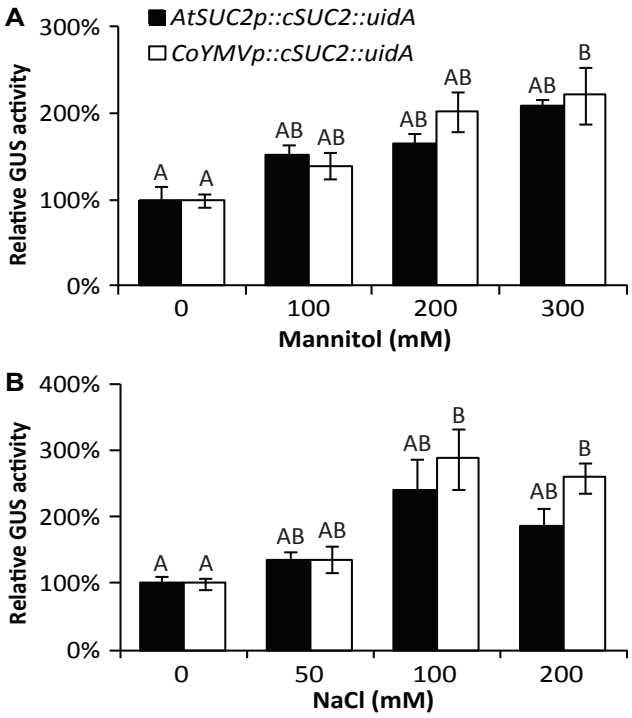
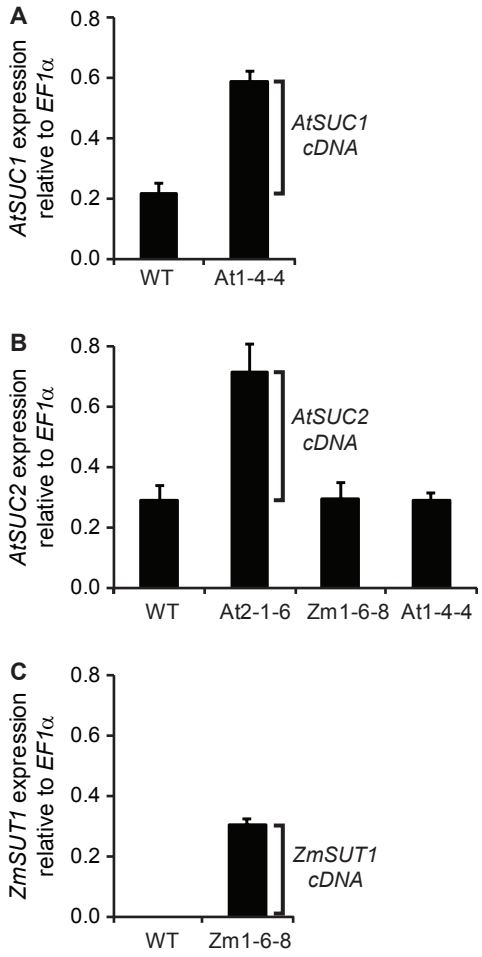
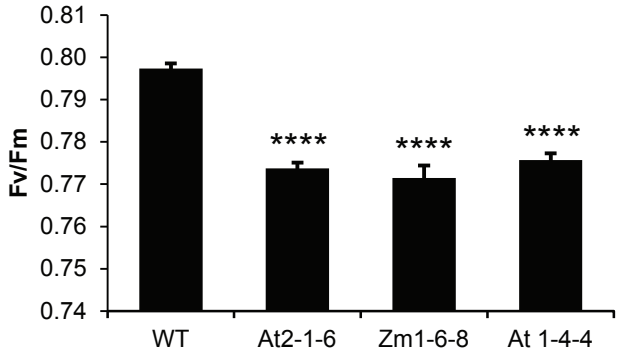


