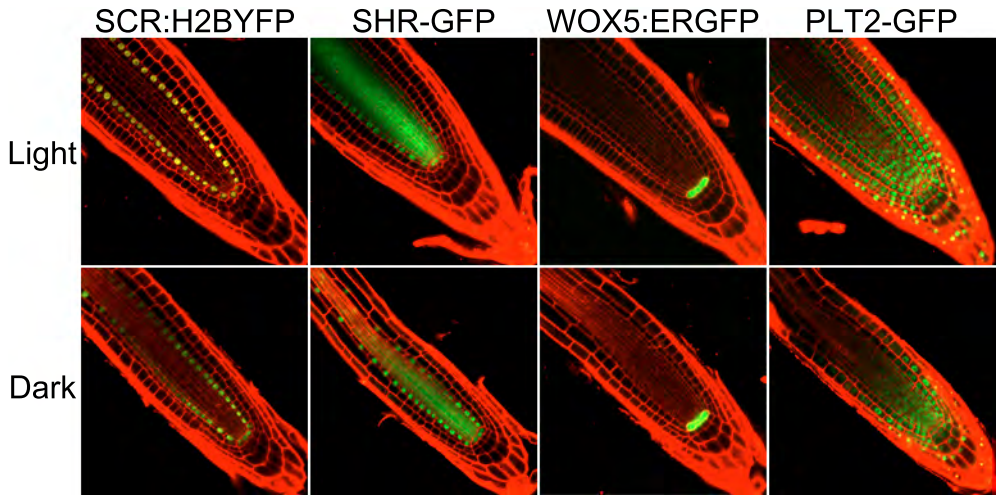

Fig. S1. The expression patterns of root-specific developmental markers are not altered upon etiolated growth. Confocal laser scanning images of 7-day-old light- and dark-grown seedling roots expressing SCR:H2BYFP, SHR-GFP, WOX5:ERGFP and PLT2-GFP. Roots were counterstained with propidium iodide (red channel).

