**Supplemental Figure 1.** Expression Patterns of *ARR1* during Shoot Regeneration. Supporting Figure 1. (A) Histological analyses on ProARR1:GUS and ProWUS:GUS. (B) Expression patterns of *ARR1* detected by *in situ* hybridization. “8D s” indicates sense probe control. Days after the callus transferred onto SIM were marked by “D”. Scale bars, 50 μm.
Supplemental Figure 2. The Effectiveness of Artificial MicroRNAs against ARR1, ARR10 and ARR12. Supporting Figure 2. After ethanol induction for 12 hours, relative transcript levels of type-B ARRs in the seedling of am-ARR1, am-ARR1/10, am-ARR1/12, am-ARR10/12, am-ARR1/10/12 transgenic lines were detected by RT-qPCR. In each panel, target ARRs were decreased, while the expression of other genes as control did not exhibit obvious changes. Mock represents non-treated control. Error bars represent standard deviations of three biological replicates.
**Supplemental Figure 3.** Defects in *ARR1, ARR10* and *ARR12* Attenuate Shoot Regeneration. Supporting Figure 3. Silencing of *ARR1, ARR10* and *ARR12* during SIM induction reduced shoot regeneration. The percentages of shoot regeneration are shown on the right. Scale bars, 2 mm. For each replicate, more than 100 individuals were used. Days after the callus was transferred onto SIM are indicated by “D”.

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Supplemental Figure 4. Transient Expression of ARR1, ARR10 or ARR12 Activates WUS Transcription. Supporting Figure 5. The effects of ARR1 (A), ARR10 (B) or ARR12 (C) on the transcription activity of WUS were detected in tobacco leaves. The quantitative analysis of fluorescence intensity is shown in (D). Error bars represent standard deviations of three biological replicates. Asterisks denote significant differences compared with the control, as determined by Student's t-test, with two asterisks denoting P < 0.01.
Supplemental Figure 5. Mutating the ARR Binding Elements in the WUS Promoter Region Reduced ARR-mediated WUS Transcription. Supporting Figure 5. (A) Transient expression assay in tobacco leaves indicates that replacing two base pairs of the ARR binding elements in the three ChIP-positive fragments or in WUS-3 (ProWUSm₁:LUC and ProWUSm₂:LUC) significantly reduced the LUC activity. Replacing one base pairs of the ARR binding elements in WUS-3 (ProWUSm₃:LUC and ProWUSm₄:LUC) resulted in moderate reduction of the LUC activity. (B) LUC/REN relative activities of (A). Error bars indicate the standard deviations of three biological replicates. Asterisks denote significant difference compared with ProWUS:LUC, as determined by Student’s t-test, with two asterisks denoting P < 0.01. (C) In wild-type explants, WUS signals became detectable at SIM6 (red arrowheads). At SIM8, WUS signals were observed in the callus protuberance. When the shoot meristems were established at SIM12, WUS signals were located in the central region of the meristem, beneath several layers of the outmost cells. In ProWUSm₂:GFP₃ transgenic lines, WUS signals were substantially reduced.
during the SIM incubation. (D) *In situ* hybridization confirming the expression pattern of *WUS* in wild-type explants. For (C) and (D), days after the callus was transferred onto SIM are indicated by “D”. Scale bars, 80 μm.
Supplemental Figure 6. Mutations in ARRs Enhanced the Signals of the ProYUC1:GUS and ProYUC4:GUS Reporters. Supporting Figure 6. (A) Histological analyses on ProYUC4:GUS are shown in wild-type (upper panels) and arr10 12 (lower panels) callus. (B) Those of ProYUC1:GUS in longitudinal sections of wild-type (upper panels), arr1 10 (middle panels) and arr1 12 (lower panels) callus. Days after the callus was transferred onto SIM are indicated by “D”. Scale bars on explants represent 2 mm, while those in the sections represent 50 μm.
Supplemental Figure 7. ARR1 Binds the Promoters of YUC1 and Regulates its Transcription. Supporting Figure 8. (A) Relative transcript levels of the WUS genes in transgenic lines with enhanced YUC expression during shoot regeneration. Error bars represent standard deviations of three biological replicates. Days after the callus was transferred onto SIM are indicated by “D”. Asterisks denote significant difference compared with the wild-type callus, as determined by Student’s t-test, with two asterisks denoting P < 0.01. (B) Scheme of the promoter regions of YUC1. YUC1-1 to YUC1-5 indicate the positions of the fragments used for the ChIP-qPCR analysis. Blue bars indicate the type-B ARR binding elements GAT(T/C). (C) ChIP was performed in ProARR1:ARR1-GFP, ProARR10:ARR10-GFP and ProARR12:ARR12-GFP lines using an antibody against GFP, followed by RT-qPCR to specifically amplify different promoter fragments of YUC1, YUC2, YUC4 and YUC6. Error bars represent the standard deviations of three biological replicates. Days after the callus was transferred onto SIM are indicated by “D”.

