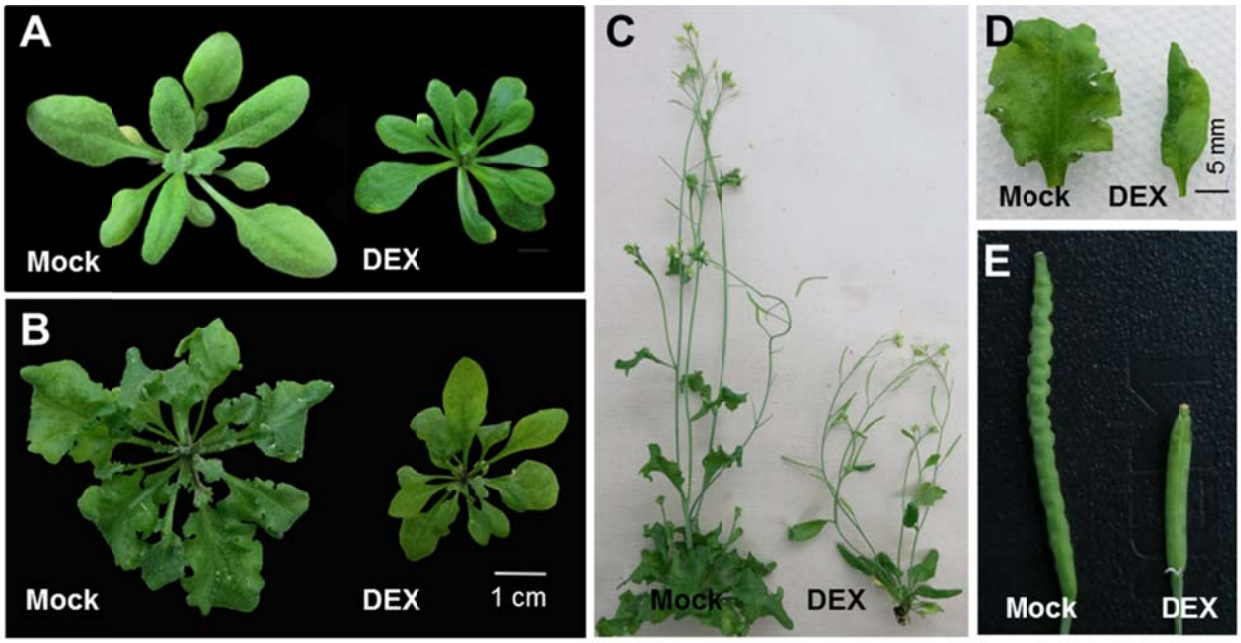
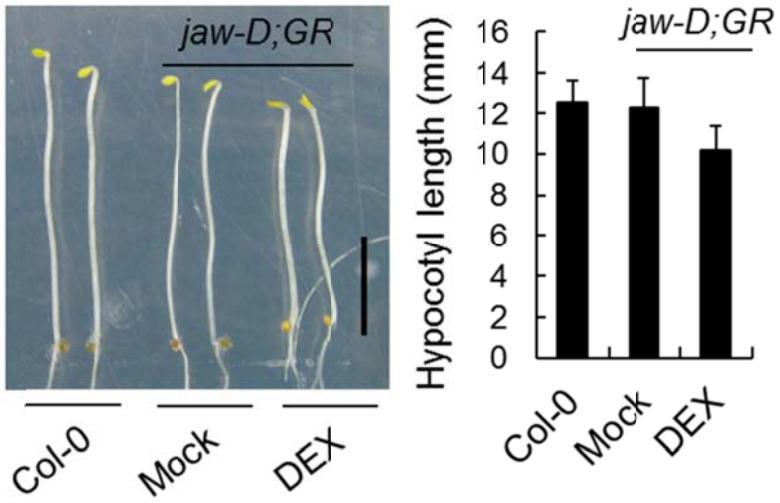
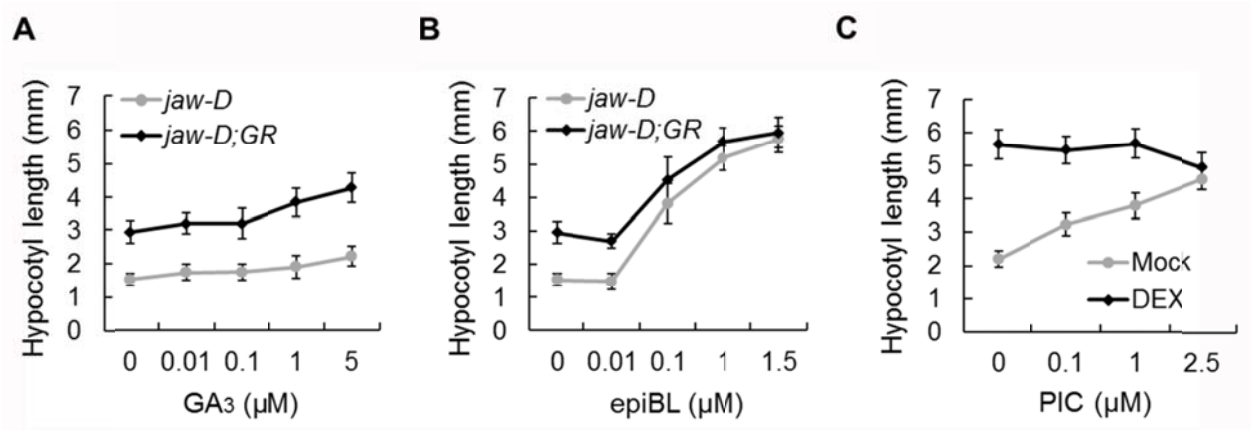


