

Supplementary Information

Drought response transcriptomics are altered in poplar with reduced tonoplast sucrose transporter expression

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Table S1. T-DNA insertion site analysis.

Figure S1. Plant-wide transcript abundance of *SUT* genes in leaf, xylem, bark and roots of wild type and *SUT4*-RNAi transgenic plants.

Figure S2. Transcript abundance of sucrose cleaving enzymes in different organs of WT and *SUT4*-RNAi plants under WW conditions.

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Figure S4. Heatmap illustration of *SUT4*-RNAi and DR effects on *LEA*, *HSP20*, *BSP/VSP* transcript abundance in roots.

Figure S5. Heatmap illustration of *SUT4*-RNAi and DR effects on transcript abundance of genes associated with abscisic acid, jasmonic acid and ethylene signaling in roots.

Dataset S1. Gene expression analysis by RNA-Seq.

Dataset S2. Root co-expression gene network analysis.

Table S1. T-DNA insertion site analysis

Line	Total read pairs (M)	Hybrid read pairs ¹	Insertion site	Nearest genome coordinate (<i>P. trichocarpa</i> v3.0)
F	32,756,771	4	Potri.009G049200	Chr09:5430076
G	29,853,306	5	intergenic (3' to Potri.004G190400)	Chr04:20513764
H	12,791,788	0	-	-

¹ Junction-flanking read pairs, with one read of the pair mapping to the T-DNA and the other to the genome.

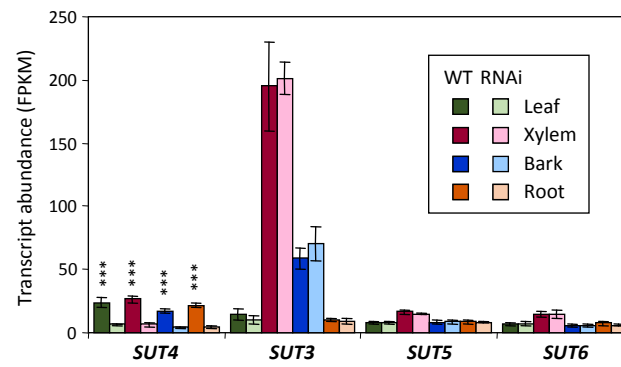


Fig. S1. Plant-wide transcript abundance of *SUT* genes in leaf, xylem, bark and roots of wild type and *SUT4*-RNAi transgenic plants. Values represent FPKM means \pm SD for n=3 biological replicates. Statistical significance of transgenic effect was determined using two-sample student's *t*-test (***, $P \leq 0.005$).

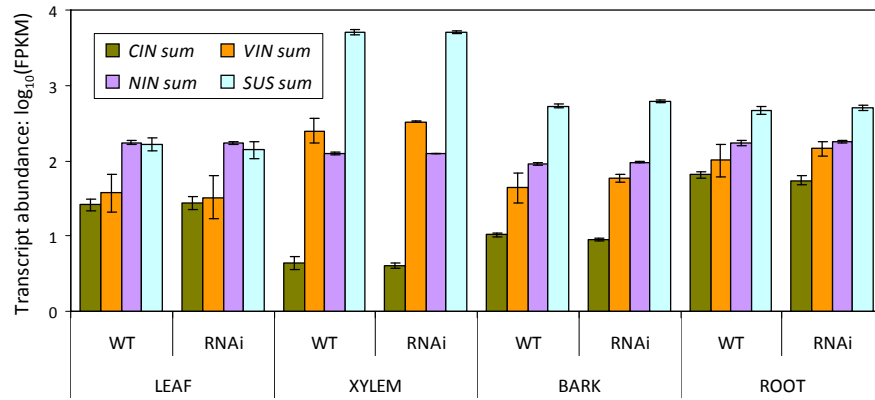


Fig. S2. Transcript abundance of sucrose cleaving enzymes in different organs of WT and *SUT4*-RNAi plants under WW conditions. FPKM values were summed from multiple gene models of each gene family for each biological replicate and log₁₀-transformed. Data are means ± SD of n=3 biological replicates. *CIN*, cell-wall invertase; *VIN*, vacuolar invertase; *NIN*, neutral invertase; *SUS*, sucrose synthase.

