

bHLH87-RIFU	<u>MDHL</u> <u>SWDGYGSRATTNT</u> <u>PPPS</u> SS..SFWSNYQQGHEQRFEMISNNNSNPNFFNSVQDLF..	56
bHLH87-C. pepo	<u>MDHL</u> <u>SWDGYGSRATTNT</u> <u>PPPS</u> SS..SFWSNFQQGHEQRFMMSSNNSNPNFFNSVQDLF..	56
bHLH87-C. maxima	<u>MDHL</u> <u>SWDGYGSRATTNT</u> <u>PPPS</u> SSLSFSWSNYQQGHEQRFMISNNNSNPNFFNSVQDLF..	58
bHLH87-C. melo	<u>MDHL</u> <u>NWNGYGSRVAKKTT</u> <u>ASTT</u> SSSSFSWSNYQQGVEERFEMISNNNSNPNFFNSVQDLF..	59
bHLH87-C. sativu	<u>MDHL</u> <u>NWNGYGSRVAKKTT</u> <u>ASTT</u> SSSSFSWSNYQQGVEERFVIVSSNNSNPNFFNSVQDLF..	59
bHLH87-N. tabacu	ME SL NWD..ESVVFQEFGASFDPIHVISNWNMPQRQEA AV RLAADS.MAAKS AAD LSRD	56
AtbHLH087-A. tha	MEGL ES VY..AQA MY GMTRE SK IMEHOGSDLIWGGNE LM ARELCS SS .SYHHQ LI NP..	55
CmbHLH87-112-2	<u>MDHL</u> <u>SWDGYGSRATTNT</u> <u>PPPS</u> SS..SFWSNYQQGHEQRFEMISNNNSNPNFFNSVQDLF..	56
Consensus	m l s s	
bHLH87-RIFUTSM MD VVGL ET QL LT SFNGDKTATATAAT...C	86
bHLH87-C. pepoTSM MD VVGL ET QL LP SFNGDKTATATAATAATC	89
bHLH87-C. maximaTSM MD VVGL ET QL LT SFNGDKTATATTTAAT...C	88
bHLH87-C. melo	VAENSSTPVLKTEDPLVMSPLTSTFTTSSNM MD VVGL EL SQ LD HGSGNGDKSATVTCS...	115
bHLH87-C. sativu	VAANSSTPVLKTENPLAMSPSLTSTFTTSSNM MD VVGL LS Q LD AGSNGDKSATVTCS...	115
bHLH87-N. tabacu	CAENGFSSSPIINMPNYIS.....DSNEMALNGIMADFSNNGVQVEIKPAPKLLSNAC	109
AtbHLH087-A. thaLSSCFMSD LG V LG EIQQQH VGN RASSIDPS...C	86
CmbHLH87-112-2TSSM MD VVGL ET QL LT SFNGDKTATATAATAATC	89
Consensus	m g	
bHLH87-RIFU	<u>SLES</u> LDCLLSATN...SNTDTSIEDDGSVSMMLSDYTNLWNFGGNAAP..SSK.....	134
bHLH87-C. pepo	<u>SLES</u> LDCLLSATN...SNTDTSIEDDGSVSMMLSDYTNLWNFGGNAAP..SSK.....	137
bHLH87-C. maxima	<u>SLES</u> LDCLLSATN...SNTDTSIEDDGSVSMMLSDYTNLWNFGGNAAB..SSK.....	136
bHLH87-C. melo	.LES LD CLLSATN...SNTDTSV ED DDGSVSMMLTDYTNLWNFGGNAAV..SSKESEKNG..	168
bHLH87-C. sativu	.LES LD CLLSATN...SNTDTSV ED DDGSVSMMLTDYTNLWNFGGNAAV..SSKESEKNG..	168
bHLH87-N. tabacu	<u>SLES</u> LDCLLSATITTTNTTSDIEDDGM S MFV DN SKGLWNFNSSSEHNASSEALKQSLGY	169
AtbHLH087-A. tha	...SLDCLLSATS...NSNNTSTEDDEGISVLFSDCQTLW SF GGVSSAESENREITTTT	141
CmbHLH87-112-2	<u>SLES</u> LDCLLSATN...SNTDTSIEDDGSVSMMLSDYTNLWNFGGNAAP..SSK.....	137
Consensus	sldcllsat ts edd lw f	
bHLH87-RIFURSHDQTHIKPTEYSVFS	151
bHLH87-C. pepoRSHDQTHIKPTEYSVFS	154
bHLH87-C. maximaRSHDQTHIKPTEYSVFS	153
bHLH87-C. meloSNSTKRSHEQTQFKAADYSIFS	190
bHLH87-C. sativuSNSTKRSHEQTQFKAADYSIFS	190
bHLH87-N. tabacu	QQLLTCHESGHKILQE EER KRKYKPINANELDETVSQSSPNKY N KRS HN QTL EN S P SE	229
AtbHLH087-A. tha	TIKP.....KPLKRN RG GGGTETTTTTTKPKSLK RN RGDE T GS	181
CmbHLH87-112-2RSHDQTHIKPTEYSVFS	154
Consensus		
bHLH87-RIFU	NNIITLSDSTSNSEGF II TDQNL PK OKKPR.....SEKPPN SS NI NF Q Q SCSSGSSCI	205
bHLH87-C. pepo	NNIITLSDSTSNSEGF II TDQNL PK OKKPR.....SEKPPN SS NI NF Q Q SCSSGSSCI	208
bHLH87-C. maxima	NNIITLSDSTSNSEGF II TDQNL PK OKKPR.....SEKPPN SS NI NF Q Q SCSSGSSCI	207
bHLH87-C. melo	NNIINLSDSTSDSGGFRIT TD HNL PK OKKPR.....SEKPPS SS NI NF Q Q SCSSGSSCI	244
