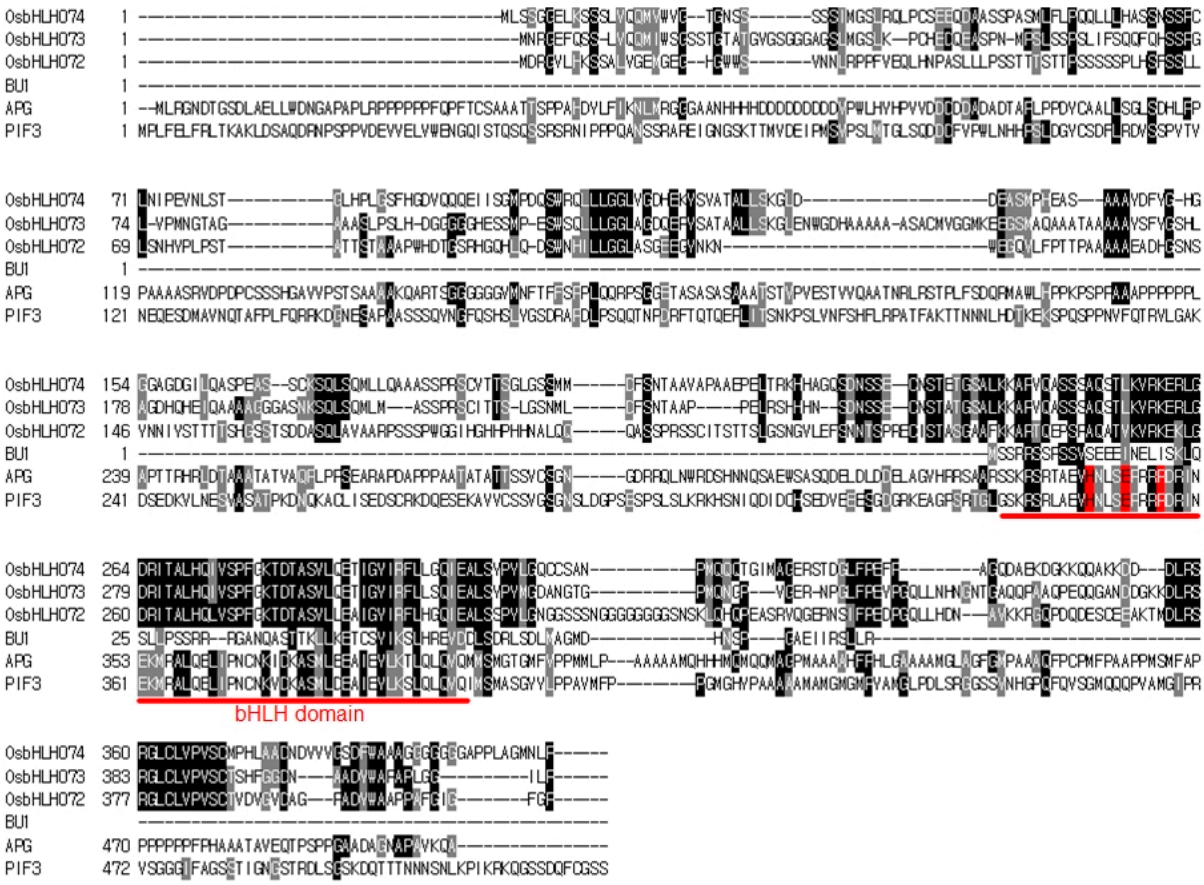

Figure S1. Multiple sequence alignment of bHLH transcription factors. The red shades refer to conserved amino acid sequence found in the typical bHLH domains. Underline indicates bHLH domain.

