Supplementary figures

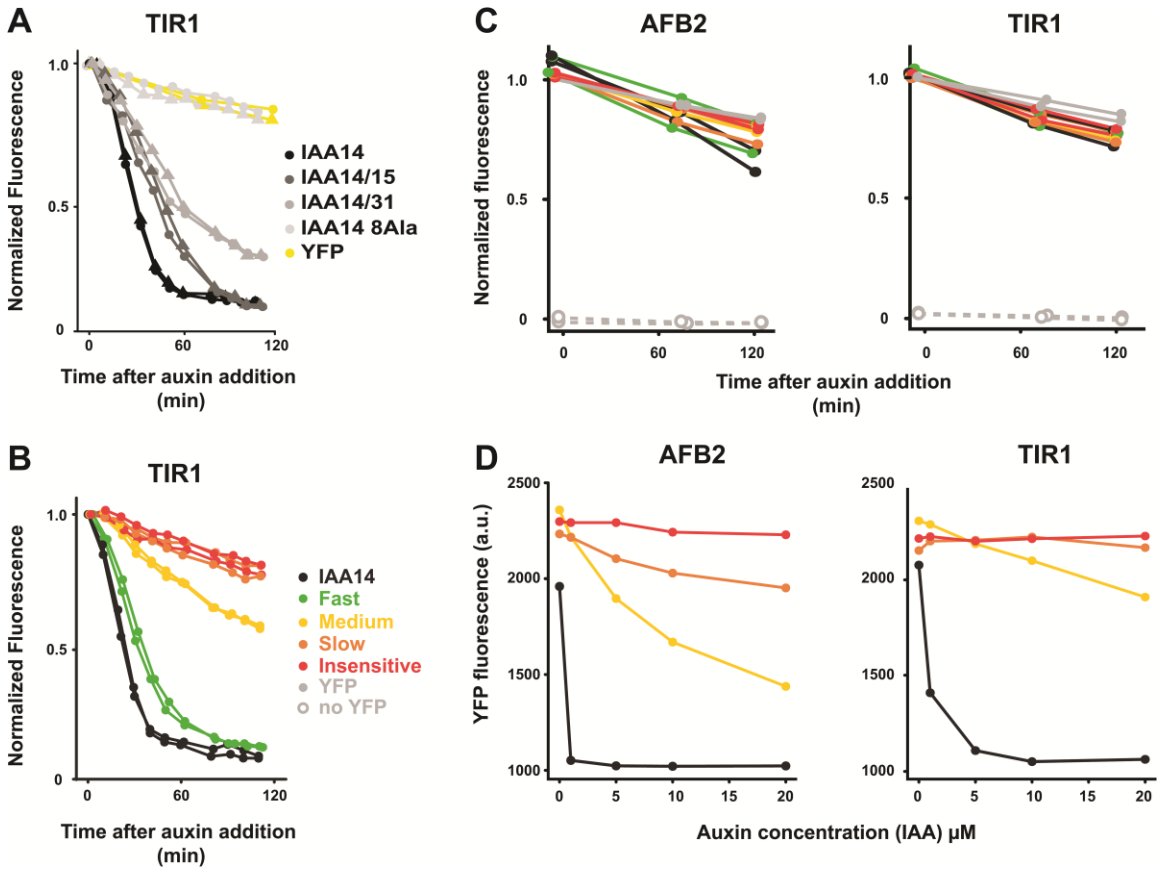

Figure S1. A synthetic system for assaying auxin-induced degradation rate variants.
(A) Chimeric IAA14 variants and a multiple-Alanine substitution variant exhibited a range of degradation rates, falling within the range of the point mutants analyzed in this study. **(B)** Degradation rates observed when IAA14 variants are co-expressed with TIR1 are similar to those observed when variants are co-expressed with AFB2. YFP-tagged variants were co-expressed in yeast with the TIR1 auxin receptor. Degradation of the YFP signal following addition of auxin at time 0 was quantified with flow cytometry. Degradation profiles were normalized to initial fluorescence. **(C)** Degradation of IAA14 variants is auxin-dependent. YFP-tagged variants were co-expressed in yeast with either AFB2 or TIR1. Fluorescence following addition of a mock treatment at time 0 was quantified with flow cytometry. All of these strains show similar fluorescence values over time as auxin-treated strains expressing YFP without an Aux/IAA fusion (YFP). A control strain without YFP was monitored to estimate levels of background fluorescence. **(D)** Degradation rates of IAA14 rate variants are correlated with sensitivity to auxin. Yeast expressing YFP-tagged IAA14 variants and either AFB2 or TIR1 was grown in media with the indicated concentrations of auxin. Fluorescence was measured by flow-cytometry 2 h after addition of mock or auxin treatment.

