

Supplementary data

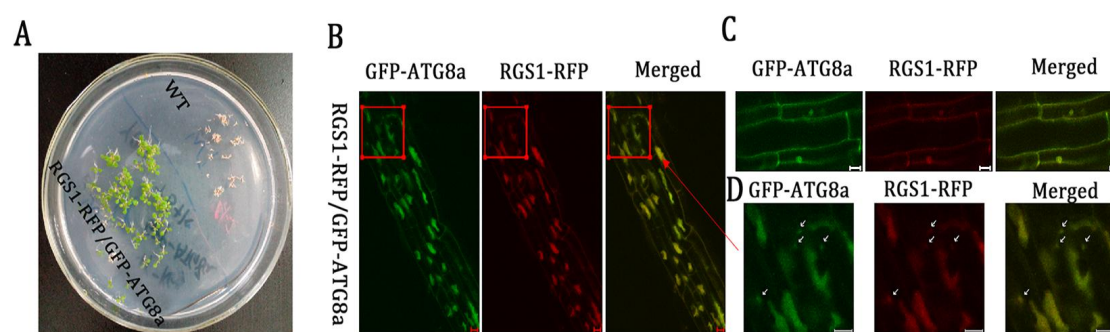


Figure S1. (A) RGS1-RFP/GFP-ATG8a were screened in Kan (100 $\mu\text{g/mL}$) and Basta (10 $\mu\text{g/mL}$) medium, and the WT was used as a control. (B) RFP-RGS1/GFP-ATG8a dark after starvation treatment for 24 h, 1 μM CA for 12 h, 6% glucose stress treatment for 30 min. (C) Normal seedlings. (D) an enlarged view of the red box mark. At least three independent experiments were performed. Scale bar = 10 μm

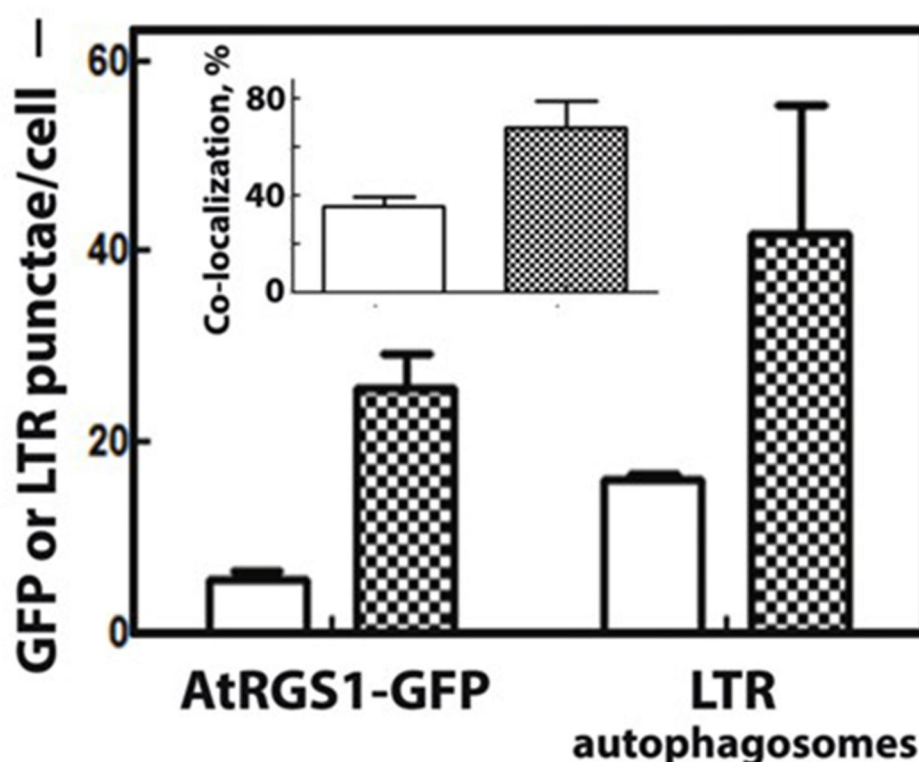


Figure S2. Quantification of (C) and (D) in Figure 4. The results showed that NtRGS1 and LTR co-localization of starvation is higher than that of normal growth conditions. (C) under MS 3% sucrose 5 days, and add 1 μM CA for 12 h (control). (D) RGS1 MS 3% sucrose 3 days, and starvation 2 days, and add 1 μM CA for 12 h (starvation).

