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.

Figure S3. Inter-organ correlations of *AQP* transcript abundance.

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 (*P. trichocarpa* 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.

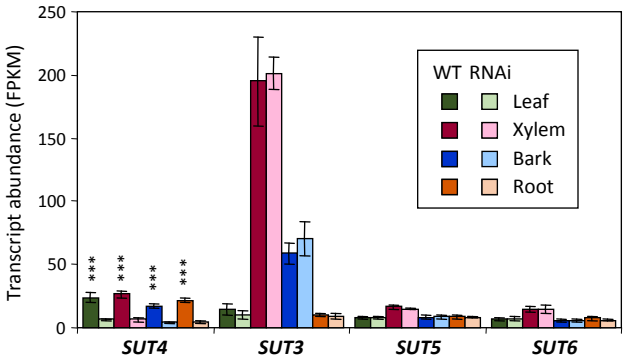

Fig. S1. Plant-wide transcript abundance of *SUT* genes in leaf, xylem, bark and roots of wild type and *SUT4*-RNAi transgenic plants. Values represent FPKM means ± SD for n=3 biological replicates. Statistical significance of transgenic effect was determined using two-sample student's *t*-test (***,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

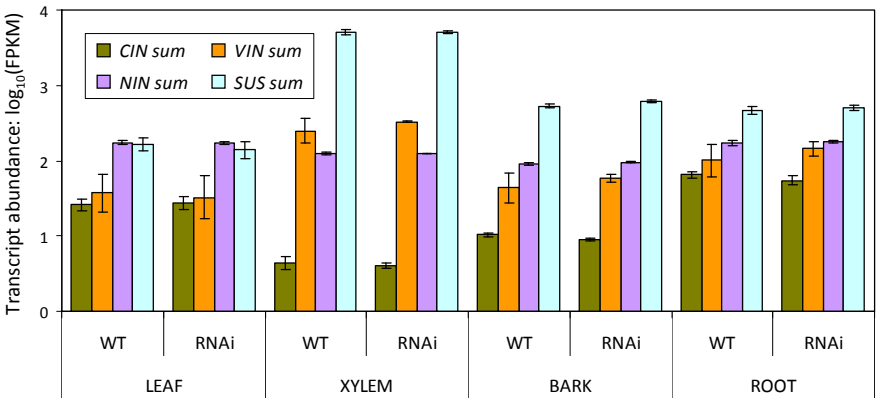

Fig. S2. Transcript abundance of sucrose cleaving enzymes in different organs of WT and *SUT4*-RNAi plants under WW conditions. FPKM values were summed from multiple gene models of each gene family for each biological replicate and log10-transformed. Data are means ± SD of n=3 biological replicates.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