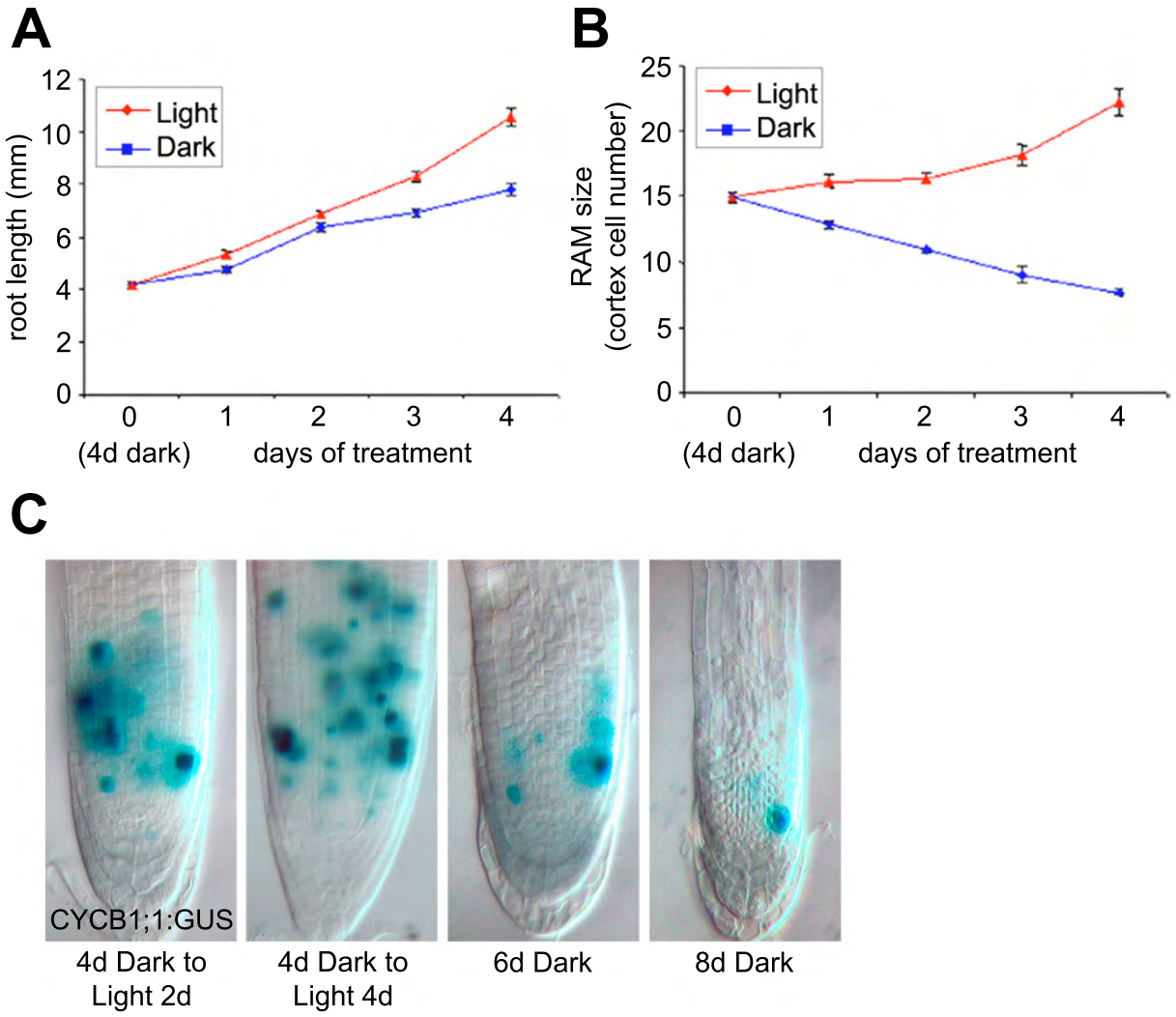

Fig. S2. Darkness reduces root growth in a reversible manner. (**A**,**B**) Primary root length (A) and RAM size (B) of WT seedlings grown for 4 days in the dark and either exposed to light or kept in the dark for additional 4 days. Measurements were taken at the indicated times. Error bars represent s.e.m. dag, days after germination. (**C**) CYCB1;1:GUS staining in seedling roots grown as indicated. The exposure of etiolated seedlings to light induces CYCB1;1:GUS expression and leads to a replenishment of the RAM, thereby allowing the recovery of root growth.

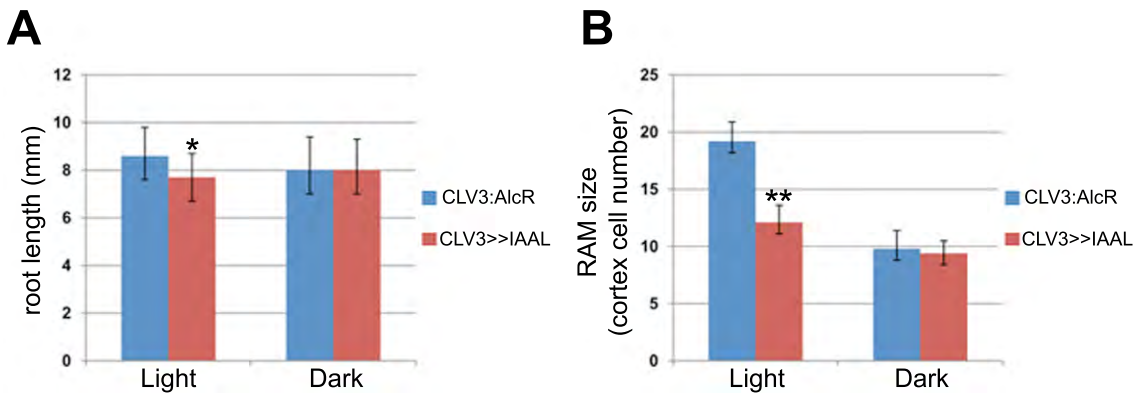

Fig. S3. Inhibition of STRAT results in reduced RAM size. (**A**,**B**) Primary root length (A) and RAM size (B) of 4-day-old light- and dark-grown CLV3:AlcR and CLV3>>IAAL seedlings upon induction by ethanol. Error bars represent s.d. **P*<0.05, ***P* <0.01, *t*-test.

