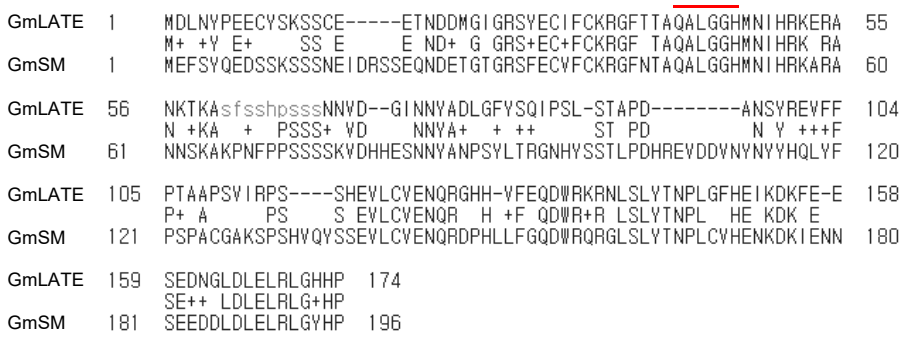


**Fig. S1** BLAST analysis of GmLATE in soybean protein sequence database.
Amino acid sequences of GmLATE were used for BLAST analysis in protein sequence database of *Glycine max*. BLAST was performed in NCBI BLAST tool. Alignment results between GmLATE and GmSM were displayed. Note that identical amino acid sequences were annotated between GmLATE and GmSM sequences. Amino acid sequences which are different between two proteins but are conservative substitutions were marked as "+". The conserved QALGGH motif is marked as a red line.

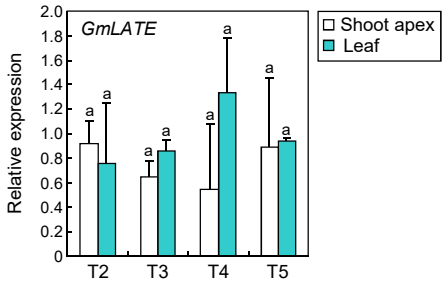


**Fig. S2** Expression of *GmLATE* in leaf and shoot apex.
Leaves and shoot apexes were harvested from the plants developing T2, T3, T4, and T5 leaves. Expression of *GmLATE* was analyzed ($n$ = 3, Tukey's test, $P < 0.05$).

| Primers | Sequences | Usage |
|---|---|---|
| GmSM SnaBI F | 5′-ccgtacgtaTCCAACCTCCTTCTTCGAGT | Cloning & RT-PCR |
| GmSM SnaBI R | 5′-ccgtacgtaGATGACCCCGTTGGTTTTCC | “ |
| GmLATE SnaBI F | 5′-ccgtacgtaACAAGCCTTAGGTGGACACA | “ |
| GmLATE SnaBI R | 5′-ccgtacgtaCTAATAACACTTGGTGCAGCGG | “ |
| GmPDS SnaBI F | 5′-CCGTACGTAATAACTGGAAAGG | “ |
| GmPDS SnaBI R | 5′-CCGTACGTAAACCAACTCTAAC | “ |
| Nb Actin F | 5′-TGGACTCTGGTGATGGTGTC | RT-PCR |
| Nb Actin R | 5′-CCTCCAATCCAAACACTGTA | “ |
| GmLATE F | 5′-GCCTTCTTCCCATGAGGTTTTG | RT-qPCR |
| GmLATE R | 5′-ATGACCAAGCCTCAGCTCCAA | “ |
| GmCOL1 F | 5′-TGTTGCTACTACTACGGACCAT | “ |
| GmCOL1 R | 5′-GAAACTGAAACACTTTGATTAACA | “ |
| GmCOL2 F | 5′-CCTAACACCAATAACAATAACA | “ |
| GmCOL2 R | 5′-GATCAGTAGTAGCAGCAG | “ |
| GmCOL13 F | 5′-AACACAACCAACCACAAGATAAGC | “ |
| GmCOL13 R | 5′-GGGAGAATCAAGAGTGCCAACG | “ |
| GmCOL5 F | 5′-CCACTAACTTGCTGCCACGATG | “ |
| GmCOL5 R | 5′-TGGAGGAAGAGAAGTGAGTGTGAG | “ |
| GmFTL2 F | 5′-ATCTCTTCTGTTAATGTACCAAAAGTG | “ |
| GmFTL2 R | 5′-GTGACCCATGAGTGTTATTATATGTAG | “ |
| GmFTL3 F | 5′-GGTTCTGGTGGAAGGAGGTTATAC | “ |
| GmFTL3 R | 5′-ACTACTAAAGAGTGTGGGAGATTGC | “ |
| GmFTL4 F | 5′-GGACAGAAGCAAAATTAAAGCAGATG | “ |
| GmFTL4 R | 5′-ACTATATACTATGATGTTTGTGTTTGGG | “ |
| GmFTL5 F | 5′-GCGACAAGCACAAGCGATTC | “ |
| GmFTL5 R | 5′-TGTTATGACACCAACTATGATGAGG | “ |
| GmACT11 F | 5′-CGGTGGTTCTATCTTGGCATC | “ |
| GmACT11 R | 5′-GTCTTTCGCTTCAATAACCCTA | “ |

**Table S1** Primers used in this work.
The primers used were designed using the NCBI primer blast (https://www.ncbi.nlm.nih.gov/tools/primer-blast). F, forward primer; R, reverse primer. Note that RT-qPCR primers for *GmCOL* and *GmFTL* genes were previously reported (Fan et al., 2014).