Supporting Information

Bell et al. 10.1073/pnas.1210789109

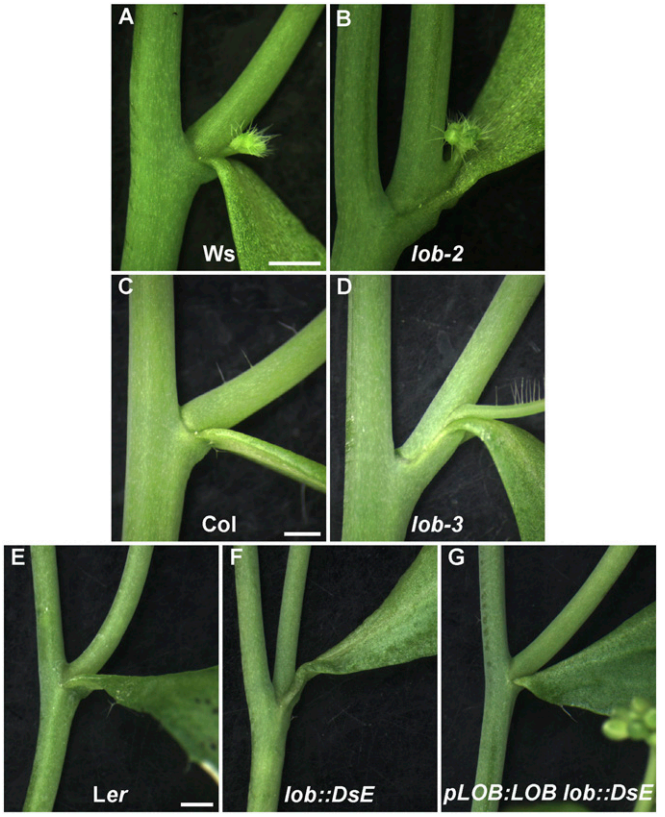

Fig. S1. LATERAL ORGAN BOUNDARIES (*lob*) mutants exhibit organ fusion. Paraclade junctions of (*A*) Ws, (*B*) *lob-2*, (*C*) Col, (*D*) *lob-3*, (*E*) Landsberg *erecta*, (*F*) *lob::DsE*, and (*G*) *pLOB:LOB lob::DsE*. The magnification is the same in *A* and *B*; *C* and *D*; and *E*–*G*. (Scale bars: 1 mm.)

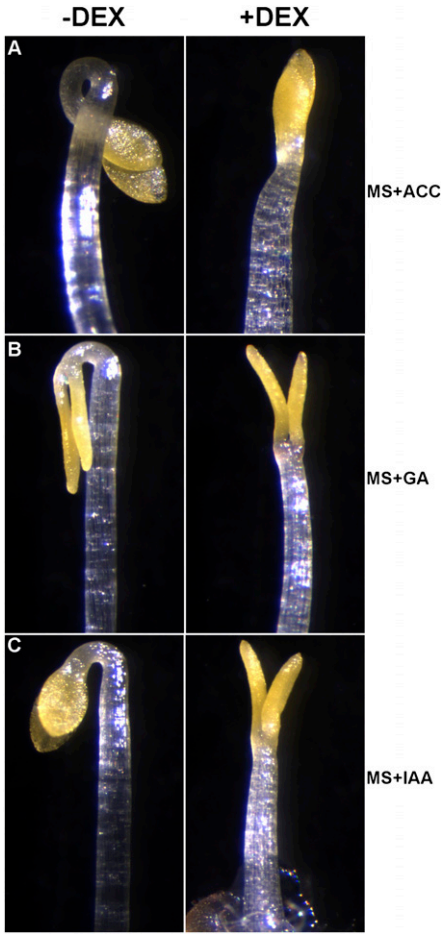

Fig. S2. Hormone responses in *35S:LOB-GR* seedlings. Dark-grown apical hook formation is suppressed in *35S:LOB-GR* seedlings grown on dexamethasone (DEX) and is not rescued by application of (*A*) 20 μM 1-aminocyclopropane-1-carboxylic acid (ACC) (*B*) 10 μM gibberellic acid (GA), or (*C*) 1 μM auxin (indole acetic acid; IAA). Seedlings were grown for 4 d in the dark on vertical plates. All images are shown at the same magnification.