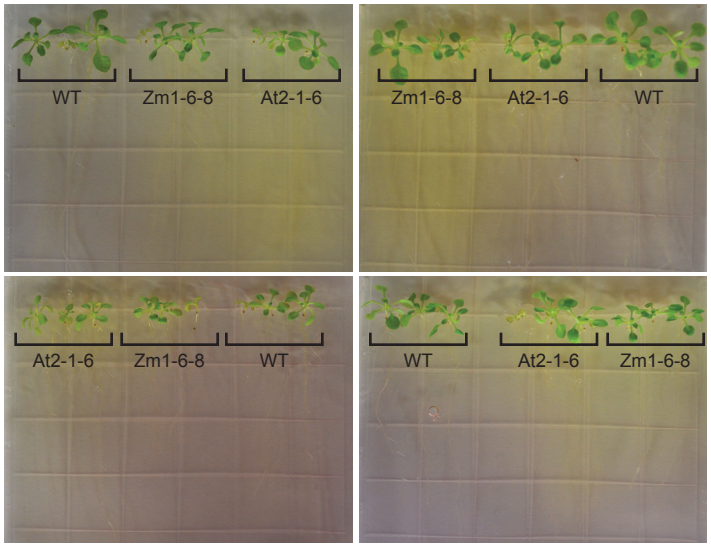
Supplemental Figure 1. Comparison of *CoYMVp* and *AtSUC2p* phloem-specific promoter activities in the presence of different stimuli (See also, Figure 1). A, Quantitative GUS analysis in *CoYMVp::cSUC2::uidA* and *AtSUC2p::cSUC2::uidA* plants grown on MS medium in the presence of 0 mM, 100 mM, 200 mM, and 300 mM mannitol to mimic osmotic / drought stress, relative to 0 mM mannitol. B, GUS activity in the presence of 0 mM, 50 mM, 100 mM, and 200 mM NaCl to mimic salt stress, expressed relative to 0 mM NaCl. Variation is expressed as standard error; n = 6; different letters represent significant differences based on univariate ANOVA with Scheffe post-hoc analysis at the 0.05 level.



Supplemental Figure 2. RT-qPCR analysis of *AtSUC1*, *AtSUC2*, and *ZmSUT1* transcript levels in WT plants and WT lines with additional companion cell-specific *SUT* expression. A, *AtSUC1* transcript abundance in WT and line At1-4-4, with additional *AtSUC1* expression attributed to the transgene. B, *AtSUC2* transcript abundance in WT and lines At1-4-4, At2-1-6, and Zm1-6-8, with the additional expression in At2-1-6 attributed to the transgene. C, *ZmSUT1* transcript levels in WT and line Zm1-6-8, which additional expression in At2-1-6 attributed to the transgene.



Supplemental Figure 3. Photosynthesis is reduced in *SUT* over-expressing lines. Photosynthesis was measured by imaging pulsed amplitude modulated fluorescence (F_v/F_m) on dark adapted leaves and revealed reductions consistent with feedback inhibition by accumulation of sugar in the rosettes; n = 12 measurements (4 fully-expanded leaves from 3 plants of each line); variation is represented as SE; significant difference from WT are based on Student's T-Test: ****, $P \leq 1 \times 10^{-5}$.



Supplemental Figure 4. Increased rhizosphere acidification by plants with additional *SUT* expression in companion cells, as demonstrated by the pH indicator dye bromocresol blue. The starting pH of the ½ strength MS medium (without added Suc or P) was 6.8. Transition of the dye from blue to yellow indicates a pH drop to below 5.0, and is most evident in the vicinity of At2-1-6 and Zm1-6-8 roots but is minimal in the vicinity of WT roots. Each panel represents a separate plate prepared from the same batch of media and plates were incubated at the same time in the same growth chamber. Each panel thus represents a biological replicate.

Supplemental Table 1: Cross reference for the most prevalent "Type", "Group" and "Clade" designations used by different authors, and the biochemical characteristics and apparent functions of representative members (adapted from (Ayre, 2011)).

