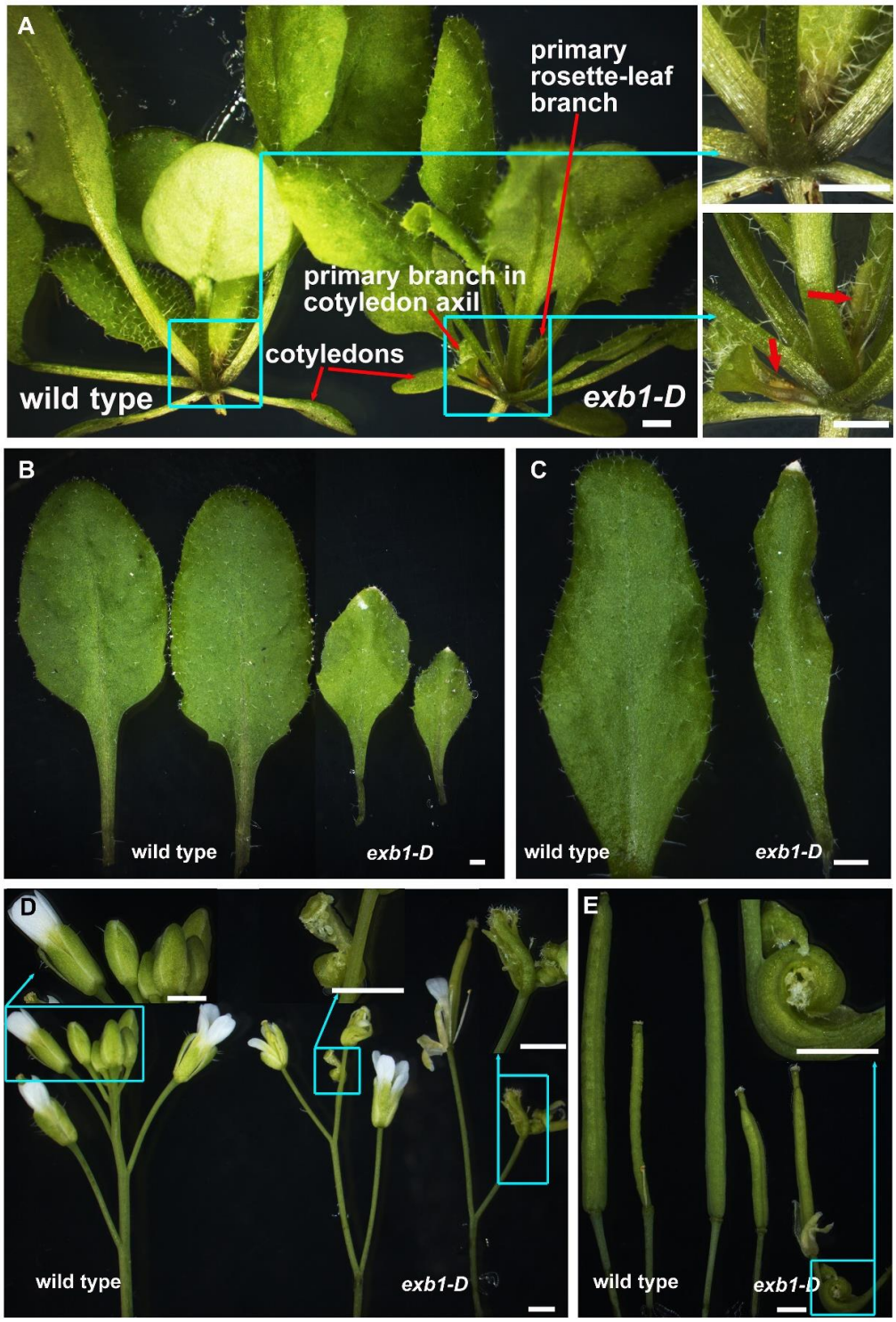
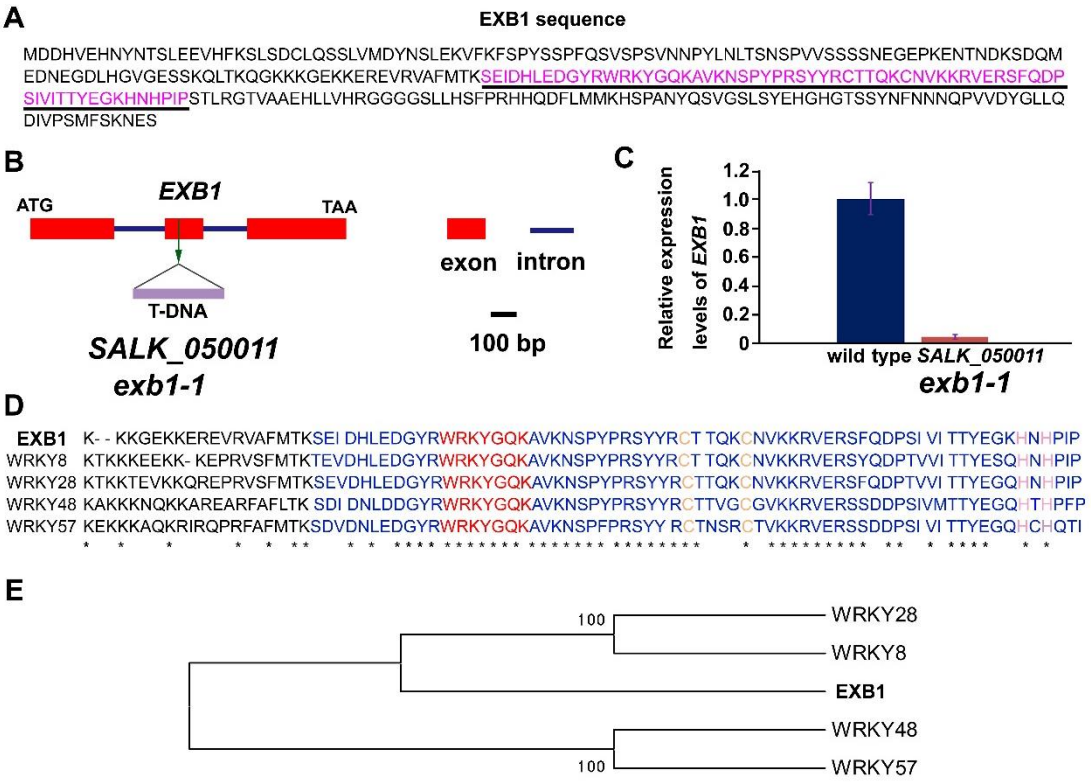


