Table S1. List of primers used in this study.

Primer ID	Primer sequence (5'-3')
GeSUT4-qPCR-F	GCAAAATTATCATACAGGTGTGA
GeSUT4-qPCR-R	GCGAGCAGAAATCAATGCATA
GeSUT3-qPCR-F	AAGGAAGATTGCAAAGCGTAT
GeSUT3-qPCR-R	AACACCACAGCAACTAAGAAT
GeINV-5712-qPCR-F	CGCATCTCAAAGCCGAGTA
GeINV-5712-qPCR-R	GGAAAAGTCACGGGGGATTA
GeSUS-4129-qPCR-F	CCCAGCTACTGGGACAAGAT
GeSUS-4129-qPCR-R	CCCTCTTCATCAGAATGCAA
GeSUS-6657-qPCR-F	TGTTGCCAA ATATCCCCAAA
GeSUS-6657-qPCR-R	CTGGAGGGCAGGTTGTCTA
GeAct7-5	TAGGGAGAGAACGGCTTGAA
GeAct7-3	GGGATGAAGCACAGTCCAAA
GeSUT4-5-BP	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCAGA TCCACCGCTTCAGTTGGC
GeSUT4D-3-BP	GGGGACCACTTTGTACAAGAAAGCTGGGTT TTA CTCAACTGCCAAAGGAACCCCA
GeSUT4-3-BP	GGGGACCACTTTGTACAAGAAAGCTGGGTATTC ATCTTCGGTCCTTCTGCTTTGC
GeSUT3-5-BP	GGGGACAAGTTTGTACAAAAAAGCAGGCTGAAT GAG ATCTACCGAGCGAGGCCG
GeSUT3-3-BP	GGGGACCACTTTGTACAAGAAAGCTGGGTGATC AGTGCATGCTGCCCATAGTTGC
AtSUC2-5-BP	GGGGACAAGTTTGTACAA AAA AGCAGGCTATGG TCAGCCATCCAATGGAGAAAGC
ATSUC2-3-BP	GGG GAC CAC TTT GTA CAA GAA AGC TGG GTT CAA TGA AAT CCC ATA GTA GCT TTG A
GeSUT4-3-BP-fusion	GGGGACCACTTTGTACAAGAAAGCTGGGTATTCATCTT CGGTCCTTCTGCTTTGC

Figure S1. Pictures of developing *G. elata* tubers.

Based on sizes, seven stages (1, 2a, 2b, 3, 4, 5 and 6) of tubers were shown. Stage 1 PLBs (protocorm-like bodies), ~1 cm in length, were derived from embryogenic callus culture. Once PLBs were inoculated with *Armillaria*, tubers started to swell (stage 2a: 1-1.5 mm in length and 1.0 mm in width) or elongate (stage 2b: 2.5 mm in length and 0.4 mm in width). With establishment of a successful symbiosis with the fungus, tubers continued to elongate and expand until reaching mature stage 6 (more than 120 mm in length). Scale bar = 1cm.

