Supplemental information to:

Uncoupling proteins 1 and 2 (UCP1 and UCP2) from *Arabidopsis thaliana* are mitochondrial transporters of aspartate, glutamate and dicarboxylates

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Running title: Transport properties of AtUCP1 and AtUCP2

Supplemental Tables S1-S4

Supplemental Figures S1-S6

Supplemental Table S1. Levels of metabolite in AtUCP transgenic plants at the absence of salt.

Metabolite	with sucrose				without sucrose			
	WT	ucp1	ucp2	dKO	WT	ucp1	ucp2	dKO
phenylalanine	1.0±0.2	0.8±0.1	0.7±0.2	0.8±0.1	1.0±0.1	0.8±0.1	1.6±0.5	1.3±0.1
tryptophan	1.0±0.1	0.7±0.2	1.1±0.1	1.0±0.1	1.0±0.1	0.9±0.1	0.8±0.2	1.1±0.1
asparagine	1.0±0.3	0.9±0.3	0.8±0.5	0.8±0.2	1.0±0.3	0.8±0.2	2.0±0.3	1.6±0.8
lysine	1.0±0.2	0.8±0.1	0.8±0.2	0.9±0.1	1.0±0.1	1.3±0.2	1.6±0.4	2.0±0.1
serine	1.0±0.1	0.9±0.1	0.9±0.1	0.7±0.2	1.0±0.1	1.2±0.1	1.4±0.1	1.3±0.1
threonine	1.0±0.1	1.0±0.1	1.1±0.1	1.0±0.1	1.0±0.1	1.0±0.1	1.1±0.1	1.1±0.1
isoleucine	1.0±0.1	1.1±0.2	1.0±0.1	0.9±0.1	1.0±0.1	1.0±0.1	1.1±0.2	1.2±0.1
methionine	1.0±0.1	0.9±0.1	1.0±0.1	1.0±0.1	1.0±0.1	1.4±0.2	1.2±0.4	1.6±0.2
leucine	1.0±0.1	1.0±0.1	1.0±0.1	0.9±0.2	1.0±0.1	1.1±0.1	1.3±0.3	1.3±0.1
alanine	1.0±0.4	1.2±0.6	1.5±0.3	1.3±0.2	1.0±0.4	1.3±0.5	0.8±0.2	1.5±0.2
beta.alanine	1.0±0.2	0.9±0.1	1.2±0.1	1.0±0.1	1.0±0.1	1.4±0.2	0.8±0.3	1.4±0.1
ornithine	1.0±0.1	1.0±0.3	0.8±0.3	0.9±0.3	1.0±0.1	1.9±0.2	2.3±0.3	**3.1±0.3**
proline	1.0±0.3	1.1±0.3	1.4±0.4	0.8±0.1	1.0±0.1	1.2±0.2	1.0±0.1	1.5±0.3
valine	1.0±0.1	1.0±0.1	1.0±0.1	0.9±0.1	1.0±0.1	1.2±0.1	1.1±0.1	1.2±0.1
glycine	1.0±0.2	1.0±0.2	0.7±0.1	0.6±0.4	1.0±0.1	1.1±0.2	1.8±0.4	1.6±0.1
glutamine	1.0±0.2	1.3±0.1	0.9±0.1	1.4±0.9	1.0±0.2	1.3±0.2	1.8±0.5	1.8±0.7
aspartate	1.0±0.1	1.1±0.2	1.3±0.3	0.9±0.1	1.0±0.1	1.1±0.1	0.8±0.1	1.0±0.1
glutamate	1.0±0.2	1.0±0.2	1.2±0.1	1.2±0.2	1.0±0.1	0.9±0.1	1.0±0.1	1.1±0.3
arginine	1.0±0.2	0.7±0.1	0.5±0.2	0.7±0.2	1.0±0.2	1.4±0.1	2.6±0.4	2.7±0.1
glucose	1.0±0.2	1.0±0.2	0.9±0.2	0.8±0.1	1.0±0.1	0.8±0.1	0.7±0.2	0.5±0.1
sucrose	1.0±0.1	1.0±0.1	1.0±0.1	1.0±0.1	1.0±0.2	0.9±0.1	0.4±0.1	0.9±0.1
maltose	1.0±0.1	0.9±0.2	0.7±0.1	1.0±0.2	1.0±0.1	1.0±0.2	0.7±0.1	0.9±0.1
raffinose	1.0±0.2	0.8±0.1	1.3±0.2	1.3±0.5	1.0±0.1	0.7±0.2	0.2±0.1	0.6±0.1
glycerol	1.0±0.2	1.0±0.2	0.9±0.1	0.9±0.2	1.0±0.1	0.9±0.1	1.0±0.3	0.7±0.1
erythritol	1.0±0.1	0.9±0.1	1.2±0.1	1.2±0.1	1.0±0.1	1.3±0.2	0.9±0.3	1.2±0.1
myo.inositol	1.0±0.2	1.0±0.1	1.3±0.2	1.1±0.3	1.0±0.1	0.9±0.1	**0.5±0.1**	0.7±0.1
malate	1.0±0.2	0.9±0.1	1.0±0.1	0.9±0.1	1.0±0.1	0.7±0.1	0.7±0.1	0.7±0.1
fumarate	1.0±0.2	1.0±0.3	0.8±0.1	0.8±0.2	1.0±0.1	0.7±0.1	**0.4±0.1**	**0.5±0.1**
citrate	1.0±0.2	0.7±0.1	1.1±0.2	0.9±0.1	1.0±0.1	**0.4±0.1**	**0.4±0.1**	**0.4±0.1**
pyruvate	1.0±0.1	0.9±0.1	1.5±0.2	1.0±0.4	1.0±0.2	1.1±0.1	0.7±0.3	1.0±0.1
glycerate	1.0±0.1	1.0±0.1	1.3±0.2	0.9±0.2	1.0±0.1	0.7±0.1	0.6±0.1	0.5±0.1
succinate	1.0±0.4	0.8±0.2	0.8±0.2	0.6±0.1	1.0±0.1	0.8±0.2	0.7±0.1	0.7±0.1
phosphate	1.0±0.7	1.9±0.6	0.7±0.3	1.4±0.8	1.0±0.1	3.3±0.6	2.9±1.7	5.2±1.1
threonate	1.0±0.4	0.8±0.2	1.0±0.1	1.0±0.4	1.0±0.2	0.8±0.2	0.4±0.1	0.7±0.2
dehydroascorbate	1.0±0.2	1.0±0.1	1.4±0.4	1.2±0.2	1.0±0.2	1.8±0.4	0.9±0.1	2.6±1.7
GABA	1.0±0.3	0.8±0.2	0.7±0.2	0.8±0.4	1.0±0.1	0.6±0.1	1.3±0.2	1.3±0.1
putrescine	1.0±0.3	0.6±0.1	0.8±0.4	1.0±0.2	1.0±0.1	1.2±0.1	1.7±0.2	1.8±0.1
AMP	1.0±0.3	1.3±0.4	1.4±0.6	1.1±0.4	1.0±0.1	1.2±0.2	1.3±0.2	0.8±0.1
benzoate	1.0±0.2	0.7±0.1	0.7±0.1	0.7±0.1	1.0±0.1	0.9±0.1	1.0±0.2	0.8±0.1
sulfate	-	3.5±1.3	-	-	-	-	-	2.3±0.9
nicotinate	1.0±0.1	**0.5±0.1**	0.7±0.1	0.7±0.1	1.0±0.1	0.7±0.1	0.8±0.3	1.3±0.1
2-oxoglutarate	1.0±0.1	0.9±0.1	0.6±0.2	1.0±0.8	1.0±0.2	0.6±0.1	1.1±0.1	0.9±0.1
fructose	1.0±0.2	0.8±0.1	0.9±0.1	0.7±0.1	1.0±0.1	0.7±0.1	0.8±0.2	0.6±0.1
shikimate	1.0±0.2	0.6±0.1	0.8±0.1	0.7±0.1	1.0±0.1	1.1±0.1	0.8±0.1	0.9±0.1
trehalose	1.0±0.2	0.8±0.3	1.3±0.4	0.9±0.1	1.0±0.1	1.1±0.2	-	0.6±0.1
galactinol	1.0±0.2	0.7±0.1	1.5±0.4	1.6±0.8	1.0±0.1	0.6±0.1	-	-