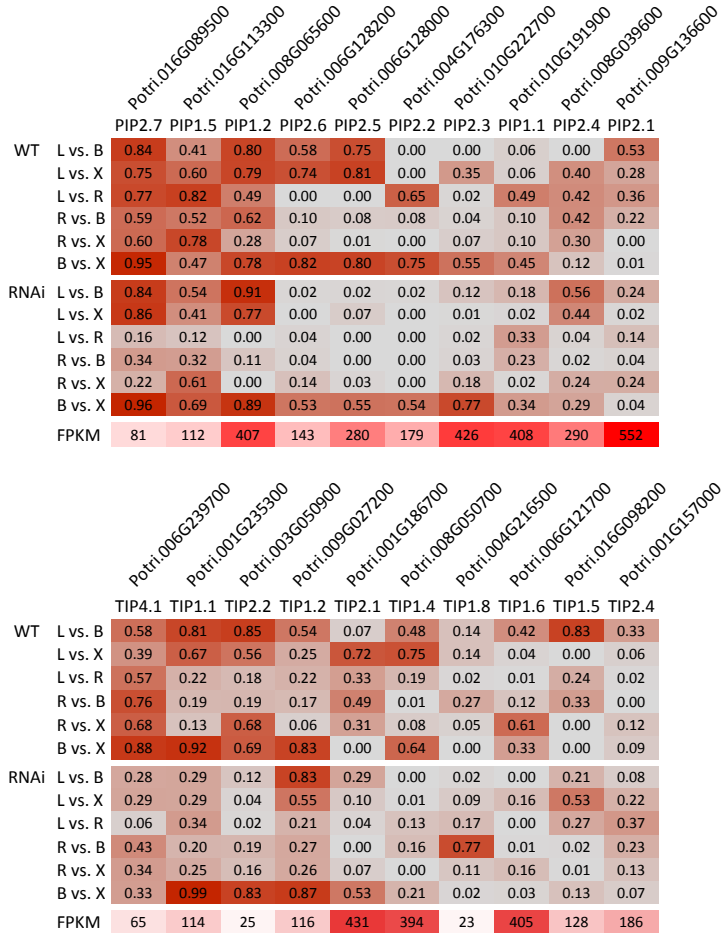

Fig. S3. Inter-organ correlations of *AQP* transcript abundance. A, *PIP* genes. B, *TIP* genes. The upper half of each panel presents correlations between WT organs, and the lower half, RNAi transgenic organs. Values are *r*2 from linear regressions with n=9 independent comparisons for each gene and 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. *LEA*

	RNAi/WT		DR/WW		FPKM
	WW	DR	WT	RNAi	
Potri.016G046400	-1.9	**2.0**	5.6	**9.4**	360
Potri.016G071600	-0.5	**1.5**	0.7	**2.7**	325
Potri.010G012100	0.2	**1.9**	0.7	**2.4**	301
Potri.007G146300	0.2	0.6	***0.9***	**1.4**	205
Potri.T111300	-1.5	**2.1**	5.7	9.4	114
Potri.002G165000	-0.3	**4.5**	**2.2**	7.0	70
Potri.009G158900	0.0	**1.5**	-0.1	**1.4**	46
Potri.006G159400	-0.1	-0.3	**1.0**	**0.8**	31
Potri.004G197600	0.1	**2.2**	0.3	**2.4**	30
Potri.009G145700	-0.2	**-2.8**	-0.4	**-3.0**	19
Potri.015G148200	-0.3	-0.3	***-1.0***	**-1.0**	18
Potri.011G127900	0.2	**-1.7**	**-1.7**	**-3.6**	16
Potri.001G173000	0.3	***0.8***	**6.7**	7.2	14
Potri.014G106100	0.2	**1.4**	**-1.5**	-0.3	13
Potri.005G122400	-1.1	0.8	**6.5**	8.4	13
Potri.001G418000	0.1	**1.5**	-0.7	0.8	12
Potri.017G108500	-0.3	**1.8**	**4.2**	6.3	12
Potri.001G173200	0.5	0.6	**7.1**	**7.2**	11
Potri.002G180000	0.0	-0.2	**-1.2**	**-1.4**	10
Potri.004G046000	0.7	0.1	**6.3**	5.7	7
Potri.009G019600	0.2	0.8	0.7	**1.2**	7
Potri.T181400	0.0	-0.5	-0.9	**-1.4**	7
Potri.017G108300	-1.2	**1.0**	**4.7**	**6.9**	7
Potri.016G142300	-1.1	**-1.3**	**1.3**	***1.1***	6
Potri.015G002400	0.4	**-1.7**	**3.0**	0.9	6
Potri.017G108400	-0.4	0.6	**5.3**	**6.3**	6
Potri.003G141200	0.1	-0.7	-0.6	**-1.4**	5

B. *HSP20*

	RNAi/WT		DR/WW		FPKM
	WW	DR	WT	RNAi	
Potri.010G195700	4.3	**4.9**	**2.6**	3.2	81
Potri.008G062300	3.7	**4.3**	0.7	1.3	60
Potri.009G039200	1.1	**1.8**	**-2.1**	**-1.4**	52
Potri.003G109200	2.8	**2.7**	-1.1	-1.1	51
Potri.019G081200	4.1	**4.8**	**-1.9**	-1.3	47
Potri.006G223900	2.6	**4.7**	-2.1	0.0	47
Potri.017G130700	0.7	**1.9**	-1.0	0.1	20
Potri.001G192600	0.3	**3.4**	**3.8**	**6.9**	19
Potri.018G140600	**1.3**	**1.3**	-1.0	***-1.0***	16
Potri.013G089200	4.3	**4.9**	1.4	2.0	14
Potri.010G175200	3.4	**2.4**	0.5	-0.5	10
Potri.T125900	3.5	**4.5**	**3.0**	4.0	6

C. *VSP/BSP*

	RNAi/WT		DR/WW		FPKM
	WW	DR	WT	RNAi	
Potri.013G100800	1.1	1.7	0.9	**1.5**	280
Potri.013G100700	1.1	**1.7**	1.0	**1.6**	105
Potri.013G101000	**1.3**	2.1	0.8	**1.6**	103
Potri.008G028500	-0.1	**-1.6**	0.0	**-1.5**	34
Potri.013G080300	**3.1**	0.5	2.6	-0.1	24
Potri.T096300	0.1	**1.8**	**1.1**	**2.8**	23
Potri.013G082800	**3.1**	1.4	2.6	***0.9***	22
Potri.019G050200	**4.3**	0.1	**2.0**	**-2.2**	9

Fig. S4. Heatmap illustration of *SUT4*-RNAi and DR effects on *LEA* (A), *HSP20* (B) and *BSP/VSP* (C) transcript abundance in roots. Values are log2-transformed fold-changes, and genes are arranged by their transcript abundance (FPKM average) in roots. Significant transgenic or DR effects are denoted by bold-underlined ($Q \leq 0.05$) or bold-italics ($P \leq 0.05$).

