Supplementary data

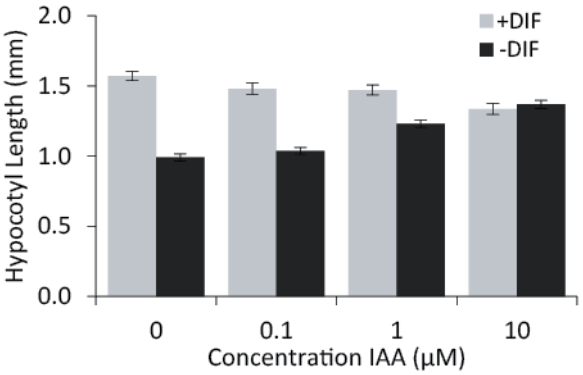

Figure S1: Average hypocotyl length of Col-0 with and without IAA. Bars represent means ± s.e. (n=5x25)

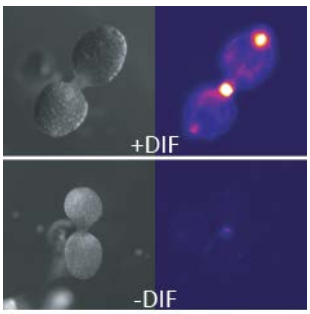

Figure S2: Auxin response as visualized by eDR5::*LUC* bioluminescence in representative seven day old seedlings grown under +DIF (top) or –DIF (bottom) at midday (t=6 h)

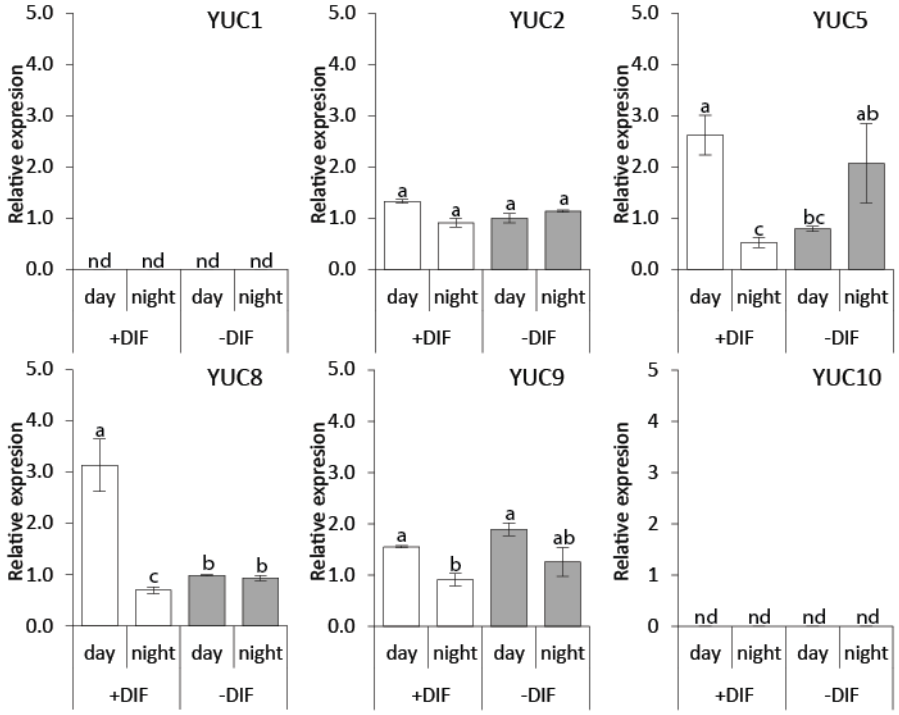

Figure S3: Expression analysis of *YUC* auxin biosynthesis genes at midday (6 hours, lights on = 0h) and midnight (18 hours, lights off = 12h) (n=3x400). Data represent means ± s.e. Bars with different letters differ significantly (P<0.05).

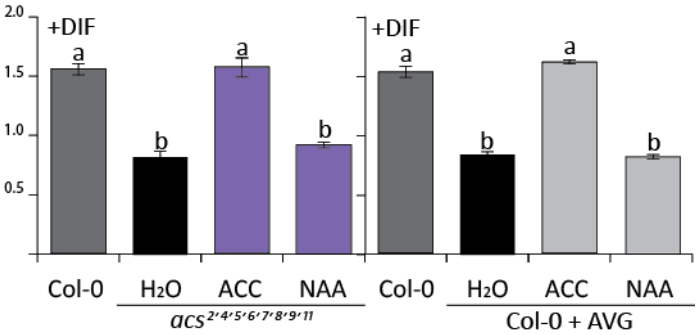

Figure S4: The effect of 10 µM ACC and 1 µM NAA application on hypocotyl elongation in *acs*^{2,4,5,6,7,8,9,11} (*acs2-1acs4-1acs5-2acs6-1acs7-1acs9-1amiRacs8acs11*) seedlings grown for seven days under +DIF and wild-type seedlings grown in the presence of AVG (n=5x25). Bars represent means ± s.e. Bars with different letters differ significantly (*P*<0.05)