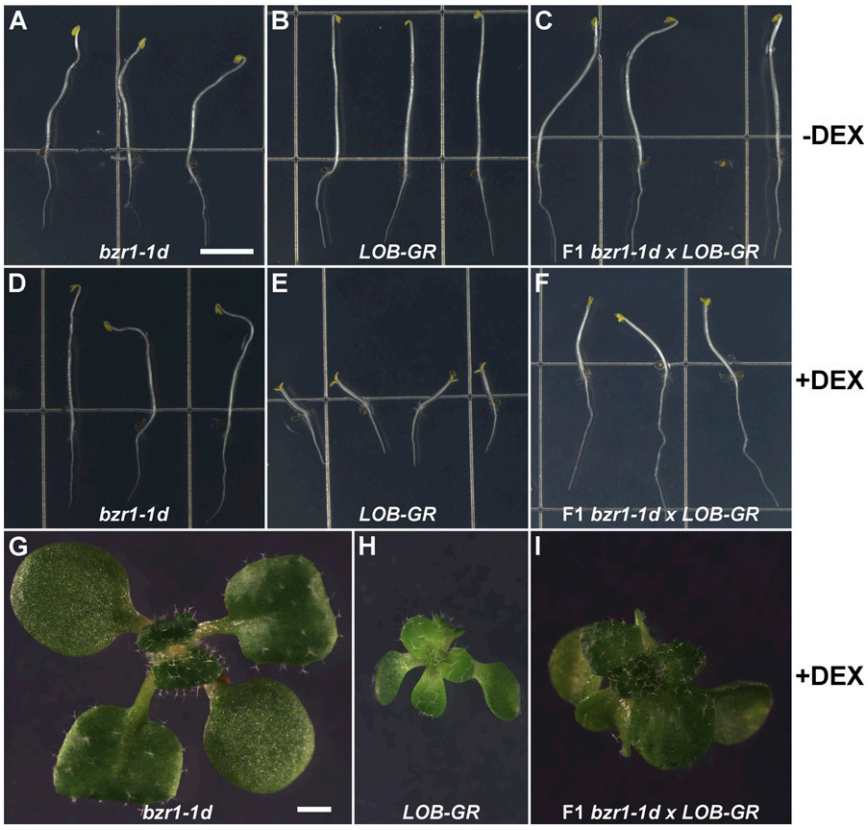

Fig. S3. Increased signaling through the brassinosteroid (BR) pathway partially suppresses the phenotype caused by ectopic *LOB* expression. (*A–F*) Dark-grown, 4-d-old *bzr1-1d* (*A* and *D*), *35S:LOB-GR* (*B* and *E*), and F1 *bzr1-1d*/+ *35S:LOB-GR*/+ (*C* and *F*) seedlings grown in the absence (*A–C*) or presence (*D–F*) of DEX. (*G–I*) Light-grown, 14-d-old *bzr1-1d* (*G*), *35S:LOB-GR* (*H*), and F1 *bzr1-1d*/+ *35S:LOB-GR*/+ (*I*) plants grown on DEX. In the presence of DEX, F1 plants exhibit a longer hypocotyl and expanded leaves compared with *35S:LOB-GR*, indicating partial suppression of the phenotype by *bzr1-1d*. Altered BR responses lead to changes in hypocotyl directional growth (1), which results in *bzr1-1d* and *35S:LOB-GR* seedlings failing to grow straight. (Scale bar in *A*: 5 mm, which corresponds to *A–F*; Scale bar in *G*: 1 mm, which corresponds to *G–I*.)

1. Gupta A, Singh M, Jones AM, Laxmi A (2012) Hypocotyl directional growth in Arabidopsis: A complex trait. *Plant Physiol* 159(4):1463–1476.

