

Supplementary Material Table 3. Subclasses of predicted E-box-binding bHLH proteins.

a. AtbHLH proteins predicted to have G-box-binding capacity.

Amino acid sequences of the bHLH domains of the proteins identified in this study which are predicted to bind G-boxes based on the amino acids located in positions 9-13-17 (K/H-E-R), highlighted in bold letters (See Functional categories section). Proteins are listed according to the Entry Number assigned and their At-bHLH number and PID number are also provided to identify them. Positions within the bHLH are numbered at the top of the figure, below the schematic that indicates the basic, helix and loop regions of the domain.

EN	AtbHLH Number	PID Number	BASIC			HELIX			LOOP			HELIX		
			K	H	E	R	0	1	2	3	4	5	6	
1	55	AAF79643	EPKMKRAKHK	ELERQRRQEN	TSLFKILRVL	LPSQYIKGKR	SSADHVLEAV	NYIKDLQKKI	K					
2	125	AAF75809	DRESKMKKHR	DIERQRRQEV	SSLFKRLRTL	LPPFYIQGKR	STSDHIVQAV	NYIKDLQIKI	K					
3	126	NM118673	NKKKKKLLHR	DIERQRRQEM	ATLFLATLRTH	LPLKYIKGKR	AVSDHVNQAV	NFIKDTQTRK	I					
4	120	NP199992	TKKEKLLHR	NIERQRRQEM	AILFASLRSQ	LPLKYIKGKR	AMSDHVNQAV	SFIKDTQTRI	K					
5	118	NM118672	...MEKLVHK	EIERQRRQEM	ASLYASLRSL	LPLEFIQGKR	STSDQVKGAV	NYIDYLQRNI	K					
6	36	NM124557	...MEKMMHR	ETERQRRQEM	ASLYASLRSL	LPLHFIQGKR	STSDQVNEAV	NYIKYLQRKI	K					
7	100	AAC78547	PVVVKLNLHN	ASERERRKKI	NTMFSSLRSC	LPPNTQTKKL	SVSATVSQAL	KYIPELQEQV	K					
8	38	CAB72167	PVVVKLNLHN	ASERDRRKKI	NTLFSSLRSC	LPASDQSKKL	SIPETVSKSL	KYIPELQQQV	K					
9	39	CAB72168	PVVVKLNLHN	ASERDRRKKI	NSLFSSLRSC	LPASGQSKKL	SIPATVSRSL	KYIPELQEQV	K					
10	101	NM120497	VVLEKLLNLHN	ASERDRRKKI	NALYSSLRAL	LPLSDQKRL	SIPMTVARVV	KYIPEQKQEL	Q					
11	67	CAB71902	EIENQRINHI	AVERNRRRQEM	NEHINSLRAL	LPPSYIQ.RG	DQASIVGGAI	NYVKVLEQII	Q					
12	57	CAB77716	EVENQRMTHI	AVERNRRRQEM	NEHLNSLRSL	MPPSFLQ.RG	DQASIVGGAI	DFIKLEQLL	Q					
13	70	AAC33499	EIESQRMTHI	AVERNRRRQEM	NVHLNSLRSL	IPSSYIQ.RG	DQASIVGGAI	DFVKILEQQL	Q					
14	97	BAB01355	EVESQRMTHI	AVERNRRRQEM	NEHLRVLRSL	MPGSYVQ.RG	DQASIVGGAI	EFVRELEQLL	Q					
15	96	AAG51804	EIENQRMTHI	AVERNRRRQEM	NEYLAVLRSL	MPPYYAQ.RG	DQASIVGGAI	NYLKELEHHL	Q					
16	94	NM102098	EIENQRMTHI	AVERNRRRQEM	NEYLAVLRSL	MPSSYVQ.RG	DQASIVGGAI	NYVKELEHHL	Q					
17	71	NM124039	EAENQRMTHI	AVERNRRRQEM	NQHLVSLRSL	MPQPFVH.KG	DQASIVGGAI	DFIKLEHKL	L					
18	99	BAB11554	DKENQRMNHI	AVERNRRRQEM	NHFLSILKSM	MPLSYSQ.PN	DQASIVGGAI	SYLKKLEQRL	Q					
19	98	BAB09783	QDQKQKMSHV	IVERNRRRQEM	NEHLTVLRSL	MPCFYVH.KG	DQASIVGGAI	EYISELQQLV	Q					
20	45	AAF30305MSHI	AVERNRRRQEM	NEHLKSLRSL	TPCFYIK.RG	DQASIVGGAI	EFIKELQQLV	Q					
21	95	AAG13058	EESPDEIHI	WTERRRRKKM	RDMFSKLHAL	LPQ.LPP.KA	DKSTIVDEAV	SSIKSLEQLT	Q					
