

A)

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BdILR3 --MASPEGSNWVFD CPLMDDLAVADFAAGPAGAFYWTTP-----MQPQMHTQAQAVSAASLPNPCAET 61
HvbHLH --MASPEGSNWVFD CPLMDDLAAADFAAVPAGGFYWNPP-----MFPQMHTLAQAVSATAPNPCAET 61
ZmbHLH --MASPEGTTWVFD CPLMDDLAVAADFAAAPAGGFFWAAPPSLQP---QAPVQS---VVAASAPNPCMET 62
SbbHLH --MASPEGTTWVFD CPLMDDLAVAADFAAAPAGGFFWAAPPSLQPQVVQAPVQS---VVAASAPNPCVET 65
OsbHLH57 --MASPEGSTWVFD CPLMDLAAAAGFDAAPAGGFYWTTPAPPQAAALQPPPPQQQPVPAPATAAPNCAET 68
OsI_26369 --MASPEGSTWVFD CPLMDLAAAAGFDAAPAGGFYWTTPAPPQAAALQPPPPQQQPVPAPATAAPNCAET 68
EcbHLH57 --MTSSEGSQWVFD CPLIDDLAADFAATPAGGFYWTTPMQAQPPQVVIQPPSPVAAAAAPSNPCSVET 68
MtILR3 --MVSRENTNWNIDYGFYDILPVPDSTFALPSS--AFTWTPQP-----PFNLSSNVSAEVT 51
GmILR3 --MVSRENTNWLFDYGLIIDIPVPDATFGVNSS--AFTWPPN-----ALNASSNVGVEIT 50
NbbHLH --MVSRENTNWLFDYGFYDIEA VPDSTFALPSS--GFNWPMQ-----NLNGSRNVSAEVT 49
VvILR3 MALDSSSENSNWLFDYGLMEDITVPGGEFPEPTPGTGFSWPSQ-----ALKSSSSVSLAET 54
AtILR3 --MVSPEINANWICDLIDADYDYG-----SFTIQGGPFSWPVQQ-----PIGVSSNSAGVT 46

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BdILR3 NSPVS LDCEHAKGHPTNKRPRSESSAQPS SKACREKVRDKNLNERFELGAVLDPGKTPKIDKCAILLNDA 131
HvbHLH NSSVS VDWDAKAGQPKNKRPRSETGAQPS SKACREKVRDKNLNERFELGAVLDPGKTPKIDKCAILLNDA 131
ZmbHLH SS--S VDCGQEKQPTNKRPRSESTTESS TKASREKIRRDKNLNERFELGAVLEPGKTPKMDKTAILLSDA 130
SbbHLH SS--S VDCGQEKQPTNKRPRSESTAEPST TKASREKIRRDKNLNERFELGAVLEPGKTPKMDKSAILLNDA 133
OsbHLH57 NG--S VDCGHGKQPTNKRPRSESGTRPS SKACREKVRDKNLNERFELGAVLEPGKTPKMDKSSILLNDA 136
OsI_26369 NG--S VDCGHGKQPTNKRPRSESGTRPS SKACREKVRDKNLNERFELGAVLEPGKTPKMDKSSILLNDA 136
EcbHLH57 NS--S VDCNQKQEPVNRKRPRSESSAQPS TKACREKIRRDKNLNERFELGAVLEPGKTPKMDKSAILLNDA 136
MtILR3 DG-SL GDSGLKESGSKKRVRSESCAATS SKACREKLRDRLNDRKFEELGSAILEPGRPAKTDKAAILLDA 120
GmILR3 DG-SL GDSDSLKESGSKKRVRSESCAATS SKACREKLRDRLNDRKFEELGSAILEPGRPAKTDKAAILLDA 119
NbbHLH DG-SI GESDYPKENGSKKRVRSESCAPTSSKACREKQRDRLNDRKFEELGSAILEPGRPPKTDKSAILLDA 118
VvILR3 DC-SF GDSGLKELGPRKRLKHESSGATG TKACREKLRDRLNERFELGSAILEPGRPPKTDKAAILLSDA 123
AtILR3 DG-SAGNSEASEKPEPGSKKRVRSESSATS SKACREKQRDRLNDRKFEELGSAILEPGRPPKTDKAAILLDA 115

