

Additional file 3 - Group and sub-group of consensus specific conserved amino acid motifs.

Numbers correspond to the motifs described in Additional file 2. Consensus sequences obtained from the analysis of the 27 Brachypodium DOF proteins with the MEME software. Motif 1 corresponds to the DOF DNA-binding domain.

Motif	E-value	Multilevel consensous sequence
1	7.5e-1149	CPRC[DN]Sx[ND]TKFCY[YF]NNY[SN]LSQPR[HY]FC[KR]ACRRYWT[AKR]GG[A S]LRNVPVGGG[CR]R[KR]
2	3.8e-062	[DEH][EDGT][KN][REGS][EN][GKN][KST][LV]W[VI]PKT[ILR]RI[DH][DGN][APT] [DA]E[AV][AT][KR]SSI[WLR][SADT][TL][LFI]GI[KEN][GPH][DG][DEKN][RNPV][GD][ELMTV][FDQ][KDIR][PSG][FGR][QGT][SCFR][KG]
3	1.1e-024	[FI]KLFG[KR][VT]I[PT]
4	1.0e-010	[VFLT][LHM][QHK][AG]NP[AV]A[FLQ][ST]R[SF][QV][SIT]F[QH]E
5	1.8e+000	MELLRSTGCV[MV]
6	7.3e-014	M[TS][ED]RAR[LM]A[ARK][VAI]P[LAHQ]PE
7	9.2e-001	D[AG]S[MT]IDLA[LM]LYSKFL[NS][HN]Q
8	2.4e+001	EL[AN]F[SV][MV]DQSC[FY]D
9	6.2e-006	Y[FY]TS[GS][IV]AIP[FI]YP[AG]A[AP][AG][AP][AG]YWG[CY]MVP[GA]W[NS][LT]P WP[PV]Q[CS]Q[PS]Q
10	2.3e+001	RPDM[LV]LEGMVGN
11	2.1e-001	RMLFPFEDLK
12	4.7e-003	KNPKL[AM][HL][HQ]HE[AG]GG[AG][AQ]HDLNL[AS]FPHH
13	4.6e-004	W[GPS][CF][][PS][GPS]WP[NA][GT][AT]W[SN][AS]PW
14	1.8e+001	FAGVDLRRPKGY
15	1.1e+002	FPSLESS[AS][IV]
16	1.3e-010	[ITV][KS][EGR]NE[TP][VA][KL]V[EKT]FG[SP][ED][VA]P[C]NE[SMA][ST][VS]L[D NR][INV][EG]EQ[NK][GKV]I
17	3.6e-005	[YC][FPY][LNP]G[PA][PA][FL][MV][YF]PW[SN][PI][GA]WN[GNS][IL][AP][VA]M
18	1.7e+000	MNGGTMWP[FY][GS]C
19	7.5e+000	C[PT]P[IV]KTN[AG]TVLSFG[HS]D
20	5.9e+001	MEEM[LM]M[GP][AT][GT]NQ
21	2.3e-024	[KES][TEG][EADQ][DSN][DE][EAGT][ASL][DSN][QER][DK][KE][VK]LKKPD[KI]I [LIV]P
22	1.0e-002	[IS][TSV][CS]S[ADEG][NPS][AGNS][SP][PL][TV]LGKH[PS]R[DE]
23	2.9e+002	FEWP[PS][AG][CF]D
24	1.1e+003	KD[LQ][GQ]HSGSS[ST][AT]E[PS][GK]VQE[IN][IT]
25	1.2e+003	L[IL][AT]QLAS[IV]KME
26	1.0e+003	[RY]H[GP]HH[AQ]Q[LQ]Q[FV]
27	4.0e+003	K[NS][IV][LS]AAS[HN]FLQR[IV]RA[AT]LP[GV]D