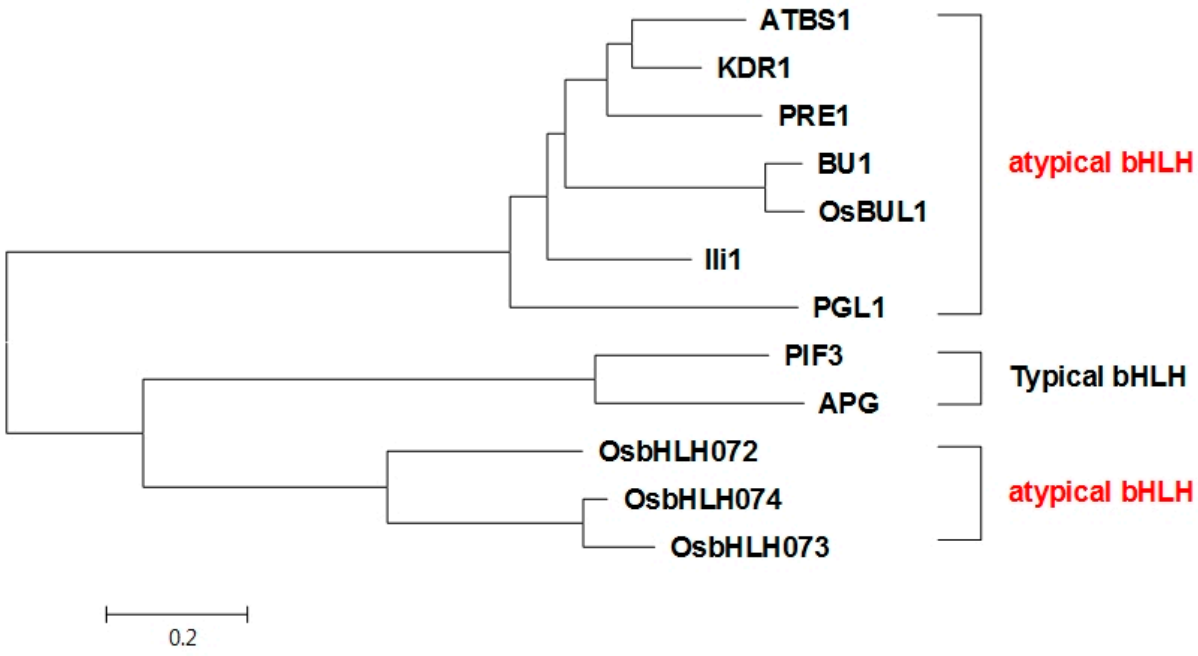

Figure S2. Phylogenetic tree of atypical and typical bHLH transcription factors from rice and Arabidopsis. Full-length amino acid residues were used from ATBS1 (AT1g74500), KDR1 (At1g26945), PRE1 (At5g39860), BU1 (Os06g12210), OsBUL1 (Os02g51320), Ili1 (Os04g54900), PGL1 (Os03g07510), PIF3 (AT1G09530) APG (Os05g04740), OsbHLH073 (Os05g14010), OsbHLH074 (Os01g13000), and OsbHLH072 (Os02g17680). Phylogenetic analyses were conducted with ClustalW and MEGA 7.0. Tree was generated by Neighbor-joining method.