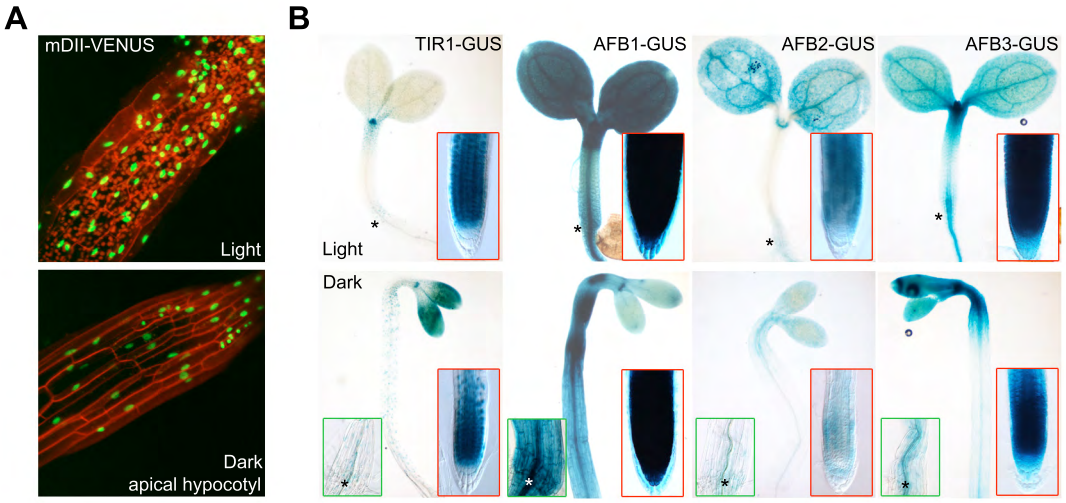

Fig. S4. Controls for DII-VENUS. (**A**) mDII-VENUS (green channel) expression in 4-day-old seedlings grown in light and in the dark. The pictures show that the mDII-VENUS auxin-insensitive version of the sensor is expressed in tissues where DII-VENUS is not detected, such as light-grown hypocotyls and the apical region of etiolated hypocotyls. Red channel, FM4-64 staining. (**B**) Expression patterns of TIR1:TIR1-GUS, AFB1:AFB1-GUS, AFB2:AFB2-GUS and AFB3:AFB3-GUS in 4-day-old seedlings grown in light or in the dark. Red-bordered insets: marker expression in the root apices of light- and dark-grown seedlings. Green-bordered insets: marker expression in the basal region of etiolated hypocotyl. Asterisks indicate the shoot-root junction. Samples were stained for 24 hours.

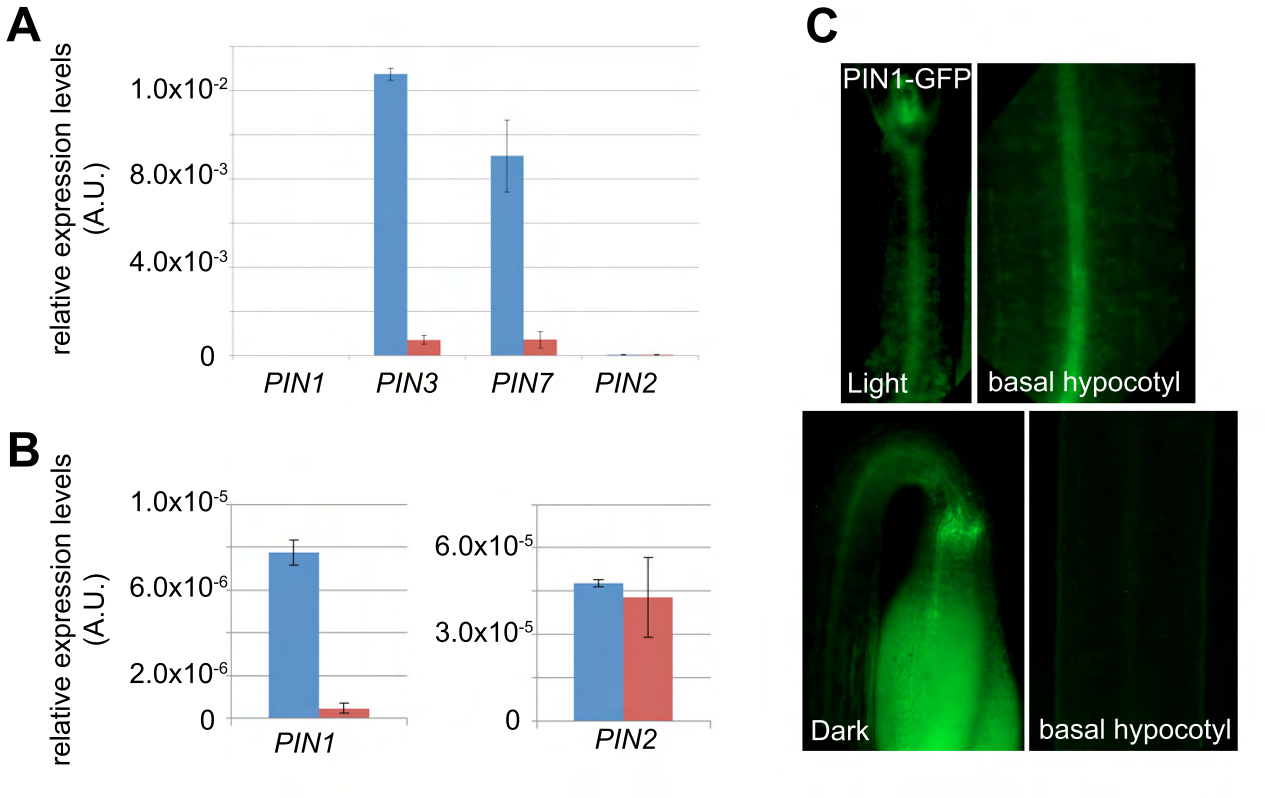

Fig. S5. Light regulation of *PIN* expression. (**A**) Expression levels of *PIN1*, *PIN2*, *PIN3* and *PIN7* determined by qRT-PCR on RNAs extracted from shoot tissues of 4-day-old seedlings grown in the light and in the dark. Note the low level of *PIN1* and *PIN2* relative expression compared with *PIN3* and *PIN7*. A.U., arbitrary units. (**B**) Expression levels of *PIN1* and *PIN2* determined as described for A, represented with the correct scales. Note that *PIN1*, but not *PIN2*, is strongly induced in the shoot tissues of light-grown seedlings compared with dark-grown ones. A.U., arbitrary units. (**C**) Epifluorescence pictures showing the expression of pPIN1:PIN1-GFP in whole-mount light and dark-grown hypocotyls. Pictures on the right show details of basal region of the hypocotyl. Note the lack of PIN1-GFP expression in the basal region of etiolated hypocotyls.