Values are mean ± SEM (n=3) peak intensities normalized by the mean of those in wild-type (WT) samples in the corresponding sucrose condition at the absence of NaCl. The values in bold are statistically significantly different from those in wild-type plants in each growth condition by ANOVA analysis (p<0.05). Abbreviation: double knockout (dKO).

Supplemental Table S2. Levels of metabolite in AtUCP transgenic plants at 50 mM NaCl.

Metabolite	with sucrose				without sucrose			
	WT	ucp1	ucp2	dKO	WT	ucp1	ucp2	dKO
phenylalanine	0.8±0.2	0.6±0.1	0.7±0.1	0.4±0.1	0.9±0.2	0.7±0.1	0.7±0.1	0.7±0.2
tryptophan	0.8±0.1	0.7±0.1	0.8±0.1	0.5±0.1	0.7±0.1	0.7±0.1	0.7±0.1	0.6±0.1
asparagine	0.5±0.1	0.4±0.1	0.5±0.1	0.6±0.1	0.5±0.1	0.5±0.1	0.5±0.1	0.6±0.1
lysine	1.0±0.2	0.7±0.1	0.9±0.1	0.9±0.1	1.2±0.1	1.2±0.1	1.2±0.1	1.6±0.2
serine	1.4±0.2	1.1±0.3	1.2±0.1	1.0±0.1	1.1±0.1	1.1±0.1	1.1±0.1	1.2±0.1
threonine	1.2±0.1	1.3±0.1	1.1±0.1	1.1±0.1	1.2±0.1	1.1±0.1	1.1±0.1	1.0±0.1
isoleucine	1.5±0.3	1.0±0.1	1.5±0.1	0.9±0.1	1.3±0.1	1.2±0.1	1.2±0.1	1.1±0.1
methionine	1.0±0.1	0.9±0.1	0.9±0.1	0.8±0.1	1.0±0.1	1.0±0.1	1.0±0.1	1.0±0.1
leucine	1.5±0.3	1.0±0.2	1.4±0.2	0.8±0.1	1.3±0.1	1.2±0.2	1.2±0.1	1.1±0.1
alanine	1.2±0.4	1.3±0.5	1.0±0.3	1.2±0.7	1.2±0.4	1.4±0.5	1.5±0.6	1.2±0.4
beta.alanine	1.4±0.1	1.1±0.1	1.1±0.1	1.2±0.1	1.5±0.4	1.8±0.3	1.6±0.4	1.6±0.2
ornithine	1.0±0.1	0.6±0.1	1.0±0.2	1.0±0.2	1.0±0.2	1.3±0.5	0.9±0.3	2.3±0.7
proline	2.7±0.2	2.8±0.7	2.4±0.3	2.3±0.3	6.1±1.0	4.5±0.4	5.2±0.8	3.4±0.6
valine	1.3±0.1	1.1±0.1	1.1±0.1	1.0±0.1	1.1±0.1	1.2±0.1	1.2±0.1	1.1±0.1
glycine	0.3±0.1	0.2±0.1	0.3±0.1	0.2±0.1	0.3±0.1	0.2±0.1	0.3±0.1	0.2±0.1
glutamine	1.5±0.3	1.6±0.3	1.4±0.4	1.2±0.3	1.1±0.1	1.3±0.1	1.3±0.2	1.2±0.3
aspartate	1.2±0.1	1.2±0.1	0.9±0.1	0.8±0.1	1.2±0.2	1.1±0.1	1.3±0.2	0.9±0.1
glutamate	1.1±0.1	1.2±0.1	1.0±0.1	1.0±0.2	1.0±0.2	0.9±0.1	1.0±0.2	0.8±0.1
arginine	0.7±0.1	0.4±0.1	0.7±0.1	0.7±0.1	0.6±0.1	0.8±0.2	0.7±0.2	1.1±0.1
glucose	0.8±0.2	0.6±0.1	0.8±0.1	1.2±0.4	0.8±0.2	0.6±0.1	1.5±1.0	0.9±0.5
sucrose	0.8±0.2	0.9±0.1	0.8±0.1	0.8±0.1	0.9±0.4	0.8±0.1	0.7±0.3	0.6±0.3
maltose	0.7±0.1	0.7±0.1	0.8±0.1	1.2±0.1	0.7±0.1	0.9±0.2	0.7±0.1	1.0±0.1
raffinose	1.2±0.3	0.9±0.4	0.9±0.1	0.9±0.3	2.2±0.9	1.5±0.2	1.3±0.3	1.0±0.1
glycerol	1.9±0.8	0.9±0.1	1.0±0.1	1.0±0.1	1.5±0.5	1.3±0.2	2.3±1.3	2.0±1.1
erythritol	1.6±0.1	1.7±0.1	1.5±0.1	1.4±0.1	1.6±0.1	1.7±0.1	1.7±0.1	1.4±0.1
myo.inositol	1.1±0.1	1.3±0.1	0.9±0.1	1.0±0.1	1.6±0.4	1.4±0.1	1.5±0.2	1.0±0.1
malate	0.6±0.1	0.4±0.1	0.4±0.1	**0.2±0.1**	0.6±0.1	0.4±0.1	0.4±0.1	**0.3±0.1**
fumarate	0.5±0.1	0.6±0.1	0.4±0.1	0.2±0.1	0.5±0.1	0.4±0.1	0.4±0.1	0.2±0.1
citrate	1.1±0.2	0.7±0.1	0.7±0.1	1.0±0.3	0.9±0.3	0.7±0.1	1.0±0.4	0.7±0.1
pyruvate	1.4±0.2	0.8±0.1	1.0±0.2	-	0.9±0.1	0.8±0.1	0.8±0.1	0.6±0.1
glycerate	0.8±0.1	0.5±0.1	0.4±0.1	0.4±0.1	1.2±0.1	0.9±0.1	1.1±0.2	0.8±0.1
succinate	0.4±0.1	-	0.4±0.1	-	0.3±0.1	-	0.3±0.1	0.3±0.1
phosphate	7.5±5.1	9.7±2.9	3.5±1.3	8.5±0.7	6.4±1.9	9.3±1.1	8.0±0.5	8.5±0.7
threonate	0.7±0.2	0.9±0.1	0.6±0.1	0.6±0.1	1.0±0.4	0.8±0.1	1.0±0.3	0.7±0.2
dehydroascorbate	0.7±0.1	1.1±0.2	0.7±0.1	0.5±0.1	0.7±0.1	0.7±0.1	0.7±0.1	0.5±0.1
GABA	0.4±0.1	0.2±0.1	0.3±0.1	0.2±0.1	0.4±0.1	0.4±0.1	0.5±0.2	0.4±0.1
putrescine	0.3±0.1	0.3±0.1	0.4±0.1	0.3±0.1	0.3±0.1	0.4±0.1	0.3±0.1	0.4±0.1
AMP	3.6±1.2	3.6±0.4	2.6±0.9	3.0±0.7	2.2±0.4	2.2±0.7	3.5±1.9	2.2±1.2
benzoate	0.7±0.1	0.7±0.1	0.7±0.1	0.8±0.1	0.9±0.1	1.0±0.1	0.9±0.1	1.0±0.1
sulfate	10±2	12±2	11±1	13±3	46±14	45±16	40±16	49±17
nicotinate	0.6±0.1	0.4±0.1	0.5±0.1	0.5±0.1	1.0±0.1	0.9±0.2	0.8±0.2	1.0±0.3
2-oxoglutarate	0.5±0.1	0.3±0.2	0.5±0.1	0.2±0.1	0.4±0.1	0.3±0.1	0.3±0.1	0.3±0.1
fructose	0.6±0.1	0.6±0.1	0.6±0.1	1.1±0.3	1.0±0.2	0.7±0.1	1.1±0.4	0.8±0.3
shikimate	0.6±0.1	0.6±0.1	0.6±0.1	0.8±0.1	0.8±0.2	0.8±0.1	0.8±0.1	0.6±0.1
trehalose	0.8±0.1	0.9±0.1	0.5±0.1	0.6±0.1	1.1±0.3	1.0±0.1	1.1±0.2	0.5±0.2
galactinol	0.8±0.3	0.5±0.1	0.5±0.1	0.4±0.1	1.7±0.9	1.0±0.1	1.1±0.4	0.7±0.1

Values are mean ± SEM (n=3) peak intensities normalized by the mean of those in wild-type (WT) samples in the corresponding sucrose condition at the absence of NaCl. The values in bold are statistically significantly different from those in wild-type plants in each growth condition by ANOVA analysis (p<0.05). Abbreviation: double knockout (dKO).

