

Table S1 Primers used in this study.

Name	Sequence (5'-3')
SIEGY2-AF	GTCGACATGAACATAACCGGCGGTTCT
SIEGY2-AR	TCTAGACTAGAGAGCAGGTTGATTAGA
SIEGY2-GFP-F	GGTACCATGAACATAACCGGCGGTTCT
SIEGY2-GFP-R	TCTAGAGAGAGCAGGTTGATTAGAGA
SIEGY2-qRT-F	CAGGAGAGCTTGATGGTGGT
SIEGY2-qRT-R	ACTTCTTCTGATAGTGGAGC
EF-1 α -F	GGAAGTTGAGAAGGAGCCTAAG
EF-1 α -R	CAACACCAACAGCAACAGTCT
35S	GACGCACAATCCCACTATCC

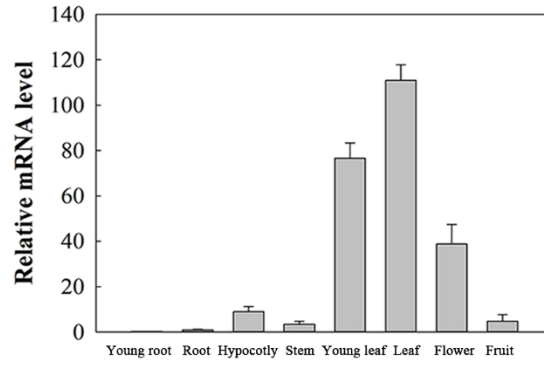


Figure S1. The expression level of SIEGY2 in different tissues.

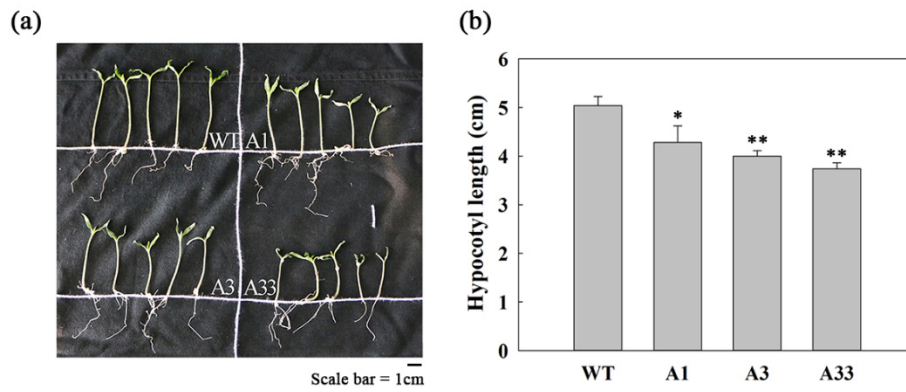


Figure S2. The phenotype of WT and AS young seedlings. The phenotype of hypocotyl (a) and the statistical analysis of the length of hypocotyl (b) in WT and AS lines.

AtEGY2.seq	MNLAVASFRGNFGVLSQCSSCCSLQFQPFVPAATSSLNHGQ	40
SlEGY2.seqMNIPAVLPCSEN	13
Consensus	a f	
AtEGY2.seq	TGTSRRKKDKIERVERKRETLVRVTETQTEFGNDDN	80
SlEGY2.seq	LQCSTPPAHLIRLVIRKKGRILWCRLSHDNNKEDDSVQDN	52
Consensus	s l l v r k l v e dn	
AtEGY2.seq	KEGKESSADDEPTKIPTLNSQSTVWNEAFGNEENKACF	120
SlEGY2.seq	NNNSHQDNDCLENTSLENN.DGPQINGLTGFEDDTDCL	91
Consensus	d p e n n g e q	
AtEGY2.seq	SSQDGDKLEVSSGSPLPGVNVSIHVIYKDDSIMFSGCL	160
SlEGY2.seq	ASE.....SPLPGV.....	100
Consensus	s splpgv	
AtEGY2.seq	SFIKSCCECHQLDDSMRLPKETIILRGQVFGFDTFFVT	200
SlEGY2.seqKECQLDESIRIPKETVEILRNQVFGFDTFFVT	132
Consensus	p qld s r pkt ilr qvfgfdtffvt	
AtEGY2.seq	SQEPYEGGVLFKGNLRGKPAISYEKIKTRMENNFGDQYKL	240
SlEGY2.seq	SQEPYEGGVLFKGNLRGQPAKTYEKVSKRMQ.....	163
Consensus	sqepyeggvlfkgnlrg a yek rm	
AtEGY2.seq	FLLTNPEDDKPVAVVVPRRSLPETTAVPEWFAAGSFGVLV	280
SlEGY2.seqDDKPVAVVVPRMILCPETTAVPEWFAAGSFGVLV	196
Consensus	ddkpavvvpr l pettavpewfaag fglv	
AtEGY2.seq	ALFTLFLRNVPALQSDILSAFDNIELLKDGLPGALVTALV	320
SlEGY2.seq	TVFTLFLRNVPALQSNFLSVFDNIELLKDGLPGALMTAFL	236
Consensus	ftlflrnvpalqs ls fdnl llkdglpgal ta	
AtEGY2.seq	LGVHELGHILVANSIGIKLGVEFVPSWQIGSFGAITRIK	360
SlEGY2.seq	LGVHEVSPRLVATEVGIKLSIFVPSWQIGCFGAITRIL	276
Consensus	lgvhe h lva gikl p fvpwqig fgaitri	
AtEGY2.seq	NIVAKREDLLKVAAAGPLAGFSTGILFLIGLFVPPSDGI	400
SlEGY2.seq	NVVPNRREDLLKVAAAGPLAGFCVGFILLISGFMLIPSDGI	316
Consensus	n v redllkvaaagplagf g il l g ppsdgi	
AtEGY2.seq	GVVVDASVFHESFLAGGIAKILGLDALKEGTSISLNPLVI	440
SlEGY2.seq	GIIIVDFSVFHESFLAGGIAKILGLVILQEGSPISVPLVI	356
Consensus	g vd svfhesflaggiakl lgd l eg is plvi	
AtEGY2.seq	WAWAGLLINGINSIPAGELDGGKIAFSIWGRKTATRTGA	480
SlEGY2.seq	WAWAGLVININSIPAGELDGGRIAFAMWGRKASARISAL	396
Consensus	wawagl in insipageldgg iaf wgrk rl	
AtEGY2.seq	SIALLGLSALESDVAFYWVVLIFFLQRGPIAPLAEDITVP	520
SlEGY2.seq	SIGLLGICSLENDVAFYWVVLIFFLQRGPIAPLSEEVTHP	436
Consensus	si llg lf dvafywvvlifflqrgpiapl ee t p	
AtEGY2.seq	DDKYVSLGILVLFISLLVCLPYPFETGNEAMMIG	555
SlEGY2.seq	QNKYMALGVVLFILGLLVCLPYPFESNQPAL...	468
Consensus	ky lg vlfl llvclpypf f a	

Figure S3. Amino acid sequence alignment of AtEGY2 and SlEGY2.