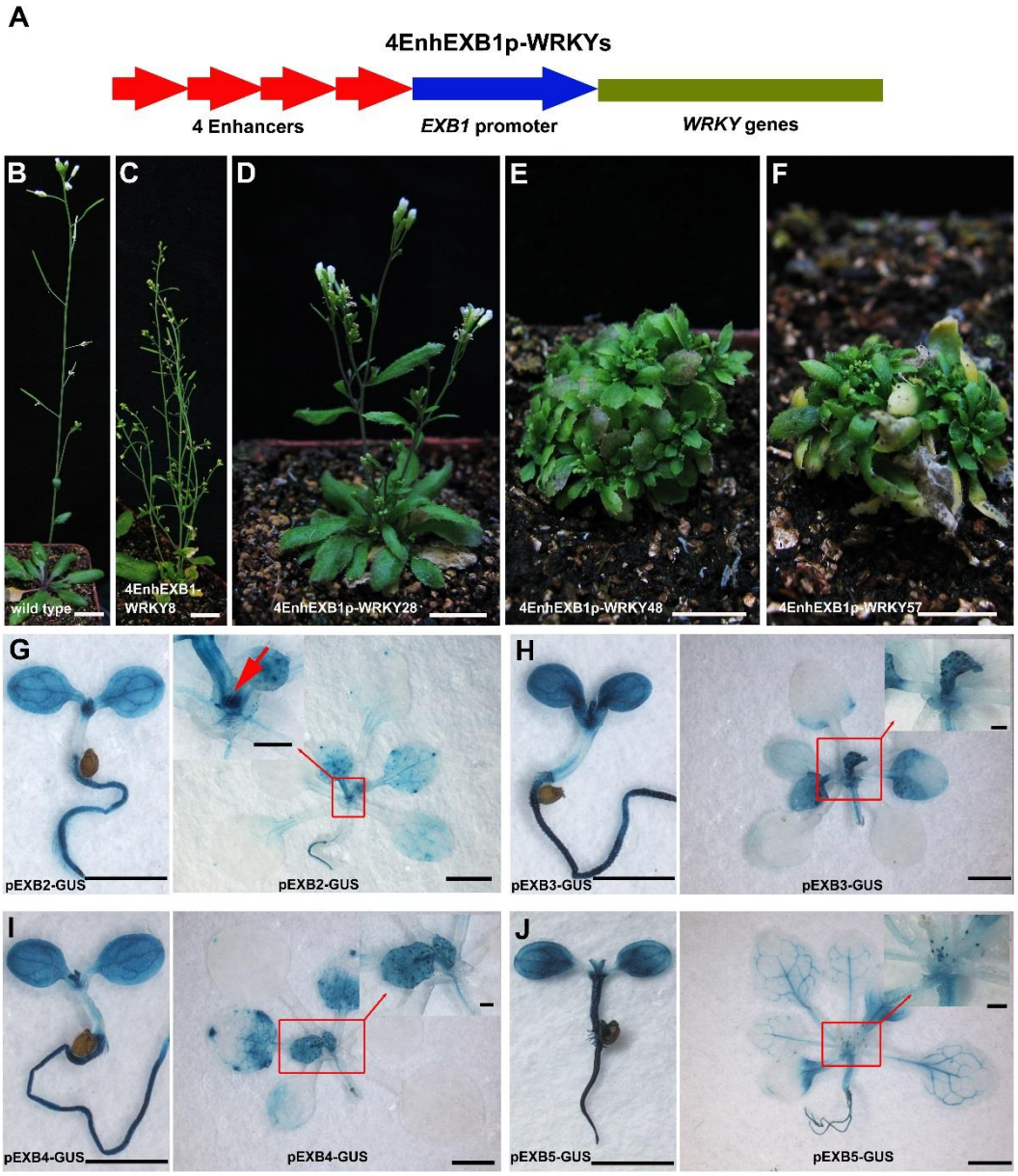
Supplemental Figure 1. The Mutant *exb1-D* Displayed Pleiotropic Phenotypes and Produced Branches in the Axils of Cotyledons.