Supplemental Figure 1. DEX-induced TCP4 activity rescues *jaw-D* phenotypes. (A) and **(B)** Rosettes of 32-day-old Col-0;*ProTCP4:mTCP4:GR* plants **(A)** and *jaw-D*;*ProTCP4:mTCP4:GR* **(B)** plants grown in mock or in the presence of 12 µM dexamethasone (DEX). **(C)** to **(E)** Mock and 12 µM DEX-treated *jaw-D*;*GR* plants highlighting the stem length **(C)**, cauline leaf size **(D),** and fruit morphology **(E)**.

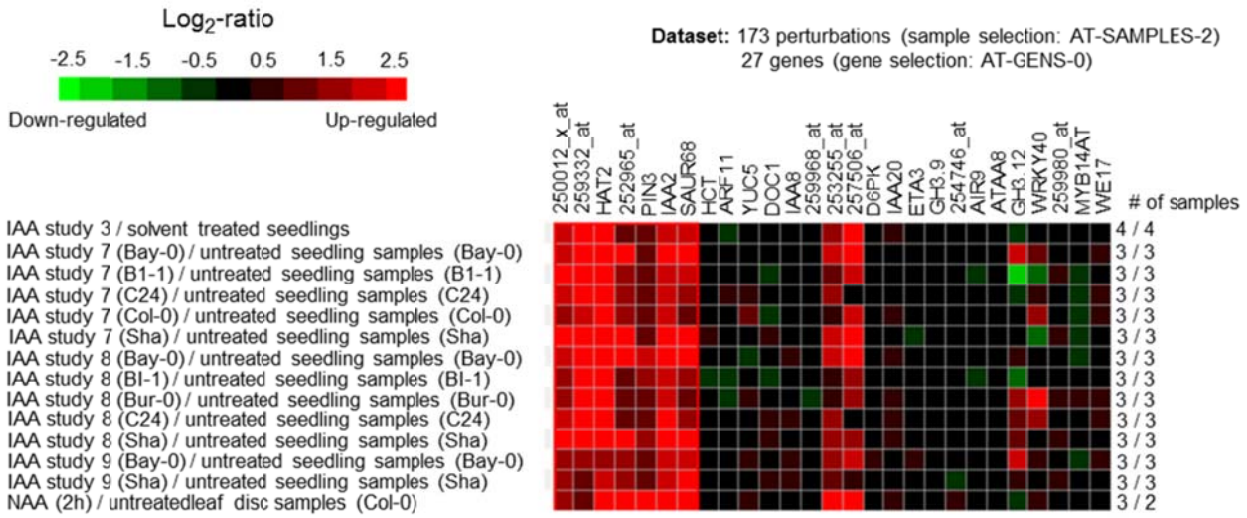


Supplemental Figure 2. Effect of TCP4 induction on hypocotyl length in seedlings grown in darkness. Five-day-old *jaw-D*;*ProTCP4:mTCP4:GR* (*jaw-D;GR*) seedlings of the indicated genotypes were grown in darkness with and without 12 µM DEX (left) and their average hypocotyl lengths were recorded (right). Error bars indicate SD; sample number n=12 - 15.

