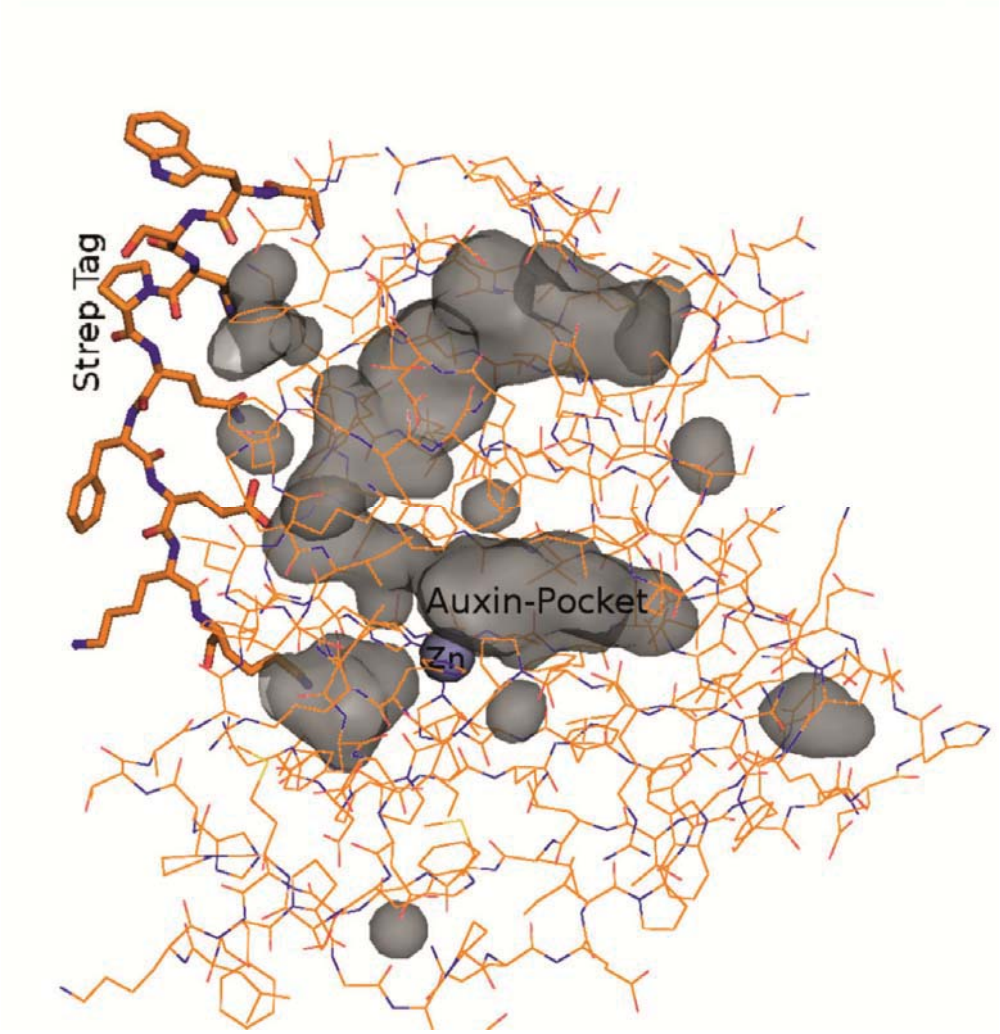
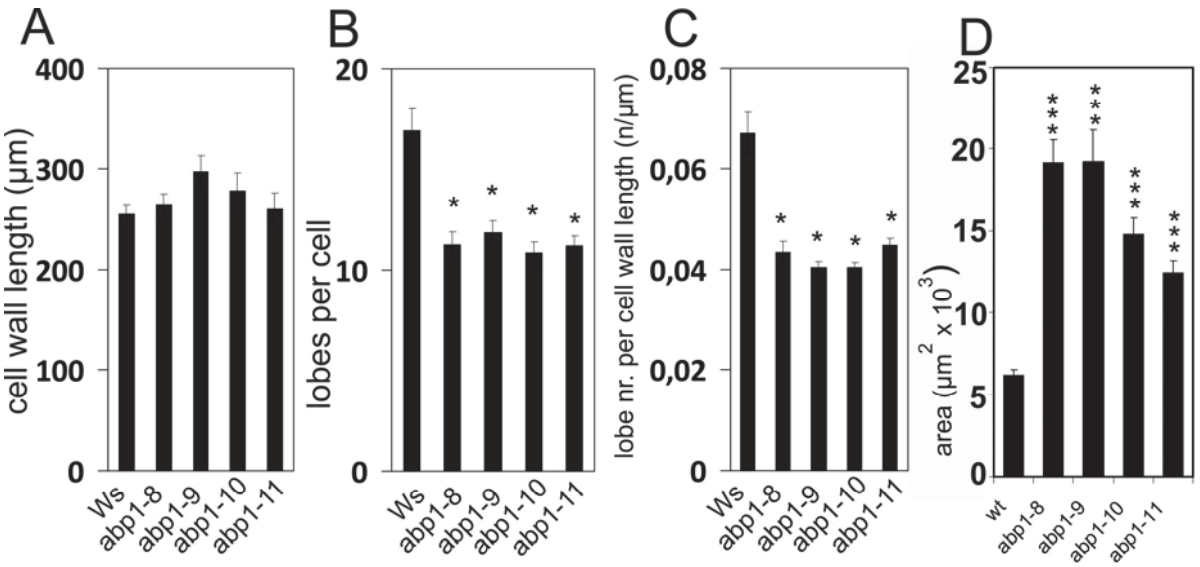
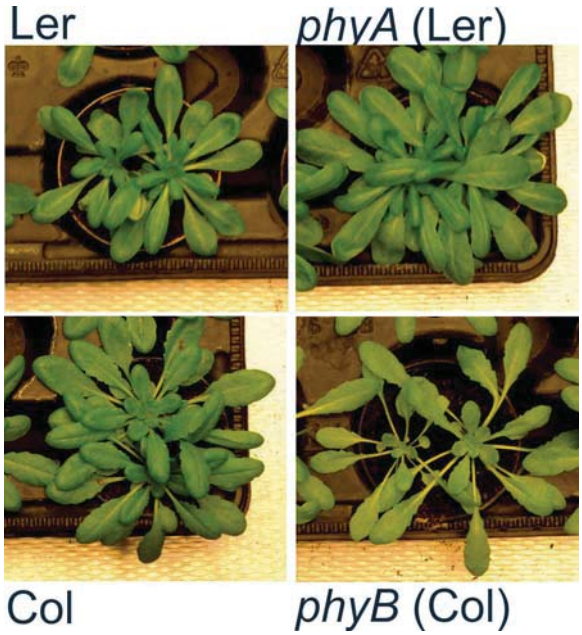
Supplemental Figures and Tables