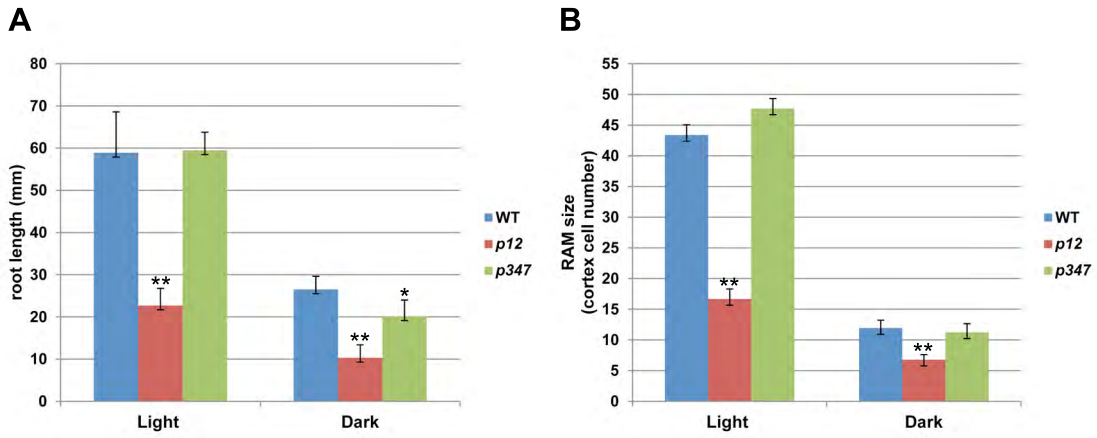

Fig. S6. A key role for *PIN1* and *PIN2*, but not *PIN3*, *PIN4* and *PIN7*, in the control of root growth. (**A**,**B**) Primary root length (A) and RAM size (B) of 6-day-old WT, *p12* and *p347* seedlings. Error bars represent s.d. **P*<0.05, ***P*< 0.01, *t*-test.

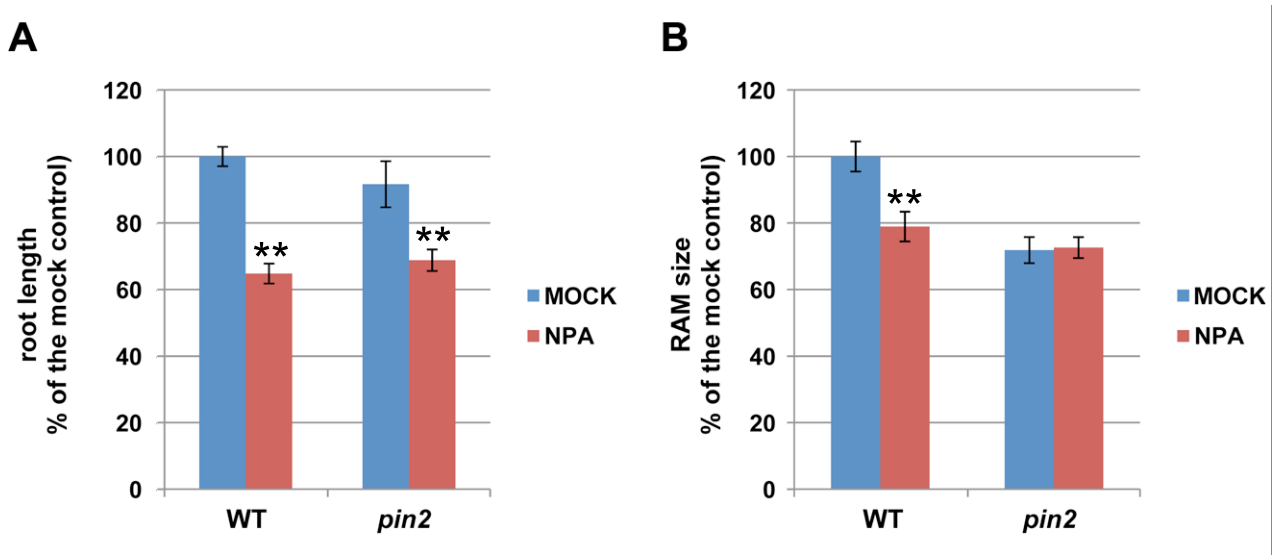

Fig. S7. The RAM of *pin2* mutants is less sensitive to NPA. (**A**,**B**) Primary root length (A) and RAM size (B) in 7-day-old light-grown WT and *pin2* (*eir1*) seedlings with and without (MOCK) NPA application on the hypocotyls. Data are expressed as percentage of the mock control, arbitrarily set to 100. Error bars represent s.e.m. **P<0.01, t-test.

