Supplementary Materials

Table S1. Primers used for qPCR, RT-PCR and gene cloning

qPCR and RT-PCR	Primer sequence (5' to 3')
GmBEH3L1 (Glyma_12G231500)	Forward: TCAGAGGGCATGGAGATAGT Reverse: GAGTCCACATTGGCGAACCG
Glyma_13G266500	Forward: CCACATTCTTCTTATAACAC Reverse: GTTGTTTTCTCTCTCCTTCGA
GmACT11 (Glyma_18G290800)	Forward: ATCTTGACTGAGCGTGGTTATTCC Reverse: GCTGGTCCTGGCTGTCTCC
GmEFL1b (Glyma_02G276600)	Forward: ATGGCTGTCACCTTCTCAGA Reverse: CATATCCCACAGGAACCAGT
Gm60S (Glyma_13G318800)	Forward: TCAACCGTATACCCCGGACA Reverse: CTTCACTGCCTCCTTCAGCA
GmFBOX (Glyma_12G051100)	Forward: ACCAGGTCTCCTCTTACCGAA Reverse: TGAGGTTCAAGGGACAAGCG
ACT8 (At1g49240)	Forward: CCTTGCTGGTCGTGACCTTACTGA Reverse: CTCTCAGCACCGATCGTGATCACT
ABF2 (At1g45249)	Forward: GAGGTCAAGAGGGTTTGCAG Reverse: GAATTTGCAGTCTCTGCACC
ERD15 (At2g41430)	Forward: CCAGCGAAATGGGGAAACCA Reverse: ACAAAGGTACAGTGGTGGC
MYB75 (At1g56650)	Forward: AGTATGGAGAAGGCAAATGG Reverse: GTAGGAATGGGCGTAATGTC
P5CS1 (At2g39800)	Forward: CGACGGAGACAATGGAATTGT Reverse: GATCAGAAATGTGTAGGTAGC
RAB18 (At5g66400)	Forward: CGATCCAGCAGCAGTATGAC Reverse: TTCGAAGCTTAACGGCCACC
RD29B (At5g52300)	Forward: CGTCCTTATGGTCATGAGC Reverse: GCCTCATGTCCGTAAGAGG

ARF4 (At5g60450)	Forward: GCACACATGGAGGCTTCTCT
	Reverse: ACCGAGGGATCAATCTCCCA
ARF8 (At5g37020)	Forward: GCAGCAGCAATCAGAGATGC
	Reverse: ATTCTGCGGATTTCCGGGTT
BAS1 (At2g26710)	Forward: GTAGCAGCTGGTTCATTCCA
	Reverse: CAGGATCGGCTACCGTTAAC
BR6OX2 (At3g30180)	Forward: CAACATAGCTGCGGTTCATG
	Reverse: GTAACCCAACATGTCTGTGA
CPD (At5g05690)	Forward: CGAAGATCGGGTACCGTTTCTG
	Reverse: CAAAGATGCTCGCACTTTCAAC
DWF4 (At3g50660)	Forward: GCTGAGATCACCGGTAACAC
	Reverse: CTCTCGCTATCTTCTTCTTGC
Gene cloning	**Primer sequence (5' to 3')**
GmBEH3L1 (*Glyma_12G231500*) for complementary transgenic line	Forward: GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGACGTCGGGGACGAGGCT
	Reverse: GGGGACCACTTTGTACAAGAAAGCTGGGTCTCATCTGGTCTTTGAGTTAC

A

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GLYMA.12G231500  4 GTRLPTWKERENNKKRERRRRAIAAKIFAGLRMYGNFKLPKHCDNNEVLKAL 55
GLYMA.13G266500  4 GTRLPTSKERENNKRRERRRRAIAAKIFAGLRMYGNFKLPKHCDNNEVLKAL 55
GLYMA.13G266600  4 VARQPTWKERENNKRRERRRRAIAAKIFSGLRMYGNYKLPKHCDNNEVLKAL 55
GLYMA.12G231400  4 GARQPTWKERENNKRRERRRRAIAAKIFSGLRMYGNYKLPKHCDNNEVLKAL 55
GLYMA.11G064300  7 TGRLPTWKERENNKRRERRRRAIAAKIYTGLRACGNYKLPKHCDNNEVLKAL 58
GLYMA.14G076900 12 SRRKPSWRERENNRRRERRRRAIAAKIYSGLRACGNFNLPKHCDNNEVLKAL 63
GLYMA.17G248900 12 SRRKPSWRERENNRRRERRRRAIAAKIYSGLRACGNFNLPKHCDNNEVLKAL 63
GLYMA.01G178000  7 TGRLPTWKERENNKRRERRRRAIAAKIYTGLRACGNYKLPKHCDNNEVLKAL 58
GLYMA.06G034000 12 HRRKPSWRERENNRRRERRRRAIAAKIYSGLRACGNYNLPKHCDNNEVLKAL 63
GLYMA.04G033800 12 NRRKPSWRERENNRRRERRRRAISAKIYSGLRACGNYNLPKHCDNNEVLKAL 63