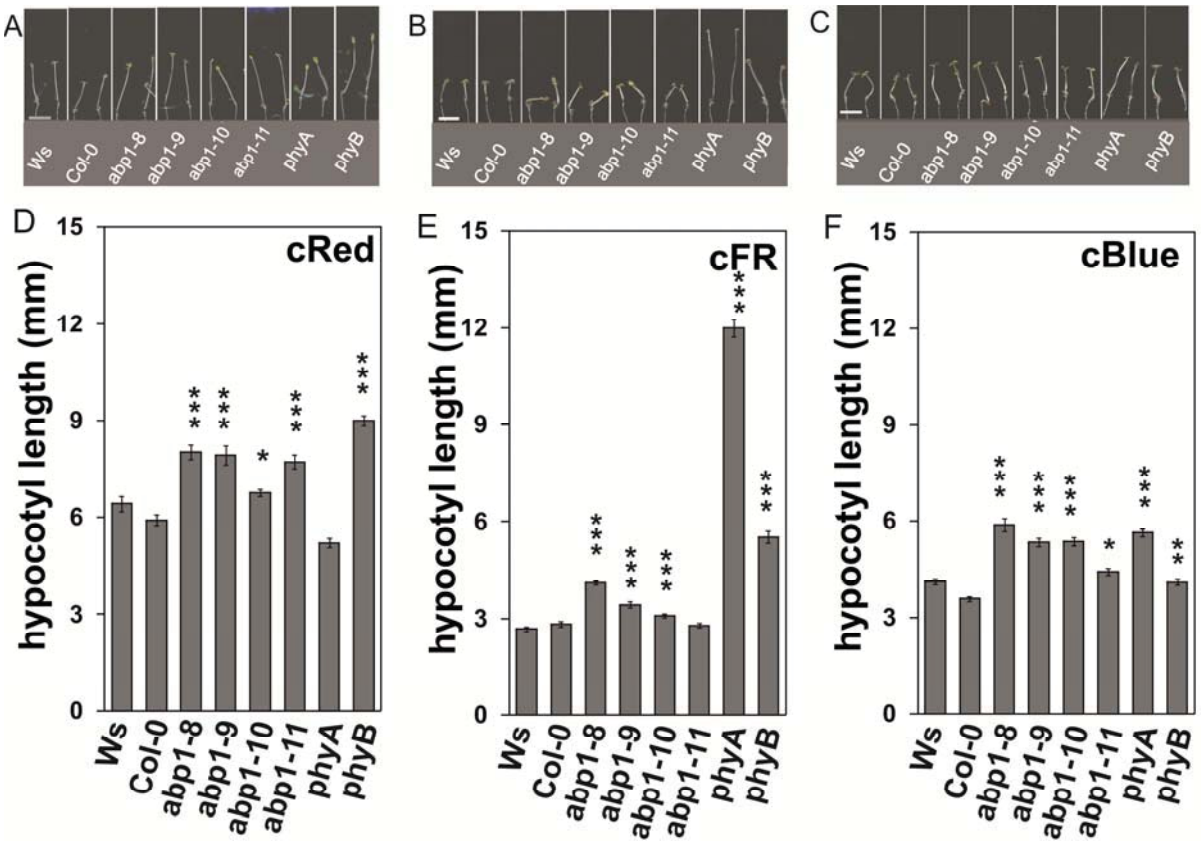
Supplemental Figure 1. 3-dimensional structure of the strep tag attached at the C-terminus of ABP1. Gray areas are all hollow spaces in the ABP1 protein which could accommodate ligands. The potential access channel for auxin is indicated and the auxin binding pocket. The large gray area in the upper part of the figure could harbor small molecules.