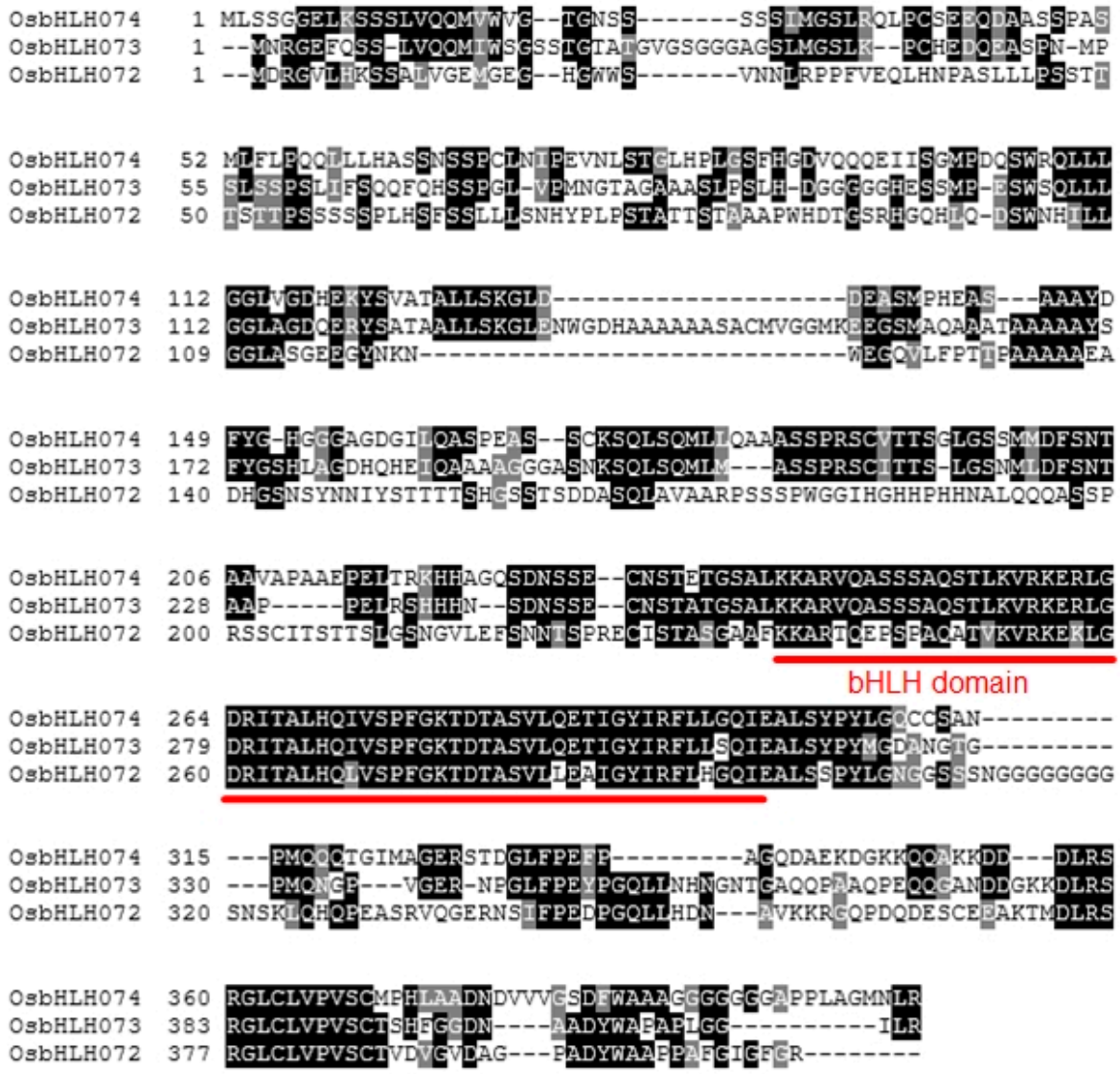

Figure S3. Multiple sequence alignment of OsbHLH072, OsbHLH073, and OsbHLH074 proteins. Black shade indicates identical amino acid and gray shade indicates similar amino acids. Underline indicates bHLH domain.

>OsKO1 (LOC_Os06g37224) promoter region (~2 kb from ATG)