1

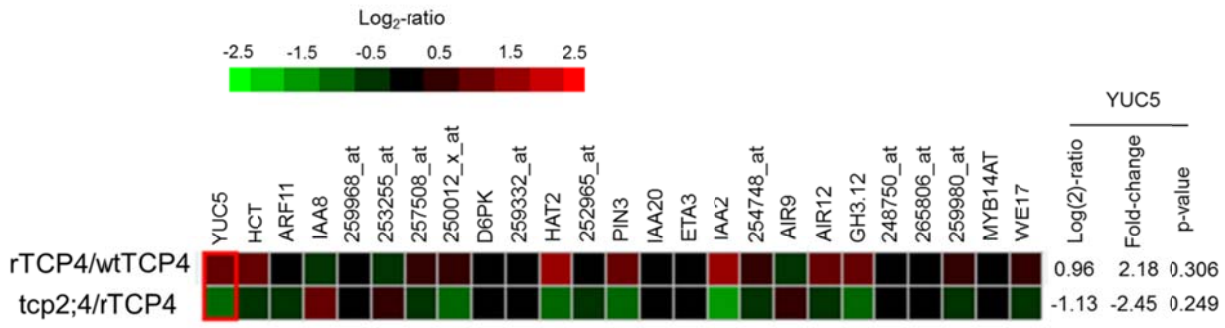


Supplemental Figure 3. Altered auxin and BR responses in TCP4-mediated hypocotyl elongation. (A) and **(B)** average hypocotyl lengths of 7-day-old *jaw-D* and *jaw-D*;*ProTCP4:mTCP4:GR* (*jaw-D;GR*) seedlings grown with 12 μM DEX and various concentrations of GA_3 **(A)** and epiBL **(B)**. **(C)** Average hypocotyl lengths of 7-day-old *Pro35S:mTCP4:GR* seedlings, grown without (Mock) or with (DEX) 12 μM DEX and various concentrations of picloram (PIC). Error bars indicate SD (n=10-15).