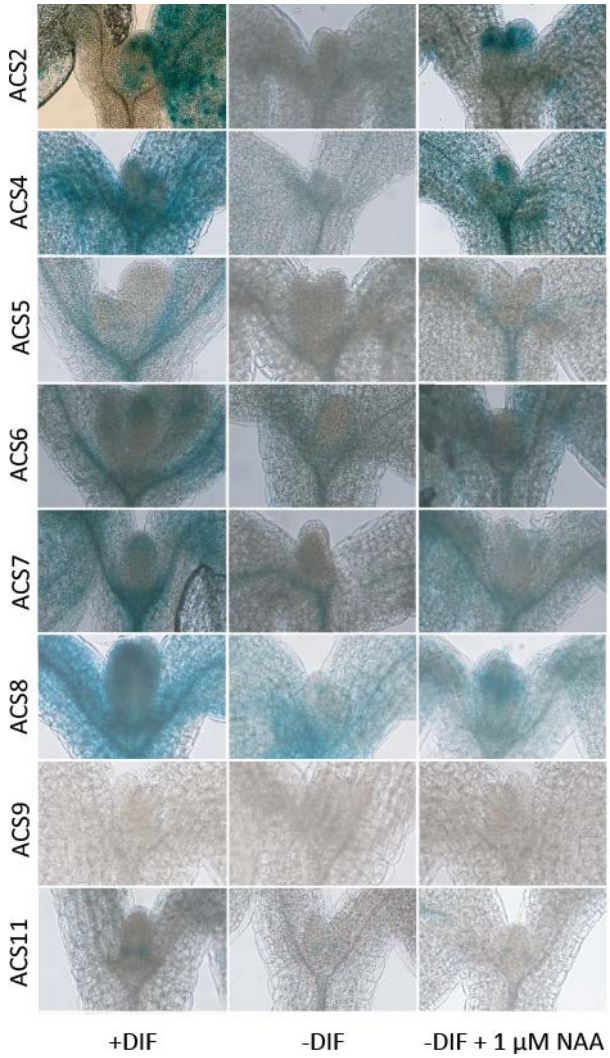

Figure S5: *ACS*$^{(2,4,5,6,7,8,9,11)}$*::GUS* promoter activity in the apex of seven day old seedlings under +DIF, -DIF and -DIF + 1 µM NAA.

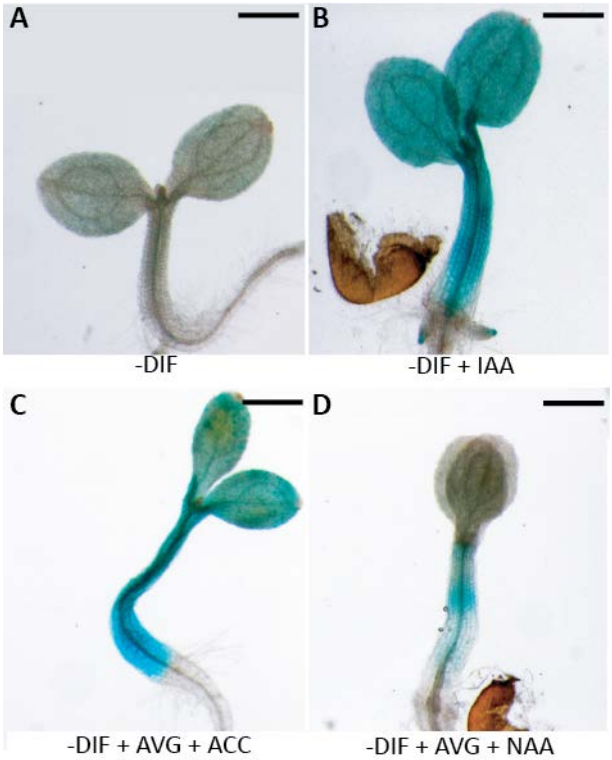

Figure S6: *PIF3::GUS* promoter activity under -DIF.
A, -DIF, **B**, -DIF + 1 µM IAA, **C**, 2.5 µM AVG + 10 µM ACC, **D**, 2.5 µM AVG + 1 µM NAA