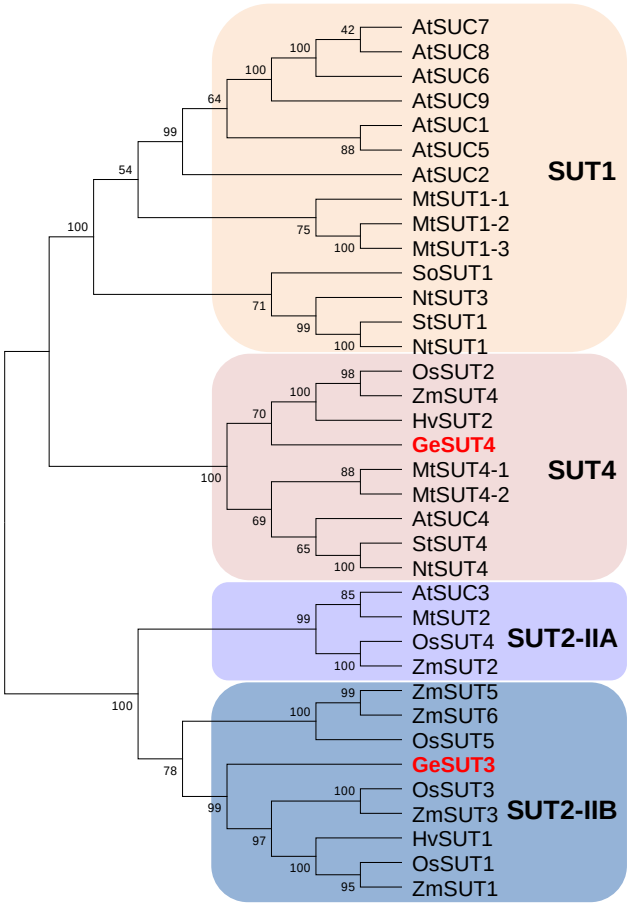


Figure S2. Phylogenetic tree of SUT transporters.

Multiple sequence alignment based on amino acid similarity between two *G. elata* SUTs and other plant species was generated using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/). Accession numbers of presented SUT genes were*: Arabidopsis thaliana*: AtSUC1 (At1g71880), AtSUC2 (At1g22710), AtSUC3 (At2g02860), AtSUC4 (At1g09960), AtSUC5 (At1g71890), AtSUC6 (At5g43610), AtSUC7 (At1g66570), AtSUC8 (At2g14670), AtSUC9 (At5g06170); *Oriza sativa*: OsSUT1 (AAF90181), OsSUT2 (BAC67163), OsSUT3 (BAB68368), OsSUT4 (BAC67164), OsSUT5 (BAC67165); *Solanum tuberosum*: StSUT1 (CAA48915), StSUT4 (AAG25923.2); *Zea mays*: ZmSUT1 (BAA83501), ZmSUT2 (AAS91375), ZmSUT3 (ACF86653), ZmSUT4 (AAT51689), ZmSUT5 (ACF85284), ZmSUT6 (ACF85673); *Nicotiana tabacum*: NtSUT1 (X82276), NtSUT3 (AAD34610), NtSUT4 (BAI60050); *Spinacia oleracea*: SoSUT1 (Q03411); *Hordeum vulgare*: HvSUT1 (Q9M422), HvSUT2 (Q9M423); *Medicago truncatula*: MtSUT1-1 (JN255789), MtSUT1-2 (JN255790), MtSUT1-3 (JN255791), MtSUT2 (JN255792), MtSUT4-1 (JN255793), MtSUT4-2 (JN255794).