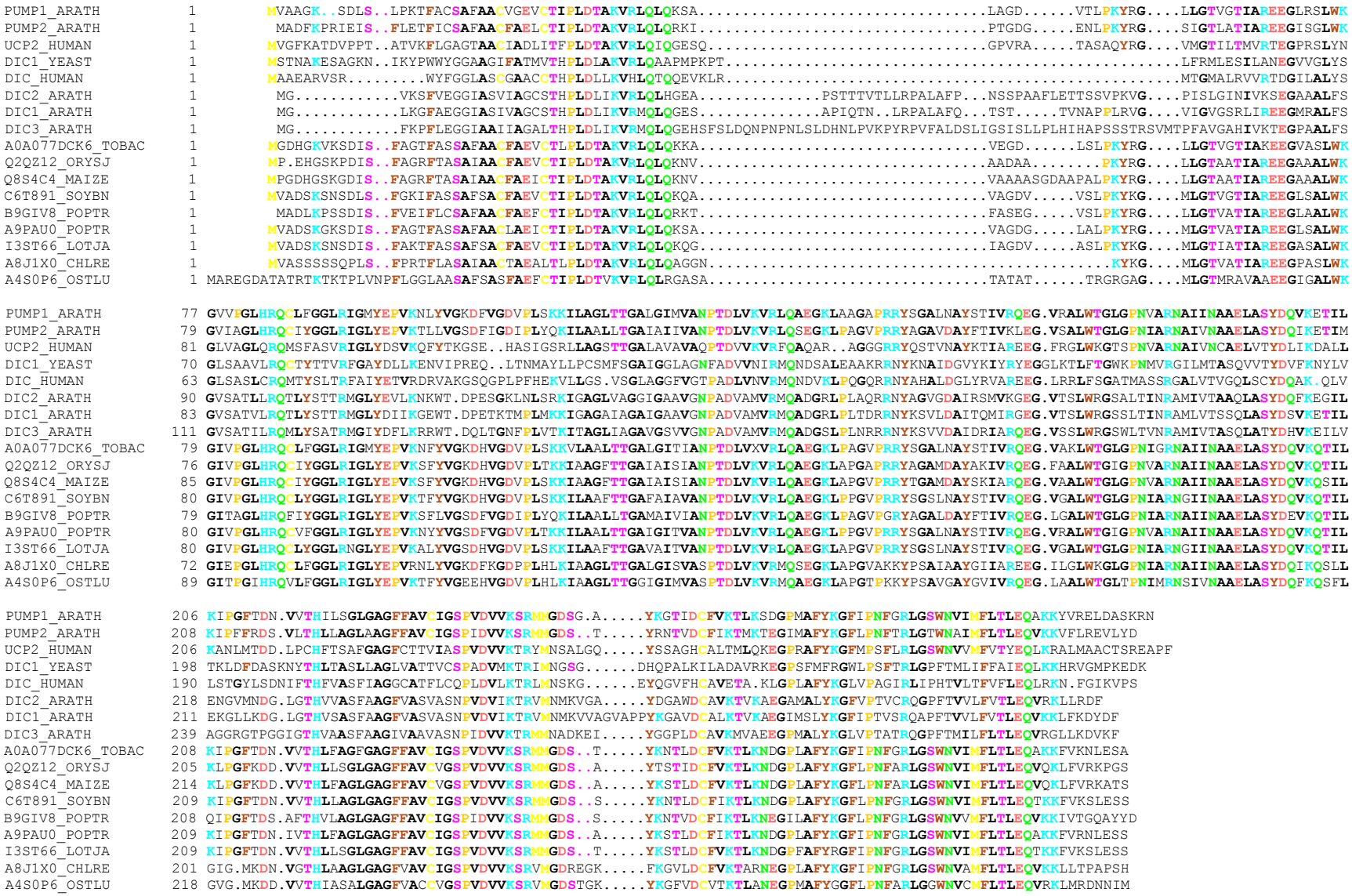
Supplemental Table S3. Levels of metabolite in AtUCP transgenic plants at 75 mM NaCl.