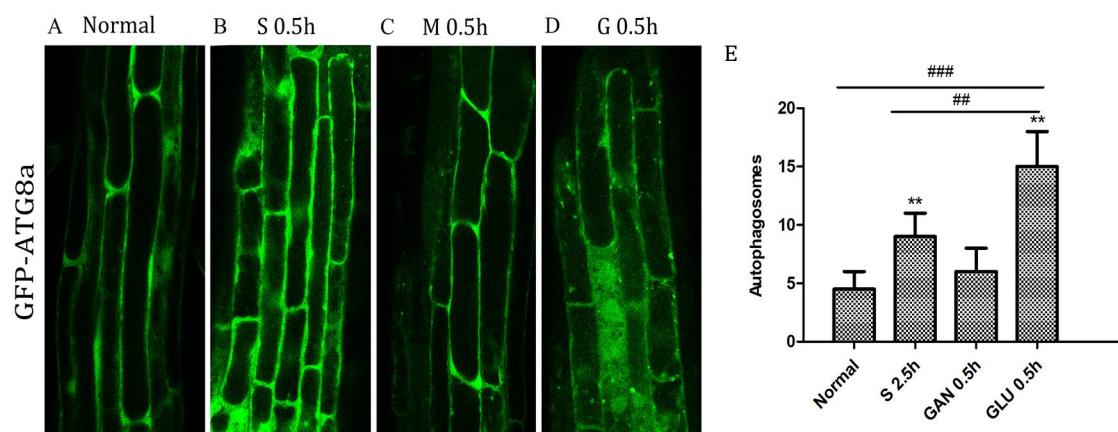


Figure S3. The observation utophagosomes. Autophagosomes labeled by GFP-ATG8a in roots of GFP-ATG8a plants with incubation in 1 μ M CA for 12 h. **(A)** Normal seedlings. **(B)** Starved seedlings treatment for 2.5 h. **(C)** Mannitol seedlings treatment for 0.5 h. **(D)** Starved seedlings treatment for 2 h stimulated by 3% glucose treatment for 0.5 h. **(E)** Quantification of the GFP-ATG8a-labeled autophagosomes per cell. roots at the indicated times was used to calculate the autophagic activity. The mean and S.D. values were calculated from roots of six seedlings per time point. Results in three parallel experiments were used for the quantification. The asterisks indicate significant differences from the starved seedlings treated with glucose for 0 h. Scale bars =10 μ m (** $P < 0.01$; ## $P < 0.01$ or ### $P < 0.001$)