		Potri.016G089500	Potri.016G113300	Potri.008G065600	Potri.006G128200	Potri.006G128000	Potri.004G176300	Potri.010G222700	Potri.010G191900	Potri.008G039600	Potri.009G136600
		PIP2.7	PIP1.5	PIP1.2	PIP2.6	PIP2.5	PIP2.2	PIP2.3	PIP1.1	PIP2.4	PIP2.1
WT	L vs. B	0.84	0.41	0.80	0.58	0.75	0.00	0.00	0.06	0.00	0.53
	L vs. X	0.75	0.60	0.79	0.74	0.81	0.00	0.35	0.06	0.40	0.28
	L vs. R	0.77	0.82	0.49	0.00	0.00	0.65	0.02	0.49	0.42	0.36
	R vs. B	0.59	0.52	0.62	0.10	0.08	0.08	0.04	0.10	0.42	0.22
	R vs. X	0.60	0.78	0.28	0.07	0.01	0.00	0.07	0.10	0.30	0.00
	B vs. X	0.95	0.47	0.78	0.82	0.80	0.75	0.55	0.45	0.12	0.01
RNAi	L vs. B	0.84	0.54	0.91	0.02	0.02	0.02	0.12	0.18	0.56	0.24
	L vs. X	0.86	0.41	0.77	0.00	0.07	0.00	0.01	0.02	0.44	0.02
	L vs. R	0.16	0.12	0.00	0.04	0.00	0.00	0.02	0.33	0.04	0.14
	R vs. B	0.34	0.32	0.11	0.04	0.00	0.00	0.03	0.23	0.02	0.04
	R vs. X	0.22	0.61	0.00	0.14	0.03	0.00	0.18	0.02	0.24	0.24
	B vs. X	0.96	0.69	0.89	0.53	0.55	0.54	0.77	0.34	0.29	0.04
FPKM	81	112	407	143	280	179	426	408	290	552	

		Potri.006G239700	Potri.001G235300	Potri.003G050900	Potri.009G027200	Potri.001G186700	Potri.008G050700	Potri.004G216500	Potri.006G121700	Potri.016G098200	Potri.001G157000
		TIP4.1	TIP1.1	TIP2.2	TIP1.2	TIP2.1	TIP1.4	TIP1.8	TIP1.6	TIP1.5	TIP2.4
WT	L vs. B	0.58	0.81	0.85	0.54	0.07	0.48	0.14	0.42	0.83	0.33
	L vs. X	0.39	0.67	0.56	0.25	0.72	0.75	0.14	0.04	0.00	0.06
	L vs. R	0.57	0.22	0.18	0.22	0.33	0.19	0.02	0.01	0.24	0.02
	R vs. B	0.76	0.19	0.19	0.17	0.49	0.01	0.27	0.12	0.33	0.00
	R vs. X	0.68	0.13	0.68	0.06	0.31	0.08	0.05	0.61	0.00	0.12
	B vs. X	0.88	0.92	0.69	0.83	0.00	0.64	0.00	0.33	0.00	0.09
RNAi	L vs. B	0.28	0.29	0.12	0.83	0.29	0.00	0.02	0.00	0.21	0.08
	L vs. X	0.29	0.29	0.04	0.55	0.10	0.01	0.09	0.16	0.53	0.22
	L vs. R	0.06	0.34	0.02	0.21	0.04	0.13	0.17	0.00	0.27	0.37
	R vs. B	0.43	0.20	0.19	0.27	0.00	0.16	0.77	0.01	0.02	0.23
	R vs. X	0.34	0.25	0.16	0.26	0.07	0.00	0.11	0.16	0.01	0.13
	B vs. X	0.33	0.99	0.83	0.87	0.53	0.21	0.02	0.03	0.13	0.07
FPKM	65	114	25	116	431	394	23	405	128	186	