22	92	BAB11628	PEKERSRRHM	LKERTRREKQ	KQSYLALHSL	LPFA...TKN	DKNSIVEKAV	DEAIKQLQRL	Q					
26	19	AAC63587	RSPVLAKEHV	LAERKRREKL	SEKFIALSAL	LPGL...KKA	DKVTILDDAI	SRMKQLQEQV	R					
27	20	AAC63588	REPHLLKEHV	LAERKRREKL	NERLIALSAL	LPGL...KKT	DKATVLEDAI	KHLKQLQERV	K					
28	18	AAC63586	SSQNSAQDHI	LAERKRREKL	TQRFVLSAL	IPGL...KKM	DKASVLDGAI	KHIKYLQESV	K					
29	25	CAB38933	RNQSNAQDHI	LAERKRREKL	TQRFVLSAL	VPGL...KKM	DKASVLDGAI	KHIKYLQERV	G					
30	2	AAB72192	HTRGKPGNHA	LSSEKRRREKL	NERFMTLRSL	IPSI...SKI	DKVSILDDTI	EYLQDLQKRV	Q					
31	1	BAB08530	EARDETGNHA	VLEKRRREKL	NERFMTLRSL	IPSI...NKI	DKVSILDDTI	EYLQELERV	Q					
32	42	CAC14865	RLPREDLSHV	VAERRRREKL	NEKFITLRSM	VFPV...TKM	DKVSILGDTI	AYVNHRLKRV	H					
33	14	AAB62853	KHHPAVLSHV	EAERQRREKL	NHRFYALRAI	VPKV...SRM	DKASVLDGAI	SYIESLKSKI	D					
34	3	CAB78685	NGREEALNHV	EAERQRREKL	NQRFYALRAV	VPNI...SKM	DKASVLDGAI	TYITDMQKKI	R					
35	17	AAD20162	NGREEPLNHV	EAERQRREKL	NQRFYALRSV	VPNI...SKM	DKASVLDGAI	SYIKELQEKV	K					
36	5	BAB08920	NGREEPLNHV	EAERQRREKL	NQRFYALRSV	VPNV...SKM	DKASVLDGAI	SYINELKSKL	Q					
37	4	CAA17131	NGREEPLNHV	EAERQRREKL	NQRFYALRAV	VPNV...SKM	DKASVLDGAI	SYISELKSKL	Q					
38	6	BAA25078	NGREEPLNHV	EAERQRREKL	NQRFYALRAV	VPNV...SKM	DKASVLDGAI	AYINELKSKV	V					
39	13	AAF97322	NGRAEALNHV	EAERQRREKL	NQRFYALRSV	VPNI...SKM	DKASVLDGAI	SYINELHAKL	K					
40	28	BAA97217	HGRDKPLNHV	EAERMRRREKL	NHRFYALRAV	VPNV...SKM	DKASVLDGAI	CYINELKSKA	E					
51	41	BAA97026	GPSATQLQHM	ISERKRREKL	NSFQALRSL	LPPG...TKK	DKASVLSIAR	EQLSSLQGEI	S					
52	134	CAB80472	SKEVAACKHS	DAERRRRLRI	NSQFATLRTI	LPNL...VKQ	DKASVLDGAI	RYFNELKMMV	Q					
53	30	AAF07352	KALAASKSHS	EAERRRRERI	NNHLAKLRSL	LPNT...TKT	DKASVLDGAI	QHVKELKRET	S					
54	32	BAA95758	KALAASKSHS	EAERRRRERI	NTHLAKLRSL	LPNT...TKT	DKASVLDGAI	QHMKELKRET	S					
55	107	CAC00740	KALASLRNHK	EAERKRREKL	NSHLNKLRSL	LSCN...SKT	DKATLLAKVV	QRVKELKQQT	L					
56	106	AAD11998	RALAALRNHK	EAERRRRERI	NSHLNKLRSL	LSCN...SKT	DKATLLAKVV	QRVKELKQQT	L					
57	51	AAD25935	KAESLSRSHR	LAERKRREKL	NSHLTALRSL	VPNS...DKL	DKAALLATVI	EYVRSKQQA	A					
75	136	AAG28811	KRGQATDSHS	LAERVRRREKL	NERLKCLQDL	VPGC...YKAM	GMVMLDVLQ	NQIEFLSMKL	S					
76	50	AAF24852	RRGQATDSHS	LAERVRRREKL	NERLKCLQDI	VPGC...YKTM	GMATMLDEII	NYVQSLQNV	E					
77	44	AAF25996	RRGQATDSHS	LAERVRRREKL	NERLRCLQDM	VPGC...YKAM	GMATMLDEII	NYVQSLQNV	E					
78	75	NP564229	KRGQATDSHS	LAERVRRREKL	NERLKCLQDL	VPGC...YKAM	GMVMLDVLQ	DYVRSKQQA	E					
79	64	AAD15506	RRGQATDRHS	LAERARREKL	SKMKYLQDI	VPGC...NKVT	GKAGMLDEII	NYVQSLQNV	E					
80	58	CAB80320	RRGQATDRHS	LAERARREKL	SKMKYLQDI	VPGC...NKVT	GKAGMLDEII	NYVQSLQNV	E					