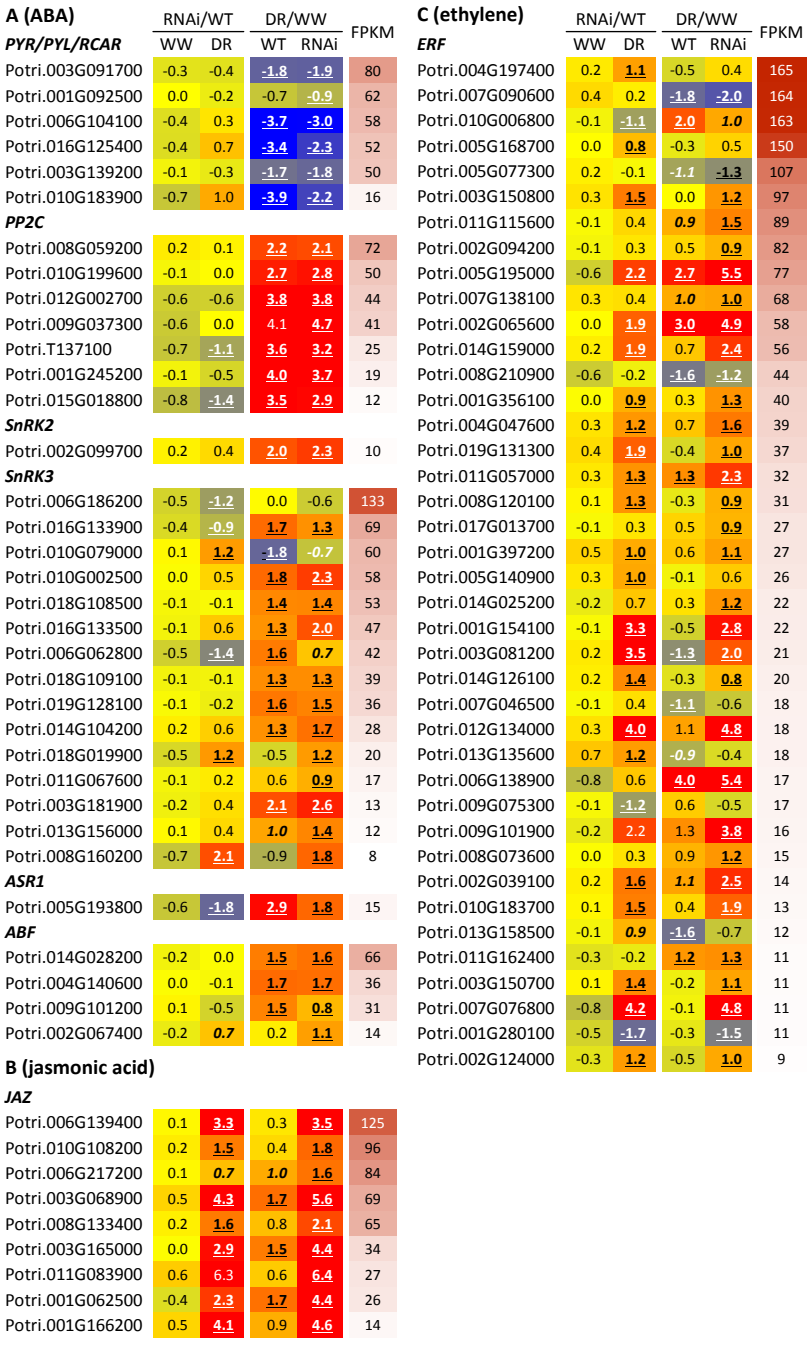

Fig. S5. Heatmap illustration of *SUT4*-RNAi and DR effects on transcript abundance of genes associated with ABA (A), JA (B) and ethylene (C) signaling in roots. Values are log2-transformed fold-changes. Genes are sorted by their transcript abundance (FPKM average) in roots. Significant RNAi or DR effects 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.