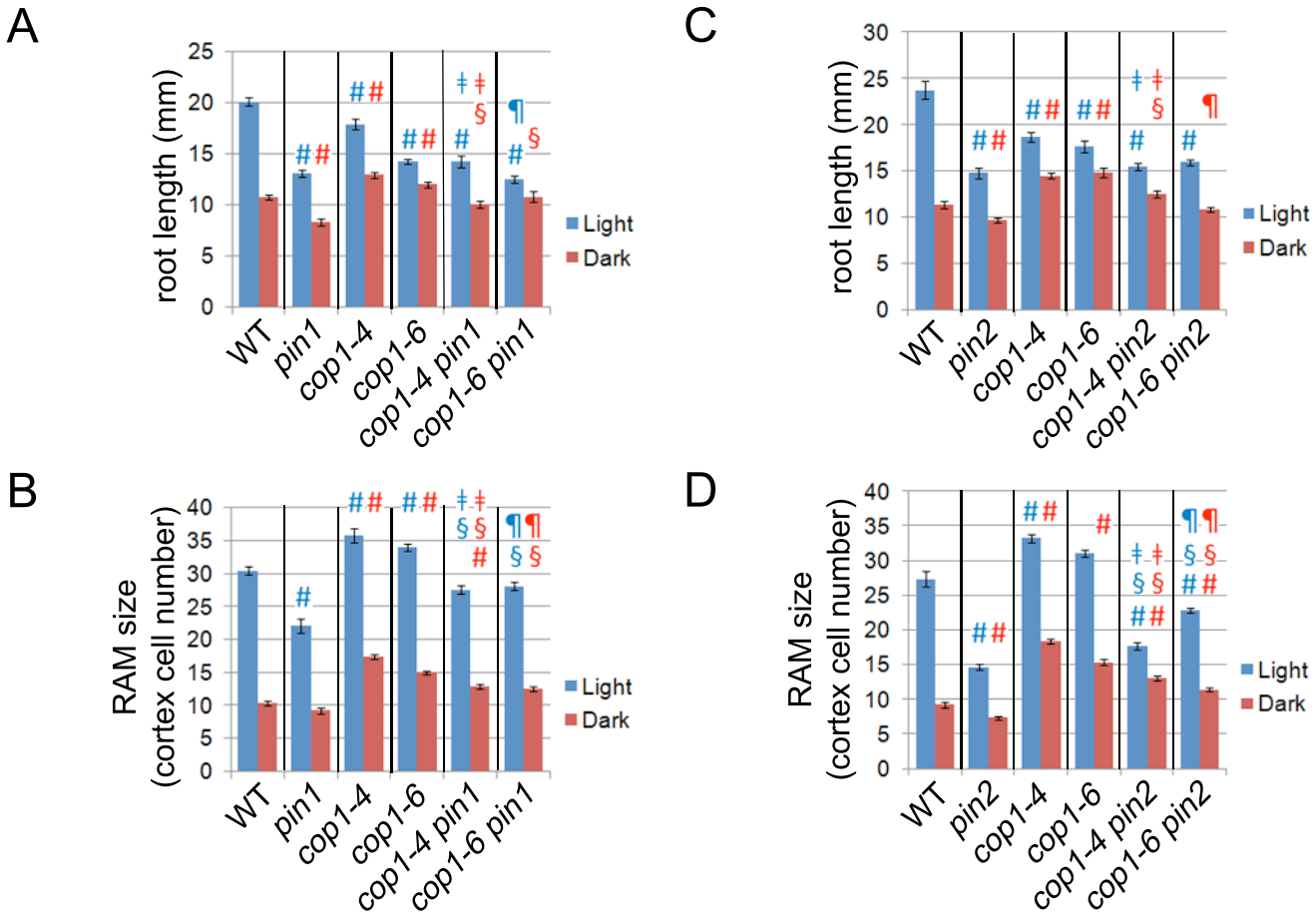

Fig. S8. *COP1* acts together with both *PIN1* and *PIN2* to regulate root growth. (**A-D**) Primary root length (A,C) and RAM size (B,D) of 8-day-old WT, *pin1*, *cop1-4*, *cop1-6*, *cop1-4 pin1*, *cop1-6 pin1*, *pin2*, *cop1-4 pin2* and *cop1-6 pin2* plants. Error bars represent s.e.m. The significance of the differences were assessed using t-tests and P-values were corrected with Bonferroni correction ($\alpha = 26$). Differences between light and dark for a given genotype were all significant (P<0.05), except for root length of *cop1-6 pin1* (panel A). Symbols highlight significant differences between genotypes (P<0.05) in the light (blue) or in the dark (red): #, genotype versus WT; §, genotype versus *pin1* (A,B) or *pin2* (C,D); ‡, genotype versus *cop1-4*; ¶, genotype versus *cop1-6*.