Metabolite	with sucrose				without sucrose			
	WT	ucp1	ucp2	dKO	WT	ucp1	ucp2	dKO
phenylalanine	0.9±0.2	0.6±0.2	0.5±0.1	0.4±0.1	1.2±0.3	0.6±0.1	0.8±0.1	0.6±0.1
tryptophan	0.8±0.1	0.7±0.1	0.7±0.1	0.6±0.1	0.7±0.1	0.6±0.1	0.6±0.1	0.6±0.1
asparagine	0.4±0.1	0.4±0.1	0.4±0.1	0.4±0.1	0.5±0.1	0.5±0.2	0.5±0.1	0.4±0.1
lysine	1.1±0.2	0.9±0.1	1.1±0.1	1.1±0.1	1.5±0.1	1.4±0.2	1.3±0.2	1.4±0.1
serine	1.4±0.2	1.1±0.2	1.3±0.1	1.1±0.1	1.4±0.1	1.0±0.2	1.3±0.2	1.0±0.1
threonine	1.7±0.1	1.8±0.1	1.4±0.1	1.3±0.1	1.6±0.1	1.3±0.2	1.5±0.2	1.4±0.2
isoleucine	1.6±0.4	1.3±0.3	1.3±0.2	1.0±0.1	1.7±0.2	1.0±0.1	1.3±0.1	1.2±0.1
methionine	1.2±0.1	1.2±0.1	1.1±0.1	1.0±0.1	1.2±0.1	1.1±0.1	1.2±0.1	1.1±0.1
leucine	1.8±0.4	1.2±0.4	1.2±0.1	0.9±0.1	1.8±0.2	1.0±0.1	1.4±0.1	1.1±0.1
alanine	1.3±0.5	1.5±0.5	1.4±0.5	1.4±0.5	1.4±0.5	1.3±0.5	1.5±0.5	1.5±0.5
beta.alanine	1.4±0.2	1.5±0.2	1.6±0.2	1.5±0.1	1.9±0.1	1.7±0.3	1.8±0.3	1.8±0.2
ornithine	0.5±0.2	0.5±0.1	1.1±0.3	1.1±0.3	1.4±0.3	1.8±0.6	1.4±0.5	1.3±0.1
proline	5.3±1.5	4.3±1.0	3.8±0.7	3.5±0.9	12±2	7.4±0.9	12±2	7±2
valine	1.4±0.2	1.2±0.1	1.2±0.1	1.1±0.1	1.3±0.1	1.0±0.1	1.3±0.1	1.2±0.1
glycine	0.2±0.1	0.1±0.1	0.1±0.1	0.1±0.1	0.2±0.1	0.1±0.1	0.2±0.1	0.1±0.1
glutamine	1.8±0.3	1.8±0.3	2.0±0.6	1.6±0.3	1.3±0.3	1.1±0.2	1.6±0.3	1.2±0.4
aspartate	1.2±0.1	1.1±0.1	0.9±0.2	0.7±0.1	1.0±0.2	0.7±0.1	1.1±0.1	0.7±0.1
glutamate	1.2±0.1	1.3±0.1	1.0±0.1	1.0±0.1	1.2±0.1	0.9±0.2	1.1±0.1	0.9±0.1
arginine	0.4±0.1	0.3±0.1	0.7±0.1	0.7±0.1	0.9±0.1	0.9±0.2	0.8±0.2	0.7±0.1
glucose	0.6±0.1	0.6±0.1	0.6±0.1	0.7±0.1	1.5±0.3	1.9±0.2	0.6±0.1	0.6±0.1
sucrose	1.0±0.1	1.0±0.1	0.9±0.1	0.8±0.1	1.0±0.1	0.5±0.2	1.3±0.3	1.3±0.3
maltose	0.5±0.1	0.5±0.1	0.5±0.1	0.6±0.1	0.6±0.1	1.1±0.3	0.6±0.1	1.0±0.2
raffinose	1.8±0.7	1.6±0.8	1.1±0.6	1.1±0.6	5.1±3.1	1.8±0.7	3.3±1.6	3.2±0.3
glycerol	1.6±0.6	1.5±0.5	1.6±0.6	1.3±0.5	1.9±0.6	1.8±0.4	1.6±0.7	1.3±0.3
erythritol	2.1±0.1	2.1±0.2	2.0±0.2	1.6±0.1	2.0±0.2	1.6±0.2	2.0±0.1	1.9±0.3
myo.inositol	1.5±0.1	1.5±0.1	1.2±0.2	1.1±0.1	2.1±0.2	1.7±0.5	2.1±0.5	2.0±0.5
malate	0.6±0.1	0.3±0.1	0.3±0.1	**0.2±0.1**	0.5±0.1	**0.2±0.1**	0.4±0.1	**0.2±0.1**
fumarate	0.5±0.1	0.4±0.1	0.2±0.1	**0.1±0.1**	0.5±0.1	**0.2±0.1**	0.4±0.1	**0.2±0.1**
citrate	0.9±0.2	0.7±0.1	0.8±0.3	0.7±0.1	0.6±0.1	**0.4±0.1**	0.7±0.1	0.5±0.1
pyruvate	1.1±0.1	0.9±0.1	0.8±0.1	0.9±0.1	1.0±0.1	0.7±0.1	0.9±0.1	**0.7±0.1**
glycerate	0.8±0.1	0.7±0.1	0.5±0.1	0.5±0.1	2.1±0.3	1.3±0.2	1.1±0.2	**0.7±0.1**
succinate	-	-	-	-	-	-	-	-
phosphate	9.4±1.4	11.0±2.2	13.5±4.1	12.0±2.4	7.8±2.7	9.1±0.5	7.0±1.7	9.5±3.1
threonate	0.9±0.2	0.7±0.1	0.5±0.1	0.4±0.1	0.8±0.2	0.4±0.1	0.8±0.1	0.6±0.1
dehydroascorbate	0.7±0.1	0.6±0.1	0.7±0.1	0.5±0.1	0.5±0.1	0.5±0.1	0.7±0.1	0.6±0.1
GABA	0.2±0.1	0.1±0.1	0.2±0.1	0.2±0.1	0.5±0.2	0.6±0.1	0.3±0.1	0.2±0.1
putrescine	0.2±0.1	0.2±0.1	0.3±0.1	0.3±0.1	0.3±0.1	0.3±0.1	0.4±0.1	0.4±0.1
AMP	5.1±1.1	4.8±1.1	4.6±1.2	4.4±1.6	3.1±0.7	3.3±0.5	2.8±1.0	2.2±0.7
benzoate	0.9±0.2	0.8±0.1	0.8±0.1	0.6±0.1	1.0±0.2	0.8±0.1	1.0±0.1	1.0±0.1
sulfate	20±4	25±8	21±7	19±5	45±15	30±10	46±23	49±15
nicotinate	0.5±0.1	0.4±0.1	0.5±0.1	0.5±0.1	0.9±0.2	0.8±0.2	1.0±0.2	0.9±0.1
2-oxoglutarate	0.2±0.1	0.2±0.1	0.2±0.1	0.1±0.1	0.3±0.1	0.2±0.1	0.2±0.1	**0.1±0.1**
fructose	0.5±0.1	0.5±0.1	0.5±0.1	0.6±0.1	1.7±0.1	1.9±0.1	0.8±0.2	0.7±0.2
shikimate	0.6±0.1	0.6±0.1	0.5±0.1	0.5±0.1	0.9±0.1	0.8±0.1	0.9±0.1	0.8±0.1
trehalose	1.2±0.1	1.0±0.1	**0.7±0.1**	**0.6±0.1**	1.2±0.2	1.0±0.2	1.1±0.3	1.4±0.3
galactinol	1.0±0.2	0.7±0.2	0.5±0.1	0.4±0.2	2.5±1.0	1.7±0.8	2.0±0.8	1.8±0.3

