
OsDREBP2A        GPENSNCAYRGVRQRTW-GKWVAEIREPNR-GRRLWLGSFPTALEAAHAYDEAARAMYG-  124
TaDREBP1         GPENSNCAYRGVRQRTW-GKWVAEIREPNR-GNRLWLGSFPTAVEAARAYDDAARAMYG-  125
DREBP1A          FRETRHPVFRGVRRRGNAGRWVCEVRVPGRRGCRLWLGTFDTAEGAARAHDAAMLAINAG  102
CRT/DREBP        FRETRHPLYRGVRRRGRLGQWVCEVRVRGAQGYRLWLGTFTTAEMAARAHDSAVLALLD-  88
OsDREB1F         FRETRHPVYRGVRARAGGSRWVCEVREPQA-QARIWLGTYPTPEMAARAHDVAAIALRGE  97
CbCBF            FRETRHPVYRGVRRNS-GKWVCEVREPNK-KSRIWLGTFPTADMAARAHDVAAIALRG-  101
BnCBF            FQETRHPIYRGVRLRKS-GKWVCEVREPNK-KSRIWLGTFKTAEIAARAHDVAALALRG-  98
CaCBF1B          FRETRHPVYRGVRKRNS-GKWVCEVREPNK-KSRIWLGTFPTAEMAARAHDVAAIALRG-  109
PaDREB1F         FKETRHPVYRGVRRRNN-DKWVCEMREPNKKKSRIWLGTYPTAEMAARAHDVAALAFRG-  110
GhDBP            APSKPTKLYRGVRQRHW-GKWVAEIRLPRN-RTRLWLGTFDTAEEAALAYDKAAYKLRG-  209
GmDREBP_NP       TAAKPTKLYRGVRQRHW-GKWVAEIRLPKN-RTRLWLGTFDTAEEAALAYDNAAFKLRG-  169
ZmDBF1           APQRPVKLYRGVRQRHW-GKWVAEIRLPRN-RTRLWLGTFDTAEQAALAYDQAAYRLRG-  90
TINY2            RDSGKHPVYRGVRMRNW-GKWVSEIREPRK-KSRIWLGTFPTPEMAARAHDVAALSIKG-  99
ERF034           RDGRKHPTYRGVRMRTW-GKWVSEIREPRK-KSRIWLGTYPTAEMAARAHDVAALAIKG-  99
ZmDBF2           GSEGKHPTFRGVRMRAW-GKWVSEIREPRK-KSRIWLGTFPTAEMAARAHDVAALAIKG-  143
ERF038           SSDGKHPVYRGVRMRAW-GKWVSEIREPRK-KSRIWLGTFPTADMAARAHDVAALAIKG-  144
GhDREBP1         RTQQKEKPFRGIRMRKW-GKWVAEIREPNK-RSRIWLGSYTTPVAAARAYDTAVFYLRG-  78
ERF_QDB64575.1   EGGAPSKTFKGVRKRAW-GKWVSEIREPNK-RSRIWLGSFPTAEMAARAYDAAVVCLRG-  97
ERF_QCF46602.1   EIVPSKTSFKGVRKRAW-GKWVSEIREPNK-RSRIWLGSFPTAEMAARAYDAAVVCLRG-  99
ERF              LHSGSPKVYKGVRKRTW-GKWVSEIREPNK-RSRIWLGSFPTAEMAAKAYDAAAVCLRG-  99
PpDBF1           KPVGSPKVYKGVRMRTW-GKWVSEIREPNK-RSRIWLGSFPTAEMAAKAYDAAAVCLRG-  96
DsDBF1           QSPACPKLYKGVRMRTW-GKWVSEIREPNK-RSRIWLGSFPTAEMAAKAYDAAVVCLRG-  99
DREBP5           ETQSSSVHYKGVRMRTW-GKWVSEIREPNK-RSRIWLGSFPTAEMAAKAYDAAVVCLRG-  95
ERF039-like      EECDSSPSYKGVRRRSW-GKWVSEIREPRK-RSRIWLGSFATPEMAAKAYDYAVFCLRG-  95
OsRAP            SPPEMEKKYKGVRRRKW-GKWVSEIRLPNS-RDRIWLGSYDSPEKAARAFDAAFVTLRG-  66
ERF_TINY-like    EESTASPRYKGVRKRQW-GKWVSEIREPRK-RSRIWLGSFPTAEMAARAYDAAVVCLRG-  92
GmDREBP3         EEHSDSKYYKGVRKRKW-GKWVSEIRLPNS-RQRIWLGSYDTPEKAARAFDAAMFCLRG-  66
ERF016           ---GNNGRYKGVRMRKW-GKWVAEVRQPNS-RGRIWLGSYKTADEAARAYDAAVVCLRG-  63
ERF016_XP        VNNNSSARYKGVRMRKW-GKWVAEVRQPNS-RRRIWLGSYKTAEEAARAYDAAVFCLRG-  68
                    ::*:* *   .:**.*:*       *:***:: :    ** *.* *   :
```

```
GmDREBP         --FC---ARLNFPNVQVSTFS---EE------PSRNSP------AAAYQS--RNSPSAKE      153