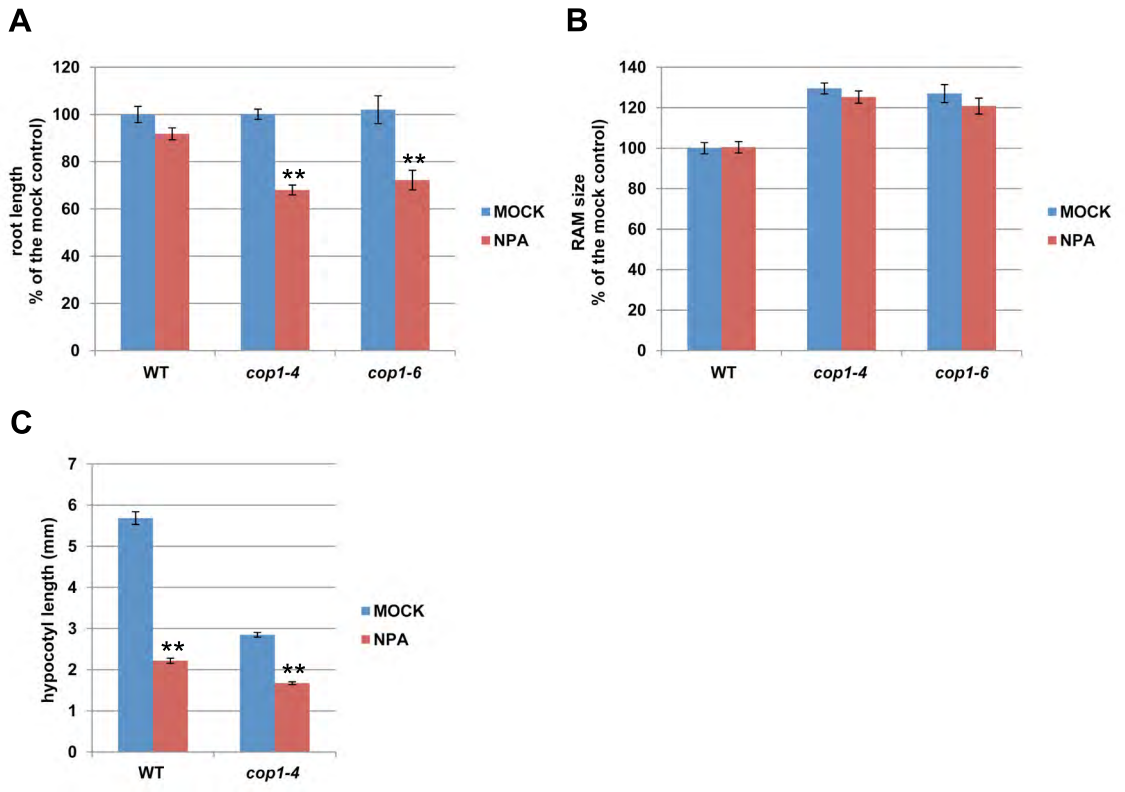

Fig. S9. COP1 regulates shoot-to-root PAT and root growth. (**A**,**B**) Primary root length (A) and RAM size (B) in 9-day-old dark-grown WT, *cop1-4* and *cop1-6* seedlings with and without (MOCK) NPA application on the hypocotyls. Data are expressed as percentage of the mock control, arbitrarily set to 100. Error bars represent s.e.m. (**C**) Hypocotyl length in 9-day-old dark-grown WT and *cop1-4* seedlings with and without (MOCK) NPA application on the hypocotyls. Note that NPA effectively inhibited hypocotyl elongation in both WT and *cop1* mutants. Error bars represent s.e.m. ***P*<0.01, *t*-test.