(**A**) Branches were developed in *exb1-D* but not in wild-type plants.
(**B**) and (**C**) Deformed rosette leaves (**B**) and cauline leaves (**C**) were formed in *exb1-D*.
(**D**) The *exb1-D* produced defective flowers with carpeloid sepals.
(**E**) The *exb1-D* formed abnormal siliques with longer styles. Bars = 1 mm.



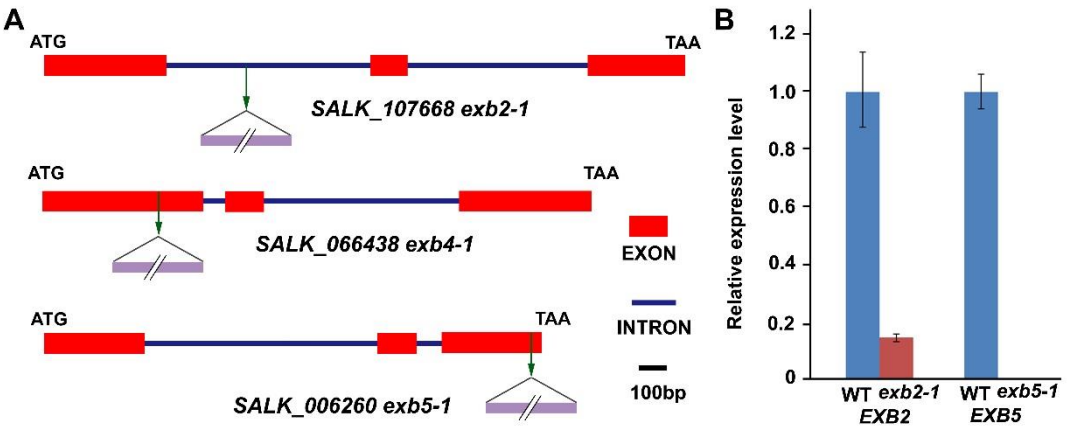
Supplemental Figure 2. *EXB1* Encoding WRKY71 Which Shares High Similarity with WRKY8, WRKY28, WRKY48 and WRKY57 in Amino Acid Sequence.