GLYMA.12G231500 56 CNKAGWTVEPDGTTYRKGCKP-SEGMEIVGGSSAAASPCSSYHPSPCASYNP 106
GLYMA.13G266500 56 CNEAGWTVEPDGTTYRKGCKP-LERMDIVGGSS-AASPCSSYHPSPCASYNP 105
GLYMA.13G266600 56 CNEAGWTVEADGTTYRKGCKPPVERMDIVGGSA-AASPCSSYHPSPCASYNP 106
GLYMA.12G231400 56 CNEAGWTVEADGTTYRKGCKPPVERMDIVGGSA-AASPCSSYHPSPCASYNP 106
GLYMA.11G064300 59 CAEAGWIVEEDGTTYRKGCKR--PSASEIGGTVANISACSSIQPSPQSSS-- 106
GLYMA.14G076900 64 CAEAGWCVEEDGTTYRKGCKP-PLAN-GAGSSMRNITFSSSQNPS------- 106
GLYMA.17G248900 64 CAEAGWCVEEDGTTYRKGCKP-PLAN-GAGSSMRNIPFSSSQNPS------- 106
GLYMA.01G178000 59 CAEAGWIVEEDGTTYRKGCKR--P-TSEIGGTPLNLSACSSIQASPQSSSY- 106
GLYMA.06G034000 64 CAEAGWTVEEDGTTYRKGCRA-PLPGDGVGTSTRNTPFSS-QNPS------- 106
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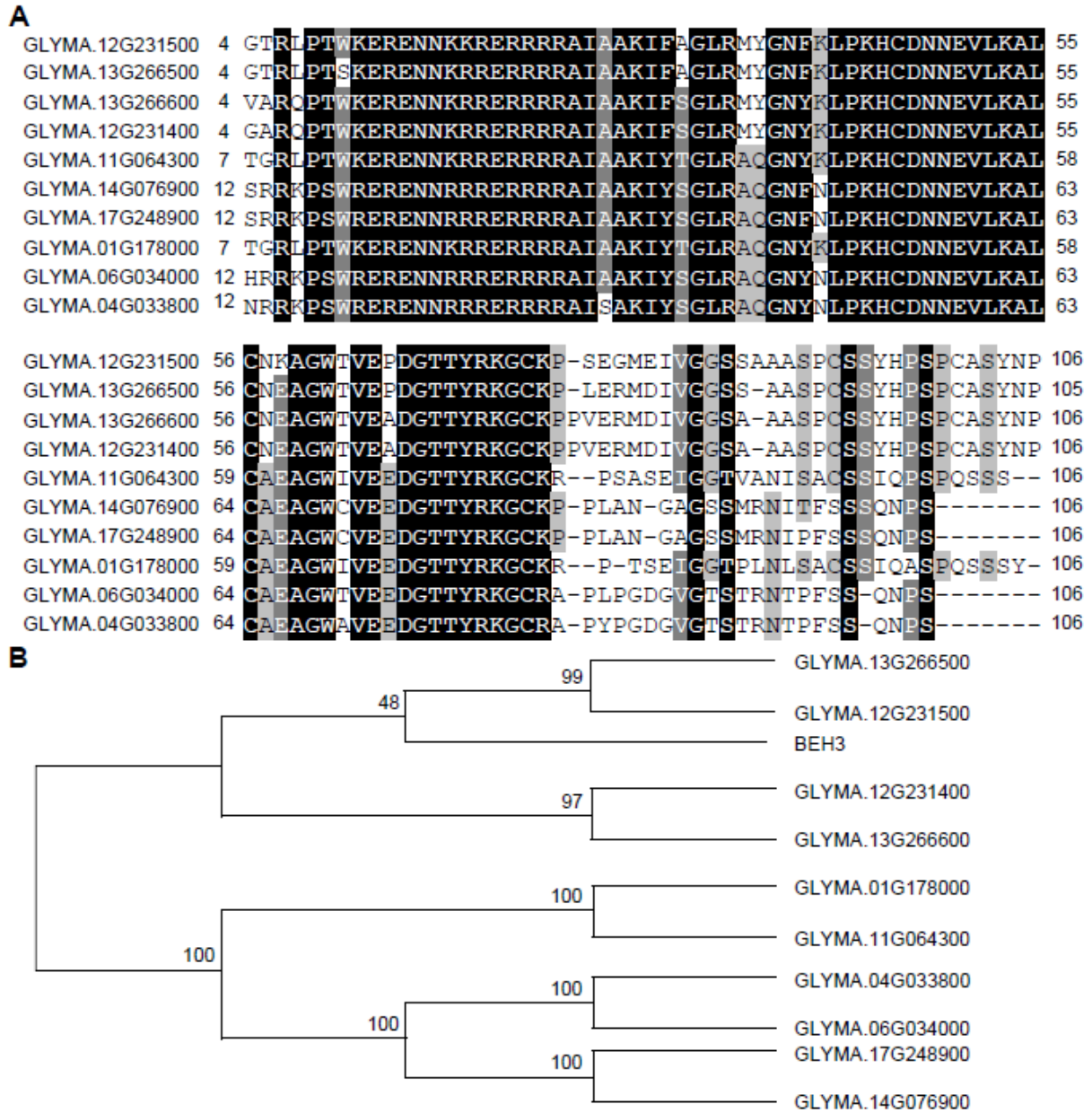
B