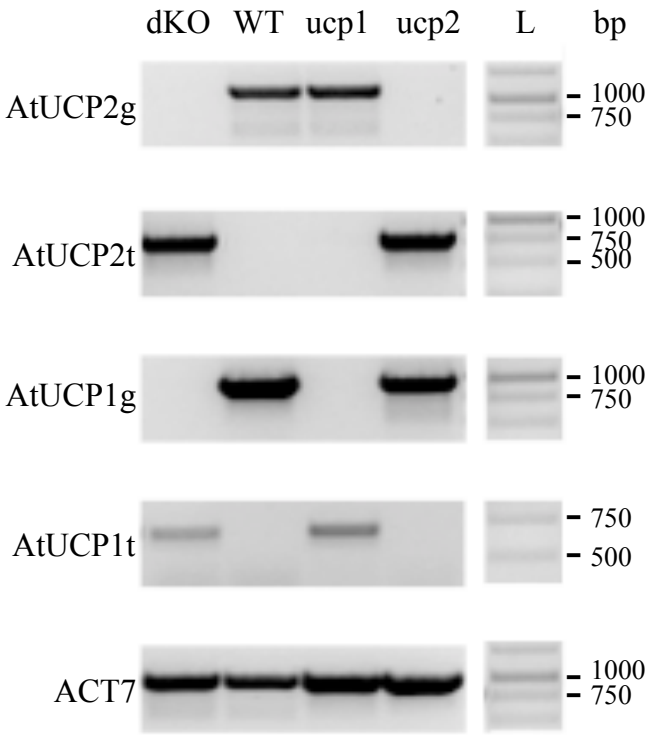
Values are mean ± SEM (n=3) peak intensities normalized by the mean of those in wild-type (WT) samples in the corresponding sucrose condition at the absence of NaCl. The values in bold are statistically significantly different from those in wild-type plants in each growth condition by ANOVA analysis (p<0.05). Abbreviation: double knockout (dKO).

Supplemental Table S4. Primer sequences used in this study

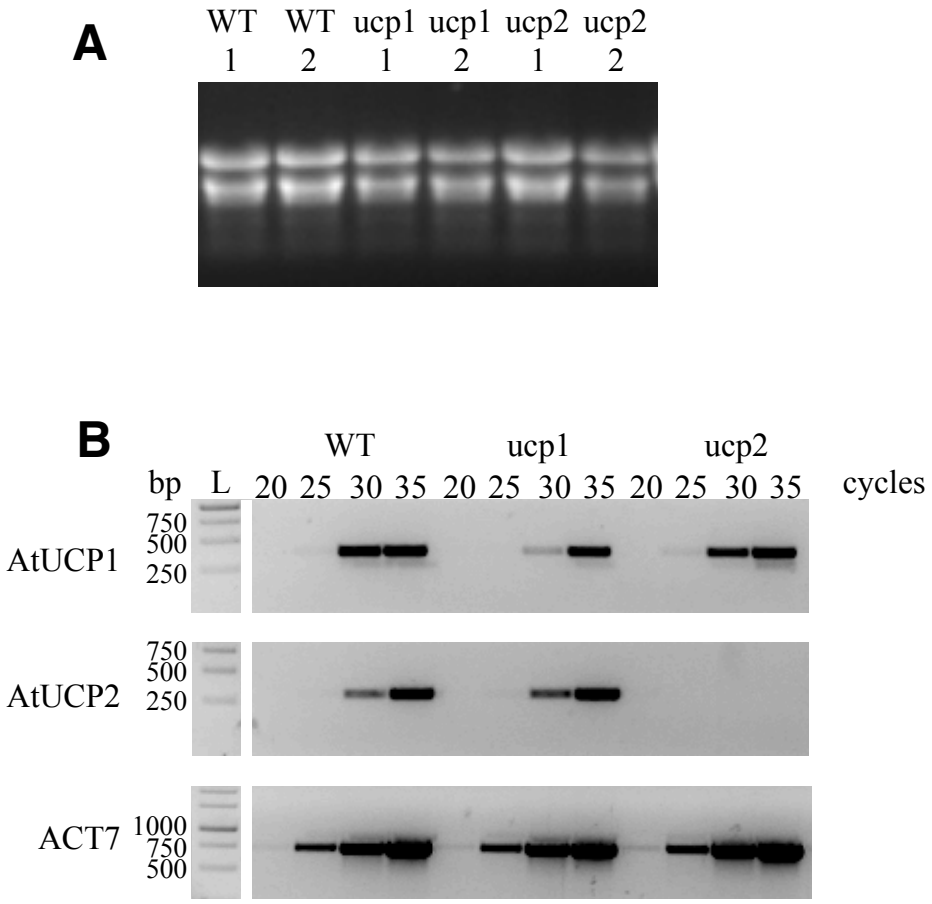
Name	Sequence (5'-3')
BH254	cgagtgcgggatcctctagagggccATGGTGGCGGCTGGTAAATC
BH255	cttgctcacgccgctccctccccgcCCGTTTCTTTTGGACGCATC
DG5	AAACAACCACCAGTAGAAGCC
DG6	TCGATCAATCACTGTCACTGG
DG8	TTCTAGCCACAGATCTGACCG
DG9	TTTATCATCGAGGGCACTCTG
DG23	CGAGGATTGTTGGGAACTGT
DG24	AAAGAGCTCGGACTCCTTCC
DG25	ATGGTGAGAATTTGCCCAAG
DG26	GCCGGTAACTTTCCTTCTGA
SALK- LBa1	TGGTTCACGTAGTGGGCCATCG
SAIL-Lba	TTCATAACCAATCTCGATACAC
UCP2_BPF	ggggacaagtttgtacaaaaaagcaggctccaccATGGCGGATTTCAAACCAAG
UCP2_BPR-s	ggggaccactttgtacaagaaagctgggtcATCGTACAAGACTTCTCTTAGAAACACTT