bHLH87-C. sativu	NNIINLSDSTSDSGGFRIT TD HNL PK OKKPR.....SEKPPS SS NI NF Q Q SCSSGSSCI	244
bHLH87-N. tabacu	FNL F ESDSLNGDCGN F OLI SE K.QSK KK PR LI AENY N KSR TI SSNI NF Q Q ASS SS .VSSI	287
AtbHLH087-A. tha	HFSLVHPQ DD SEKGG KL IY DE NQSK KK PR.....TEKERGGSSNI SF Q H STCL...SD	233
CmbHLH87-112-2	NNIITLSDSTSNSEGF II TDQNL PK OKKPR.....SEKPPN SS NI NF Q Q SCSSGSSCI	208
Consensus	f i k kkpr ssnifq	
bHLH87-RIFU	DQEPDEAIAQMKEMIYRAAAF RPV NGLEAIEKPKRKNV RI STDPQTVAARQRRERISE	265
bHLH87-C. pepo	DQEPDEAIAQMKEMIYRAAAF RPV NGLEAIEKPKRKNV RI STDPQTVAARQRRERISE	268
bHLH87-C. maxima	DQEPDEAIAQMKEMIYRAAAF RPV NGLETIEKPKRKNV RI STDPQTVAARQRRERISE	267
bHLH87-C. melo	DQEPDEAIAQMKEMIYRAAAF RPV NGLEMIIEKPKRKNV RI STDPQTVAARQRRERISE	304
bHLH87-C. sativu	DQEPDEAIAQMKEMIYRAAAF RPV NGLEMIIEKPKRKNV RI SSDPQTVAARQRRERISE	304
bHLH87-N. tabacu	DQEPDEAIAQMKEMIYRAAAF RPV NGPDAIEKPKRKNV RI STDPQTVAARQRRERISE	347
AtbHLH087-A. tha	NVEPDAEIAQMKEMIYRAAAF RPV NGLEIVIEKPKRKNV RI STDPQTVAARQRRERISE	293
CmbHLH87-112-2	DQEPDEAIAQMKEMIYRAAAF RPV NGLEAIEKPKRKNV RI STDPQTVAARQRRERISE	268
Consensus	epd ealaqmkiyraaafipvn g e ekpkrknv is dpqtvaarqrrerise	
bHLH87-RIFU	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNTIAFSFN	325
bHLH87-C. pepo	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNTIAFSFN	328
bHLH87-C. maxima	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNSTIAFSFN	327
bHLH87-C. melo	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNTIAFSFN	364
bHLH87-C. sativu	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNTIAFSFN	364
bHLH87-N. tabacu	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL RSQV EA LEAIGQ QDEFSSIQFNY.	402
AtbHLH087-A. tha	KIRVLCTLVPGGCKMDTASMLDEAANYL KFL RAQV KA LENL R PKLD....QTNL S FSSA	348
CmbHLH87-112-2	FIRVLQRIVPGGSKMDTASMLDEAANYL KFL KSQIKALENLGOKIESLNCPSNTIAFSFN	328
Consensus	irvlq vpgg kmdtasmldeaanylkfl q ale k f	
bHLH87-RIFU	P.SFPPIQTSSSSSHNNFSLQNPYDQLM.....	352
bHLH87-C. pepo	P.SFPPIQTSSSSSHNNFSLQNPYDQLM.....	355
bHLH87-C. maxima	P.SFPPIQTSSSSSHNNFSLQNPYDQLM.....	354
bHLH87-C. melo	P.SFPPIQTSS...SHNNFTLLNPNH LI NQYPQN	393
bHLH87-C. sativu	P.SFPPIQTSS...SHNNFTLLNPNH LI NQYPQN	393
bHLH87-N. tabacu	..PFP ML PH.....FPV Q NP PI HGPKS..	424
AtbHLH087-A. tha	PTS F PL F HS.....FL PL QNP Q IHHPEC..	373
CmbHLH87-112-2	P.SFPPIQTSSSSSHNNFSLQNPYDQLM.....	355
Consensus	fp np	

FIGURE S2 Amino acid sequences alignment of pumpkin CmbHLH87 with others. The conserved domains (bHLH) are shown by thin underlines. The genes included are

bHLH87-like (*C. moschata* cv. 'Rifu', XP_022953326.1), bHLH87-like (*C. pepo*, XP_023547764.1), bHLH87-like (*C. maxima*, XP_022992322.1), bHLH87-like (*C. melo*, XP_008462383.1), bHLH87-like (*C. sativus*, XP_004141799.1), bHLH87-like (*Nicotiana tabacum*, XP_016504990.1), AtbHLH087 (*Arabidopsis*, AAM10960.1) and CmbHLH87 (*C. moschata* cv. '112- 2', MH105822).