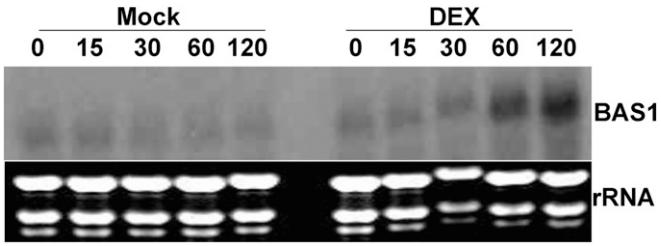

Fig. S4. *BAS1* transcript accumulation in response to altered LOB activity. Northern blot analyses of *BAS1* transcript levels. Eight-day-old *35S:LOB-GR* seedlings were exposed to mock or DEX treatment for the indicated time (minutes). *BAS1* transcripts were elevated in *35S:LOB-GR* seedlings within 60 min of DEX treatment.

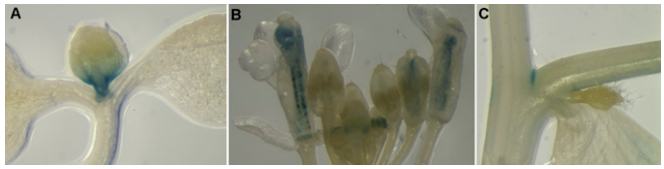

Fig. S5. Beta-glucuronidase (GUS) activity in *pBAS1:BAS1-GUS* plants. (*A*) Eight-day-old seedling. (*B*) Inflorescence showing expression in young carpels, ovules, developing seeds, and the base of floral organs. (*C*) Paraclade junction.

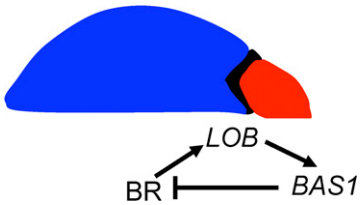

Fig. S6. Model for feedback loop involving LOB and BR activities in organ boundaries. As organ primordia (red) become distinct from the shoot apical meristem (blue), the boundary domain (black) forms between them. BR activity induces *LOB* expression, and in turn, LOB activity induces transcription of *BAS1*, which acts to reduce active BRs in boundary cells.

Table S1. Oligonucleotide sequences

Purpose	Gene	Primer name	Sequence
pLOB:GUS:3′IGR	*LOB*	LOButrF	5′-TCTAGAACATGTGAGAGTTT-3′
pLOB:GUS:3′IGR	*LOB*	LOBigrR	5′-CTGCAGGTTTGGTATGAATC-3′
RT-PCR	*BAS1*	BAS1-F	5′-CCATGGAGGAAGAAAGTAGCAG-3′
RT-PCR	*BAS1*	BAS1-R	5′-GGATCCTCAATCCTCATGATTGGTCA-3′
ChIP and EMSAs	*BAS1 A*	BAS1A-F	5′-CCCGGGAAACCTCAATTCGTTGACCTTCAC-3′
ChIP and EMSAs	*BAS1 A*	BAS1A-R	5′-CCCGGGTTTGCTTGCTGGACTATTTGAGC-3′
ChIP	*BAS1 B*	BAS1B-F	5′-CCCGGGAGTCGTTGTTGAAGCTGATAGAGC-3′
ChIP	*BAS1 B*	BAS1B-R	5′-CCCGGGTGCCTGAATCATTAATCCCAAC-3′
ChIP	*BAS1 C*	BAS1C-F	5′-AGCTTCAATTTGGGGTTTTCGGT-3′
ChIP	*BAS1 C*	BAS1C-R	5′-GACTTAATCCATGAGGTAGAGACAAC-3′
ChIP	*At3g26980*	UBQL-F	5′-TGGAGAAAGAGATAATCAA-3′
ChIP	*At3g26980*	UBQL-R	5′-CCAAAAGATTGTGCTCGGTG-3′

Underlined sequences indicate introduced restriction enzyme sites.

Dataset S1. Genes differentially expressed in DEX-treated *35S:LOB-GR* seedlings compared with mock treated

Dataset S1

Dataset S2. Gene Ontology (GO) term enrichment data for genes differentially expressed in DEX-treated *35S:LOB-GR* seedlings compared with mock treated

Dataset S2