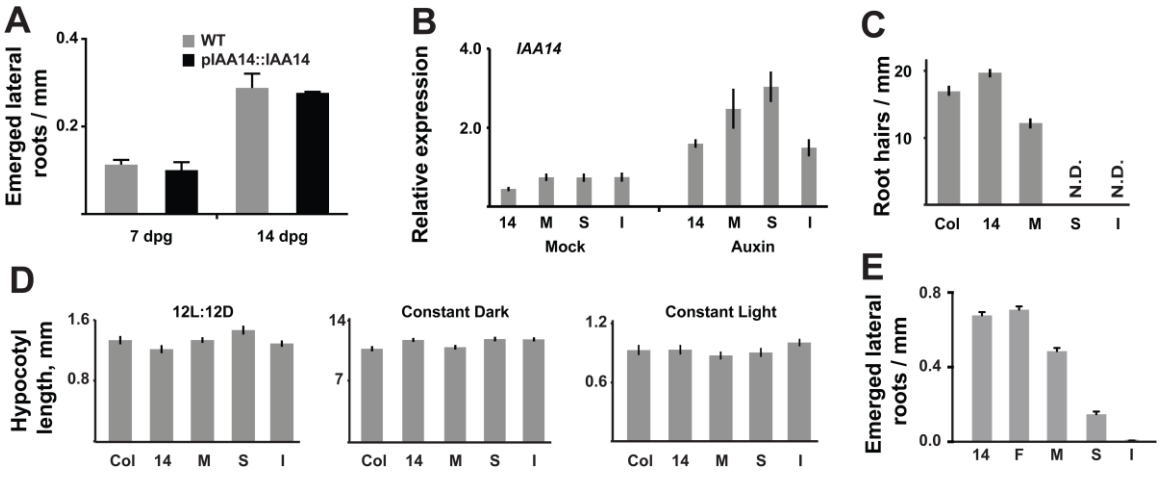

Figure S2. **Effects of IAA14 are specific and not dose-dependent.**
(A) Additional copies of wild-type IAA14 do not affect lateral root densities. Lateral root phenotypes were compared between plants transformed with wild-type IAA14 expressed from its own promoter (pIAA14::IAA14) and untransformed plants (Col). Emerged lateral roots were counted at the end of 7dpg or 14dpg. Error bar represent S.E.M. **(B)** Variant lines exhibit similar levels of IAA14 mRNA expression. Plants transformed with IAA14 variants were treated for 3 h with either mock or auxin treatments. Levels of *IAA14* mRNA in isolated roots were quantified by qPCR. **(C)** Effects of variation in IAA14 degradation rate are tissue-specific Root hair density decreased when IAA14 degradation rate was slowed. **(D)** Hypocotyl length of plants grown in light/dark cycles or constant conditions was not correlated with IAA14 degradation rate. Error bars represent S.E.M. **(E)** Auxin treatment increased lateral root densities in all variants, but the relative LR densities were maintained. 7dpg seedlings were transplanted onto plates containing 1µM IAA and emerged lateral roots were counted 7 days later. Error bars represent S.E.M. of two replicates of six plants each.