OsDREBP2A       --PT---ARVNFADNSTDANS---GCTSAPSLMMSNGP------A--TIP--SD--EKDE      164
TaDREBP1        --AK---ARVNFSEQSPDANS---GCTLAPPLPMSNGA------TAASHP--SD--GKDE      167
DREBP1A         GGGGGGGACCLNFADSAWLLAVPR-----------SYRTLADVRHAVAEAVEDFFRRRLAD      151
CRT/DREBP       -----RAACLNFADSAWRMLPVLAAG------SSRFSSAREIKDAVAIAVLEFQRQRPVV      137
OsDREB1F        --RG---AELNFPDSPSTLPR-----------ARTASP-EDIRLAAAQAAELYRRPPPPL      140
CbCBF           --RS---ACLNFADSAWRLRI-------PESTGA-KEIQKAAAEAALAFQDEMMMS      144
BnCBF           --RG---ACLNFADSAWRLRI-------PETTCA-KDIQKAAAEAALAFEAEKSDT      141
CaCBF1B         --RS---ACLNFADSAWRLPV-------PASSDT-KDIQKAAAEAAEAFRPLKLEG      152
PaDREB1F        --KL---ACINFADSAWRLPV-------PASMDT-MDIRRAAAEAAEGFRPVEFGG      153
GhDBP           --DF---ARLNFPNLRHHGSH---VGDYKPLPSSVD--AKLQAICESLVQNPKQGSKKK      258
GmDREBP_NP      --EF---ARLNFPHLRHHGAFVFGEFGDYKPLPSSVD--SKLQAICESLAKQEEKPCCSV      222
ZmDBF1          --DA---ARLNFPDNAE---------SRAPLDPAVD--AKLQAICATIAAASSSSKNSK      133
TINY2           --TA---AILNFPELADSFPR-----------PVSLSP-RDIQTAALKAAHMEPTTSFSS      142
ERF034          --QS---AYLNFPDLAHQLPR-----------PATASP-KDIQFAAAKAAAAPKSDGRH-      141
ZmDBF2          --RA---AHLNFPDLAGALPR-----------AASAAP-KDVQAAAALAAAFTSPSS-EP      185
ERF038          --RA---AHLNFPDLAGVLPR-----------AASASP-KDVQAAAALAAAFTTSPSSSP      187
GhDREBP1        --PS---ARLNFPDLIFQED------------EL-RDISAASIRKKATEVGAKVDA      116
ERF_QDB64575.1  --SN---ATLNFPDSPPSSLL-----------LPHCLSP-RDIQAAAAAAAAAAPPA-DE      140
ERF_QCF46602.1  --SN---ATLNFPNSPPSSL-----------PLCGSP-RQIQAAAAAAAAAAPDP-DE      140
ERF             --QS---VKLNFPDSPPQGV-----------QRCTSP-RDVQAAAAAAAACILPA-SA      140
PpDBF1          --RS---VKLNFPDSPPRCA-----------ARCNSP-REVQAAATAAAVACIPSA-TA      137
DsDBF1          --QS---ATLNFPDSPPQCI-----------SPSRAP-KDVQAAAAAAAACASAS---      138
DREBP5          --QS---ATLNFPDSPPQCV-----------SPSREP-KDVQAAAAAAAACCTSS-AT      136
ERF039-like     --PS---AMLNFPDSPPVISP-----------GKKLTSSKDIQAAAAAAAKKKAVPRPAS      139
OsRAP           --HGAAGADLNFPDSPPSCD-----------ARSSDP-RQVQAAALSHANRAHVTPQQA      111
ERF_TINY-like   --PS---AALNFPDSPPLSL-----------PECHTP-REIQVVAAAAATAAESCTPLN      134
GmDREBP3        --RN---AKFNFPDNPPDIAG-----------GTSMTP-SQIQIAAAQFANAGPHEG---      106
ERF016          --SS---ATLNFPDNPPEIPL-----------ADEMTP-VQIQEFAFRHARRAPAQS---      103
ERF016_XP       --SS---GKLNFPDNPPDIAD-----------ASELTP-EQIQEAAFRHARKDITEE---      108
                      .**  .