EN	AtbHLH Number	PID Number	BASIC				HELIX			LOOP	HELIX			
			H	1	0	E	R	2	0	3	0	4	0	5
81	79	BAA97208	RRGQATDRHS	LAERARREKI	SEKMTALQDI	IPGC..NKII	GKALVLDEII	NYIQSLQRQV	E					
82	49	AAF07355	RRGQATNSHS	LAERVRREKI	SERMKFLQDL	VPGC..NKVT	GKAVMLDEII	NYVQSLQRQV	E					
83	76	AAG29214	RRGQATNSHS	LAERVRREKI	SERMKFLQDL	VPGC..DKVT	GKAVMLDEII	NYVQSLQCCI	E					
84	63	CAA18832	RRGQATDSHS	LAERVRREKI	SERMKFLQDL	VPGC..DKIT	GKAGMLDEII	NYVQSLQRQI	E					
85	62	AAF02164	RRGQATDSHS	LAERVRREKI	SERMKLLQDL	VPGC..NKVT	GKALMLDEII	NYVQSLQRQV	E					
86	78	BAB10689	RRGQATDSHS	LAERVRREKI	SERMKLLQDL	VPGC..NKVT	GKALMLDEII	NYVQSLQRQV	E					
87	77	BAB01846	RRGQATDSHS	LAERARREKI	SERMRTLQDL	VPGC..NRIT	GKAVMLDEII	NYVQSLQRQV	E					
88	31	BAA87957	RRGQATDSHS	LAERARREKI	SERMKILQDL	VPGC..NKVI	GKALVLDEII	NYIQSLQRQV	E					
89	137	AF428350	RRGQATDSHS	LAERVRREKI	SERMRTLQNL	VPGC..DKVT	GKALMLDEII	NYVQTLQTQV	E					
90	74	AAC34336	RRGQATNSHS	LAERVRREKI	SERMRLQEL	VPGC..NKVV	TGAVMLDEII	NYVQSLQQQV	E					
91	60	CAB67608	RRGQATDSHS	LAERARREKI	NARMKLLQEL	VPGC..DKIQ	GTALVLDEII	NHVQSLQRQV	E					
92	7	AAD25805	RRGQATDPHS	LAERLRREKI	AERIRSLQEL	VPTV..NK.T	DRAAMIDEIV	DYVKFLRLQV	K					
93	59	CAB80752	RRGQATDPHS	LAERLRREKI	AERIRALQEL	VPTV..NK.T	DRAAMIDEIV	DYVKFLRLQV	K					
94	69	CAA18195	RRGQATDPHS	LAERLRREKI	AERMKSLQEL	VPNG..NK.T	DKASMLDEII	DYVKFLRLQV	K					
95	66	AAD03387	RRGQATDPHS	LAERLRREKI	AERMKALQEL	VPNG..NK.T	DKASMLDEII	DYVKFLRLQV	K					
96	82	BAA97525	RRGQATDPHS	LAERLRREKI	AERMKSLQEL	VPNT..NK.T	DKASMLDEII	EYVRFLLQV	K					
98	73	BAB10945	KRNIDAQFHN	LSEKRRRSKI	NEKMKALQKL	IPNS..NK.T	DKASMLDEAI	EYLKQLQLQV	Q					
99	24	CAB80359	KRCRAAEVHN	LSEKRRRSKI	NEKMKALQSL	IPNS..NK.T	DKASMLDEAI	EYLKQLQLQV	Q					
100	8	AAC33213	KRSRAAEVHN	LSEKRRRSKI	NEKMRALQEL	IPNC..NK.V	DKASMLDEAI	EYKLSLQLQV	Q					
