**Supplementary file: Material and Methods**

**Generation of *SlSUT2* RNAi plants**

A 761 bp *Xho*I*-Xba*I fragment of the SlSUT2 coding region was isolated and cloned first in sense orientation in pUC-RNAi linearized by *Xho*I*-Spe*I, and subsequently in antisense orientation using *Sal*I and *Xba*I. The whole fragment including the intron sequence was cut out using *Pst*I and ligated in pBinAR linearized with *Sbf*I. Tomato transformation of variety Moneymaker was performed as described previously using the Agrobacterium strain 3101 kindly provided by Caterina Brancato. Tomato plants were grown in the greenhouse with a light/dark cycle of 16 h light (22°C) and 8 h dark (15°C).

**Sugar determination**

Determination of soluble sugar was performed enzymatically according to Stitt et al. 1989 [20](#_ENREF_20" \o "Stitt, 1989 #14895).

**Mycorrhization of tomato plants**

For mycorrhization experiments, seedlings of tomato wild type plants and the corresponding transgenic lines were planted in 4 L pots with expanded clay (2-5 mm; Lamstedt Ton, Gärtnereibedarf Kortmann GmbH, Germany). Half of the pots were inoculated with *Rhizoglomus irregularis* QS 81 (INOQ, Schnega, Germany) in a ratio of 1.5: 8.5 inoculum: substrate. The control plants were grown in the same substrate without inoculum. The plants were grown in the greenhouse in a randomized design and watered every day with 200 - 400 mL of nutrient solution (De Kreij, 1997), containing 10% of the standard phosphate concentration (0.1 mM). 8 WT plants and 4 SlSUT2-RNAi plants for each transgenic line (#7, #10, #11, #27) were inoculated and 4 control plants per line were not. Plants were harvested 15 weeks after transfer to the greenhouse.

**Analysis of arbuscule morphology**

After clearing of the colonized roots for 2 h at 50°C in 10% KOH as described by Banhara et al. [21](#_ENREF_21" \o "Banhara, 2015 #8719), they were stained with WGA-FITC (Sigma Aldrich, St Louis, USA) over night at a concentration of 10 µg ml-1 in PBS buffer. Root samples were analyzed by confocal microscopy (LSM800; Zeiss, Jena, Germany) with excitation at 488 nm and detection at 500 – 540 nm. Tubule diameter of 15 tubules per arbuscule and 4 arbuscules in 4-8 plants per genotype (WT: *n* = 480; *SlSUT2*-RNAi: *n* = 180) was quantified using the Zeiss confocal software blue edition ZEN2.0.

**Real time qPCR**

Quantitative real time PCR was performed after RNA isolation from mycorrhizal and non-mycorrhizal roots as described previously 19 using following primers: RiGAPDH fwd: GAC GTC TCA GTT GTT GAT TTA; RiGAPDH rev: TTT GGC ATC AAA AAT ACT AGA; SlPT4 fw: agc ccc agg cag att atg tt; SlPT4 rev: cat gtt aat cgc ggc ttg tt; SlTEF fw: TGG AAC TGT GCC TGT TGG TC; SlTEF rev: ACA TTG TCA CCA GGG AGT GC; SlSUT2 fw: GGC ATT CCT CTT GCT GTA ACC; SlSUT2 rev: GTT TGC ACA GCT CGA GAT CC.

**Pollen germination and pollen viability**

Pollen germination rate was determined as described previously [18](#_ENREF_18" \o "Hackel, 2006 #18) by incubating pollen grains overnight in the dark at 26°C in 20 mM MES buffer, pH 6.0 containing 15% PEG 4000, 2% sucrose, 0.07% Ca(NO3) x 4 H2O, 0.02% MgSO4 x 7 H2O, 0.01% KNO3 and 0.01% H3BO3 . Pollen was scored as geminated when the pollen tube was longer than the pollen grain diameter. For each transgenic line 500 pollen grains were counted. Pollen viability was tested in Brewbaker and Kwack Medium (146.1 mM sucrose, 1.6 mM boric acid, 1.2 mM Ca(NO3), 0.8 mM MgSO4 x 7H2O, 1.0 mM KNO3, 0.7µM aniline blue). Pollen grains were classified as viable when they showed uniform and bright fluorescence.