(**A**) The protein sequence of EXB1. The WRKY domain is indicated by pink color.
(**B**) The location of T-DNA insertion mutant *exb1* (*SALK_050011*). The exons are indicated by red boxes, and introns by blue lines.
(**C**) The relative expression level of *EXB1* in wild-type plants and *SALK_50011*. The expression level in the wild type was set to 1.0. The error bars represent the SD of three replicates.
(**D**) The alignments of WRKY domain of EXB1 with that of WRKY8, WRKY28, WRKY48 or WRKY57. Letters in red indicate the high conserved WRKYGQK peptide sequence and letters in orange and pink indicate the zinc finger motif. Asterisks indicate the same amino acid residues.
(**E**) Phylogenetic tree of EXB1, WRKY8, WRKY28, WRKY48 and WRKY57 were generated based on the full-length protein sequences using maximum likelihood (ML) method.



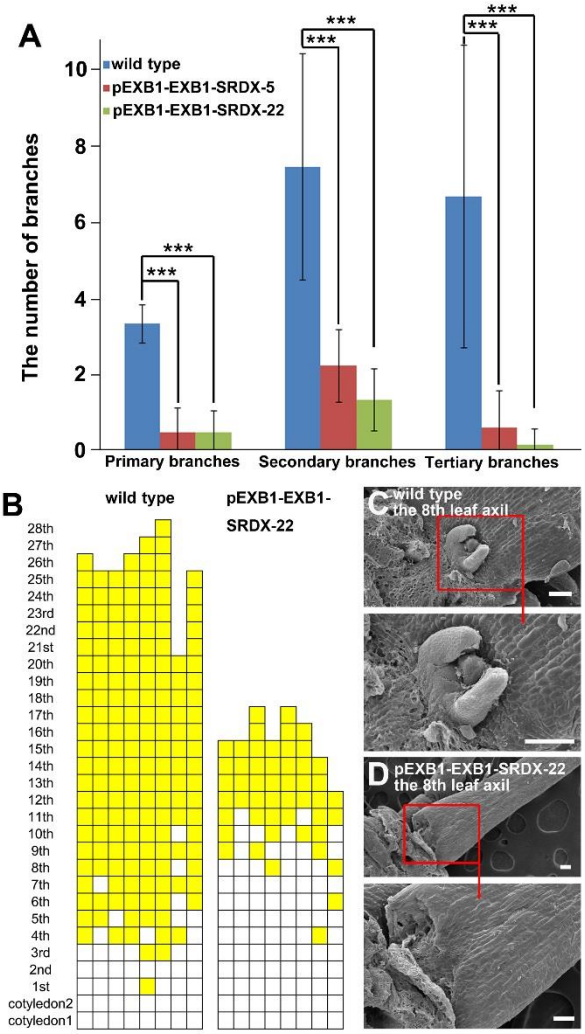
Supplemental Figure 3. EXB1 Had Highly Redundant Function With EXB2, EXB3, EXB4 and EXB5.

(**A**) Schematic representation of 4EnhEXB1p-WRKYs constructs.
(**B**) to (**F**) The phenotypes of 4EnhEXB1p-WRKY8 (**C**), 4EnhEXB1p-WRKY28 (**D**), 4EnhEXB1p-WRKY48 (**E**), and 4EnhEXB1p-WRKY57 (**F**) transgenic plants. The transgenic plants displayed excessive branching similar to that observed in *exb1-D* when compared to wild-type plants (**B**).
(**G**) to (**J**) The expression patterns of *EXB2* (**G**), *EXB3* (**H**), *EXB4* (**I**), and *EXB5* (**J**). The four genes had overlapping expression patterns with *EXB1*. Bars = 1 cm in (**B**) to (**F**), 1 mm in (**G**) to (**J**), and 100 μm in the insets of (**G**) to (**J**).