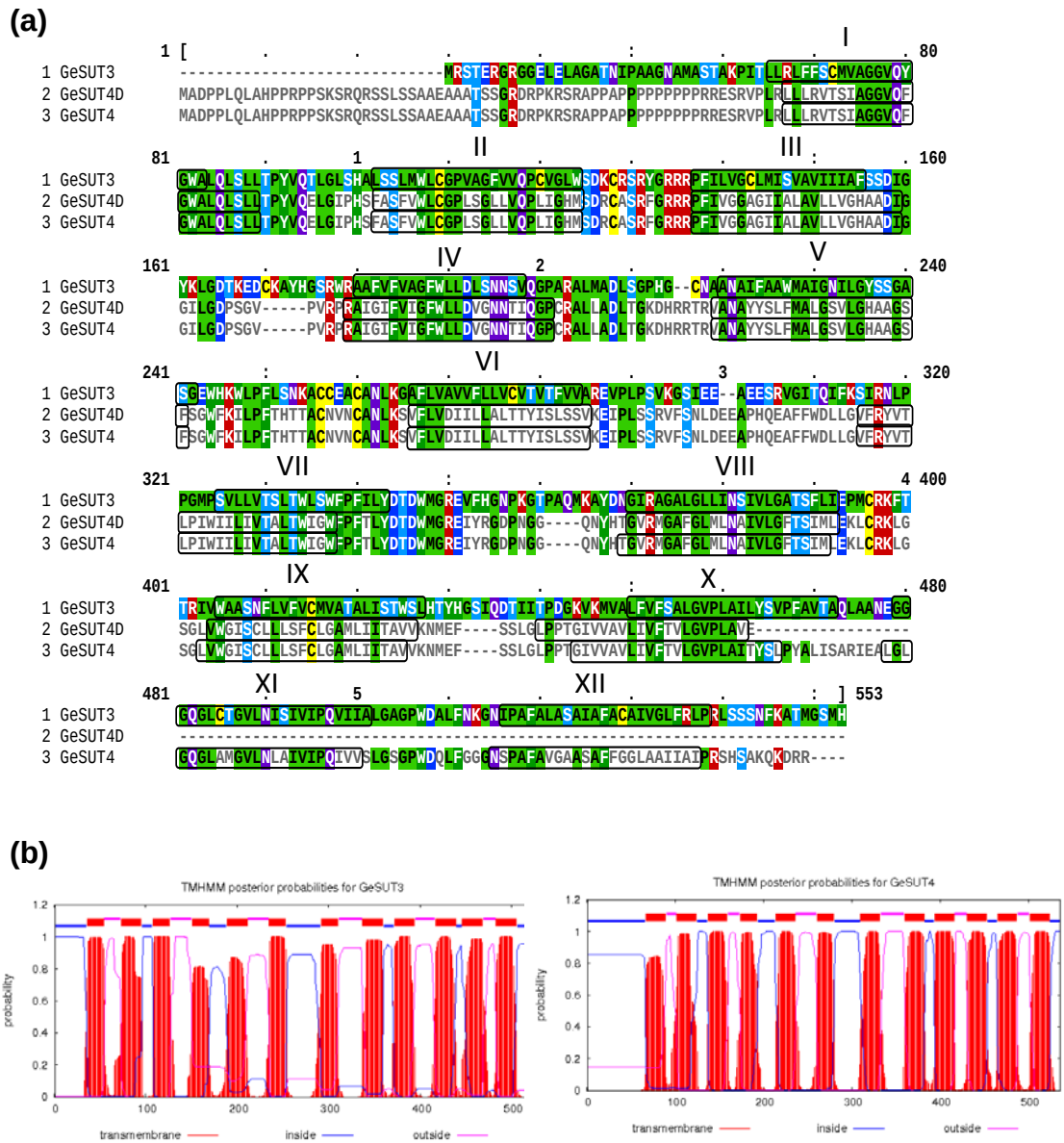
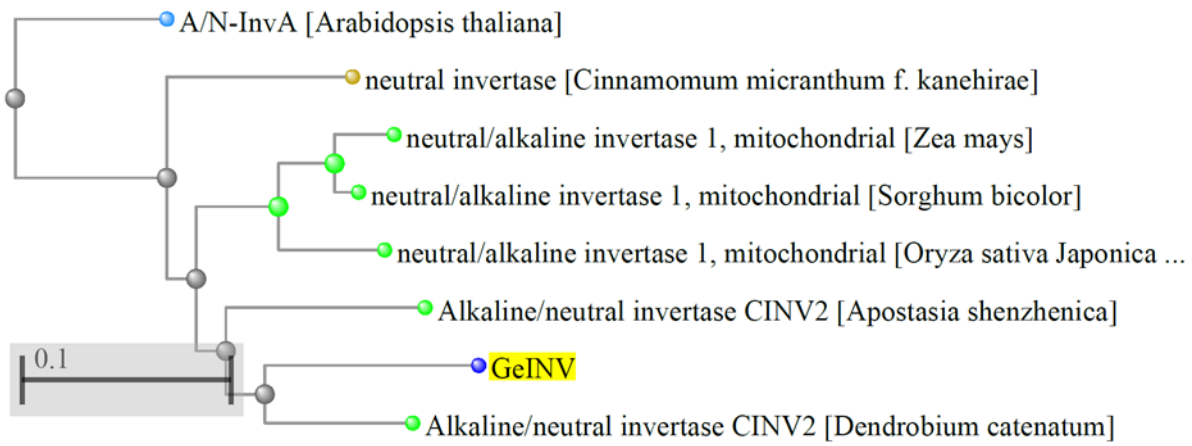


Figure S3. Gene properties of *Gastrodia GeSUT* genes.

