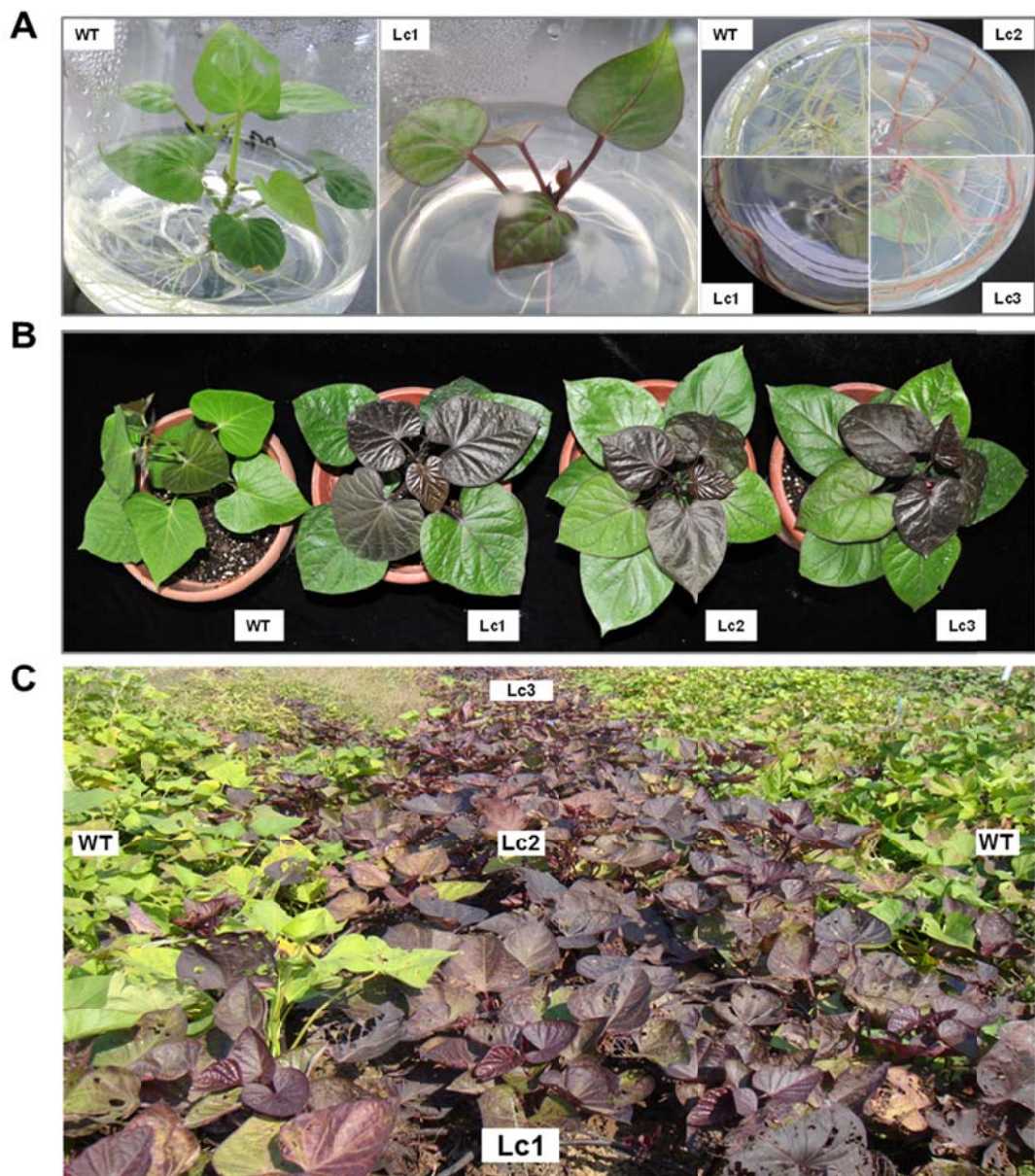


Altered Phenylpropanoid Metabolism in the Maize *Lc*-Expressed Sweet Potato (*Ipomoea batatas*) Affects Storage Root Development. Hongxia Wang, JunYang, Min Zhang, Weijuan Fan, Nurit Firon, Sitakanta Pattanaik, Ling Yuan and Peng Zhang

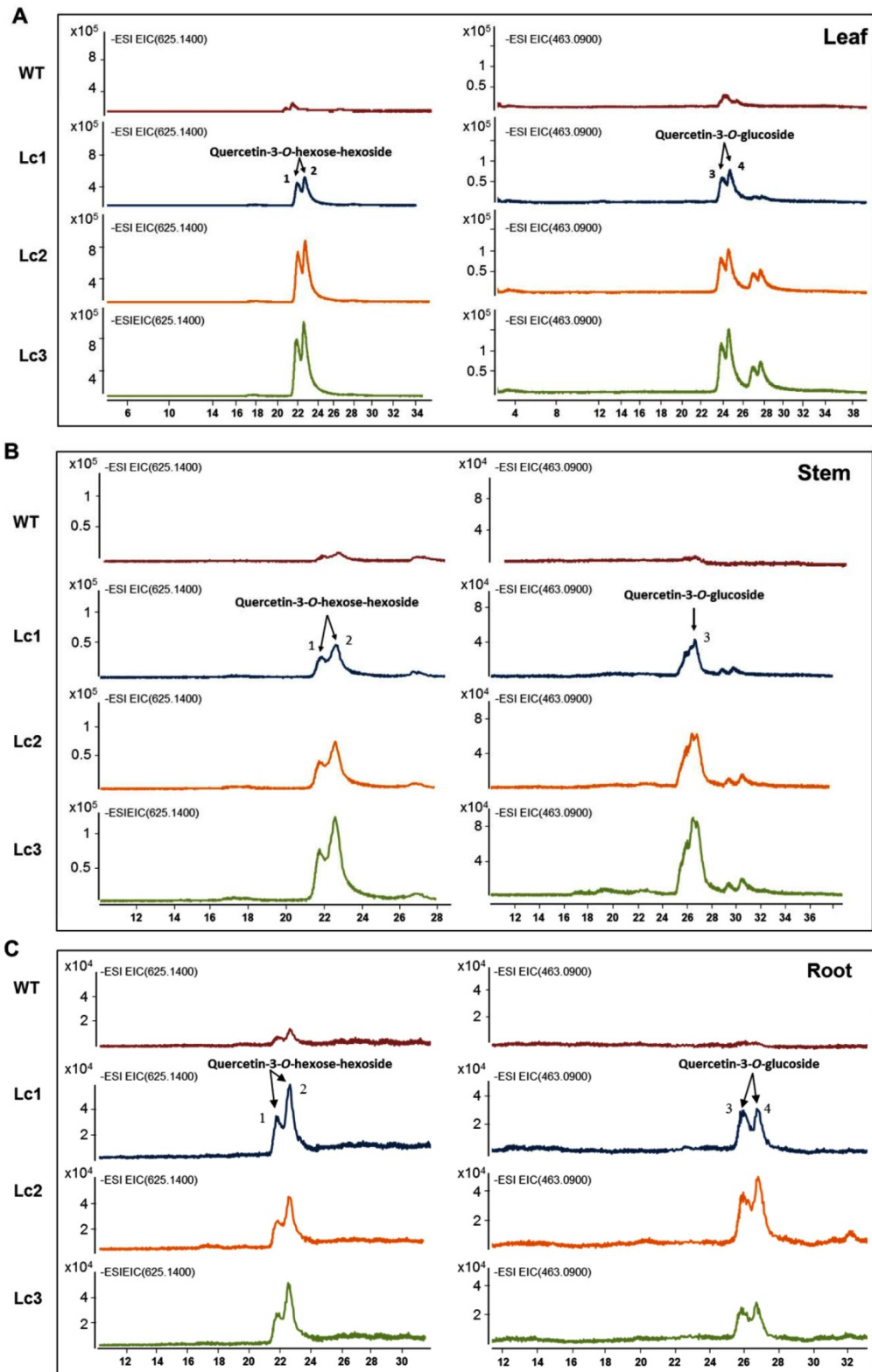
SUPPLEMENTARY INFORMATION

Supplementary Table S1 | qRT-PCR primers for the genes related to the flavonoid, lignin and starch metabolism pathways

