

**Table S3. Recapitulation of *iaa18-1* phenotypes in T1 seedlings**

Transgene	Number screened	Number in each phenotypic class (Number surviving to adulthood)			
		No root	Aberrant phyllotaxy	Unopened cotyledons	Curled leaves
<i>iaa18-1:GUS</i>	15,000	34 (0)	41 (2)	14 (4)	3 (3)
<i>iaa18-1</i>	4,000	3 (0)	8 (0)	0	nd

T1 seedlings selected for hygromycin resistance carrying either the *iaa18-1* or *iaa18-1:GUS* genomic constructs either failed to survive, or they had no morphological phenotype or GUS activity suggesting that the transgene had been silenced. We therefore screened without antibiotic selection among T1 seedlings for those with aberrant cotyledon placement. T1 seeds from *Ler* plants infiltrated with *iaa18-1:GUS* or from Columbia plants infiltrated with *iaa18-1* were plated without selection, and the number of seedlings with each phenotype counted. Seedlings in the 'no root' category generally also had aberrant phyllotaxy. Fig. S2 shows *iaa18-1:GUS* seedlings representative of different phenotypic classes. For representative *iaa18-1:GUS* transformants, we confirmed by subsequent X-Gluc staining that seedlings with phenotypes indeed carried the *iaa18-1:GUS* transgene. Numbers in parentheses indicate the number of seedlings in each category that survived to adulthood. Phenotypes of these surviving transformants often disappeared late in development and in subsequent generations. nd, not determined.