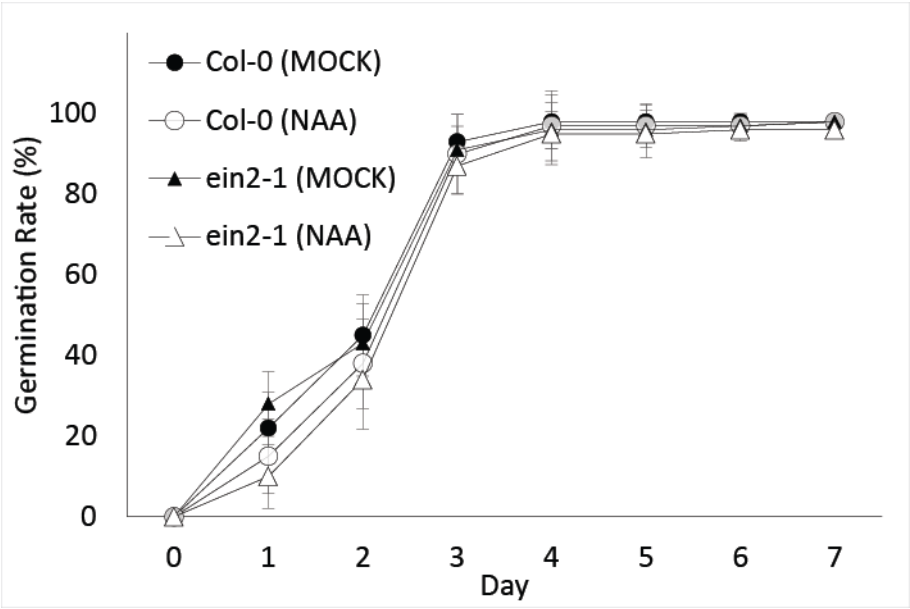

Figure S7: Germination rate of **Col-0 (circles) and *ein2-1* (triangles) seeds treated with 1 µM NAA (white) compared to mock (black)**. Radicle emergence over 1 mm is referred to as germination. Germination rates were counted as germinated seeds/total germinated seeds at day 10. The results shown are the means ± SD of three independent experiments (n=3x50).

Table S1: Primer sequences used for gene expression analysis

CYP79B2	F	CAACCGAAACATCGTCCTTT	Franklin et al., 2011
CYP79B2	R	TTGGGATCCGTCATCAATTT	Franklin et al., 2011
IAA29	F	CTTCCAAGGGAAAGAGGGTGAC	Sun et al., 2013
IAA29	R	TTCCGCAAAGATCTTCCATGTAAC	Sun et al., 2013
SAUR19	F	CTTCAAGAGCTTCATAATAATTCAAACTT	Franklin et al., 2011
SAUR19	R	GAAGGAAAAAATGTTGGATCATCTT	Franklin et al., 2011
SAUR21	F	TAAGCTTCAAAAACCTTTTCGTACA	Franklin et al., 2011
SAUR21	R	CCAAATGTCGGATCATCATGATCA	Franklin et al., 2011
SAUR22	F	GACAAATAGAGAATTATAAATGGCTCTG	Franklin et al., 2011
SAUR22	R	ATGAATTAAGTCTATATCTAACTCGGAAA	Franklin et al., 2011
SAUR23	F	ATTCAAACTTTCAGACAAAAGAAATGG	Franklin et al., 2011
SAUR23	R	ACAAGGAAACAACTCTATCTCTAACT	Franklin et al., 2011
SAUR24	F	GAGATATTTGGTGCCTGTCTCATATTTAAACC	Franklin et al., 2011
SAUR24	R	CAAGAAGAAAGAGGAAAAAGGGCTCATC	Franklin et al., 2011
TAA1	F	CAAGAAGCATGTCCGAGTCA	Franklin et al., 2011
TAA1	R	AGCTTCATGTTGGCGAGTCT	Franklin et al., 2011
YUC8	F	CCTTGAGCGTTTCGTGGGTTGTTT	Sun et al., 2012
YUC8	R	CCTGCAATCAAACAGTTCTCGCGT	Sun et al., 2012
YUC1	F	TGGAGAGTAAAGACTCATGAT	Sun et al., 2012
YUC1	R	GTACTCACTCGCGTGAACGAT	Sun et al., 2012
YUC2	F	GGTGACACGGATCGGTTAGGGT	Sun et al., 2012
YUC2	R	TGCCGAATAATGCATTACCCGT	Sun et al., 2012
YUC5	F	TTCAACGAGTGTGTCCAGTCTGCT	Sun et al., 2012
YUC5	R	TCTCTGGAACAACTTTCTCCGCGT	Sun et al., 2012
YUC9	F	CCTGCAATCAAACAGTTCTCGCGT	Sun et al., 2012
YUC9	R	TGAAGCCAAGAAGGGACGTTGCTA	Sun et al., 2012
YUC10	F	TTCTGAAGTATGCTCCAGTGGCGA	Sun et al., 2012
YUC10	R	GTTTGGTGGCGAAAGGACCTTGTT	Sun et al., 2012
UBQ5	F	AAGGTTCAGCGTTTGAGGAAGG	Zhong et al., 2012
UBQ5	R	TCTTTCTGGTAAACGTAGGTGAGTC	Zhong et al., 2012

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