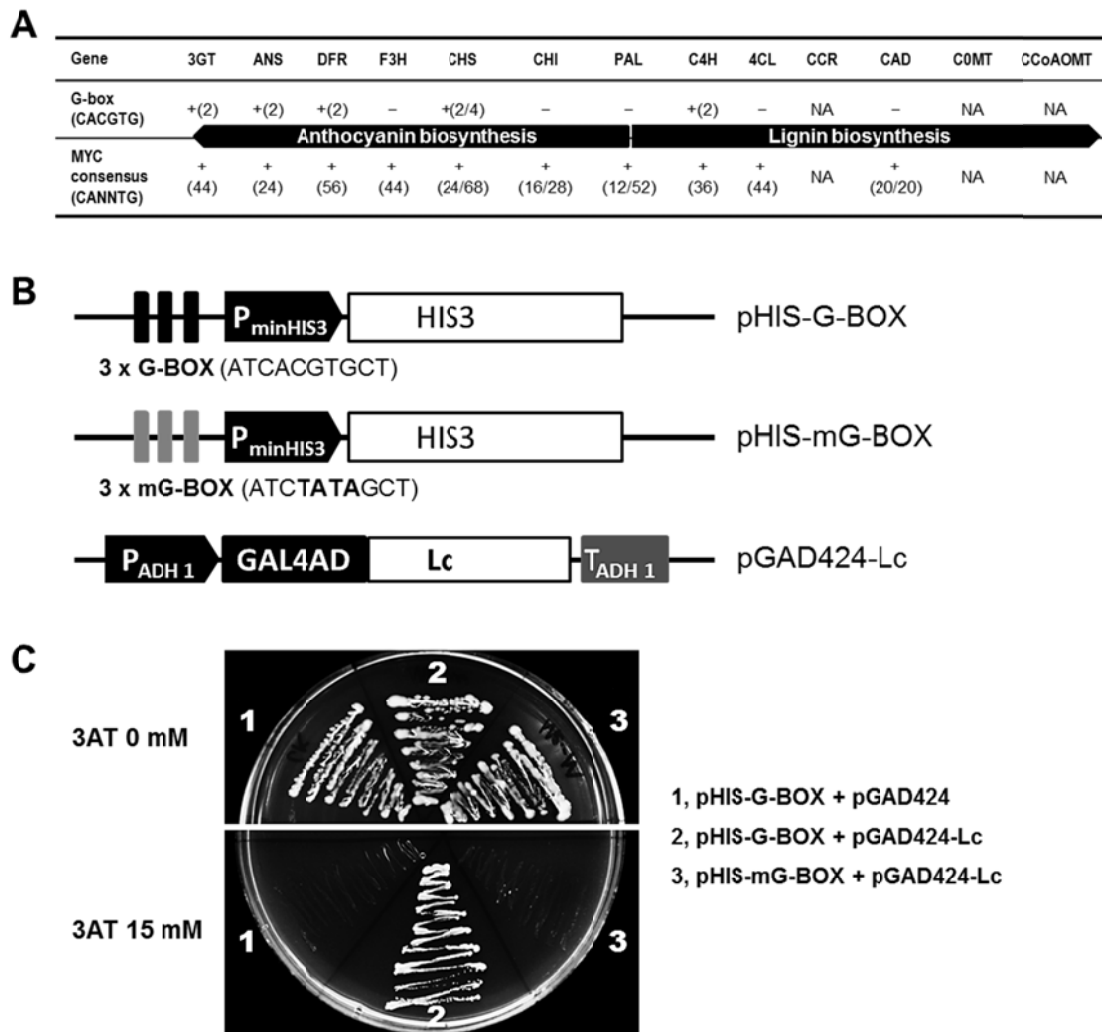
Primer	Forward primer (5'→3')	Reverse primer (5'→3')
<i>qlbPAL</i>	GCGGAGCACGAGAAGAATGT	ATGGCAGGGTTCCGTTCTC
<i>qlbCHI</i>	GCCGAAGTCAAAGTGGAGAG	CGCCTATCGCCGTGAACTTG
<i>qlbCHS</i>	CGCACTTGGATAGCCTGGTC	ATCGGGAGCCAAGGTCTGCG
<i>qlbF3H</i>	CATCGTTTCCAGCCATCTCC	TTTCCGTTACTGCCCTCCAC
<i>qlbFLS</i>	CCTCCTTCTGCGGTGAACTA	CCTGCAGCTTCCTTCAACTC