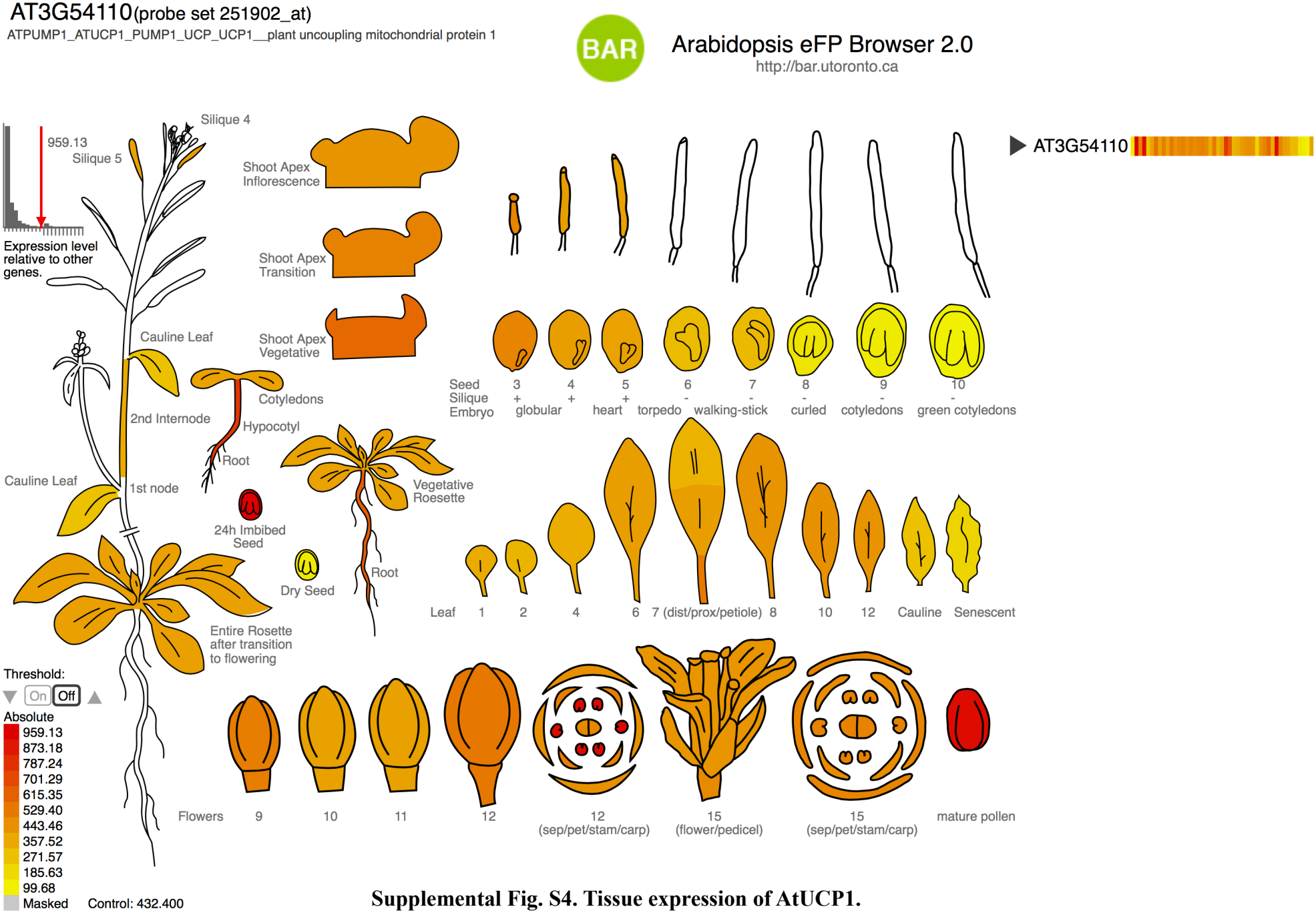
Supplemental Fig. S1. Sequence alignment of AtUCP1, AtUCP2 and their homologues. Protein sequences nominated with their UniProtKB entry names were selected based on their sequence identity with AtUCP1 (PUMP1_ARATH) and AtUCP2 (PUMP2_ARATH). They include their closest human, *S. cerevisiae* and Arabidopsis homologues as well as their homologues in other plants. The alignment was done with ClustalW.



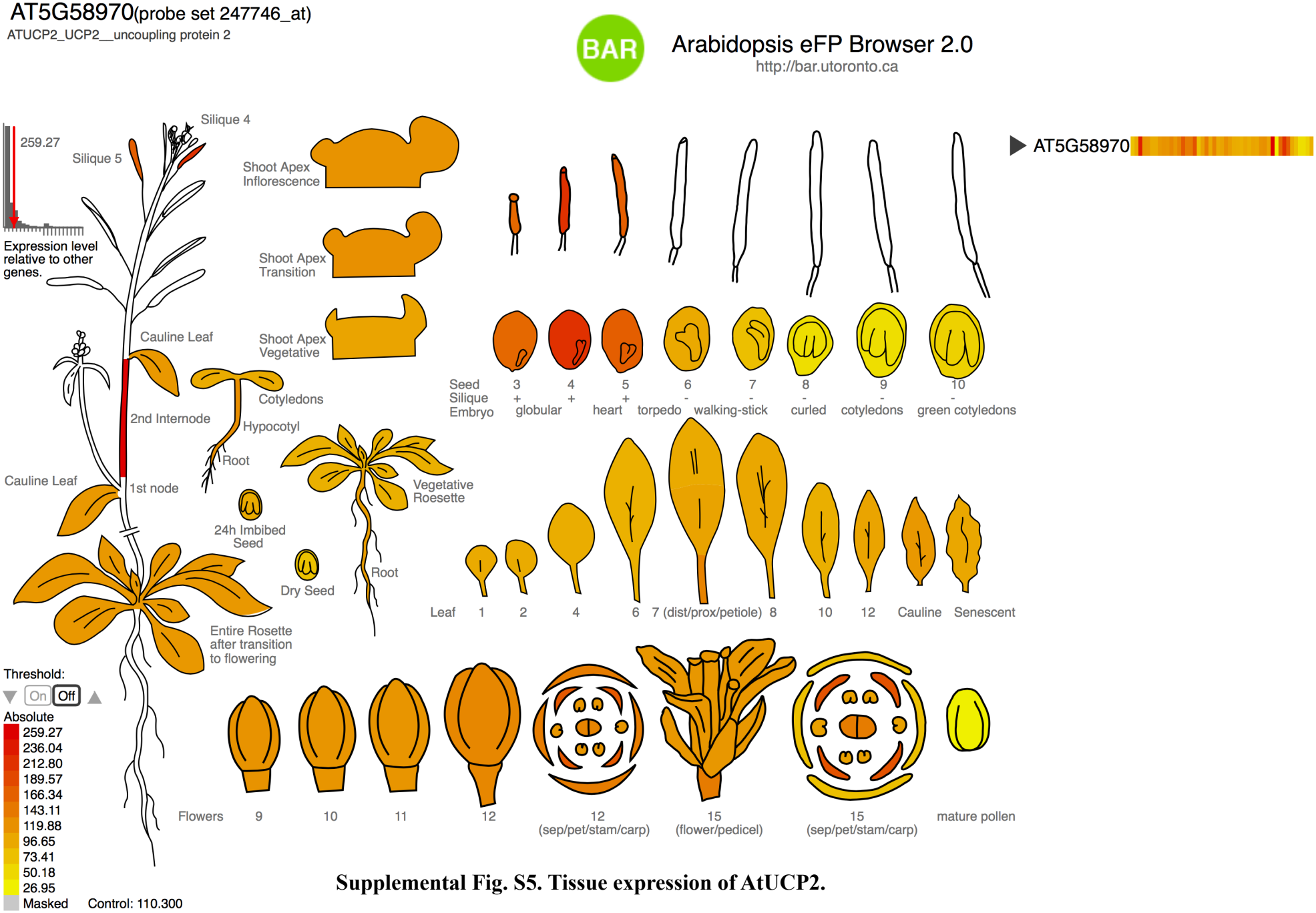
Supplemental Fig. S2. Isolation of ucp1 and ucp2 T-DNA homozygous insertion lines and ucp1/ucp2 double mutants. Genomic DNA PCR analysis of wild-type *A. thaliana* Col-0 plants (WT), ucp1, ucp2 and double knockout (dKO). A DNA ladder (L) with the number of base pairs (bp) is shown to the right. The g letter (in AtUCP1g and AtUCP2g) indicates PCR reaction with primers surrounding the T-DNA insertion and the letter t (in AtUCP1t and AtUCP2t) indicates PCR reaction with primers specific for T-DNA/gene flanking region. ACT7 refers to ACT7 control gene amplification.