cattttgggataagtttttctaggggtctacttgcgaaataagtttttcaaaaggactaaaatgtgaaaaatccagatg
gtctctaatcattaatgtattcaaatacttttttcttactcttctttccttcctttcaccaccatgcaacaaaatttactctaata
aatgctaagagtcaactctgagccgttgtcatgcataacaaccatacttctttctctttcttccatatcatcaaatttactt
gtatgacaatagagagagaccactaataaataccattgtacatgctctagttgcctgggaagacagttaatcggtgg
attttaccgcatacaaatcgctgcgccttgatgggtcgagcgcttgacacccgggcagccgcgtgctgccccagg
aggtaaatcctccactgatccctgctcgtattataagatgtttgatttttttttcctaatcaaactttcttaagtttcatcaaa
tttataaaaaaatttaacagcatacactagtggagaaatgctttgtagtcccggttggtaacatcctgtagtcccggttt
tttaaccgggactacgaatctgggactaaagatcgctatctttagtcccggttcaaatactcaggactaaaaatatgg
tcccagttgttgttaccgaccgggacttttttttctttttctttttcatccggttggtatttttccttttttttttctttcgcccaaatct
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ccatattcttttacacttattcacatctacaacaaagcatccatgttcttttacacttattcacagtacaacatcttcagaa
caacgagcattcattacagagaatagagaaagaaaaaaaagttcacatctacaacaacatcttcagcattcatcag
ataacacagagaagagaagaaaaaaaaatgttcgtccgccagccgccgcctcctgaccggcgccggcctccat
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gaggagataaggatgggaggatagaggctttttttttttacccgttgtttaacaaccgggactaaaaatagatctttgg
tcccggttggtgttactaactgggactaaagatcaccgtgatctttggtcccggttggtaatatcaaccgggacaaa
agttaggttactaaccgagactaaaaaccccaggagggcctgacagcccatgaaaacatgcaaaccaggactaa
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ttttattggaaccgggactattgtggaatttggtcgaccgaccaaagatgatttctccgatagtgatagaaaatataaa
ttggttttaataaattgaacattaaatatatttttataatatgtttctttttaatattactatatttttttataaatttagtcaatttaa
ataagtttgactagtaaaatactagctagtcaaacaactacatgcatcgtgcatggatattacttcccgacgacaact
attgtaaaagtctgatcttaagttcaaaccacgtgagctgaccgcatgatcaacgcattatgcggataccttaattaa
gttcccaagtcaatcaaattgagggtacaagacgaaattgattcccccacacacttgctccttcttccacttccatcct
gccctatataatatatatatatatatatatatatatatatatatatatatatatatatatactagtactgtacgtactaaaccgggga
ttgatcaggagagtgcagtgcaaactcgcagtgaacctgtgtgatcgatcggccATG

Figure S4. Information of *OsKO1* promoter region from start codon (ATG). We manually found E-boxes in the promoter regions using conserved nucleotide sequences. Red letter indicate predicted E-box sites.

> OsKO2 (LOC_Os06g37300) promoter region (~2 kb from ATG)

attggctaagggtgtgtttagttcgcgaaaaggatgattagaaggaaatatatatcctatgtacataaacttctcgtac
acactccatgcatatcaaatagcaaatgccatagaaaattctagaaaaaatcggacaaatactaaaaatcttagttct
ctgattggaaatttatgttgcgaagtttttttttcacttttaagacgccagtactgattatgaataaataaaagaaaagg
gacatcatctgctatcccactatcatatcggagttgagagagcggagataaagaaaggatggagatggtcatcagt
gtcattcctcccacttcgggacggtgacgaggaagcgctcaagcggtgccaaatccgatggccaaggatctcgg
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agttctgattttgatcgcaatgaccgcttcctccctcgccatgaccctaggcaagaggaggaggaggaccaggaa
actttatcgatactatgctattagccattaatacgagcacatgtgccacgtctaaaacttgaatttgggtaggcaagttt
caccataagaaatctaaacaattgagttatgctcactttacagttatataacttttaattaacccgttccaatggtcatat
cttagttttattttgaatggcgtagttcctatataatattattataaaatatatgtgttttctattcggtattttagtctgcatatt
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acagagatactgtttttattattaaaaattgatcgggccttaatgaaaactatcatggtcggactaatttataacttctgtg
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aactactatagtgtaattccaatataactatactataactacactaaaaattttatgtaacttgtatatatataagtattaaa
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accacagttacattgaaaaatcttttaagtcgatatttagcaattaccaagtggtattaataacgaggagaacagca
aaagtaattagtcgaaactcgaaaatcaggtgtacttgcatatgggtattacttggcataaaggctggtcttaatttca
aagcacgtgagctgaccgcgcgatgaatacctacctactacatgtggctcccaaggagtacagaagaaattaaac
gcaaattaatgaatgtgcaagcgtatgtgtacatggccctaccaaacaatgacgacaacgacactacaagaacga
cgtaatatttttaattgaggtagctgctacacgtgttaaatttgtattacaaagctcttaaaaaattaatgatatattcacat
cgtgaaacaaagtgatgttaagactttatttttttttaagaatagtacgtatagacttattattctagtgtgtttgaaagaa
gaaagaagattaagaaaataaaccattaaatatgattaattaagtattaattattttaaacataaaaaacaaattagtgt
aatttatttatagaaaaaattataaaagaaaaatgatgattactactccctccgtccaataaaaaatctatcagaggttg
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aaagcaacaaaaaagacttcaagttggtacagcgacgacgccgccctttcttatttcctcgctcttcgacgtgctgc
ggcctctataaataagaaagccgggattaattaaagagtgcgtgtgatcagatcgtgtgccATG

Figure S5. Information of *OsKO2* promoter region from start codon (ATG). We manually found E-boxes in the promoter regions using conserved nucleotide sequences. Red letter indicate predicted E-box sites.