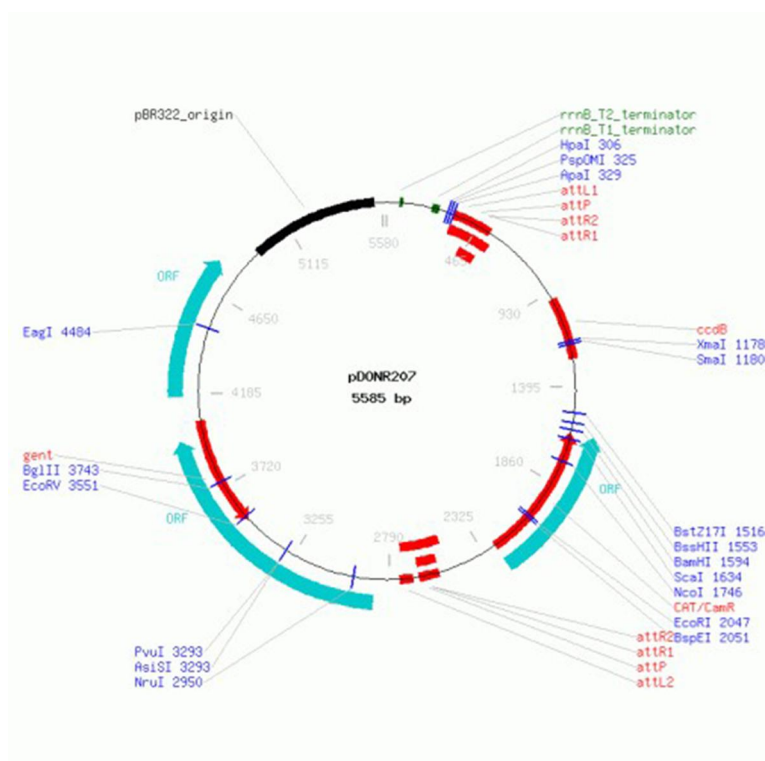


Figure S4. Vector pDONR207

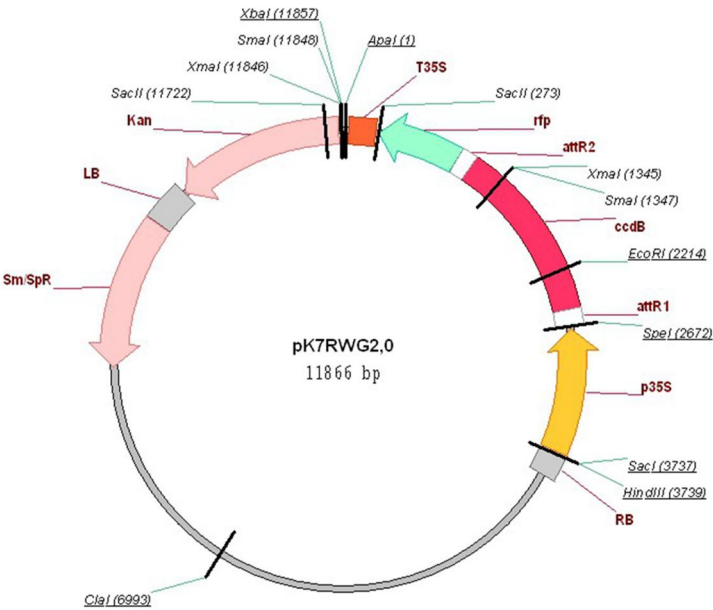


Figure S5. Vector pK7RWG2

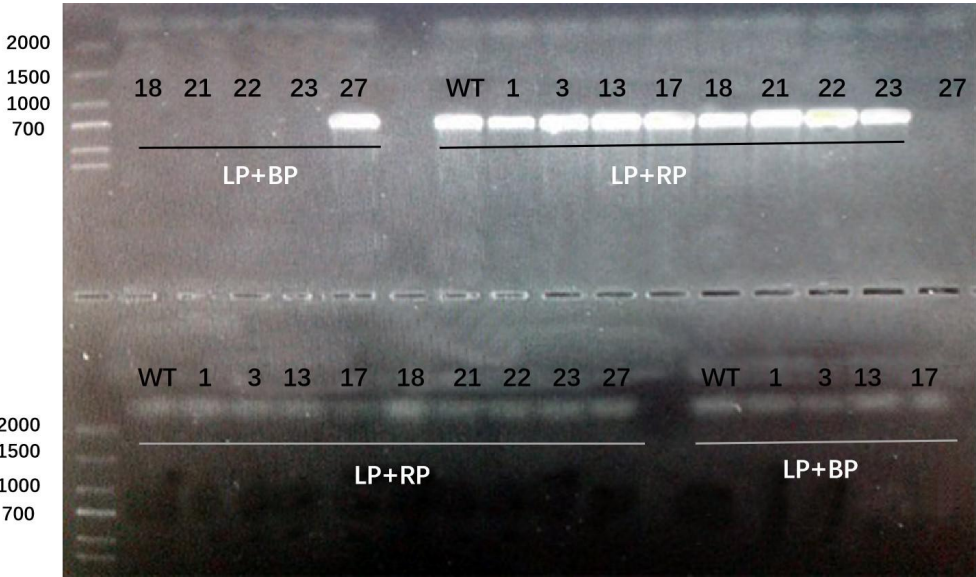


Figure S6. 1% agarose gel electrophoresis was observed and photographed using a gel imaging system. When the LP+BP or RP+BP primers were added, only one lane appeared as a homozygous mutant, as shown in Figure No. 27. The numbers are plant code, LP: insert left gene primer; RP: insert gene right primer; BP: insert gene primer. Maker: DL2000 Marker (TaKaRa) *rgs1* Primers