(a) Amino acid alignment of three identified SUT. *GeSUT3*, *GeSUT4D*, *GeSUT4* were derived from RNAseq contigs 5219, 4177-1, and 4177-2, respectively. Full-length coding sequences of *Ge*SUT4 and *Ge*SUT3 were amplified and cloned using rapid amplification of cDNA ends (RACE) strategy. Transmembrane domains I to XII were indicated. Conserved amino acids were marked in green. (b) Transmembrane topologies of *Ge*SUT3 and *Ge*SUT4 analyzed by the TMHMM2.0 program (www.cbs.dtu.dk/services/TMHMM).

(a)



(b)

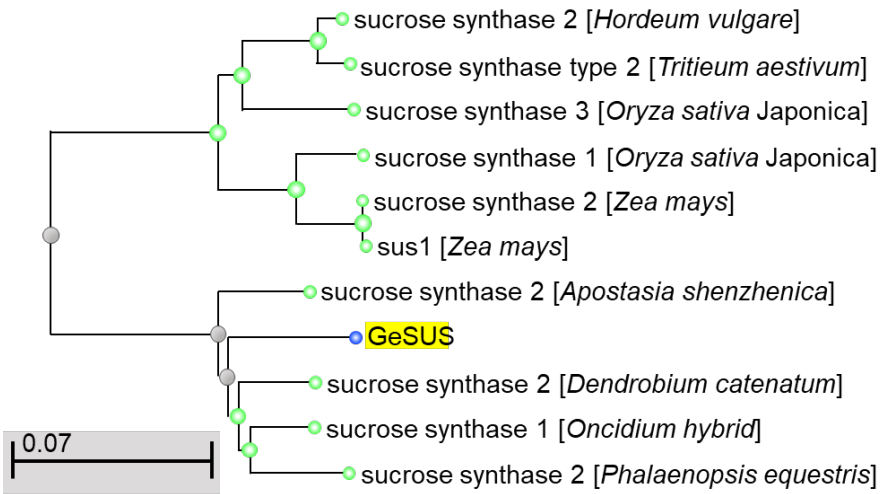


Figure S4. Phylogenetic tree of genes involved in sucrose metabolism from *Gastrodia*. (a)) GeINV was derived from RNAseq contig 5712. (b) GeSUSs were derived from RNAseq contigs 4129 and 6657. Amino acid alignment of genes from Gastrodia and other plant species was generated using NCBI blast.

