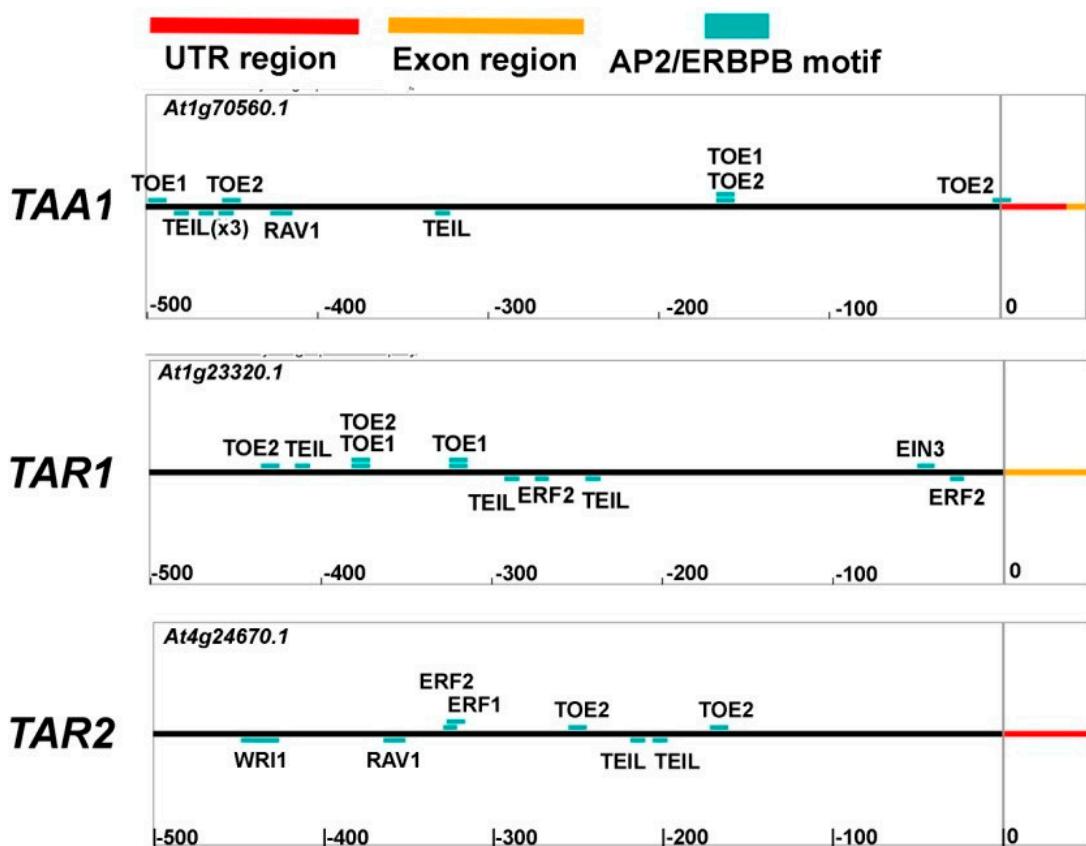


Supplementary materials

The Diverse Salt Stress Response of *Arabidopsis ctr1-1* and *ein2-1* Ethylene Signaling Mutants is Linked to Altered Root Auxin Homeostasis