GmDREBP         SGSALVILERSECMMLWNNSGGDAAEDD----------G-----MED------LSLSLSVK      193
OsDREBP2A       LESPPFIVANGPAVLYQ-PDKKDVLERV---------V-----PEVQDVKTEGSNGLKRV      209
TaDREBP1        SESPPSLISNAPTAALHRSDAKDESESA----------G-----TVARKVKKEVSNDLRST      213
DREBP1A         DALSATS------------SSSTTP---------STPRTDDDEESAATDGDESSSPAS--      188
CRT/DREBP       ST--------------------------------SEMHDGEKDAQGSPTPSELSTS--      161
OsDREB1F        ALP--------------------------------------EDPQEGTS-----      151
CbCBF           -------------------DTTTT--D--HGFDMEETFVE--AIVTAEQ----------      168
BnCBF           TTNDHGMNMA-----S-QVEVNDTT--D--HDLDMEETIVE--AVFREEQREGFYMAE--      187
CaCBF1B         ISKESSS--------------------------S------------------------      160
PaDREB1F        VCSGSSD---------------------------EKERMVV--QV-EEKNKKGSVN----      179
GhDBP           SS-KVTADTK----SR-NNKKSDMAE-----PKPEEN----------TAKVENSSSLS--      295
GmDREBP_NP      EDVKPVIHAA----EL-AEVESDVAKSNAEYVYPEFE----------DFKVEHENPMF--      265
ZmDBF1          AKSKAMPINA----S--------VLEAAA--ASPSN-----------SSSDEGSGSGF--      166
TINY2           STSSS--------SSL-SSTSS-LE--SLVL------V---------MDLSR--T-----      168
ERF034          --------------------------------------------SPADR--AP----      148
ZmDBF2          GAG-----------A-HEEP-------AAK------D-------GAAPE--------      202
ERF038          SSS------------L-SADD--VA--PCVV------H--------ADADE--QPAAAA      213
GhDREBP1        LQTS-LHHAS----AS-SSESS-NP--TRVFRKPDLNKYPD-------SSDED-------      153
ERF_QDB64575.1  GSTPSSSTVP----S-----AS-PP--PRPN-----------------------S--      160
ERF_QCF46602.1  ASNPASDPAS----SQ-PDEGS-NP--TRPFSIPELGIVKR--EAFDSQPNEGSNPAKPF      190
ERF             LPMVN-HS-V-----T-PSFES-TP--LN--SLHSSSGMSS------DDEAEDIDRSHHV      181
PpDBF1          LTVAN-FQSP-----A-QTLES-SP--LH--SSPSSSDMSS------GDEDSGEDSVQSF      179
DsDBF1          -PLA--EPTN-----T-PTFES-TT--V--ESLHSPLHC----------EA--------      165
DREBP5          PSIG--EPAN-----I-PTFES-SS--SAVESFSASSSQ----------EA--------      166
ERF039-like     VTSKPV------------------------PLPSSS--------KQAQEEEAPVTPL      164
OsRAP           AAAL--------------------MS--P-----PSLSPP--------PGFATGSEVVAPA      137
ERF_TINY-like   FQVKEEAQSLGFQLSI-RNETN-VS--PRSHLRPVESEN--------SSTSEGRS-----      177
GmDREBP3        ----------------------HS--GRPEHPPMESPS--------PSVSEGTI-----      128
ERF016          ----------------------VE--DLGSNEA---AV-------------------      114
ERF016_XP       ----------------------AE--VKEEMAA---GG-------------------      119
```

```
GmDREBP        HEE----------------------GE---DESGTS-----SSYLSLS-----------  211
OsDREBP2A      CQERKNMEVC-------------ESEGIVLHKEVNIS-----YDYFNVHEVV-----EMI  246
TaDREBP1       HEEHKTLEVS-------------QPKGKALHKAANVS-----YDYFNVEEVL-----DMI  250
DREBP1A        ----------------------------DLAFELDVLSDMGWDLYYASLAQGML       214
CRT/DREBP      ----------------------------SDLLDEHWFGGMDAGSYYASLAQGML       187
OsDREB1F       -----------GGG----ATATSGRPAAVFVD---------EDAIFDMPGLIDDMARGMM  187
CbCBF          ------------------------SASLYID---------EEDMFGMPSLMASMAEGML   194
BnCBF          --ET-----T-VVG----VVPEEQMSKGFYMD---------EEWMFGMPTLLADMAAGML 226
CaCBF1B        ------------------------TPESMFFMD---------EEALFCMPGLLTNMAEGLM 188
PaDREB1F       -------------------LERSRSLSLSYWD---------EEEVFHMPRLLHDMAEGLL  211
GhDBP          ----------------------------TVQSESE-------------GSAV-----    306