Supplemental Figure 4. The Identification of *exb2-1*, *exb4-1*, and *exb5-1* Mutants.

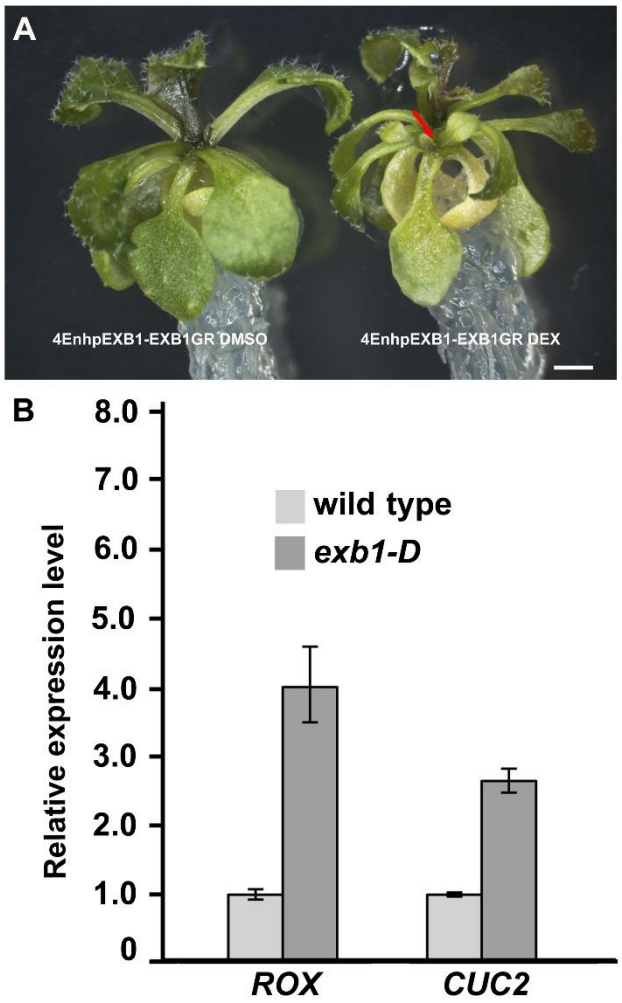
(**A**) Schematic representation of T-DNA locations in the *exb2-1*, *exb4-1*, and *exb5-1* mutants.
(**B**) The relative expression level of *EXB2* or *EXB5* in the *exb2-1* or *exb5-1* mutants. *EXB2* was knocked down in *exb2-1* and *EXB5* was knocked out in *exb5-1*. The expression level of *EXB2* or *EXB5* in wild type was set to 1.0. The error bars represent the SD of three biological replicates.



Supplemental Figure 5. Disruption of EXB1 Caused Fewer Branches in pEXB1-EXB1-SRDX Transgenic Plants.

(**A**) The number of branches of 45-day-old wild type and pEXB1-EXB1-SRDX transgenic lines. Branch numbers were the average of more than ten plants. Two-tailed t-test was used to test the significance. Three asterisks represent $p<0.001$.

(**B**) The statistic analysis of AMs in each leaf axil of 50-day-old wild type and pEXB1-EXB1-SRDX-22 transgenic line in a short-day condition. Each column represents one independent plant and each row presents the position of the axils. The typical leaf axil morphologies represented by the two color grids were shown in (**C**) and (**D**). The white grids represent the absence of AMs; the yellow ones represent the AMs with leaf primordia. (**C**) and (**D**) The representative leaf axils of wild-plant and pEXB1-EXB1-SRDX-22. Bars = 100 μm.



Supplemental Figure 6. 4EnhEXB1p-EXB1GR Transgenic Plants Produced More Branches after DEX Treatment and the RAX Downstream Gene *ROX* and *CUC2* Were Up-regulated Significantly in *exb1-D*.