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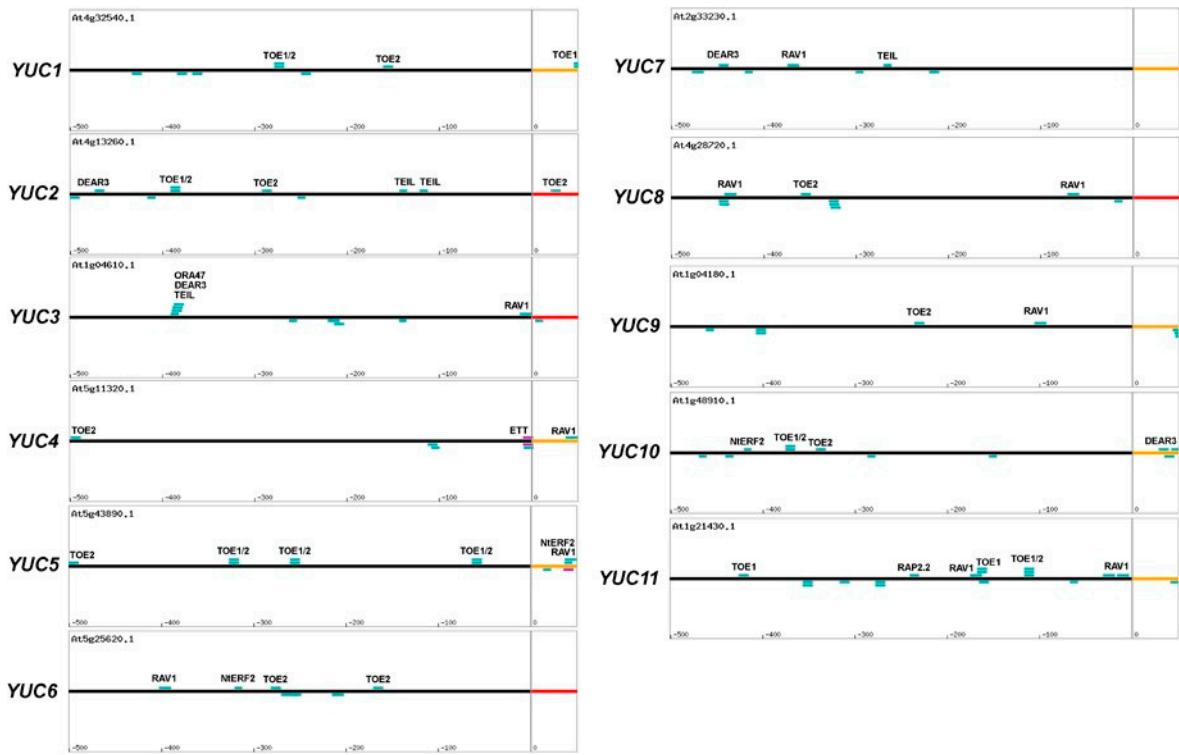


Figure S1. AthaMap analyses of promoter regions (-500 to $+50$ b.p.) of the genes coding for TAA1, TAR1, TAR2, and YUCs (1-11).

Table S1. TF DeCON in silico screen of the auxin Trp-dependent biosynthesis TAA1 (At1g70560), TAR1 (At1g23320), TAR2 (At4g24670) and YUC1-11 (resp. AT4G32540, AT4G13260, AT1G04610, AT5G11320, AT5G43890, AT5G25620, AT2G33230, AT4G28720).

TF ID	Family	Gene name	Genome count	Genome ratio	Query count	Query ratio	logFC	P value	adjP value
AT1G46768	AP2-ERE吕布	RAP2.1	1889	0.068306	5	0.357143	2.386419	0.001757	0.018726
AT4G06746	AP2-ERE吕布	RAP2.9	2105	0.076116	5	0.357143	2.230221	0.002841	0.023911
AT5G25810	AP2-ERE吕布	TINY	1602	0.057928	4	0.285714	2.302239	0.007028	0.036683

AT1G04180, AT1G48910, AT1G21430) using public database. The data analysis was done by setting the maximum p -value at 0.05 and the logFC filter at 2 to narrow down the displayed results