GmDREBP_NP     -----------------------------------------------SGES-----    269
ZmDBF1         -----------------------------GSDDE-M-------------SSSS-----   176
TINY2          -E---SEELGEIVELPSLGAS-YDVDSANLGNE---------FVFYD-------------  201
ERF034         -----------------------SSPTADNDDDD---------AALFDLPDLL-------- 169
ZmDBF2         -EAAADAQAPVPVALPPPAASRPGTPSSGVEDE---------RQLFDLPDLL-------- 244
ERF038         KNDDDDGSTTAPV---------AAAAAAAAADE---------QQLFDLPDLL-------- 247
GhDREBP1       ----------------------------------------------------------- 153
ERF_QDB64575.1 -------------------PVKKEVQ-EDGEDDH-----NLQGLFDMPMSPEDL-----  189
ERF_QCF46602.1 SIELG----------HE-EGTVKREIM-E--EEDNHLQGLLMDGILNLPLSPDF------ 230
ERF            TKF---CS-------HVDVVPVE------------------------------------- 194
PpDBF1         VAEGSQIS-------PSEVVPVLEWVKVEFGDK-----ETVAAGDVDFDCDYSFI-----  222
DsDBF1         SSALAMAE-------PQSSFEVEEWIQAEFGDL-----EPLIDNAFRFPELPPC------  207
DREBP5         SSAVT-LT-------SSSTVPLEEWINSEFGEL-----EPLLDNAFRFPELPPL------  207
ERF039-like    LVSE----------SSPSSLRRTWSL------QLDEDFAAMA-MLLPPLPPLP-----   200
OsRAP          VRADGSIDWRPVMAHPPPLYSPPGWGG-------GHAYDFLQPP-------PPSP-----  178
ERF_TINY-like  -RKI---DLS-------------SKD------EHDEELDYTG-------ESCP-----   200
GmDREBP3       -QTDS--DVP-------------TLN------GSVTD-LFTP-------VGSS-----   151
ERF016         -----------------------------VSAS-------GSSS-----          122
ERF016_XP      -----------------------------NFNG-------ECYF-----          127


GmDREBP        ----------------------------------------------------------- 211
OsDREBP2A      IVELSADQKTE-------------VHEEYQ---EGD----------------------- 266
TaDREBP1       IVELSADVKME-------------AHEEYQ---DGD----------------------- 270
DREBP1A        MEPPSAALG--DDGD-----------------------AILADVPLWSY---------- 238
CRT/DREBP      MEPPSARTWSEDGGE-----------------------YSAVYTPLWN---------- 212
OsDREB1F       LTPPAIGRSLDDWAAID----------------DDDDHYHMDYKLWMD---------- 219
CbCBF          LPLPSVQ--WNHNYDID----------------GDDD-----VSLWSY---------- 219
BnCBF          LPLPSVQ--WGHNDDFE----------------GDAD-----MNLWNY---------- 251
CaCBF1B        LPPPQCAEIGDHV--ET----------------ADAD-----TPLWSYSI-------- 215
PaDREB1F       LSPSQCLGGYMNLDDMG----------------TDAD-----VKLWSFSI-------- 240
GhDBP          -SSPLSDLT---FSDFDE---QPWPEVVSSSE-TFMLSKYP-SEIDWDSILKA------- 350
GmDREBP_NP     -SSPESSVTFLDFSDFSDS-NNQWDE----ME-NFGLEKFPSVEIDWEAI--------- 312
ZmDBF1         -PTPVVAPPVADMGQLDFS-EVPWDE----DE-SFVLRKYPSYEIDWDALLSN------- 222
TINY2          ----------------SVDYCLYPPPWGQSSEDNYGHGISPNF-GHGLSWDL----------- 236
ERF034         ----------LDLKWSSW------LSSSSSE--YFAEIRLDHEPFLWEPFQLGENIHVFD 211
ZmDBF2         ----------LDIRDGFGRFPPMWAPLTDVEDVVNAELRL-EEPLLWE------------ 281
ERF038         ----------FDIQDGPFGFPAMWAPLADVDE-VNAELRL-EEPLLWDLGVTDA------ 289
GhDREBP1       ----------------------------------------------------------- 153
ERF_QDB64575.1 -ALPAAAM--------------------EF-APSTSEFWELDNLWSFSR--------- 216
ERF_QCF46602.1 --IPVAAI--------------------EP-AAAASEFWELDNLWGFAR--------- 256
ERF            ----------------------------------------------------------- 194
PpDBF1         -SEFAADS------LLACSYNSKG--RTEYLP-IETHDAALYDSTLWFF---------- 261
DsDBF1         --------------VFDSQFQI-F--QPSAGP-LEADNRALYDS-LWCFS---------- 238
DREBP5         --------------DQICQ-------LPSGAF-LDTESRMLYDS-LWCFS---------- 234