<i>qlbDFR</i>	TTTATCGGCTCCTGGTTGGT	CGTGTCGGCTTTCCGGTAGTT
<i>qlbANS</i>	GCGTCCCTAACTCCATCATC	AGAACACCGCCCAAGAAACC
<i>qlbGT</i>	CGCCCTAAAAGCCCCATT	CTCACAAAGCAGCCCACAGAT
<i>qlbC4H</i>	TGGTGATTTTCATCCCCATTT	TTTTGCTGGGCTTCAAGAAT
<i>qlb4CL</i>	TATTTTCCGATCGAGGTTGC	ACTTTCCGGCAAATCAAATG
<i>qlbCCR</i>	GCAGAGATAACGGCCAGAAG	TTGCTACAACCCACCATCAA
<i>qlbCAD</i>	AGCTGGTAATGGTTGGCATC	TCCAAAGCCGTGTTGACATA
<i>qlbCOMT</i>	AAACGGGAAAGTGATCGTTG	CCATGATCCAAGTGTTGACG
<i>qlbCCoAOMT</i>	CCGTTCTTGACCAGATGAT	TTCCACAGGGTGTTGTCGTA
<i>qlbAGPa</i>	TCGACGGTGATGTTAGCAAG	AACAGCCTTTGGAGAAACGA
<i>qlbAGPb</i>	GACAAGAACGTAAGGATTGGGA	CGAATGGTTGCTTTCTCCAT
<i>qlbGBSSI</i>	CAGTTGGTTTGCCAGTTGAC	ACGTTGAACTTTGCCACTCC
<i>qlbSBEI</i>	GGTTTACGGGTCTTGATGGA	AACAGCCTGCTATCCCACAC
<i>qlbSBEII</i>	CTTCCCTGAAGCCATAACCA	CCATTTGCCAATCCTCATCT
<i>qlbSS</i>	CGGTTCACTTTGCTTTGTCA	CATTGTGTGGGCGATACTTG