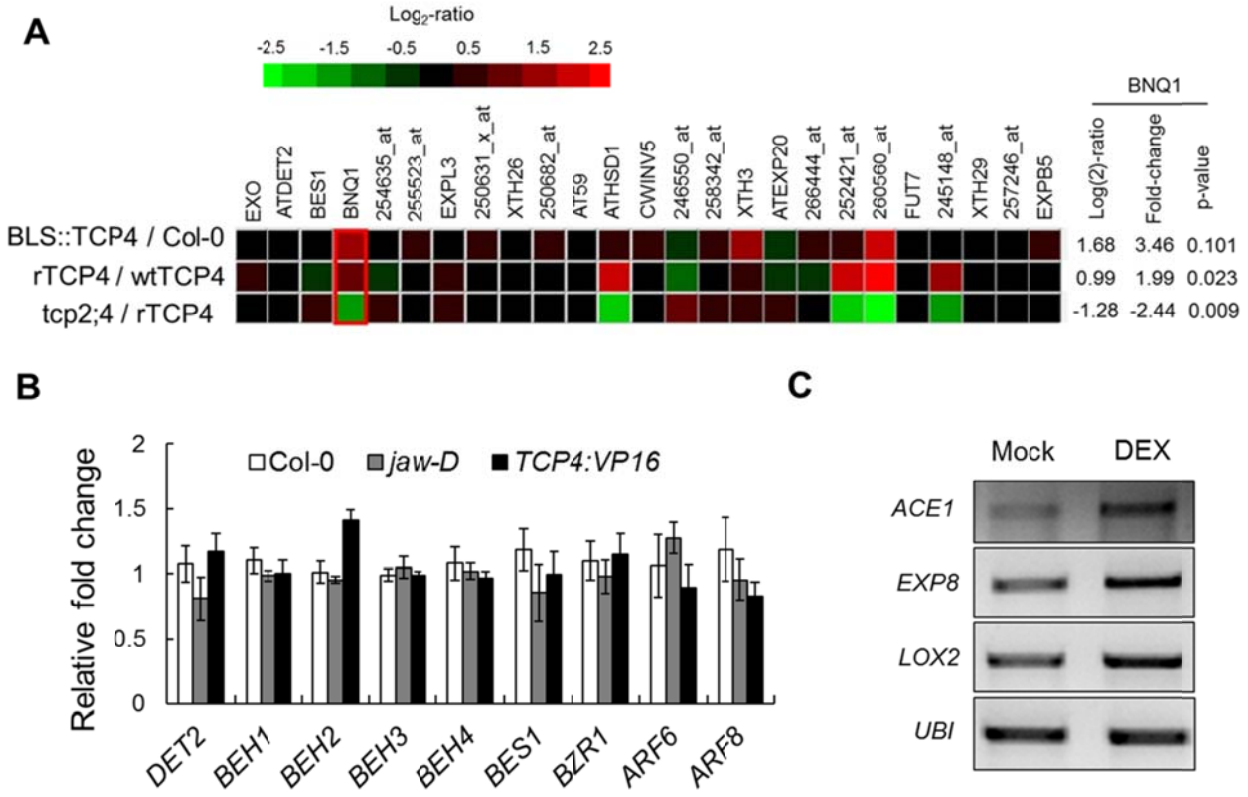


Supplemental Figure 4. GENEVESTIGATOR analysis of auxin-related genes in the *jaw-D*;*ProTCP4:mTCP4:GR* microarray. GENEVESTIGATOR (https://genevestigator.com/gv/) analysis comparing the expression levels of the auxin-related genes altered in the microarray experiment on the *jaw-D;ProTCP4:mTCP4:GR* seedlings compared with the previously reported transcriptome profiles of indole acetic acid (IAA)-treated and naphthaleneacetic acid (NAA)-treated seedlings. Top 14 correlated transcriptome profiles of IAA/NAA-treated microarrays are shown. An abridged version of this result is shown in Figure 3.

2

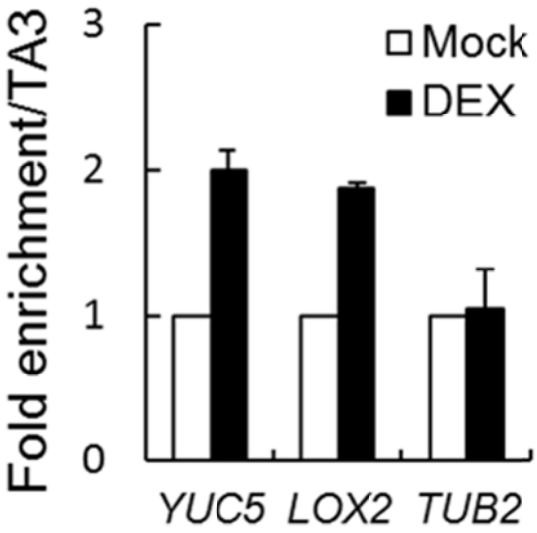


Supplemental Figure 5. GENEVESTIGATOR analysis of differentially expressed, auxin-related genes in the *jaw-D;ProTCP4:mTCP4:GR* microarray. Comparison of differentially-expressed, auxin-related genes in the *jaw-D*;*GR* microarray with those in the *TCP4* microarrays available in the public database using the GENEVESTIGATOR tool (*https://genevestigator.com/gv/*). *YUC5* is indicated with a red rectangle to highlight significant expression difference.