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BdILR3 IRVVT EIRSEAEK LKDSNES LQDKIKELKSEKNELRDEKQRLKAEKESLEQQIKFMNARQSLVPHPSVIP 201
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ZmbHLH IRVVG EIRSEAKKLKDSNES LQDKIKELKAEKNELRDEKQRLKAEKESLEQQIKFLNARPSLVPHHPVIP 200
SbbHLH IRVVG EIRSEAEK LKDSNES LQDKIKELKAEKNELRDEKQRLKAEKESLEQQIKFLNARPSLVPHHPVIS 203
OsbHLH57 IRVMA EIRSEAQKLKDSNES LQDKIKELKAEKNELRDEKQRLKAEKESLEQQIKFLNARPSFVPHPPVIP 206
OsI_26369 IRVMA EIRSEAQKLKDSNES LQDKIKELKAEKNELRDEKQRLKAEKESLEQQIKFLNARPSFVPHPPVIP 206
EcbHLH57 IRVVS EIRTEAQKLKDSNES LQDKIKELKAEKNELRDEKQRLKAEKENLEQQIKFMNARPSLVPHPPVIP 206
MtILR3 VRMVT QIRGEAQKLKDANSGLQDKIKELKVEKNELRDEKQRLKAEKELQQLKSMNAP-PSFLPTPTAL 189
GmILR3 VRMVT QIRGEAQKLKDTNQGLQDKIKELKAEKNELRDEKQRLKAEKELQQLKSLNAQ-PSFMPPPAAM 188
NbbHLH VRMVT QIRGEAQKLKDSNLNLQDKIKELKAEKNELRDEKQRLKAEKELQQLKTTNAQ-PGFLPP--AI 185
VvILR3 VRMVT QIRSEAEQKLKESNGDLQDKIKELKAEKNELRDEKQRLKAEKELQQLKSAQ-PGFLPHPSAM 192
AtILR3 VRMVT QIRGEAQKLKDSNSSLQDKIKELKTEKNELRDEKQRLKTEKELQQLKAMNAPQPSFFPAPMM 185

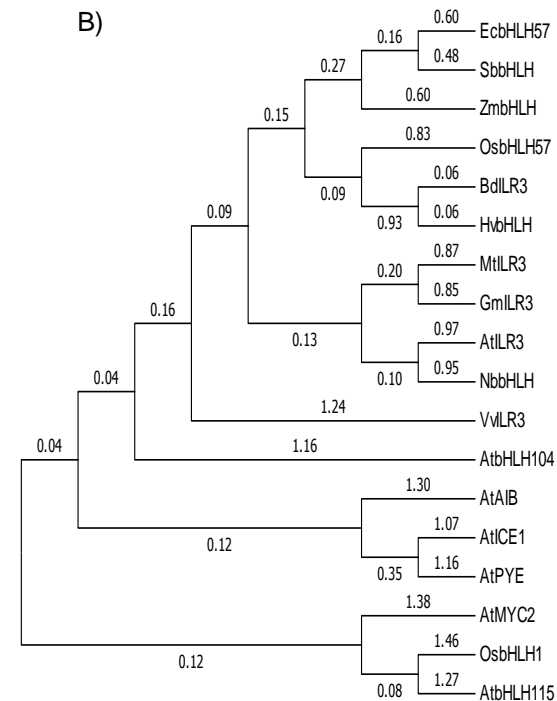
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HvbHLH ATAFAAAQG--QAAGHKLMFPVMSYPGFPMWQFMPPSDVDTSDDPKSCPPVA 251
ZmbHLH ASAFPAPQGPAAAARHKLMFPVIGYPGFPMWQFMPPSDVDTSDDPKSCPPVA 252
SbbHLH ASAFPAPQGPVAG-HKLMFPVLGYPGFPMWQFMPPSDVDTSDDPKSCPPVA 254
OsbHLH57 ASAFPAPQG--QAAGQKLMFPVIGYPGFPMWQFMPPSDVDTSDDPKSCPPVA 256
OsI_26369 ASAFPAPQG--QAAGQKLMFPVIGYPGFPMWQFMPPSDVDTSDDPKSCPPVA 256
EcbHLH57 ASAFPAPQGP--AAGQKLMFPVIGYPGFPMWQFMPPSDVDTSDDPKSCPPVA 256
MtILR3 PAAFAAQG----QAHGKLVFFISYPGVAMWQFMPPAAVDTSDHVLRRPPVA 237
GmILR3 PAAFAAQG----QAHGKLVFFISYPGVAMWQFMPPAAVDTSDHVLRRPPVA 236
NbbHLH PAAFAPHG----QVPGSKLVFFISYPGVAMWQFMPPAAVDTSDHVLRRPPVA 233
VvILR3 PAAFAAQG----RAPGNKLMFFIGYPSVAMWQFMPPAAVDTSDHVLRRPPVA 240
AtILR3 PTAFAAQG---QAPGNKLVFFISYPGVAMWQFMPPASVDTSDHVLRRPPVA 234

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B)



S2 Figure: Comparison of EcbHLH57 with its close homologs. A) Alignment of deduced amino acid sequences of bHLH genes. box- bHLH domain, *- leucine residues. B) Phylogenetic analysis of EcbHLH57 with closely related members of bHLH family. Multiple sequence alignment was performed using ClustalW and phylogenetic tree was constructed.