ERF039-like    -PIQMTD--------------------E-EDSDHGVLEHLDLW------------- 221
OsRAP          -PLPSCDDDMVDVVD--------------------ESSASLWSFDTRD------- 205
ERF_TINY-like  -PLLTADDYYVSLDDVELAWDNMKVDDL----------NFLDLPPLEDFFEDGPRKLTKT 249
GmDREBP3       -GYASDYGIFPGFDDFSGDFYVPEMPNVNYGE-ENGEGFIVDESFLWNF---------- 198
ERF016         -GYGVDD------V--------------------GVDGAFYQSPGLWTF---------- 144
ERF016_XP      -GGGSVG------D--------------------GSGGTYYHSSGFWTF---------- 149
```

```
GmDREBP          --------------------------------   211
OsDREBP2A        --DGFSLFSY----------------------   274
TaDREBP1         --DGFSLFSY----------------------   278
DREBP1A          --------------------------------   238
CRT/DREBP        --------------------------------   212
OsDREB1F         --------------------------------   219
CbCBF            --------------------------------   219
BnCBF            --------------------------------   251
CaCBF1B          --------------------------------   215
PaDREB1F         --------------------------------   240
GhDBP            --------------------------------   350
GmDREBP_NP       --------------------------------   312
ZmDBF1           --------------------------------   222
TINY2            --------------------------------   236
ERF034           L---HSLV------------------------   216
ZmDBF2           --------------------------------   281
ERF038           --------------------------------   289
GhDREBP1         --------------------------------   153
ERF_QDB64575.1   --------------------------------   216
ERF_QCF46602.1   --------------------------------   256
ERF              --------------------------------   194
PpDBF1           --------------------------------   261
DsDBF1           --------------------------------   238
DREBP5           --------------------------------   234
ERF039-like      --------------------------------   221
OsRAP            -----SYFRY----------------------   210
ERF_TINY-like    NSGRQSLVQYCRQFSSNYERVDSMHLVCDVFTM   282
GmDREBP3         --------------------------------   198
ERF016           --------------------------------   144
ERF016_XP        --------------------------------   149
```

Figure S2. Sequence alignments of DsDBF1 and other known ERF/DREB proteins from mosses and vascular plants such as *Syntrichia caninervis* (DREBP5_AMT92109.1), *Physcomitrium patens* (ERF RAP2-1-like_XP 024372564.1; PpDBF1 ABA43687.2; ERF_TINY-like_XP 024390306.1), *Gossypium hirsutum* (GhDREBP1_AAO43165.1; GhDBP_RAP2-4-like_NP 001314591.1), *Glycine max* (GmDREBP3_ABB36646.1; GmDREBP_NP 001345276.1; GmDREBP_NP 001345278.1), *Oryza sativa* (OsRAP_XP 468111.1; OsDREBP2A_XP 025878770.1; DREBP1A_XP 015610912.1; OsDREB1F_NP 001359120.1; ERF038_XP 015614793.1), *Triticum aestivum* (TaDREBP1_AAL01124.1; CRT/DREBP_XP 044398325.1), *Zea mays* (ZmDBF1_AAM80486.1; ZmDBF2_AAM80485.1), *Capsicum annuum* (CaCBF1B_AAQ88400.1), *Capsella bursa-pastoris* (CbCBF_AAR26658.1), *Brassica napus* (BnCBF_AAL38243.1), *Prunus avium* (PaDREB1F_XP 021803652.1), *Arabidopsis thaliana* (TINY2_NP 196720.1), *Bryum argenteum* (ERF_QDB64575.1), *Pohlia nutans* (ERF_QCF46602.1), *Selaginella moellendorffii* (ERF039-like_XP 024530345.1), *Citrus sinensis* (ERF016_XP 006474696.1), *Apostasia shenzhenica* (ERF034_PKA61103.1) and *Theobroma cacao* (ERF016_XP 007012585.2). Multiple alignment was performed using Clustal Omega. Amino acid sequences are highlighted with different colors. Sequences marked by (*) show conserved amino acid residues.