<i>qlba-amlyase</i>	CTGCATTTTTGTTCCCTGCAA	TTCGATGCGTCCAAGTCATA
<i>qlbB-amlyase</i>	AGACTGGAAGGAGGCTGTGA	TGTTGGCTTCTTCGAGGACT
<i>lbactin</i>	CTGGTGTTATGGTTGGGATGG	GGGGTGCCTCGGTAAGAAG



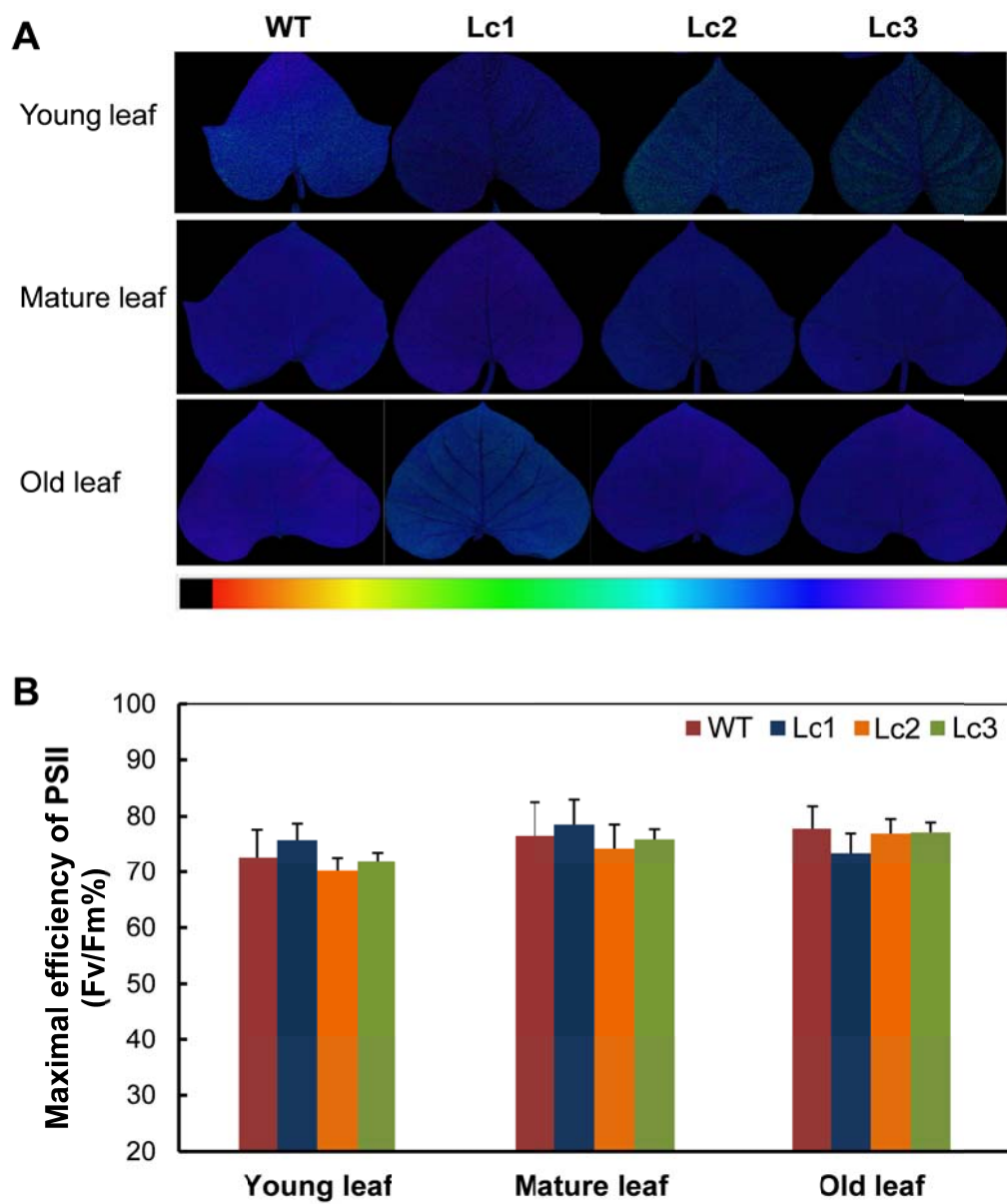
Supplementary Figure S1 | Enhanced pigmentation in Lc transgenic plants. (A) *In vitro* shoot culture. (B) Plantlets in the pots. (C) Plants in field before harvest.