(**A**) The phenotypes of 16-day-old 4EnhEXB1p-EXB1GR transgenic plants treated with DMSO or DEX for one week. The red arrow indicates one branch in a leaf axil. Bars = 1 mm.
(**B**) The expression level of *ROX* and *CUC2* was increased in *exb1-D*. The expression level of *ROX* or *CUC2* in wild type was set to 1.0. The error bars represent the SD of three biological replicates.

A

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B

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C

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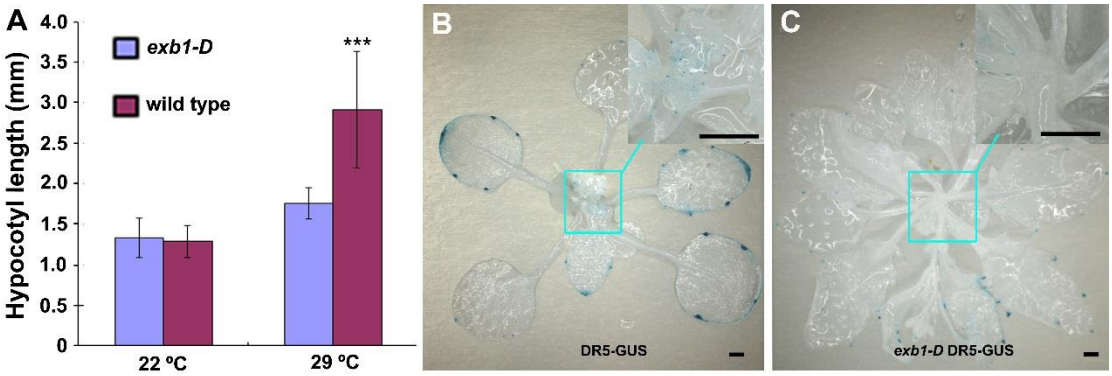
ACAAGT**ATG**

Supplemental Figure 7. The Possible W-box *Cis*-elements in the Promoters of *RAX* Genes.

(**A**) The possible W-box *cis*-elements in the promoter of *RAX1*.
(**B**) The possible W-box *cis*-elements in the promoter of *RAX2*.
(**C**) The possible W-box *cis*-elements in the promoter of *RAX3*. Red bold letters represent possible W-box *cis*-elements. Purple bold letters represent start codons of *RAX* genes.



Supplemental Figure 8. The Auxin Homeostasis Was Compromised by *EXB1* Overexpression .

(**A**) The hypocotyl elongation of *exb1-D* was compromised in the treatment under 29 ºC. (**B**) and (**C**) Auxin reporter DR5-GUS analysis showed that auxin pathway was affected by *EXB1* overexpression. Bars = 1 mm.

Supplemental Table 1. The transcript alteration of genes in auxin pathway by EXB1 induction.

Gene ID	Gene product	Value of mock-treated plants	Value of DEX-treated plants	Log2(fold change)	*p*_value
AT1G70560	TAA1	6.130240	1.939510	-1.7	0.000378
AT4G13260	YUC2	0.878797	0.455587	-0.9	0.158667
AT1G04610	YUC3	0.077682	0.039684	-1.0	0.469674
AT5G16530	PIN5	5.950950	1.099360	-2.4	0.000043
AT5G15100	PIN8	0.494479	0.249029	-1.0	0.250873
AT2G46530	ARF11	3.966420	1.745610	-1.2	0.007063
AT3G61830	ARF18	13.58180	5.873470	-1.2	0.000174
AT1G34410	ARF21	0.029921	0.000405	-6.2	0.578522
AT1G52830	IAA6	1.556270	0.613108	-1.3	0.064486
AT4G14550	IAA14	2.936580	1.232950	-1.3	0.0274252
AT5G57420	IAA33	0.407542	0.078609	-2.4	0.1609220
AT4G28720	YUC8	0.102336	0.551910	2.4	0.0045511
AT3G23050	IAA7	104.1030	222.0350	1.1	0.0002182
AT3G17600	IAA31	0.059568	0.188590	1.7	0.2857590