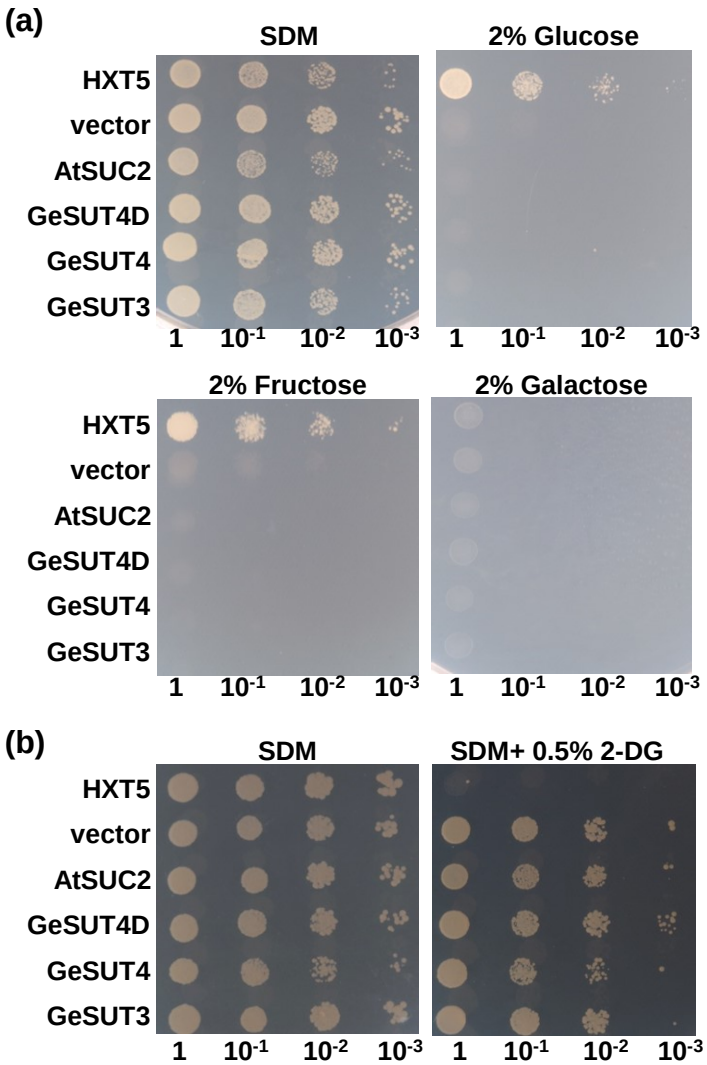


Figure S5. Transport activity of *Ge*SUT4 to hexoses in yeast.

(a) Analysis of transport activity to hexoses in YSL2-1. (b) Analysis of transport activity to toxic glucose analog in EBY. VW4000. The YSL2-1 (a) or EBY. VW4000 (b) yeast cells were transformed to express *GeSUT* genes, an empty vector, a yeast hexose transporter HXT5 and an Arabidopsis sucrose transporter, *At*SUT1. Then transformed cells were diluted in series and plated on solid media (pH 5 or 7) supplemented with various sugars. Selective media containing 2% of maltose (SDM), glucose, fructose, galactose, or 1% of maltose with 0.5% 2-deoxyglucose (2-DG) were used. Images were taken after incubation at 30 ˚C for 4-6 days.

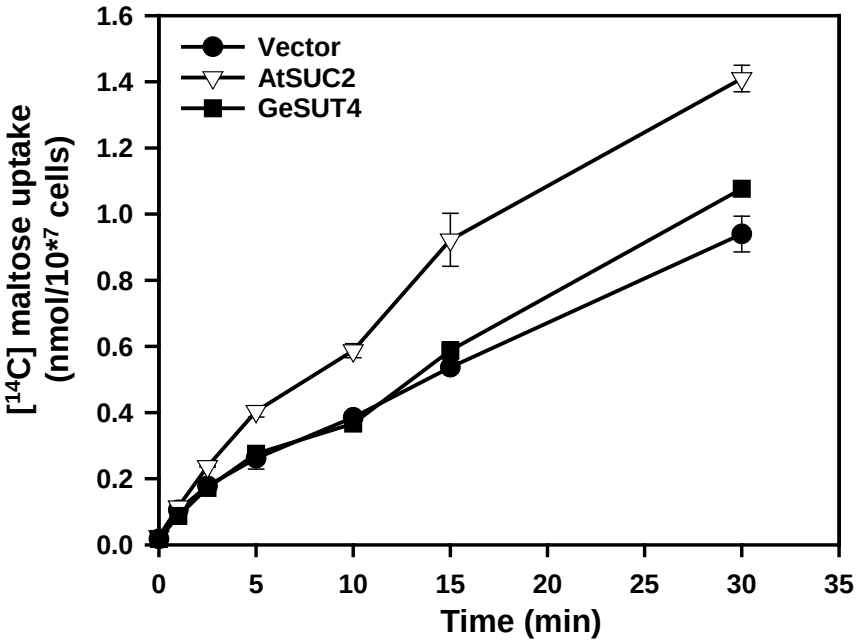


Figure S6. The uptake activity of *Ge*SUT4 to maltose.

YSL2-1 yeast cells expressing *G*eSUT4, or *At*SUT1 or the empty vector were incubated with 1 mM maltose containing 1.5 uCi [^{14}C]maltose. For indicated time period, cells were harvested for radioactivity measurement. Results are mean from two independent colonies.