Figure S1. Analysis of amino acid sequences of BES1-ND domain in BES1/BZR1 family homologous genes and phylogenetic relationship of BEH3 orthologs from soybean (*Glycine max*). (**A**) Alignment of BES1-ND domain sequences of GLYMA_12G231500 and other BES1/BZR1 homolog genes from *G. max* species. Shown are the BES1-ND domain sequences of GLYMA_12G231500, GLYMA_13G266500, GLYMA_13G266600, GLYMA_12G231400, GLYMA_11G064300, GLYMA_14G076900, GLYMA_17G248900, GLYMA_01G178000, GLYMA_06G034000, and GLYMA_04G033800 (https://phytozome-next.jgi.doe.gov). Gray and black shading describe similar and identical amino acids, respectively. Gap (-) is introduced to optimize the amino acid sequence alignment. (**B**) Phylogenetic relationship of BEH3 orthologs from soybean (*G. max*). The bootstrap values are

shown near the corresponding branch (MEGA-X program).

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BEH3             1  MTSGTRTPTWKERENNKRRERRRRAIAAKIFAGLRIHGNFKLPKHCDNNEVLKALCNEAGWTVBDDGTTYRKGC
GLYMA.12G231500  1  MTSGTRLPTWKERENNKRRERRRRAIAAKIFAGLRMYGNFKLPKHCDNNEVLKALCNKAGWTVBDDGTTYRKGC
GLYMA.13G266500  1  MTSGTRLPTSKERENNKRRERRRRAIAAKIFAGLRMYGNFKLPKHCDNNEVLKALCNEAGWTVEFDGTTYRKGC

BEH3            75  KEMDPMDLMNGS-TSASPCSSYQHSPRASYNPSPSSS------SFPSPTNPFGDANSLIPWLKNLSSNSPS---
GLYMA.12G231500 75  KESEGMEIVGGSSAAASPCSSYHPSPCASYNPSPGSS------SPYYTQIPNPDGNSLIPWLKNLSTASSSASS
GLYMA.13G266500 75  KELERMDIVGGS-SAASPCSSYHPSPCASYNPSPGSSSFPSPSSSPYYTQIPNADGNSLIPWLKNLSTASSSASS