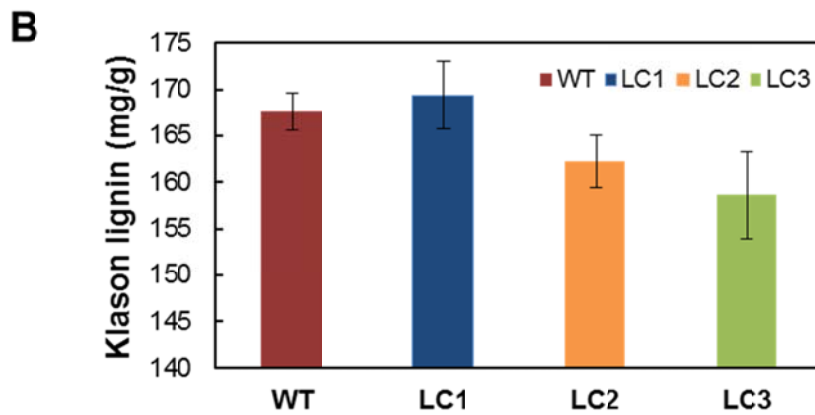
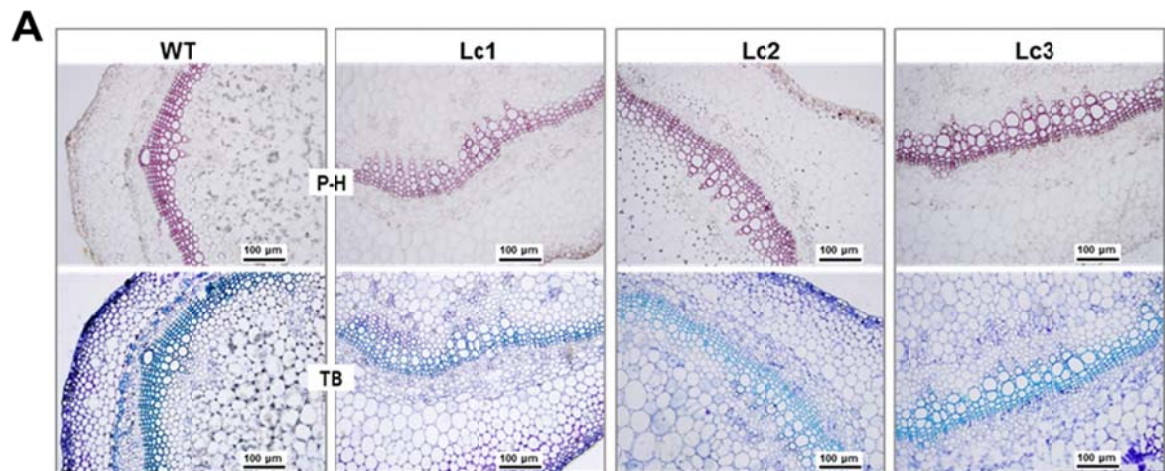
Supplementary Figure S2 | HPLC-MS analyses of flavonols in wild-type and *Lc* transgenic sweet potato. Leaf (A), stem (B) and developing storage root (C) were measured. Quercetin-3-O-hexose-hexoside (molecular weight, 625.14) and quercetin-3-o-glucoside (molecular weight, 463.09) are indicated by arrows.