Type[1]	Group[2] / Clade[3]	Distribution, function	Affinity ($K_{0.5}$ mM) in yeast or (oocytes)	Representative members	Location, apparent physiological function	Antisense/mutant phenotype	Reference[4]
Type I	Group 2 / SUT1	Dicot, high affinity uptake	0.5 0.77 (1.44) 0.5 (0.066) 1.0 (0.5)	AtSUC1 AtSUC2 AtSUC9 Solanaceae SUT1	Numerous sinks, uptake Phloem, loading/retrieval Broadly, high affinity retrieval Phloem & sinks, loading/retrieval	Pollen defects Stunted, accumulate carbohydrate Early flowering Stunted, accumulate carbohydrate	(Feuerstein et al., 2010) (Srivastava et al., 2008) (Sivitz et al., 2007) (Schmitt et al., 2008)
Type IIA	Group 3 / SUT2	Monocot and Dicot, low affinity	Not active 1.9	Solanaceae SUT2 AtSUC3/AtSUT2	Sink organs, pollen tube growth Sinks & wounded tissue	Reduced pollen growth None apparent	(Hackel et al., 2006) (Meyer et al., 2004)
Type IIB	Group 1 / SUT3	Monocot, high affinity uptake	(7.5) (3.7)	OsSUT1 ZmSUT1	Broadly, seed filling, not loading Phloem & sinks, loading	Shriveled seeds Stunted, accumulate carbohydrate	(Scofield et al., 2002) (Slewinski et al., 2009)
	Group 5 / SUT5	Monocot, high affinity uptake	(2.3)	OsSUT5	Broadly	Unknown	(Sun et al., 2010)
Type III	Group 4 / SUT4	Dicot and monocot, low affinity	Unknown (16.0) 6.0	HvSUT2 LjSUT4 StSUT4	mesophyll, tonoplast transport Nodules, tonoplast transport Broadly, plasma membrane	Unknown Unknown Early flowering & tuberization	(Endler et al., 2006) (Reinders et al., 2008) (Chincinska et al., 2008)

1. Based on (Aoki et al., 2003; Reinders et al., 2012)
2. Based on (Braun and Slewinski, 2009)
3. Based on (Kühn and Grof, 2010)
4. Only the most recent or thorough references are provided here, see (Ayre, 2011) for more thorough descriptions and citations.

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Supplemental Table 2: Oligonucleotides used to create the indicated SUT cDNA by PCR for TOPO directional cloning.

cDNA	Forward Primer (5'→3')	Reverse Primer (5'→3')
AtSUC2	CACCATGGTCAGCCATCCAATGGAGAAAGCTGC	ATGAAATCCCATAGTAGCTTTGAACGCAGGAGC
NtSUT3	CACCATGGAGAGTGGTAGTATGGGAATG	AAACTTGTTTTGTGATGTCCAGTATTTTGTC
LeSUT2	CACCATGGATGCGGTATCGATCAGAGTACCGT	ACCAAAATGGAAGCCAGTTGATTTG
LeSUT4	CACCATGCCGGAGATAGAAAGGCATAGAACAAGG	TGCAAAGATCTTGGGTCTCTCAACCCGGTGTTCG
LeSUT1	CACCATGGAGAATGGTACAAAAGGGAAACT	AATGGAAACCGCCCATGGCGACTGCTGG

Supplemental Table 3: Oligonucleotides used for RT-qPCR analysis of expression for the indicated genes

cDNA	Forward Primer (5'→3')	Reverse Primer (5'→3')
AtSUC1	GTCGTCCTTTCATCGCCACC	TTGTTGGCTACGTCGAGGAT
AtSUC2	TAGCCATTGTCGTCCCTCAGATG	ATGAAATCCCATAGTAGCTTTGAAGG
AtSUC3	TTCGGCTGATGGTGAATCTGTGT	AAGCATGCGATATTCCAAGGGTCT
AtSUC9	CCCTTCCTACCAATGCCATCAGA	GGCACCGGAACTGCTTGAAATAATG
EF1α	GAGCCCAAGTTTTTGAAGA	CTAACAGCGAAACGTCCCA
LeSUT1	CCATAGCTGCTGGTGTTCAA	ACCAGAAATGGGTCCACAAA
LeSUT2	CCGCTATCATTAGCGTGGTT	GCAAGAGGAATGCCAAGAAG
LeSUT4	CAGCCTCTAGATCCCAGTCG	ACAAGCAGGATCACCCAAAC
NtSUT3	CAGAAGCCTGTGGTGTTCAA	TGATCTTTCTGTGGCAGCAC
PAP14	TGTGCGAGACAAGTGACGTGG	GATTCGATCGCAGGAGCAAA
PAP24	CCACCAATGATTGGTATGGCA	AGGCTTTCTCTTCCCATAGGCT
PHT2;1	CATTCTCCAAAACGGAGCAG	CGAGAACATCCATTGGGATAA
PT2	CGAAGCTCCTCGGTCGTAT	GGAGAGTCCCAGGCTTTTGT
ZmSUT1	AGACGCAGGCCATTTATCC	GGAGAAGTCAAGGAGCCAAA