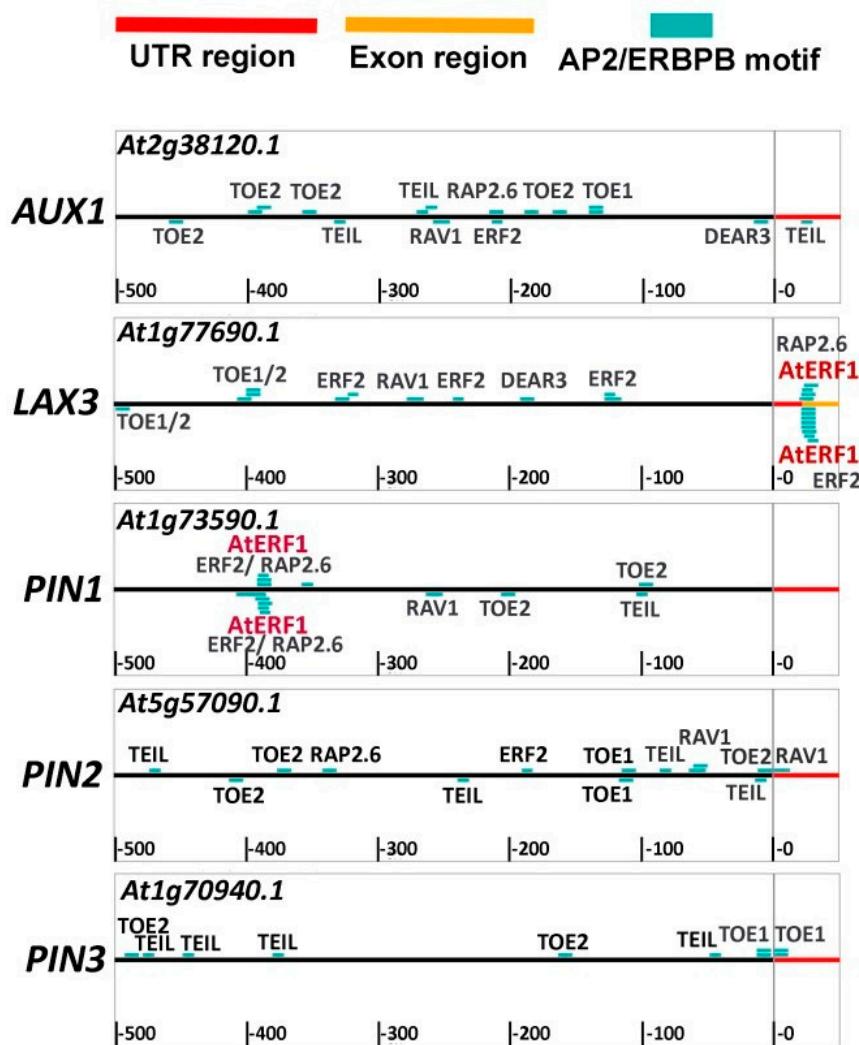


Figure S2. AthaMap analyses of promoter regions (-500 to +50 b.p.) of the auxin transporter genes *AUX1*, *LAX3*, *PIN1*, *PIN2*, and *PIN3*.

Table S2. TF DeCON in silico screen of the auxin transport genes PIN1-8 (resp. AT1G73590, AT5G57090, AT1G70940, AT2G01420, AT5G16530, AT1G77110, AT1G23080, AT5G15100), AUX1/LAX1/ 2 / 3 (AT2G38120, AT5G01240, AT2G21050, AT1G77690) and ABCB1/4/19.

TF ID	Family	Gene name	Genome count	Genome ratio	Query count	Query ratio	logFC	Pvalalue	adj.P value
AT1G46768	AP2-EREBP	RAP2.1	1889	0.068305912	6	0.4	2.549917643	0.000294507	0.0254 99675
AT1G44830	AP2-EREBP	ERF014	1398	0.050551437	5	0.333333333	2.721141586	0.000642796	0.0308 85482
AT5G25810	AP2-EREBP	TINY	1602	0.057928042	5	0.333333333	2.524631787	0.001193024	0.0341 608

The data analysis was done by setting the maximum *p*-value at 0.05 and the logFC filter at 2 to narrow down the displayed results.

Table S3. Primers used in the qRT-PCR analyses.

Gene Name	Locus	Amplicon	
		Length (b.p.)	Forward Primer (5'-3') Reverse Primer (5'-3')
AUX1	AT2G38120	151	GAGGTCACGCCGTTACTGTT GAGAGAAAGCGTTGGAGTGG
LAX3	AT1G77690	185	CACAACCTGGGATGATGTCG AATGTTCCCCAACAAATCCA
PIN1	AT1G73590	224	TAAGGTGATGCCACCAACA A GCCATGAACAAACCCAAAGACT
PIN2	AT5G57090	235	CTTTCTTGCGAGGCCTTA ACTGCTCGGAGATGAGAAC
PIN3	AT1G70940	209	ATCTTCTCACCCGACCAATG GATGCTCCACTCGAGGCTAC
ACTIN2	AT3G18780	67	CTTGCACCAAGCAGCATGA CCGATCCAGACACTGTACTTC A CTT
EF1ALPHA	AT5G60390	151	AGCACCGCTCTTCTGCTTTC GGGTTGTATCCGACCTCTTC