BEH3           139  --KLP--FFHGNSISAPVTPPI----ARSP----------------TRDQVT--IPDSG-----------WLS
GLYMA.12G231500 143 PKLPHLYLHSGSISAPVTPPLSSPTARTBRINAEWDEQSARPGPGWTRQQHYSFLPSSSPPSPGRQVVDPEWFA
GLYMA.13G266500 148 PKLPHLYLHSGSISAPVTPPISSPTSRTBRINVEWDEQSARPG--WTRQQHYSFLPSSSPPSPGRQVVDPEWFA

BEH3           175  GMQTPQSGPSSPTFSLVSPNPFFIKEAFKMGDCNSPMWTPGQSGNCSPAIPAGVIQNSDVPMADGMTAEFAFGC
GLYMA.12G231500 217 GIKLPHVSPTSPTFSLVSSNPFAFKEH-ALPSSGSPMWTPAQSGTCSPAVPFGSYQNADIPMSDAVSDEFAFGC
GLYMA.13G266500 220 GIKLPHVSPTSPTFSLVSSNPFAFKED-GLPGSGSPMWTPAQSGTCSPAIPFGSIQNADIPMSEAVSDEFAFGC

BEH3           249  NPMAANGMVKPWEGERIHGECVSDDLELTLGNSRTR
GLYMA.12G231500 290 NVI---GLVKPWEGERIHBEFGSDDLELTLGNSKTR
GLYMA.13G266500 293 NTI---GLVKPWEGERIHBEFGSDDLELTLGNSKTR
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Figure S2. Alignment of amino acid sequences of two soybean BEH3 orthologs (GLYMA_12G231500 and GLYMA_13G266500) and *Arabidopsis thaliana* BEH3. Shown are the amino acid sequences of *Glycine max* GLYMA_12G231500, GLYMA_13G266500, and *A. thaliana* BEH3 (At4g18890). Black shading describes identical amino acids. Gap (-) is introduced to optimize the amino acid sequence alignment.
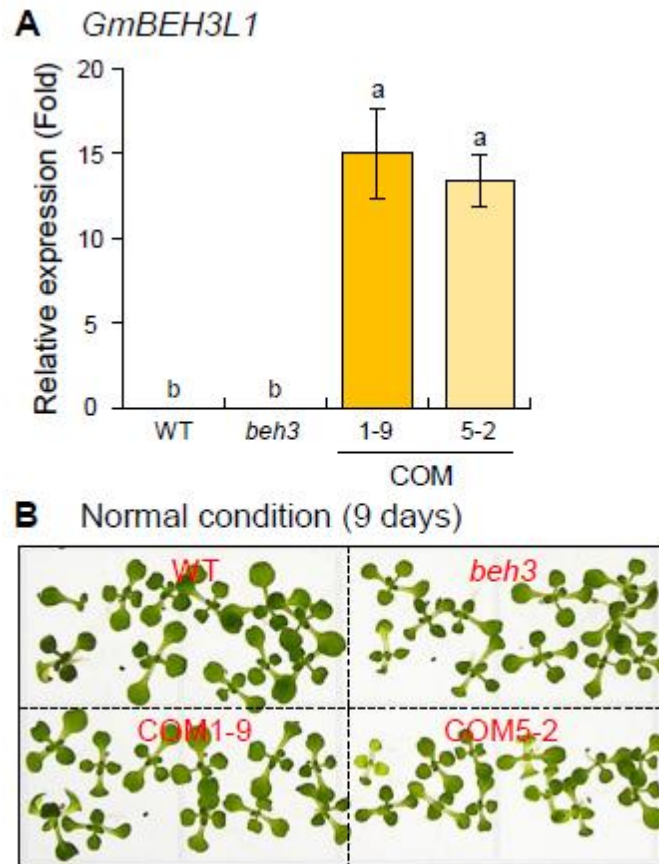
Figure S3. Genotype analysis of *GmBEH3L1*-expressing complementary lines. (A) Genotype analysis of WT, *beh3*, and two individual *GmBEH3L1*-expressing complementary (COM1-9 and COM5-2) seedlings. The expression level of the *GmBEH3L1* gene was quantified by qPCR using mRNAs obtained from 10-day-old seedling samples. Error bars represent the standard deviation of three independent biological replications. Lowercase letters indicate significant differences ($P < 0.05$) by Tukey's multiple range test. **(B)** Photos of WT, *beh3*, and *GmBEH3L1*-expressing complementary (COM1-9 and COM5-2) seedlings at 9 days under the normal condition.