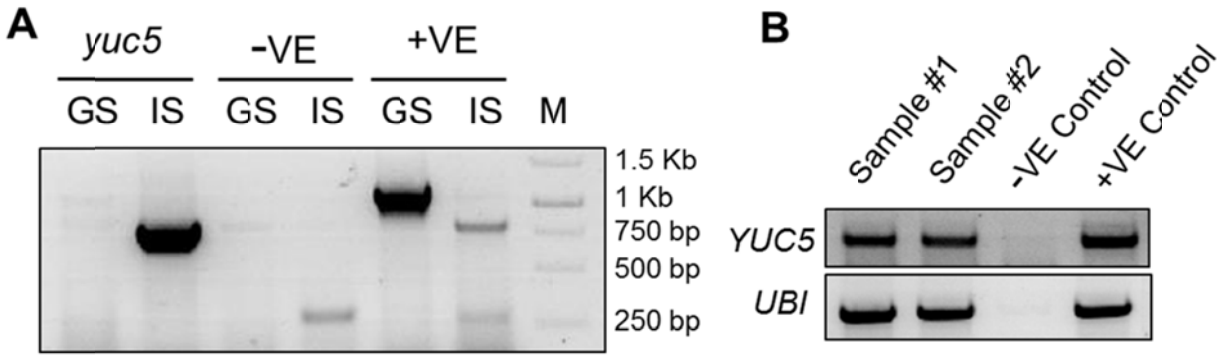
3

Supplemental Figure 6. Transcriptional analysis of cell expansion genes in the mutants of *TCP* genes. (A) Comparison of differentially expressed cell expansion genes in the *jaw-D*;*GR* microarray with those in previously reported *TCP4* microarrays available in the GENEVESTIGATOR database (*https://genevestigator.com/gv/*). The gene of interest, *BNQ1*/*PRE1*, is boxed. **(B)** RT-qPCR analysis of the relative transcript levels of BR biosynthesis/signaling genes in cDNA prepared from 9-day-old seedlings of the indicated genotypes. Transcript levels were normalized to *PP2A* or *TUB2*. Average values from biological triplicates are shown. Error bars indicate SD. **(C)** RT-PCR analysis of the indicated genes carried out on cDNA samples prepared from 9-day-old *jaw-D;GR* seedlings grown in continuous mock or continuous DEX. *LOX2* is a positive control and *UBI* (*UBIQUITIN10*) is a loading control.

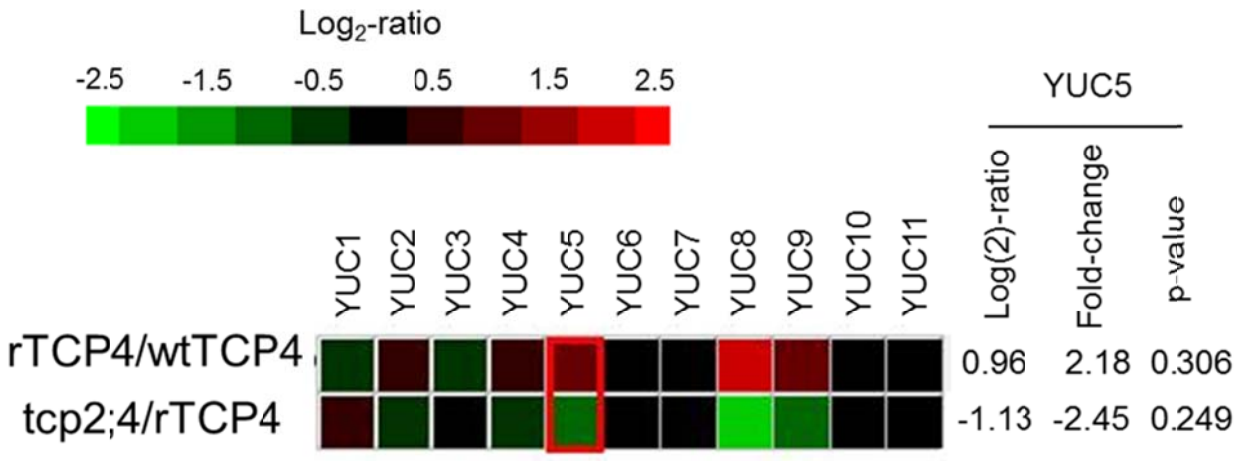


Supplemental Figure 7. DEX-induced TCP4 promotes *YUC5* promoter accessibility for transcription *in vivo*. Quantitative PCR results of the promoter regions of the indicated genes as analyzed by FAIRE experiment. Ten-day old seedlings of *Pro35S:mTCP4:GR* plants were treated with mock and 12 µM DEX for 3 h and the*YUC5* promoter was analyzed for accessibility for transcriptional activation. A direct target gene of TCP4, *LOX2,* was used as a positive control; *TUB2* was used as a negative control; and *TA3* was used as an internal control. This experiment was repeated twice and one set of representative data is shown. Error bars indicate SD (sample size, 3).