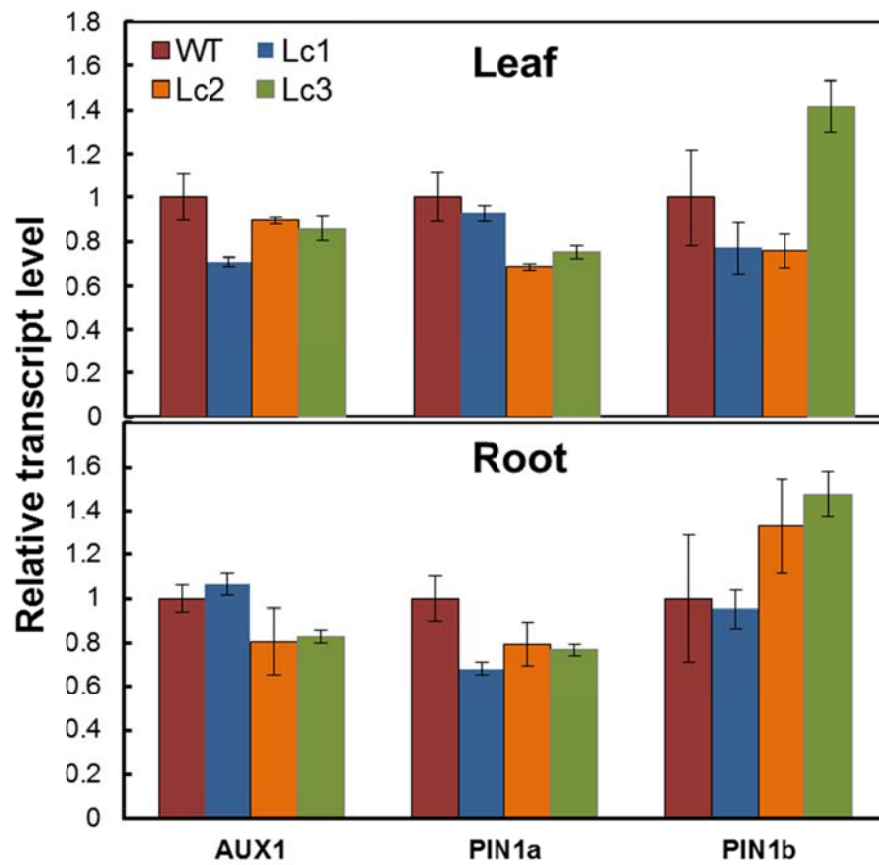
Supplementary Figure S3 | The Lc-binding element G-box and MYC consensus in the promoter regions of sweet potato anthocyanin and lignin biosynthetic genes and G-box binding activity by the yeast one hybrid assay. (A) Promoters containing G-box (5'-CACGTG-3') and MYC consensus (CANNTG) are indicated by "+"; their numbers are indicated within parenthesis and different available homologous gene separated by "/". NA, not available. (B) The bait vector pHIS-G-box and pHIS-mG-box harbor three copies of the regular G-box and mutant (5'-ATCTATAGCT-3') sequences, respectively; the prey vector pGAD424-G-BOX-Lc contains the *Lc* sequence. pGAD424 was used as the negative control. (C) The growth status of the transformed yeast report strain with prey and bait vectors. Only the strain transformed with pHIS-G-box and pGAD424-G-BOX-Lc showed resistance on the SD/-His-Leu plate supplemented with 30 mM 3-amino-1,2,4-triazole (3-AT).



Supplementary Figure S4 | Photosynthesis capacity of young, mature and old leaves in wild-type and *Lc* transgenic sweet potato. (A) Chlorophyll fluorescence. (B) Maximal quantum yield of PSII (Fv/Fm). Error bars represent the SE of three replicates.



Supplementary Figure S5 | Lignin deposition patterns (A) and Klason lignin content (B) in wild-type and *Lc* transgenic sweet potato. Stem sections of 1.5-month-old plants were stained with two dyes, phloroglucinol-HCl (P-H) and toluidine blue (TB). WT, wild type; Lc1–3, independent *Lc* transgenic lines. Error bars represent the SE of three independent replicates.



Supplementary Figure S6 | qRT-PCR analysis of the changes in the transcript levels of genes related to auxin transport in leaves and developing storage roots (S16) of 2-month-old wild-type (WT) and *Lc* transgenic sweet potato. Lc1–3, independent *Lc* transgenic lines. AUX1, auxin transporter protein 1; PIN1a, PIN-FORMED1a; PIN1b, PIN-FORMED1b. Error bars represent the SE of three independent replicates.