101	15	AAD24380	KRSRAAEVHN	LSERKRRDRI	NERMKALQEL	IIRC..NK.S	DKASMLDEAI	EYMKSLQLQI	Q					
102	9	AAD22130	RRSRAAEVHN	LSERKRRDRI	NERMKALQEL	IPHC..SK.T	DKASILDEAI	DYKLSLQLQL	Q					
103	65	CAB86934	RRSRAAEVHN	LSERKRRDRI	NERMKALQEL	IPHC..SR.T	DKASILDEAI	DYKLSLQMLQ	Q					
104	119	CAA22971	KRSRAADMHN	LSERKRRREKI	NERMKTLQEL	LPRC..RK.V	DKVSMLEDAI	EYVKSLQLQI	Q					
105	138	CAA2297B	KRSRAAEVHN	LAERVRREKI	MERNKTLQEL	LPRC..NK.V	DKVSMLEDAI	EYVKSLQEMQI	Q					
106	56	CAA22972	KRSRAAEVHN	LAERVRREKI	NEKMKTLQEL	LPRC..NK.V	EKVSTLDDAI	EYVKSLQSQI	Q					
107	23	CAB81467	KRSRAAEVHN	LSERKRRQKI	NEMMKALQEL	LPRC..TK.T	DRSSMLDDVI	EYVKSLQSQI	Q					
108	16	CAB80763	KRSRAAEVHN	QSERKRRDKI	NQRMKTLQKL	VPNS..SK.T	DKASMLDEVI	EYKQLQLQAV	Q					
109	72	BAB08482	RRGRAAAIHN	QSERKRRDRI	NQRMKTLQKL	LPTA..SK.A	DKVSILDDVI	EHLKQLQAV	Q					
110	124	AAC34226	KRKRSTEVHK	LYERKRRDEF	NKKMRALQDL	LPNC..YK.D	DKASMLDEAI	KYMRTLQLQV	Q					
125	102	AAF07356	KASAIRSKHS	VTEQRRRSKI	NERFQILREL	IPNS..EQKR	DTASFILLEVI	DYVQYLQEKV	Q					
126	46	CAB93714	KLNTPRSKHS	ATEQRRRSKI	NDRFQMLRQI	IPNS..DQKR	DKASFLLEVI	EYIQFLQEKA	H					
127	141	BAB08642	NRNSCRSKHS	ETEQRRRSKI	NERFQSLMDI	IPQNQNDQKR	DKASFLLEVI	EYIHFLQEKV	H					
133	105	BAB09934	CESSATSSKA	CREKQRRDRL	NDKFMELGAI	LEPG..NPPKT	DKAAILVDVAI	RMVTQLRGEA	Q					
134	115	AAG50538	ESCTGSNSKA	CREKQRRDRL	NDKFTELVSSV	LEPG..RTPKT	DKVAIINDAI	RMVNQARDEA	Q					
135	34	BAA95734	SCSKPG.TKA	CREKLRREKL	NDKFMDLVSSV	LEPG..RTPKT	DKSAILDDAI	RVVNQLRGEA	H					
136	104	CAB78483	SCSRGGGTKA	CREKLRREKL	NERFMDLVSSV	LEPG..RTPKT	DKPAILLDDAI	RILNQLRDEA	L					
137	11	AAL55718	KKEAVCSQKA	EREKLRDRL	KEQFLVGLGNA	LDPN..R.PKS	DKASVLTDTI	QMLKDVMMNQV	D					
138	121	NM112876	DVSARKSQKA	GREKLRREKL	NEHFVLELGNV	LDPE..R.PKN	DKATILTDTV	QLLKELTSEV	N					
139	47	NM114632	GKVPKRINKA	VRELRKREHL	NELFIELADT	LELN..Q.QNS	GKASILCEAT	RFLKDVFGQI	E					