LP: TGTTGATGAAAAGCCTTAGCG

RP: TAGCTGCTACGCTGGAGAAAC

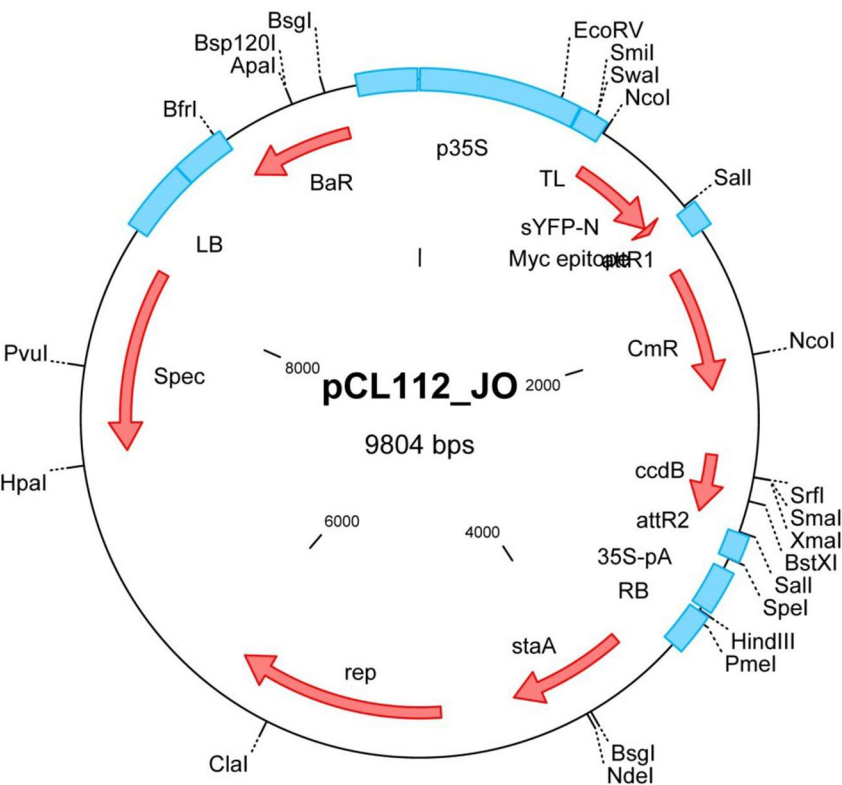


Figure S7. Vector pCL112_JO

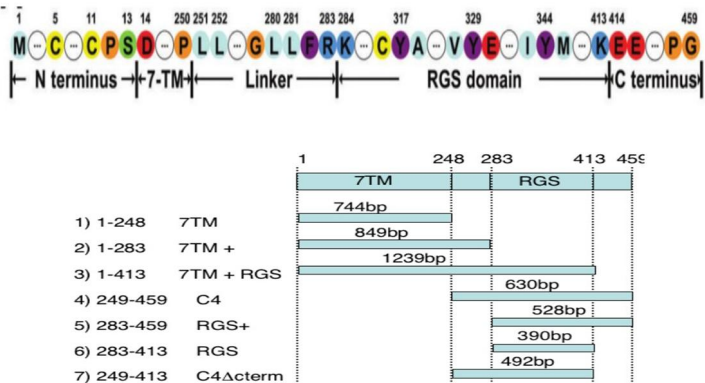


Figure S8. Domain structure of the RGS1 protein, NtRGS1 is expressed under 35S promoter in our constructs. The gene was cloned from BY-2 cDNA incl. 12 bp, of Kozak sequence in order to make the expression smoother. The following is the sequence of the construct