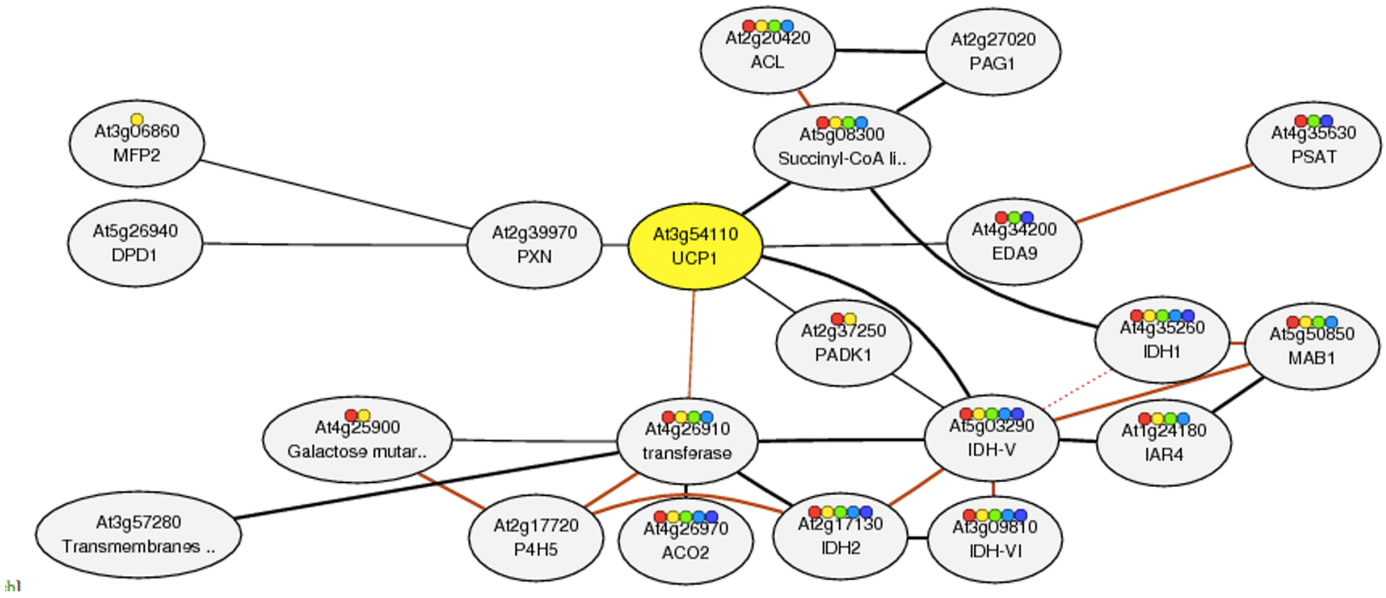
Supplemental Fig. S3. Semiquantitative RT-PCR in wild-type (WT), ucp1 single mutant and ucp2 single mutant. A: Agarose gel of total RNA for qualitative and quantitative assessements. Total RNA extractions have been done on 2 independent plants (WT1 and 2, ucp1-1 and 2 and ucp2-1 and 2). B: RT-PCR with AtUCP1 specific primer pair, AtUCP2 specific primer pair or Act7 specific primer pair as a control. A DNA ladder (L) with the number of base pairs (bp) is shown to the left. Note: All reactions have been done at the same time and loaded on the same gel.



Supplemental Fig. S4. Tissue expression of AtUCP1.



Supplemental Fig. S5. Tissue expression of AtUCP2.



Supplemental Fig. S6. Gene co-expression networks of AtUCP1. The microarray data from the ATTED database show the genes co-expressed with At3g54110 (AtUCP1). Among these genes are several citric acid cycle enzymes such as aconitase (At4g26910), isocitrate dehydrogenase (At4g35260, At2g17130, At5g03290 and At3g09810), α-ketoglutarate dehydrogenase (At4g26910) and succinyl-CoA ligase (At2g20420 and At5g08300) as well as the peroxisomal transporter for NAD^+ (At2g39970).