Supplemental Table 2. The primer list used in this work

Primer name	Primer sequences (5' - 3')
EXB1-1	atgGATGATCATGTTGAGCACAATT
EXB1-2	tcaAGACTCGTTCTTGGAGAACATT
EXB1-2N	AGACTCGTTCTTGGAGAACATT
EXB1-3	caccATGGATGATCATGTTGAGCACAATT
Enh-1	CTAGAGCTAGTAGATCCCCAACATG
Enh-2	AACACTGATAGTTTCGGATCTAG
EXB1-SRDX	ctaAGCGAAACCCAAACGGAGTTCTAGATCCAGATCCAGAGACTCGTTCTTGGAGAACA
EXB1P-1	GGGGACAACTTTGTATAGAAAAGTTGCTGAAGGTTTTTTGGCTCCCTAA
EXB1P-2	GGGGACTGCTTTTTTGTACAAACTTGCTGAAGAAGAGGAGAAAGA
EXB1P-3	caccGAAGGTTTTTTGGCTCCCTAA
EXB1P-4	TGAAGAAGAGGAGAAAGA
GR-1	atgATTCAGCAAGCCACTGCAGGAG
GR-2	TGCTCAACATGATCATCCATTCATTTTTGATGAAACAGAA
GR-3	TTCTGTTTCATCAAAAATGAATGGATGATCATGTTGAGCA
RAX1P-1	AACACCAATGAGTCAATACTGTTTT
RAX1P-2	TTCTCTCGTTAGTGAATTGAAGTTT
RAX2P-1	TCTTCCCATAAGAATATATGTATGT
RAX2P-2	CTCTCTATCTGTCTCTCTTGGTCTA
RAX3P-1	TCTTTTAGCCTTTTGTTTTTTTCAATA
RAX3P-2	ACTTGTACTCCTAGTGAAGTCTTGTTCT
FLUC-1	caccATGGAAGACGCCAAAAACATAAAGA
FLUC-2	ttaCAATTTGGACTTTCCGCCCTTC
35S-1	GCCAACATGGTGGAGCACGACACTC
35S-2	AAGCTCGAGAGAGATAGATTTGTAG
VP16-1	GCCCCCCCGACCGATGTCAGCCTGG
VP16-2	ctaCCCACCGTACTCGTCAATTCCA
VP16-3	caccGCCCCCCCGACCGATGTCAGCCTGG
G4DBD-1	caccATGAAGCTACTGTCTTCTATCGAAC
G4DBD-2	ttaTTGATTCGACCTCGACGATACA
EXB1 RT-1	CCATGGGACCTCTAGTTACAATTTT
EXB1 RT-2	TAATGCAACCATAACGATACGATCT
EXB2 RT-1	CATCTCCCTCCTCCATTACCA
EXB2 RT-2	TCAAGGGTTGCGCATAGTTT
EXB5 RT-1	CTCGAAGACGGCTATCGTTGGAGAA
EXB5 RT-2	CGGATGGTTGTGTTGACTCTCGTAGG
Actin8 RT-1	TCCAGGCATTGTCCACAGAA
Actin8 RT-2	ACCTGCTCCTCCTTAGACAT