Fig. S3. Inter-organ correlations of *AQP* transcript abundance. A, *PIP* genes. B, *TIP* genes. The upper half of each panel presents correlations between WT organs, and the lower half, RNAi transgenic organs. Values are r^2 from linear regressions with $n=9$ independent comparisons for each gene and organ pair. The FPKM value for each gene is presented as average transcript abundance across all organs. L, leaf; B, bark; X, xylem and R, root.

A (ABA)					C (ethylene)						
	RNAi/WT		DR/WW		FPKM		RNAi/WT		DR/WW		FPKM
	WW	DR	WT	RNAi			WW	DR	WT	RNAi	
PYR/PYL/RCAR						ERF					
Potri.003G091700	-0.3	-0.4	-1.8	-1.9	80	Potri.004G197400	0.2	1.1	-0.5	0.4	165
Potri.001G092500	0.0	-0.2	-0.7	-0.9	62	Potri.007G090600	0.4	0.2	-1.8	-2.0	164
Potri.006G104100	-0.4	0.3	-3.7	-3.0	58	Potri.010G006800	-0.1	-1.1	2.0	1.0	163
Potri.016G125400	-0.4	0.7	-3.4	-2.3	52	Potri.005G168700	0.0	0.8	-0.3	0.5	150
Potri.003G139200	-0.1	-0.3	-1.7	-1.8	50	Potri.005G077300	0.2	-0.1	-1.1	-1.3	107
Potri.010G183900	-0.7	1.0	-3.9	-2.2	16	Potri.003G150800	0.3	1.5	0.0	1.2	97
PP2C						Potri.011G115600	-0.1	0.4	0.9	1.5	89
Potri.008G059200	0.2	0.1	2.2	2.1	72	Potri.002G094200	-0.1	0.3	0.5	0.9	82
Potri.010G199600	-0.1	0.0	2.7	2.8	50	Potri.005G195000	-0.6	2.2	2.7	5.5	77
Potri.012G002700	-0.6	-0.6	3.8	3.8	44	Potri.007G138100	0.3	0.4	1.0	1.0	68
Potri.009G037300	-0.6	0.0	4.1	4.7	41	Potri.002G065600	0.0	1.9	3.0	4.9	58
Potri.T137100	-0.7	-1.1	3.6	3.2	25	Potri.014G159000	0.2	1.9	0.7	2.4	56
Potri.001G245200	-0.1	-0.5	4.0	3.7	19	Potri.008G210900	-0.6	-0.2	-1.6	-1.2	44
Potri.015G018800	-0.8	-1.4	3.5	2.9	12	Potri.001G356100	0.0	0.9	0.3	1.3	40
SnRK2						Potri.004G047600	0.3	1.2	0.7	1.6	39
Potri.002G099700	0.2	0.4	2.0	2.3	10	Potri.019G131300	0.4	1.9	-0.4	1.0	37
SnRK3						Potri.011G057000	0.3	1.3	1.3	2.3	32
Potri.006G186200	-0.5	-1.2	0.0	-0.6	133	Potri.008G120100	0.1	1.3	-0.3	0.9	31
Potri.016G133900	-0.4	-0.9	1.7	1.3	69	Potri.017G013700	-0.1	0.3	0.5	0.9	27
Potri.010G079000	0.1	1.2	-1.8	-0.7	60	Potri.001G397200	0.5	1.0	0.6	1.1	27
Potri.010G002500	0.0	0.5	1.8	2.3	58	Potri.005G140900	0.3	1.0	-0.1	0.6	26
Potri.018G108500	-0.1	-0.1	1.4	1.4	53	Potri.014G025200	-0.2	0.7	0.3	1.2	22
Potri.016G133500	-0.1	0.6	1.3	2.0	47	Potri.001G154100	-0.1	3.3	-0.5	2.8	22
Potri.006G062800	-0.5	-1.4	1.6	0.7	42	Potri.003G081200	0.2	3.5	-1.3	2.0	21