Total 89 proteins

b. AtbHLH proteins predicted to be Non-G-box binding proteins.

Amino acid sequences of the bHLH domains of proteins predicted to retain the capacity to bind an E-box, based on the conservation of the residues E13 and R16, but lacking the amino acids K/H9 important for the recognition of a G-box.

EN	AtbHLH Number	PID Number	BASIC				HELIX			LOOP	HELIX		
			1	0	E	R	2	0	3	0	4	0	5
23	10	AAD20667	GRGSRKSRST	PTERRRVHF	NDRFFDLKNL	IPNP...TKI	DRASIVGEAI	DYIKELLRTI	E				
24	89	AAF80214	GRGSKKRKIF	PTERRRVHF	KDRFGDLKNL	IPNP...TKN	DRASIVGEAI	DYIKELLRTI	D				
25	91	AAD20666	GRGKRKNKPF	PTERRRCHL	NERYALKLL	IPSP...SKG	DRASILQDGI	DYINELRRRV	S				
41	35	BAA97365	AASSPASKNI	VSERNRQKL	NQRLFALRSV	VPNI...TKM	DKASIIKDAI	SYIEGLQYEE	K				
42	27	CAB43668	ATSPASSKNV	VSERNRQKL	NQRLFALRSV	VPNI...SKL	DKASVIKDSI	DYMQELIDQE	K				
43	29	AAC98450	KTCTDRSRTL	ISERRRRGRM	KDKLYALRSL	VPNI...TKM	DKASIVGDAI	LYVQELQSQA	K				
44	33	AAF78492	KKKGMPAKNL	MAERRRRKRL	NDRLYMLRSV	VPKI...SKM	DRASILGDAI	DYIKELLQRI	N				
45	116	NM113586	KKKGMPAKNL	MAERRRRKRL	NDRLYMLRSV	VPKI...SKM	DRASILGDAI	DYIKELLQRI	N				
46	61	CAB89386	KLEGQPSKNL	MAERRRRKRL	NDRLSLLRSI	VPKI...TKM	DRASILGDAI	DYMKELLDKI	N				
47	93	NM125962	KLEGQPSKNL	MAERRRRKRL	NDRLSMLRSI	VPKI...SKM	DRASILGDAI	DYMKELLDKI	N				
48	21	AAC64222	SGKGSQAKNL	MAERRRRKRL	NDRLYALRSL	VPRI...TKL	DRASILGDAI	NYVKELQNEA	K				
49	22	CAB79132	EDENFKSPNL	EAERRRREKL	HCRILMALRSH	VPIV...TNM	TKASIVEDAI	EYIGELQNNV	K				
50	90	AAD39586	PTENFKSKNL	HSERKRRERI	NQAMYGLRAV	VPKI...TKL	NKIGIFSDAV	DYINELLVEK	Q				
62	103	CAA20199	IDYIKFLQEQ	ITEKVRKEKL	GDRITLQQL	VSPF...GKT	DTASVLHDAI	DYIKFLQEQI	D				
69	130	AAB88652	KRGCATHPRS	LAERVRRTRI	SERMKLLQEL	VPNM..DKQT	NTSDMLDLAV	DYIKDLQRQY	K				
70	122	AAG50543	KRGCATHPRS	LAERVRRTRI	SERMKLLQEL	VPNM..DTQT	NTADMLDLAV	DYIKDLQRQY	K				
71	80	AAG12608	KRGCATHPRS	LAERVRRTRI	SDRIRRLQEL	VPNM..DKQT	NTADMLLEEAV	EYVKALQSQI	Q				
72	81	CAB78042	KRGCATHPRS	LAERVRRTRI	SDRIRKLQEL	VPNM..DKQT	NTADMLLEEAV	EYVKVLQRQI	Q				
73	129	AAC64303	KRGFATHPRS	LAERVRRTRI	SGKLLKLQEL	VPNM..DKQT	SYADMLDLAV	EHIKGLQHQV	E				
74	128	AAF29386	KRGCATHPRS	LAERVRRTRI	SGKLLKLQDL	VPNM..DKVT	SYSDMLDLAV	QHIGLQHQV	Q				