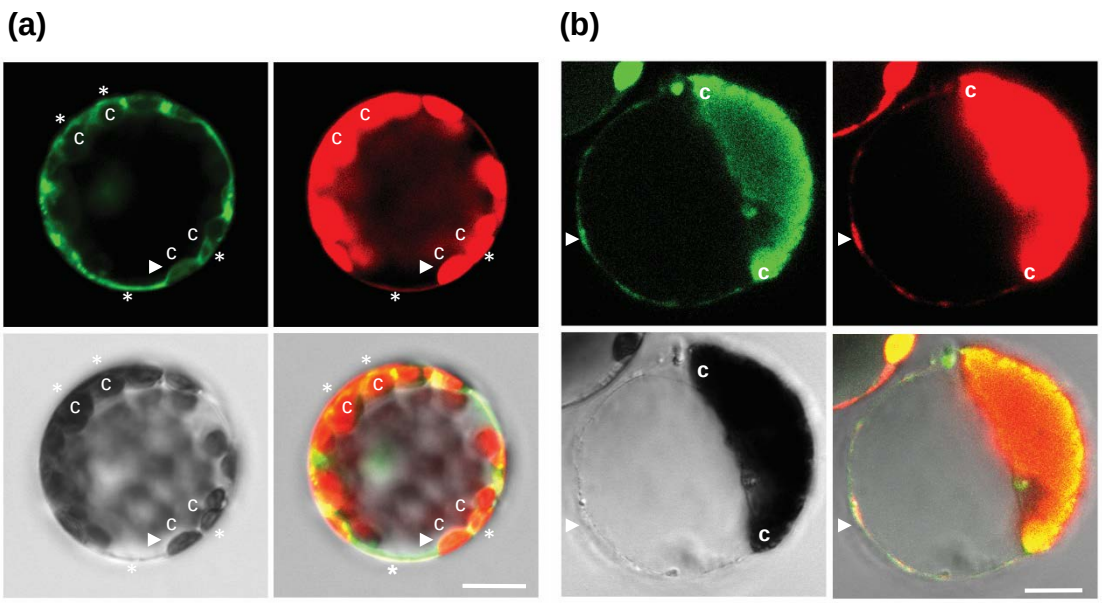


Figure S7. Localization of *Ge*SUT4 expression.

Expression of GeSUT4-GFP fusion proteins in Arabidopsis protoplasts. (a) fluorescence images derived from GeSUT4-GFP fusions, a membrane marker (FM4-64 stain), bright-field and merged signals in a intact protoplast were shown. (b) fluorescence images derived from GeSUT4-GFP fusions, a tonoplast marker, AtγTIP-RFP, bright-field and merged signals in a lysed protoplast were shown. Cells were observed shortly after treated the lysis buffer. Letter (c) indicates locations of chloroplasts. Asterisks (*) and arrowheads indicated merged signals at the plasma membrane or tonoplast, respectively. ales are 10 μm.