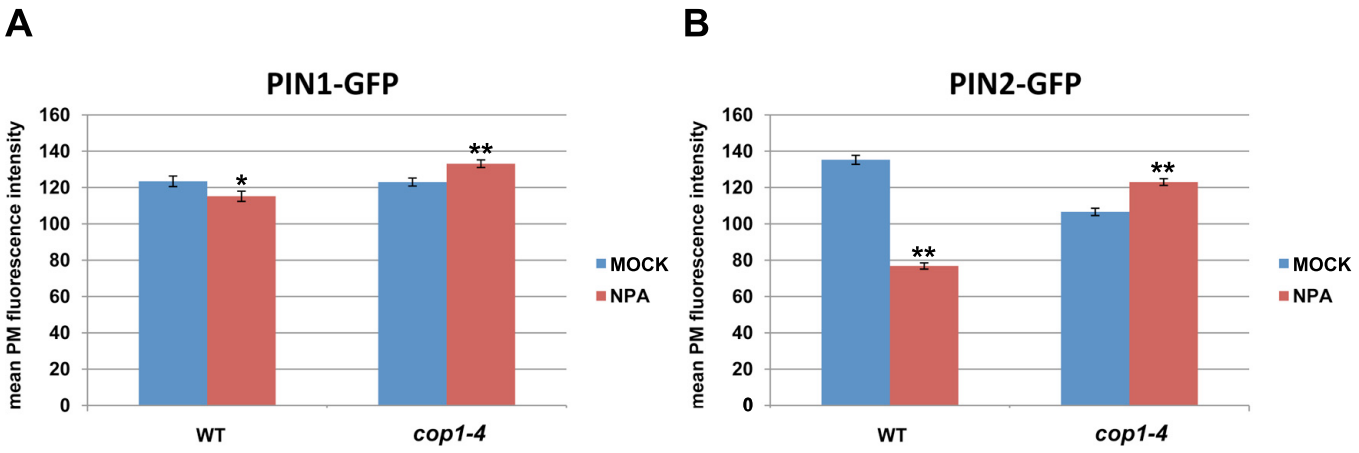

Fig. S10. COP1 function in the root regulates PIN1 and PIN2 stability. (**A**,**B**) Quantification of PM intensity of PIN1-GFP (A) and PIN2-GFP (B) in 7-day-old WT and *cop1-4* seedling roots with and without (MOCK) NPA application on the hypocotyls. Note that NPA application at the hypocotyls of *cop1-4* seedlings did not cause any reduction in the amounts of PM-localized PIN1-GFP and PIN2-GFP as observed for WT plants. Error bars represent s.e.m. **P*<0.05, ***P*<0.01, *t*-test.

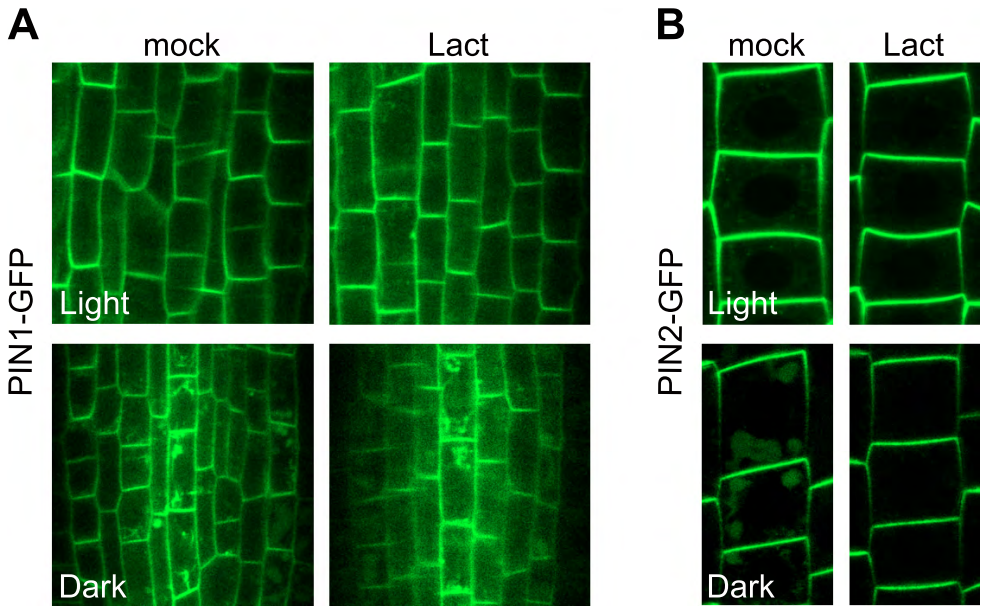

Fig. S11. The vacuolar targeting of PIN2-GFP, but not that of PIN1-GFP, is blocked by proteasome inhibition. (**A**) PIN1-GFP localization in RAMs of 5-day-old light-and dark-grown seedlings untreated (mock) or treated with 50 µM lactacystin for 4 hours (Lact). (**B**) PIN2-GFP localization in RAMs of 5-day-old light-and dark-grown seedlings untreated (mock) or treated with 50 µM lactacystin for 4 hours (Lact).