GGAGAATAAATTATCGCAGCTTGTC

TAGCAAAGGAGGGTGTCCAAGCGACTATATGGCGCTTTCAATTGCCGTAGTGCCATGATCTTACTTCTC

CTGAAAGCGA

CATTACCATACCTGATTCACAAGATTCCGAGGCCCAAAGGCAGTAGCTTTTGGCTTGTTGGCAATTCAAG

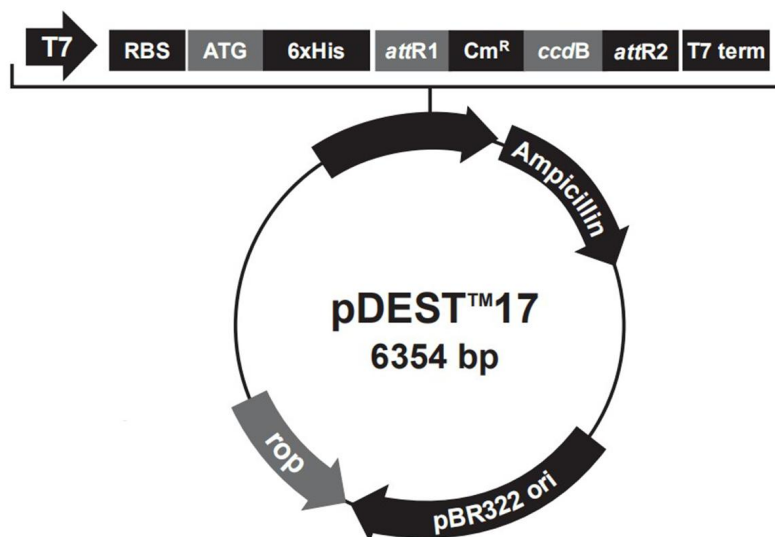
TTCTAGCAAGC

TTCAATCTGTTGTTGTCAATTGTGATAGCTCTCAATTTCTAAAGTTCAGAAAGAGACATTGGTGGAGGT

CTTGCTATCT

TTGGGCAGTCTGGATTGAAGGTCCACTCGGATTGGTTTGCTGTTGAGCTGCCGTATTACACAGATATTC

46 CAACTATATT
 47 ATATATTTGTGAAGAGACGTCTGCCACCAATTAGATCCTATATTTTCTTTTCGCTGATTCTCTTGCCGTGG
 48 ATAGCTAGT
 49 GCTGCCTTTTATTCATATAAGAAAGCCTCTAAATTACCGATGTCACATGGGGACTGTGTGGATCATCCCTG
 50 TTATGGGCCT
 51 TCATGCATTATATGTTGTAGCTTTGATTGCTTTTACTGGGGCTGTGCGTCATGTGGAATTCAGATTTTCATG
 52 AACTCAAAG
 53 ACCTTTGGAGAGGAATTCTTGTATCTGCAGCTTCCATTGGAATTTGGGTGGCTGCTTATGTTATGAATGA
 54 AGTTCGCGAG
 55 GATATATCATGGCTAGAAA
 56 TTGCCTCTAGATTTTTGCTATTGGTTATGACAAGTGTCCTTGTGCTGGCATTCTTCTCTT
 57 TCTCAATTTCTCAACCTCTTATCTCACTTATGAGCTTGAGGAAGAAGGATCATAAGGAGT
 58 ACAAGACAATGAGCCAGGCATTAGGCATACATGATAGTGGGATTCATCTACAGAGGGAAC
 59 CGATAAGCATTATAGATCCAGATGAACCTTTGGATAAGCTCCTGCTGAACCGAAGGTTCC
 60 GGCAGTCCTTCATGGAATTTGCAGACAGTTGTTTGGCTGGGGAGAGTGTCATTCTCTATG
 61 ATGAAGTGCAACAGTTTGATAAAATTCCTATTCAAGATCCAGTTAGGAGAATTTACATAG
 62 CGCGCCACATAATAGAGAAGTATATAGCTGCAGGAGCACCAATGGAGGTGAACATTTCTC
 63 ACAGAATTCGGCAGGAAATTTTGAGTACTAATGATCTCTCCATACTAATCTCTTCAAAA
 64 ATACTCTAGGTGAACTGATGCAGCTGATGAACTGAATTTAGCAAAGGATTACTGGTCAT
 65 CGATATATTTTCATGAAGCTGAAAGACGAGGTCAGTATGAGAACAGTTGATCATGAGCTGG
 66 AACATGCTAGCGGTTGGAACTTTTCTCCAAGATTGAGTTCTGTCCATTGTAGTGATGACC
 67 CTTTTCAGCATGAACATAGCCCCAGGTATTCTGCTTGCCATAGTCATGATTCAAAACTGC
 68 AATCTGAATTCGTCGACAAGCTTATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGG
 69 ...GFP to be continued
 70 Kozak sequence
 71 ATG-NtRGS start
 72 TCT-NtRGS stop
 73 GFP
 74 pENTR RGS pieces-BY-2
 75 *Nicotiana tabacum* NtRGS1¹⁻²⁴⁸(7TM), NtRGS1²⁴⁹⁻⁴⁵⁹(RGS domain), NtRGS1²⁴⁹⁻⁴¹³(RGS domain not included C
 76 terminus)



77

78 **Figure S9.** Vector pDEST17

79 **SVideo.**