Potri.018G109100	-0.1	-0.1	1.3	1.3	39	Potri.014G126100	0.2	1.4	-0.3	0.8	20
Potri.019G128100	-0.1	-0.2	1.6	1.5	36	Potri.007G046500	-0.1	0.4	-1.1	-0.6	18
Potri.014G104200	0.2	0.6	1.3	1.7	28	Potri.012G134000	0.3	4.0	1.1	4.8	18
Potri.018G019900	-0.5	1.2	-0.5	1.2	20	Potri.013G135600	0.7	1.2	-0.9	-0.4	18
Potri.011G067600	-0.1	0.2	0.6	0.9	17	Potri.006G138900	-0.8	0.6	4.0	5.4	17
Potri.003G181900	-0.2	0.4	2.1	2.6	13	Potri.009G075300	-0.1	-1.2	0.6	-0.5	17
Potri.013G156000	0.1	0.4	1.0	1.4	12	Potri.009G101900	-0.2	2.2	1.3	3.8	16
Potri.008G160200	-0.7	2.1	-0.9	1.8	8	Potri.008G073600	0.0	0.3	0.9	1.2	15
ASR1						Potri.002G039100	0.2	1.6	1.1	2.5	14
Potri.005G193800	-0.6	-1.8	2.9	1.8	15	Potri.010G183700	0.1	1.5	0.4	1.9	13
ABF						Potri.013G158500	-0.1	0.9	-1.6	-0.7	12
Potri.014G028200	-0.2	0.0	1.5	1.6	66	Potri.011G162400	-0.3	-0.2	1.2	1.3	11
Potri.004G140600	0.0	-0.1	1.7	1.7	36	Potri.003G150700	0.1	1.4	-0.2	1.1	11
Potri.009G101200	0.1	-0.5	1.5	0.8	31	Potri.007G076800	-0.8	4.2	-0.1	4.8	11
Potri.002G067400	-0.2	0.7	0.2	1.1	14	Potri.001G280100	-0.5	-1.7	-0.3	-1.5	11
Potri.002G124000	-0.3	1.2	-0.5	1.0	9						
B (jasmonic acid)											
JAZ											
Potri.006G139400	0.1	3.3	0.3	3.5	125						
Potri.010G108200	0.2	1.5	0.4	1.8	96						
Potri.006G217200	0.1	0.7	1.0	1.6	84						
Potri.003G068900	0.5	4.3	1.7	5.6	69						
Potri.008G133400	0.2	1.6	0.8	2.1	65						
Potri.003G165000	0.0	2.9	1.5	4.4	34						
Potri.011G083900	0.6	6.3	0.6	6.4	27						
Potri.001G062500	-0.4	2.3	1.7	4.4	26						
Potri.001G166200	0.5	4.1	0.9	4.6	14						

Fig. S5. Heatmap illustration of *SUT4*-RNAi and DR effects on transcript abundance of genes associated with ABA (A), JA (B) and ethylene (C) signaling in roots. Values are log₂-transformed fold-changes. Genes are sorted by their transcript abundance (FPKM average) in roots. Significant RNAi or DR effects are denoted by bold-underlines ($Q \leq 0.05$) or bold-italics ($P \leq 0.05$). *ASR*, ABA stress ripening; *ABF*, ABA-responsive element binding factor; *ERF*, ethylene response factor; *JAZ*, jasmonate ZIM-domain; *PP2C*, protein phosphatase 2C; *PYR/PYL/RCAR*, pyrabactin resistance/PYR-like/regulatory components of ABA receptor family; *SnRK*, sucrose non-fermenting-1 (SNF1)-related protein kinase.