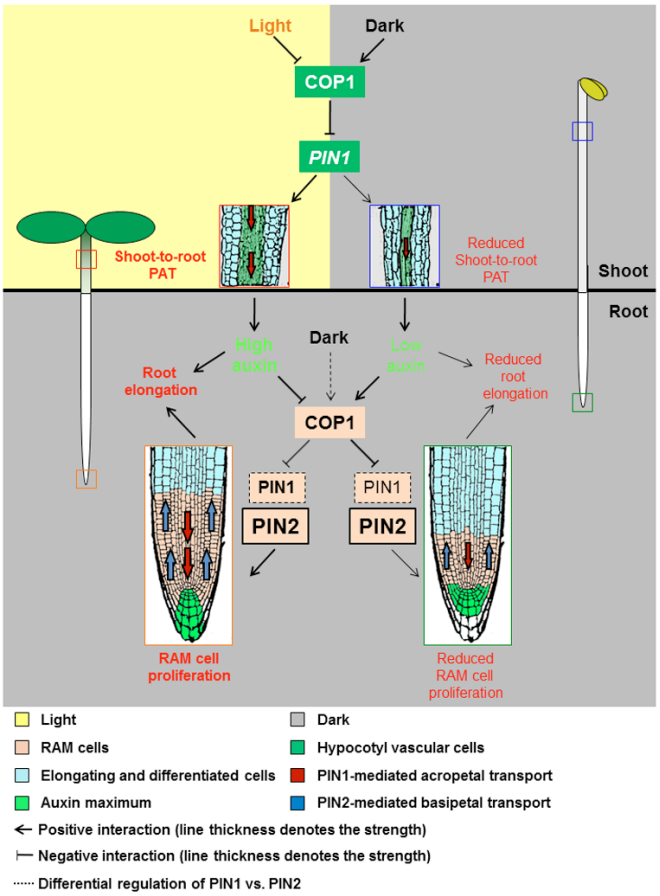

Fig. S12. Model for COP1-mediated coordination of root and shoot growth to changing light environments. The master photomorphogenesis repressor COP1 coordinates *Arabidopsis* root and shoot growth in response to changes of light condition. COP1 function in the shoot regulates shoot-to-root PAT by controlling the transcription of the auxin efflux carrier gene *PIN1*, resulting in an appropriately tuned level of shoot-derived auxin in the root, which directly influences primary root elongation and also adapts auxin transport and cell proliferation in the RAM by modulating root COP1-dependent PIN1 and PIN2 stability, thus permitting rapid and precise modulation of root growth in changing light environments.

Table S1. List of mutants and transgenic lines used in this study

Line	Ecotype	Reference
pin1-1	Originally derived from the En-2, backcrossed many times into Col-0	Okada et al., 1991
pin1-6	Ws-2	Vernoux et al., 2000
pin2 (*eir1-1*)	Col-0	Luschnig et al., 1998
pin3-5	Col-0	Benková et al., 2003
pin7-1	Ler	Benková et al., 2003
pin1 pin2	Col-0	Blilou et al., 2005
pin3 pin4 pin7	Col-0	Blilou et al., 2005
cop1-1	Col-0	McNellis et al., 1994
cop1-4	Col-0	McNellis et al., 1994
cop1-6	Col-0	McNellis et al., 1994
CYCB1;1:GUS	Col-0	Colon-Carmona et al., 1999
CLV3:AlcR	Ws-2	Deveaux et al., 2003
PIN1:GUS	Col-0	Vieten et al., 2005
PIN2:GUS	Col-0	Vieten et al., 2005
PIN3:GUS	Col-0	Vieten et al., 2005
PIN7:PIN7-GUS	Col-0	Vieten et al., 2005
DR5:GUS	Col-0	Ulmasov et al., 1997
DR5rev:GFP	Col-0	Friml et al., 2003
35S:DII-VENUS	Col-0	Brunoud et al., 2012
35S:mDII-VENUS	Col-0	Brunoud et al., 2012
PIN1:PIN1-GFP	Col-0	Xu et al., 2006
PIN2:PIN2-GFP	Col-0	Xu and Scheres, 2005
VAM3:mRFP-VAM3 PIN1:PIN1-GFP	Col-0	Ebine et al., 2008; Shirakawa et al., 2009
SCR:H2BYFP	Col-0	Heidstra et al., 2004
SHR-GFP	Col-0	Nakajima et al., 2001
WOX5:ERGFP	Col-0	Blilou et al., 2005
PLT2-GFP	Col-0	Aida et al., 2004
TIR1:TIR1-GUS	Col-0	Parry et al., 2009
AFB1:AFB1-GUS	Col-0	Parry et al., 2009
AFB2:AFB2-GUS	Col-0	Parry et al., 2009
AFB2:AFB2-GUS	Col-0	Parry et al., 2009

Table S2. qPCR primers used in this study

Gene	Agi Code	Left primer sequence	Right primer sequence	Amplicon length (nt)	UPL	Primer efficiency
PIN1	At1g73590	cctcaggggaatagtaacgaca	tcatcgtctttgttaccgaaact	71	103	1.891
PIN2	At5g57090	ggcgaagaaagcaggaaga	ggtgggtacgacggaaca	78	29	1.792
PIN3	At1g70940	cccagatcaatctcacaacg	ccggcgaaactaaattgttg	90	42	1.904
PIN7	At1g23080	tgggctcttgttgctttca	tcacccaaactgaacattgc	110	159	1.843

The table show primers couples, amplicon length, UPL probes as obtained by the software ProbeFinder by Roche Diagnostic (v 2.41; http://qpcr.probefinder.com/organism.jsp) with the intron-spanning assay option checked on. Primer efficiencies were calculated with the LightCycler480 software (Roche) on the basis of standard curves obtained by serially diluting a cDNA obtained from 4 day-old light-grown seedlings. Details on the ACTIN2 (Eff = 1.80) primer sequences and UPL can be found in Ciarbelli et al. (Ciarbelli et al., 2008).