Supplemental Figure 8. Expression Patterns of ProDR5:GFP were Disturbed in YUC4ox Lines. Supporting Figure 8. As described previously, ProDR5:GFP signals were progressively confined to a pattern apical and peripheral to the WUS-accumulating region at SIM8. After the formation of shoot meristem, GFP signals were located in the L1 cell layer. By contrast, the GFP signals spread into the whole explant of YUC4ox lines and were enriched in the root apical meristem at SIM12. Days after the callus was transferred onto SIM are indicated by “D”. Scale bars, 100 μm.
Supplemental Figure 9. YUCs Act Downstream of ARRs. Supporting Figure 8. (A) Shoot induction in yuc 1 4 double and arr10 12 yuc 1 4 quadruple mutants. Besides reduced shoot regeneration, both mutants gave rise to filaceous structures. The number of days of SIM incubation is indicated above each column of panels. Scale bars, 2 mm. (B) Shoot regeneration frequencies of yuc1 4 and arr10 12 yuc1 4 mutants were significantly decreased compared with those of the wild type. For each replicate, more than 100 individuals were used. (C) Transcript levels of ARR10 and ARR12 in the yuc1D, YUC4ox, and yuc1 4 double mutants examined by RT-qPCR. Error bars in (B) and (C) indicate the standard deviations of three biological replicates.
**Supplemental Figure 10.** Expression of YUC4 under Mutated YUC4 Promoter Reduced Shoot Regeneration. Supporting Figure 8. (A) Shoot induction in ProYUC4m:YUC4 transgenic lines. The number of days of SIM incubation is indicated above each column of panels. Scale bars, 2 mm. (B) Shoot regeneration frequencies of ProYUC4m:YUC4 transgenic lines were significantly reduced compared with those of the wild type. For each replicate, more than 100 individuals were used.
Supplemental Figure 11. ARR1, ARR10 and ARR12 Bind the Promoters of YUCs and Regulate Their Expression in the SAM. Supporting Figure 10. (A) Distribution patterns of ARR1, ARR10 and ARR12 in the SAM. Expression regions of ProARR1:ARR1-GFP, ProARR10:ARR10-GFP and ProARR12:ARR12-GFP reporters (green) overlap with WUS signal indicated by ProWUS:dsRED (yellow). Scale bars, 50 μm. (B) Scheme of the promoter regions of YUC2 and YUC6 are shown on the top. YUC2-1 to YUC2-6 and YUC6-1 to YUC6-5 indicate the positions of the fragments used for the ChIP-qPCR analysis. The blue bars indicate the type-B ARR binding elements GAT(T/C). ChIP analysis showed that ARR1 could bind to the promoter of YUC1 and YUC4, while ARR10 and ARR12 could bind to the YUC4 promoter.
The positions of fragments in the *YUC4* promoter are shown in Figure 8A, and those of the *YUC1* promote are shown in Supplemental Figure 7B. ChIP assays were performed in *ProARR1:ARR1-GFP*, *ProARR10:ARR10-GFP* and *ProARR12:ARR12-GFP* transgenic lines using antibodies against Myc or GFP followed by RT-qPCR. Specific primers were used to amplify different promoter fragments from *YUC1*, *YUC2*, *YUC4* and *YUC6*. Error bars represent the standard deviations of three biological replicates.
Supplemental Figure 12. Phenotypes of ProARR10:YUC4 Transgenic Lines. Supporting Figure 10. (A) Seedlings of WT and ProARR10:YUC4 transgenic line. (B) and (C) show longitudinal sections of the SAM in WT and ProARR10:YUC4 transgenic seedling, respectively. Scale bars, 50 μm.
Supplemental Figure 13. *ARR1, ARR10* and *ARR12* are Involved in Axillary Meristem Initiation. Supporting Figures 2, 3 and 4. Scheme of axillary bud formation in leaf axils of the wild-type and the *arr1 10 12* triple mutant seedling. The black line represents the border between the rosette leaf (lower) and the cauline leaf (upper). Each column represents a single seedling. Each square within a column represents an individual leaf axil. Green squares indicate the presence of an axillary bud, while red squares indicate their absence.