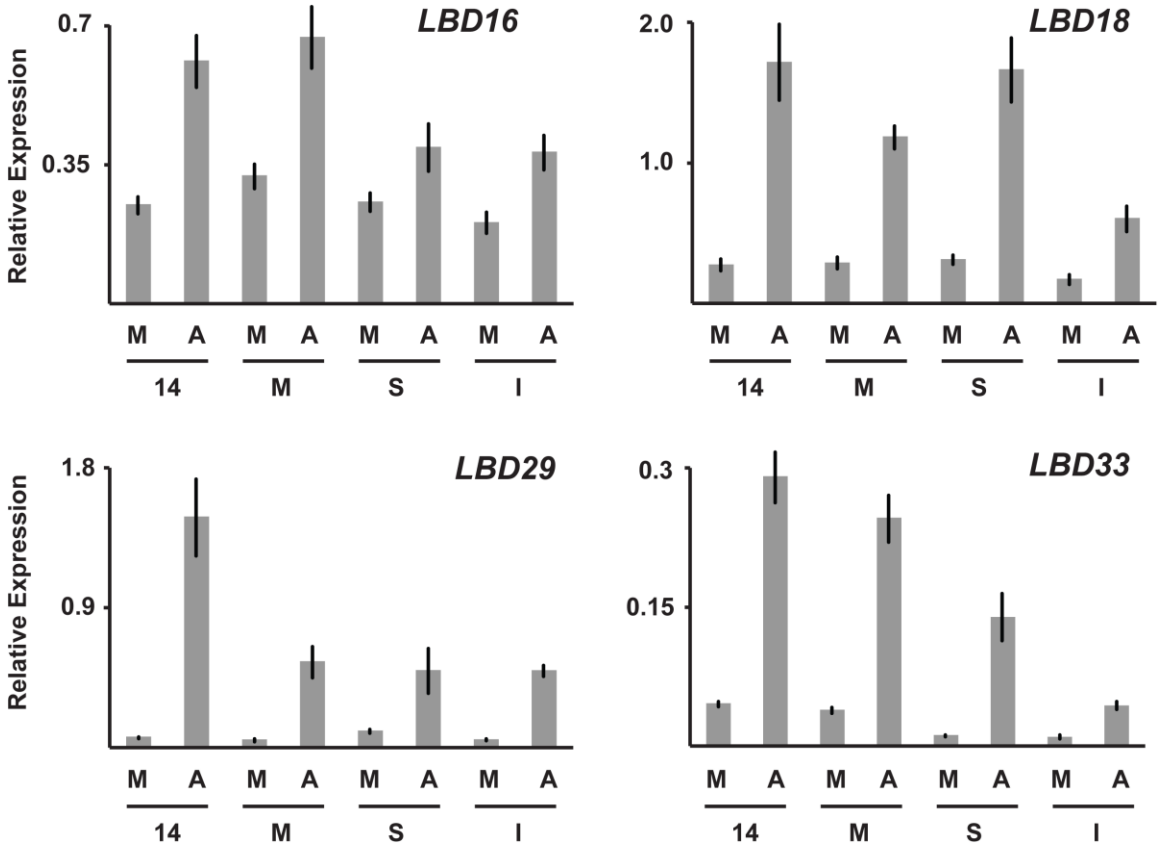

Figure S3. Expression of genes downstream of IAA14 is decreased in an uncoordinated manner in slower rate variants plants.
The *LATERAL ORGAN BOUNDARY DOMAIN (LBD)* genes *LBD16*, *LBD18*, *LBD29*, and *LBD33* act downstream of the IAA14-ARF7-ARF19 signaling module. Auxin-induced expression of LBD genes was decreased when IAA14 degradation rate was slowed. Plants were treated for 3 hours with either Mock or 1µM IAA. M: mock, A: auxin.