ROX RT-1	TCCACCACTTCCTCATCCTC
ROX RT-2	ACCAGGGACCATGCTTTGTA
RAX1 RT-1	CTCTCGGACAGCAACAACAA
RAX1 RT-2	CCTCTGGTCAATGTGGTGGT
RAX2 RT-1	TGGAAGCAGGTGGTCAGTAA
RAX2 RT-2	GCAATGGCTAAGTGGTGATG
RAX3 RT-1	TCTATCTTGAGCGCCAACAC
RAX3 RT-2	GGAGGCTCCTGAGAACAAGT
CUC2 RT-1	AAGCTCCAAGGATGAATGGG
CUC2 RT-2	TTGTTGAGGGTACTTTCGTC
DL1	GACAACATGTCGAGGCTCAGCAGG
EXB1 Co-1	GTGTATGATGGTCGATGATCTGAGAT
EXB1 Co-2	TTGACGAGTAGAAAGAGTTGGAAGTA
SPL-1	caccATGGCGACTTCTCTCTTCTT
SPL-2	ttaAAGCTTCAAGGACAAAT
WRKY8-1	ATGTCTCATGAAATCAAAGA
WRKY8-2	TCAAGGCTCTTGTTTGAAGA
WRKY28-1	ATGTCTAATGAAACCAGAGA
WRKY28-2	TCAAGGCTCTTGCTTAAAGA
WRKY48-1	ATGGAGAAGAAAAAAGAAGA
WRKY48-2	TCATTTCTTATTCTCTTCAT
WRKY57-1	ATGAACGATCCTGATAATCC
WRKY57-2	TCAAGGGTTGCGCATAGTTT
EXB2p-1	caccTAATACACATTACAACATGATTGAA
EXB2p-2	GACGAAGAACAAAGAGAAAAAACTT
EXB3p-1	caccTCAATCCTCTGCAACTTTTTGTTTT
EXB3p-2	GGTGAAGAACAATGAAGAGAGAGGT
EXB4p-1	ccacACTTTTGAGACCCATGGTATGTATT
EXB4p-2	GTAATAGAGAAAAGATGGAATCTAT
EXB5p-1	caccCGTTGTGGAGAGAGAGAGAGAGATC
EXB5p-2	GATGATTGATCGGCGAGAGAAGTAG
LBb1.3	ATTTTGCCGATTTCGGAAC
050011LP	GTAGCAGTGCCAGTGTGTCAG
050011RP	AATGAAGGCGAGCCTAAAGAG
107668LP	TTGACTGCTTTTTGGCCATAC
107668RP	CTCGATCAAGAGAACGGTTTG
066438LP	TTACCGGTGACCAGTGTTTTC
066438RP	CTTTTTGGCCGTATTTTCTCC
006260LP	TTTCCGTGGTGTTTTGACTG
006260RP	CTGGCCGACATATCTATCGAG

Supplemental Methods

Plant Materials

Arabidopsis T-DNA insertion mutants were ordered from the *Arabidopsis* Biological Resource Center (ABRC, http://abrc.osu.edu). Homozygous mutants were genotyped by PCR using gene specific primers and T-DNA specific primer LBb1.3.

DR5:GUS line was crossed to *exb1-D* and the homozygous lines in the T3 generation were used for analysis.

The High Temperature-induced Hypocotyl Elongation Assay

To perform the high temperature-induced hypocotyl elongation assay, the 5-day-old seedlings of wild type (Col-0) and *exb1-D* were transferred to new plates containing 1/2 MS (Murashige and Skoog) media. Then the plates were put vertically at 29°C or 22°C under long-day conditions for 7 days. The hypocotyl length of the seedlings was measured for statistical analysis. Two-tailed t-test was used to test the significance.

Generation of Binary Constructs

To generate 4EnhEXB1p-WRKYs, the coding sequences of WRKY8, WRKY28, WRKY48 and WRKY57 were amplified from wild-type *Arabidopsis* genomic DNA using primer pairs: WRKY8-1 and WRKY8-2, WRKY28-1 and WRKY28-2, WRKY48-1 and WRKY48-2, and WRKY57-1 and WRKY57-2, respectively. The fragments were then cloned into pQDR2L3 vector to generate pQDR2L3-WRKYs. 4EnhEXB1p-WRKYs were generated by the LR reactions using the plasmids including pQDL4R1-4Enh, pENTR/D-pEXB1, pQDR2L3-WRKYs and pK7m34GW.

To analyze the expression patterns of *EXB2*, *EXB3*, *EXB4* and *EXB5*, the corresponding promoter regions were amplified from wild-type *Arabidopsis* genomic DNA using primer pairs EXB2p-1 and EXB2p-2, EXB3p-1 and EXB3p-2, EXB4p-1 and EXB4p-2, and EXB5p-1 and EXB5p-2, respectively. The fragments were cloned into pENTR/D-TOPO to generate pENTR/D-EXB2p, pENTR/D-EXB3p, pENTR/D- EXB4p and pENTR/D-EXB5p, respectively. pEXB2-GUS, pEXB3-GUS, pEXB4-GUS and pEXB5-GUS were generated by LR reactions between and pKGWFS7 and pENTR/D-EXB2p, pENTR/D-EXB3p, pENTR/D-EXB4p or pENTR/D- EXB5p.