Table S1. Primers used in this study

Name	Primer sequence (5′→3′)	Remarks
CPS1-qF	GCGTGCATTTTCGAACCAA	qPCR
CPS1-qR	TTGGCCAGCACTGACACTCT	qPCR
GA20ox1-qF	GCCACTACAGGGCCGACAT	qPCR
GA20ox1-qR	TGGTTGCAGGTGACGATGAT	qPCR
GA20ox2-qF	CCAATTTTGGACCCTACCGC	qPCR
GA20ox2-qR	GAGAGAAGCCCAACCCAACC	qPCR
GA3ox2-qF	TCCTCCTTCTTCTCCAAGCTCAT	qPCR
GA3ox2-qR	GAAACTCCTCCATCACGTCACA	qPCR
GA2ox1-qF	TGACGATGATGACAGCGACAA	qPCR
GA2ox1-qR	CCATAGGCATCGTCTGCAATT	qPCR
GA2ox3-qF	TGGTGGCCAACAGCCTAAAG	qPCR
GA2ox3-qR	TGGTGCAATCCTCTGTGCTAAC	qPCR
Slr1-qF	CTTCGAGCCCGTGCACCTGG	qPCR
Slr1-qR	CCGTAAGCCCGATCGGTCGC	qPCR
KO1-qF	AGTAGCCAAGGAGGCGATGA	qPCR
KO1-qR	CGGCTTATCACAGACAATGCT	qPCR
KO2-qF	TGAAGTAGCCAAGGAGGCGA	qPCR
KO2-qR	CGCTGATTGCGACCATACTTT	qPCR
OsbHLH073-qF3	CCTCCTCTTCAGCACAATCTAC	qPCR
OsbHLH073-qR3	GCCAATGGTCTCTTGCAGTA	qPCR
Actin-qF	CAGCCACACTGTCCCCATCTA	qPCR
Actin-qR	AGCAAGGTCGAGACGAAGGA	qPCR
OsbHLH073-OE-F1	GTTAACatgaatagaggagaattccagagctc	Overexpression, Localization
OsbHLH073-OE-R1	ACTAGTGGTACCcgtaggatcccgccgag	Overexpression, Localization
4A-02508-F	TTACCCCTAGGTACAGGGGTG	*OsbHLH073-D* genotyping
4A-02508-R	TACTGTAATAAGCAAGCCGGC	*OsbHLH073-D* genotyping
LB	CTAGAGTCGAGAATTCAGTACA	T-DNA border for genotyping
3A-17056-F	GCGTCTGTACTGCAAGAGACC	*OsbHLH073* KO-Genotyping
3A-17056-R	AATACCGGATGTGACACATTC	*OsbHLH073* KO-Genotyping
5A-00405-F	GAGCAACTGGTCCTCCCTG	*OsbHLH074* KO-Genotyping
5A-00405-R	CAATTTGCAAAACGCCTCTAC	*OsbHLH074* KO-Genotyping
OsbHLH073-RT-F1	CCTCCTCTTCAGCACAATCTAC	RT-PCR for *OsbHLH073*
OsbHLH073-RT-F1	GTAAGGTTGATTGCTCTTGATGC	RT-PCR for *OsbHLH073*
OsbHLH074-RT-F1	CATGCAGGCCAGTCAGATAA	RT-PCR for *OsbHLH074*
OsbHLH074-RT-F1	TCAGGTCGTCGTCCTTCTTC	RT-PCR for *OsbHLH074*
Actin-RT-F1	AGGCTCCTCTCAACCCCAAGGCCAATCG	RT-PCR for *OsActin*

Actin-RT-R1	AGGTAATCAGTGAGATCACGCCCAGC	RT-PCR for *OsActin*