4

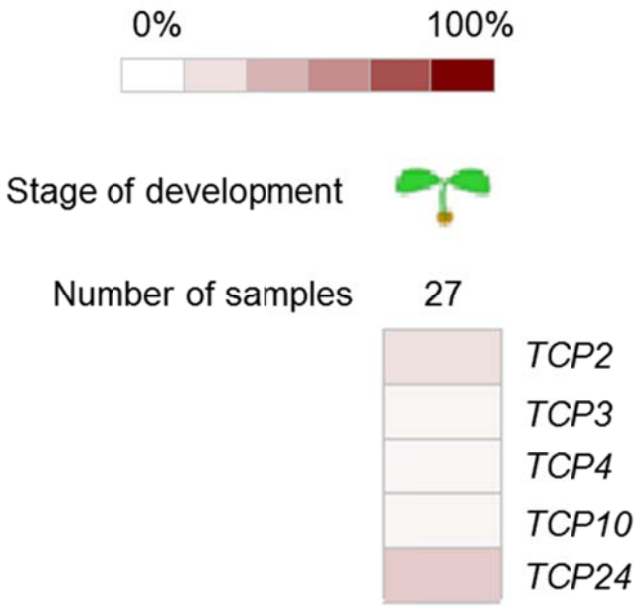


Supplemental Figure 8. Genotyping and characterization of *yuc5*. (A) EtBr-stained agarose gel showing the PCR-based genotyping of the *yuc5* T-DNA insertion line. GS indicates gene-specific primer combination; IS indicates T-DNA insertion-specific primer combination. The list of primers for GS and IS is provided in Supplemental Data Set 2, –VE and +VE indicate distilled water and Col-0 genomic DNA, respectively, as PCR templates. M, size markers. **(B)** RT-PCR analysis of *YUC5* transcript on RNA samples prepared from 9-day-old *jaw-D;ProTCP4:mTCP4:GR;ProDR5:GUS;yuc5* seedlings. *UBIQUITIN* (*UBI*) was used as the loading control, –VE and +VE indicate distilled water and wild type cDNA, respectively, as templates. Samples #1 and #2 indicate two independent samples used for RT-PCR analysis.



Supplemental Figure 9. GENEVESTIGATOR (*https://genevestigator.com/gv/*) analysis of *YUC1* to *YUC11* expression in the mutant lines of *TCP* genes. *YUC5* is highlighted by a red box.

5



Supplemental Figure 10. GENEVESTIGATOR analysis of miR319-targetd *TCP* transcripts in wild-type hypocotyl. Expression analysis of miR319-targetd *TCPs* in publicly available hypocotyl microarrays by GENEVESTIGATOR (*https://genevestigator.com/gv/*). Number of microarray data sets used for this analysis and percentage of expression potential from 0 (white) to 100 (dark brown) are shown.

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Supplemental Table 1. List of auxin-related genes differentially regulated after 2 and 4 h of DEX treatment in the *jaw-D;ProTCP4:mTCP4:GR* microarray. A 1-kb region upstream of the predicted transcriptional start site was scanned for the presence of TCP4 DNA-binding motifs. The known direct target of TCP4, *LOX2* (Schommer et al., 2008), is highlighted by a dashed rectangle. The transcription start site was defined based on TAIR database information (*www.arabidopsis.org*). NA indicates not analyzed.

Gene ID	Description	Fold change after DEX treatment		TCP4 DNA-binding motif	
		2 h	4 h	TGGNCC	GTGGNCC
AT5G43890	*YUCCA5*	3.0	3.6	+	-
AT5G48930	*HCT*; Auxin homeostasis	3.8	2.3	+	-
AT2G46530	*ARF11*	3.2	1.7	-	-
AT2G22670	*IAA8*	2.5	1.9	+	+
AT1G76530	Auxin efflux carrier	2.3	0.3	-	-
AT4G34760	*SAUR50*	2.3	1.7	+	+
AT5G18020	*SAUR20*	2.3	1.9	-	-
AT1G29440	*SAUR63*	2.2	2.0	+	+
AT5G18030	*SAUR*-like	2.0	1.3	+	+
AT5G18060	*SAUR23*	2.0	1.3	-	-
AT5G18010	*SAUR19*	1.9	1.2	-	-
AT5G55910	*D6PK* ; Polar auxin transport	1.8	-1.6	-	-
AT5G18050	*SAUR22*	1.8	0.9	-	-
AT3G03830	*SAUR28*	1.7	0	+	+
AT5G47370	*HAT2*	1.7	1.1	-	+
AT4G38860	*SAUR16*	1.7	1.1	+	-
AT1G70940	*PIN3*	1.6	2.0	-	-
AT2G46990	*IAA20*	1.6	-0.2	-	+
AT3G23030	*IAA2*	1.4	2.1	-	-
AT4G12980	Auxin-responsive gene	1.2	1.6	+	-
AT2G34680	*AIR9*	0.5	-2.1	-	-
AT3G07390	*AIR12*	0	-1.7	-	-
AT5G13320	*GH3.12*	-1.3	2.7	NA	NA
AT5G47530	Auxin-responsive gene	-1.7	0	+	-
AT2G18010	*SAUR10*	-2.2	1.4	-	-
AT1G76520	Auxin efflux carrier	-2.3	-1.8	-	-
AT2G31180	*MYB14*	-2.5	-2.2	+	-
AT1G25220	*ASB1*	-2.8	-0.2	+	-
AT3G45140	*LOX2*	2.5	1.7	+	+

