Transcriptional repression of *BODENLOS* by HD-ZIP transcription factor HB5 in *Arabidopsis thaliana*

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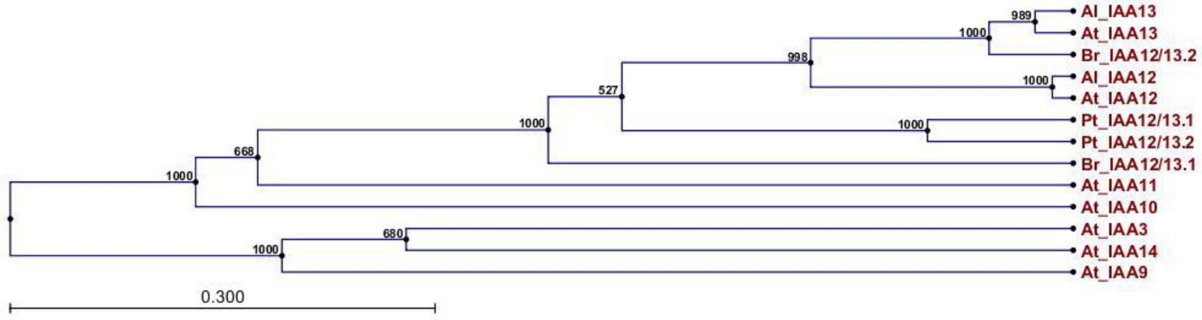

Figure S1. Phylogenetic relationship of IAA12 and IAA13 homologs and AtIAA3, AtIAA9, AtIAA10, AtIAA11 and AtIAA14. Al, *Arabidopsis lyrata*, At, *Arabidopsis thaliana*, Br, *Brassica rapa*, Pt, *Populus trichocarpa*.

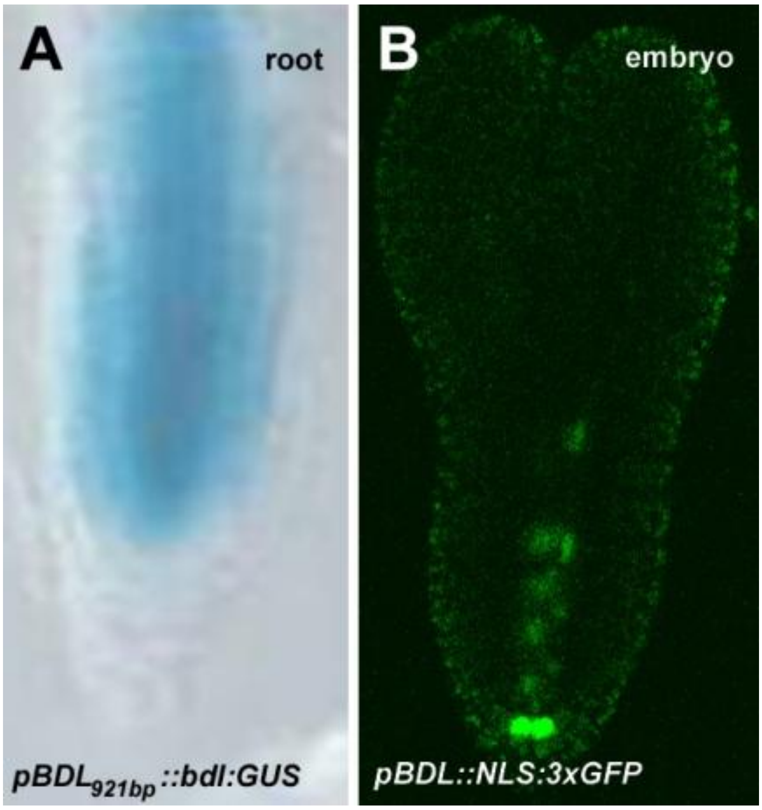

Figure S2. (A) *pBDL*$_{1000bp}$*::bdl:GUS* expression in the root meristem (B) *pBDL::NLS:3xGFP* expression in torpedo-stage embryo.