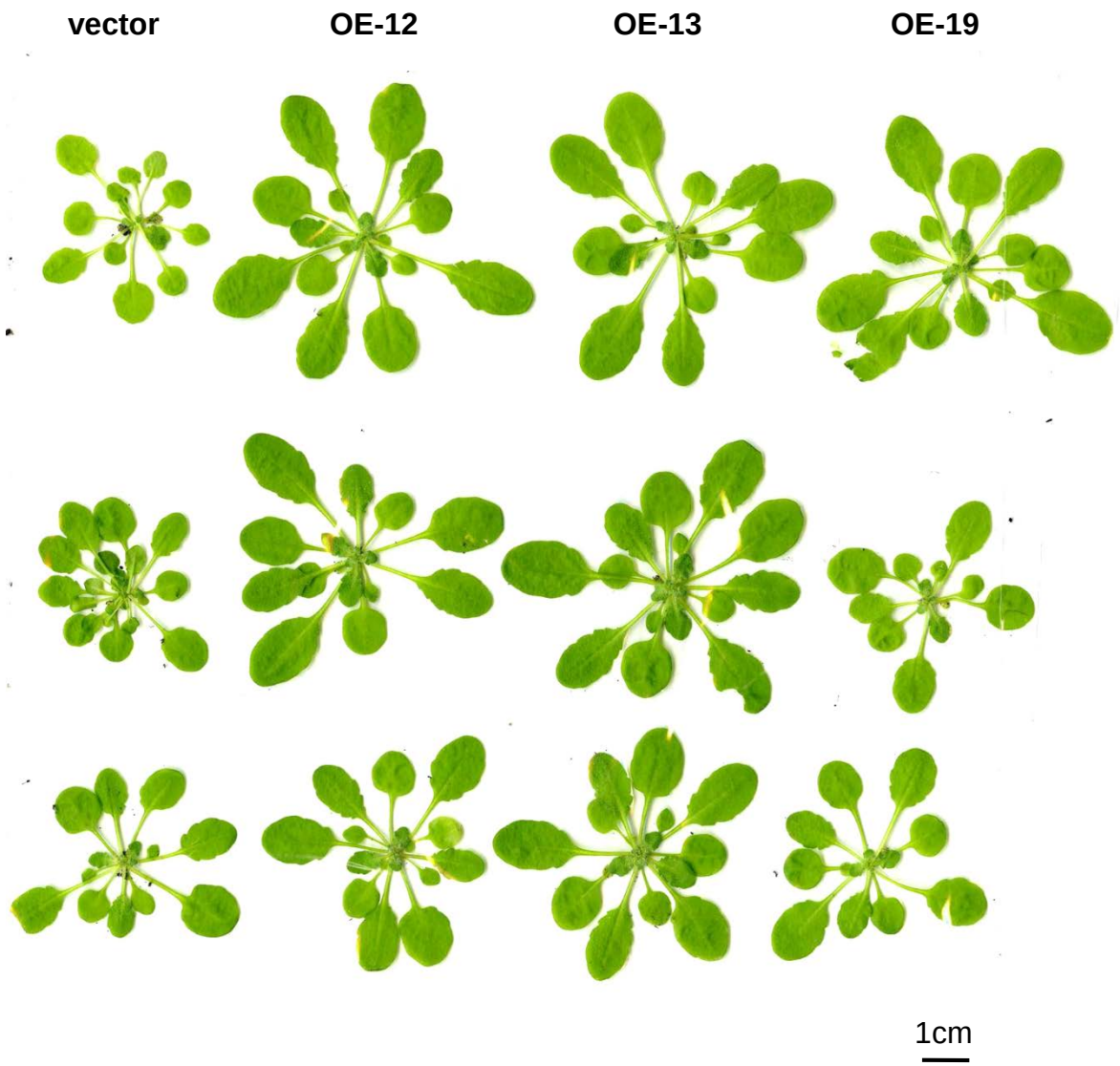


Figure S8. Leaf areas of transgenic Arabidopsis overexpressing *GeSUT4*.

Transgenic seedlings overexpressing *GeSUT4* (OE-12, -13, -19) or the empty vector (vector) were grown on solid selected media for 7 d. Then, seedlings of similar sizes were transferred to soils to grow another 3 weeks. The whole aerial parts from three representative plants were shown.

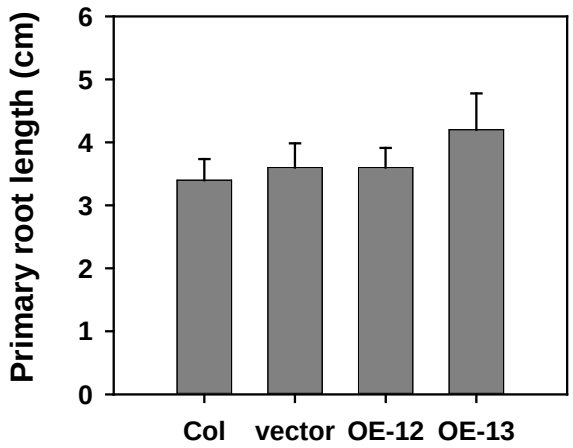


Figure S9. Roots growth of transgenic Arabidopsis overexpressing *GeSUT4*.

Nine-day-old seedlings of Arabidopsis seedlings overexpressing *GeSUT4* (OE-12, -13) or the empty vector (vector) were grown on solid 1/2MS media and pictured before symbiosis analysis. Seedlings from non-transformed wild type (Col) were also measured. Primary root lengths were measured using image J. Results are mean ± SE (n=6).