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Supplemental Table 2. List of genes known to be involved in cell expansion and differentially expressed after 2 and 4 h of DEX induction in the *jaw-D;ProTCP4:mTCP4:GR* microarray. The 1-kb region upstream of the predicted transcription start site was used to analyze the TCP4 DNA-binding motif. The transcription start site was defined based on TAIR database information (*www.arabidopsis.org*).

Gene ID	Description	Fold change after DEX treatment		TCP4 DNA-binding motif	
		2 h	4 h	TGGNCC	GTGGNCC
AT4G08950	*EXO*; Cell Expansion regulator	1.9	2.3	+	-
AT2G38050	*DET2*; Cell Expansion regulator	1.6	1.9	-	-
AT5G39860	*PRE1*; Cell Expansion regulator	3.2	0	-	+
AT3G45960	*EXLA3*; Cell wall loosening	2.1	0	-	-
AT4G28850	*ATXTH26*; Xyloglucosyl transferase	1.7	-4.4	-	-
AT5G14920	*GASA14* ; GA mediated cell elongation	0	-2.5	+	-
AT3G44990	*XTH31*; XYLOGLUCAN	0	-1.6	+	-
AT4G38210	*EXPA20* ; Cell wall loosening	0	2.0	+	+
AT1G14070	*FUT7*; Xyloglucan fucosyltransferase family	-1.9	0	+	-
AT4G18990	*XTH29*; Xyloglucan	-2.8	0	-	-
AT5G28646	*WVD2*; Cell Expansion	-2.3	-2.8	+	+
AT3G60570	*EXPB5*; Cell wall loosening	-4.1	0	-	-

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Supplemental Table 3. Transcript abundance of *YUC* genes in *TCP* mutant lines. Transcript abundances of the indicated *YUCCA* genes in 5-day-old *jaw-D;GR;DR5-GUS* and *jaw-D;GR;DR5-GUS;yuc5* seedlings treated with mock and 12 µm DEX. Statistical significance and p-values are shown; ns indicates not significant. Unpaired Student's *t*-test was used.

jaw-D;GR; ProDR5:GUS			*YUC2*	*YUC3*	*YUC4*	*YUC5*	*YUC6*	*YUC8*	*YUC9*
	Mock	AVER	7.04	3.44	6.25	7.60	3.11	3.47	6.52
		STDEV	0.10	0.13	0.22	0.17	0.07	0.04	0.11
	DEX	AVER	5.17	3.23	6.49	5.55	3.33	2.23	7.27
		STDEV	0.08	0.08	0.19	0.19	0.03	0.08	0.35
		p-value	< 0.0001	ns	ns	0.0002	ns	< 0.0001	0.02
jaw-D;GR; ProDR5:GUS;yuc5			*YUC2*	*YUC3*	*YUC4*	*YUC5*	*YUC6*	*YUC8*	*YUC9*
	Mock	AVER	7.44	3.66	6.25	3.06	4.17	2.71	6.78
		STDEV	0.09	0.11	0.14	0.07	0.05	0.16	0.29
	DEX	AVER	5.48	3.91	6.15	2.76	4.05	1.64	7.14
		STDEV	0.20	0.14	0.09	0.21	0.07	0.11	0.20
		p-value	0.0001	ns	ns	ns	ns	0.0008	ns

Supplemental References

Schommer, C., Palatnik, J.F., Aggarwal, P., Chetelat, A., Cubas, P., Farmer, E.E., Nath, U., and Weigel, D. (2008). Control of jasmonate biosynthesis and senescence by miR319 targets. PLoS Biol **6,** e230.