Supplemental Figure 2. Quantification of lobe formation in *abp1* mutants. (A) Length of cell walls of epidermal cells. (B) Number of lobes per cell. (C) Lobes per length of circumference. (D) Epidermal cell areas. (n>20; S.E.; *= p<0.05; ***=p<0.001).



Supplemental Figure 3. Rosettes of *phyA* and *phyB* mutants grown side by side with respective wt plants. Shown were plants grown for 55 d in short days (8h/16h).



Supplemental Figure 4. Elongation in monochromatic continuous light (R, FR, B) of 4 d old seedlings (1 µmol m^{-1} s^{-2} each). Seedlings were grown for four days. (A-C) Representative images of seedlings grown in FR, R, B respectively. (D-F) Hypocotyl lengths (n>80; S.E.; *: p<0.05;**: p<0.01; ***: p<0.001).

Supplemental Table 1. Quantum chemical modeling of auxin binding pocket in the wt and several *abp1* mutants.

dE energies resemble binding energies, the auto values of the Overlap (representing electron density of he binding box) and Coulomb (representing the charge surface of the binding box) matrix are given in the second and third row, respectively. In the bottom part of the table, for clarity, only the differences are presented. When comparing different mutations the differences of the surface charges (Coulomb) and the electron density (Overlap) of the box rather than the total values are important. The three values together have a strong influence on the biological efficacy. (ΔE (Kcal/mol); X^{wt} = X – WT).

	wt	**H106>N106**	**T25>Y25**	**L54>I54**	**W151>A151**
		abp1-10	*abp1-9*	*abp1-8*	not realized
dE(Kcal/mol)	-41.10	-37.51	-42.14	-35.90	-37.56
Overlap	13740.29	13705.01	13918.43	13722.70	13430.28
Coulomb	111916.90	109955.50	115202.40	112869.60	101709.00
dE^{wt} (Kcal/mol)	0.00	3.59	-1.04	5.20	3.53
$Overlap^{wt}$	0.00	-35.28	178.14	-17.59	-310.01
$Coulomb^{wt}$	0.00	-1961.40	3285.50	952.70	-10207.90

Supplemental Table 3. Primers for PCR

Auxin treatment:

18S rRNA forw	5'-GGC TCG AAG ACG ATC AGA TAC C-3';
18S rRNA rev	5'-TCG GCA TCG TTT ATG GTT-3';
ABP1 forw	5'-ACG AGA AAA TCA TAC CAA TTC GGA CTA ACC-3';
ABP1 rev	5'-GTA TCT ACG TAG TGT CAC AAA ACC TCA AC-3';
IAA2 forw	5'-GGT TGG CCA CCA GTG AGA TC-3';
IAA2 rev	5'-AGC TCC GTC CAT ACT CAC TTT CA-3';
IAA3 forw	5'- CAAAGATGGTGATTGGATGCT-3';
IAA3 rev	5'- TGATCCTTAGTCTCTTGCACGTA-3';
IAA11 forw	5'-CCT CCC TTC CCT CAC AAT CA-3';
IAA11 rev	5'-AAC CGC CTT CCA TTT TCG A-3';
IAA14 forw	5'-CCT TCT AAG CCT CCT GCT AAA GCA C-3';
IAA14 rev	5'-CCA TCC ATG GAA ACC TTC AC-3';
IAA19 forw	5'-GGT GAC AAC TGC GAA TAC GTT ACC-3';
IAA19 rev	5'-CCC GGT AGC ATC CGA TCT TTT CA-3';
IAA20 forw	5'-CAATATTTCAACGGTGGCTATGG-3';
IAA20 rev	5'-GCC ACA TAT TCC GCA TCC TCT A-3';
GH3.5 forw	5'-AGC CCT AAC GAG ACC ATC CT-3;
GH3.5 rev	5'-AAG CCA TGG ATG GTA TGA GC-3';
SAUR9 forw	5'-GAC GTG CCA AAA GGT CAC TT-3';
SAUR9 rev	5'-AGT GAG ACC CAT CTC GTG CT-3';
SAUR15 forw	5'-ATG GCT TTT TTG AGG AGT TTC TTG GG-3;
SAUR15 rev	5'-TCA TTG TAT CTG AGA TGT GAC TGT G-3';

SAUR23 forw	5'-ATG GCT TTG GTG AGA AGT CTA TTG GT-3;
SAUR23 rev	5'-TCA ATG GAG CCG AGA AGT CAC ATT GA-3'.
PIN1-forw	5’GGA GAC TTA AGT AGG AGC TCA GCA-3’;
PIN1-rev	5’-CCA AAA GAG GAA ACA CGA ATG-3’;
PIN2-forw	5’-TAT CAA CAC TGC CTA ACA CG-3’;
PIN2-rev	5’-GAA GAG ATC ATT GAT GAG GC-3’;
PIN3-forw	5’-GAG TTA CCC GAA CCT AAT CA-3’;
PIN3-rev	5’-TTA CTG CGT GTC GCT ATA GT-3’;
PIN5-forw	5’-ACC CTG CCG CTC TTC ACC A-3’;
PIN5-rev	5’-GCC CAC AAC GCT AAG ACC G-3’;

Light experiments:

*ATHB2*_F	5’-GAG GTA GAC TGC GAG TTC TTA CG 3’
*ATHB2*_F	5’-GCA TGT AGA ACT GAG GAG AGA GC-3’
*HFR1*_F	5’-CAC AAG ACG GAC AAG GTT TCG-3’
*HFR1*_R	5’-GTC AGC ATG TGG TTG TGC ATT C-3’
*PIL1*_F	5’-TGG TGC CTT CGT GTG TTT CTC A-3’
*PIL1*_R	5’-GGA CGC AGA CTT TGG GAA TTG-3’
*PIF5*_F	5’-GAT GCA GAC CGT GCA ACA AC-3’
*PIF5*_R	5’-CTT TTA TGC TTG CTT AGG CG-3’
*PIF1*_F	5’- CCCGTCAAGAGTCTTTGTACC-3’
*PIF1*_R	5’- CCCGAGGTTGGATCATACTG-3’
*IAA29*_F	5’- TCCTCTGGAATCCGAGTCTTC-3’
*IAA29*_R	5’- GGTGGCCATCCAACAACTT-3’
*IAA19*_F	5'-GGT GAC AAC TGC GAA TAC GTT ACC-3';
*IAA19*_R	5'-CCC GGT AGC ATC CGA TCT TTT CA-3';
*PIN3*_F	5’-GAG TTA CCC GAA CCT AAT CA-3’;
*PIN3*_R	5’-TTA CTG CGT GTC GCT ATA GT-3’;
*FIN219*_F	5’- GTCATCACAAATTACGCAGGGTTG-3’
*FIN219*_R	5’- TCTCTTTCGGTGTTCTTGTCGATG-3’
*TAA1*_F	5'-TGG ATC ATG GTG ATC CAA CG-3'
*TAA1*_R	5'-GCT CAA GCA ACC AAC ACA AG-3'

PCR genotyping was done using reverse ABP1 genomic primer (5'-CCT GAG ATC TCA AGT AGG AAG CGT C-3') and right border primer (5’-TCC CAA CAG TTG CGC ACC TGA ATG-3’) primer (Chen et al., 2001b).

Literature describing the shade marker genes:

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