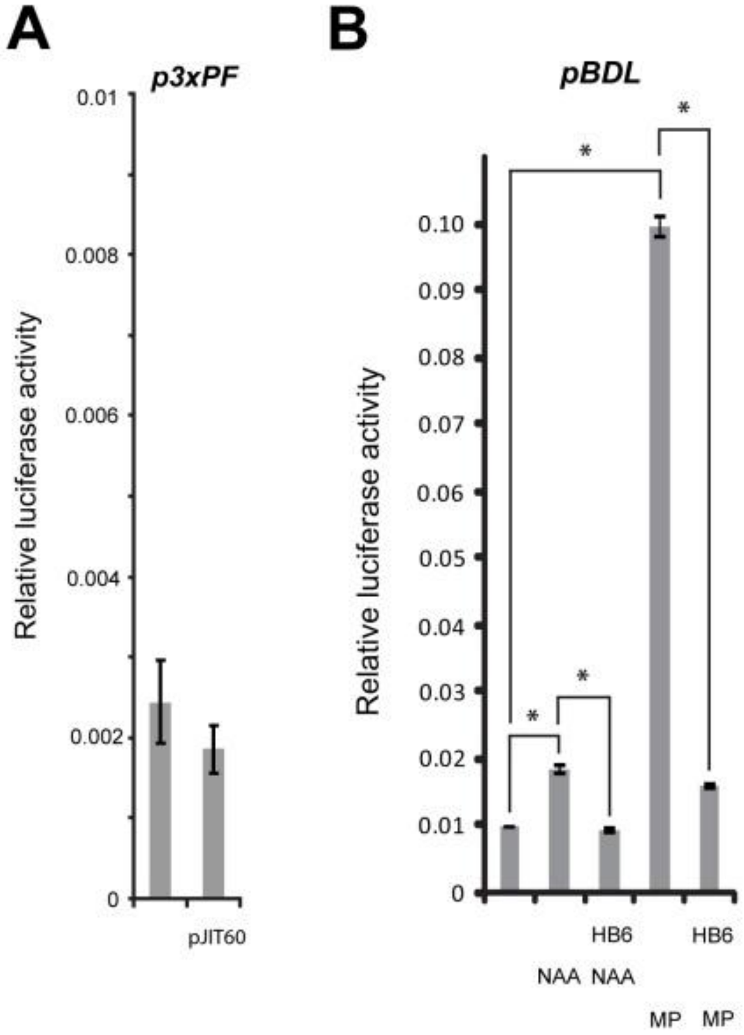

Figure S3. (A) Empty vector (*pJIT60*) does not significantly repress *p3xPF::LUC* expression. (B) HB6 represses auxin- or MP-induced expression of *pBDL::LUC*. Transient activity assay using *pBDL::LUC* as reporter construct in the presence or absence of HB6, MP and NAA as indicated. Values represent mean ± s.e.m. *, statistically significant differences for values as indicated by black lines, as determined by Student's *t* test ($p < 0.05$); for statistical details see Table S1.

Table S1. Statistical details, i.e. number of biological replicates (n), the statistical test that was used, and p- values.

Transient Activity Assays (Student's t-test, two-tailed distribution, two-sample unequal variance)		
	n	**p-value**
p3xPF::LUC	17	
p3xPF::LUC + HB5	4	0.023982777417344 (vs. p3xPF::LUC)
p3xPF::LUC + NAA	13	0.00511018361506801 (vs. p3xPF::LUC)
p3xPF::LUC + HB5 + NAA	12	0.0172479925742428 (vs. p3xPF::LUC + NAA)
p4xPF36::LUC	14	
p4xPF36::LUC + HB5	3	
p4xPF36::LUC + NAA	12	0.000071208885780171 (vs. p4xPF36::LUC)
p4xPF36::LUC + HB5 + NAA	9	0.000111681769431711 (vs. p4xPF36::LUC + NAA)
pBDL::LUC	6	
pBDL::LUC + NAA	3	0.00562278511084931 (vs. pBDL::LUC)
pBDL::LUC + HB5 + NAA	3	0.00980249790102142 (vs. pBDL::LUC + NAA)
pBDL::LUC + MP	3	0.000211341066818974 (vs. pBDL::LUC)
pBDL::LUC + HB5 + MP	3	0.000255057508922423 (vs. pBDL::LUC + MP)
pBDL::LUC	3	
pBDL::LUC + NAA	3	0.00399308644606912 (vs. pBDL::LUC)
pBDL::LUC + HB6 + NAA	3	0.000379475036834726 (vs. pBDL::LUC + NAA)
pBDL::LUC + MP	3	0.000298979203607784 (vs. pBDL::LUC)
pBDL::LUC + HB6 + MP	3	0.0000970250859890226 (vs. pBDL::LUC + MP)

List S1. Sequences used for the phylogenetic and the VISTA analysis.

Protein sequences used for the phylogenetic analysis

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GYSELLKALEVMFKFSVGEYFERDGYKGSDFVPTYEDKDGDWMLIGDVPWEMFICT
CKRLRIMKGSEAKGLGCGV*

At_IAA9
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*

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1 kb 5’ upstream regions used for the VISTA analysis

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