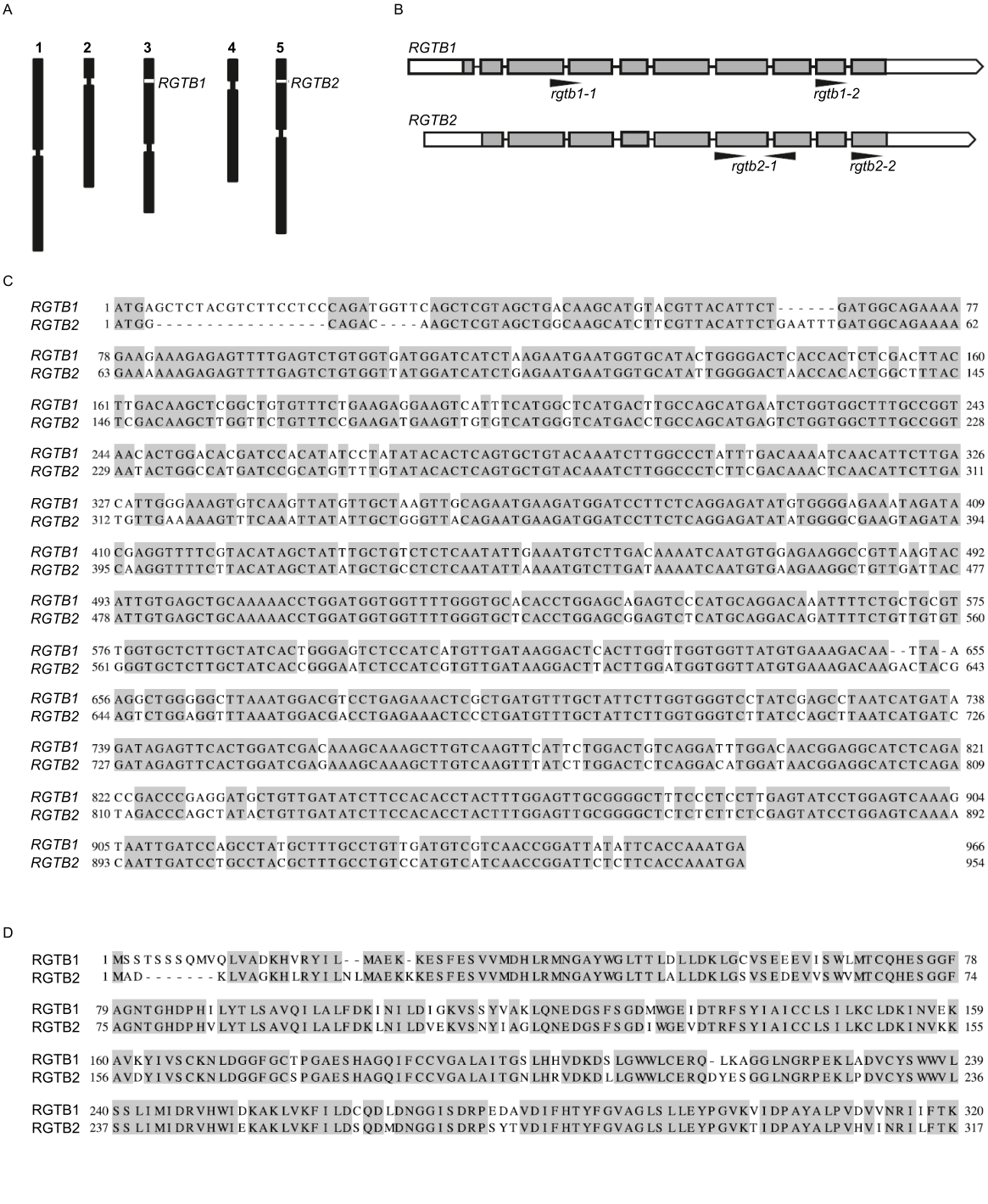
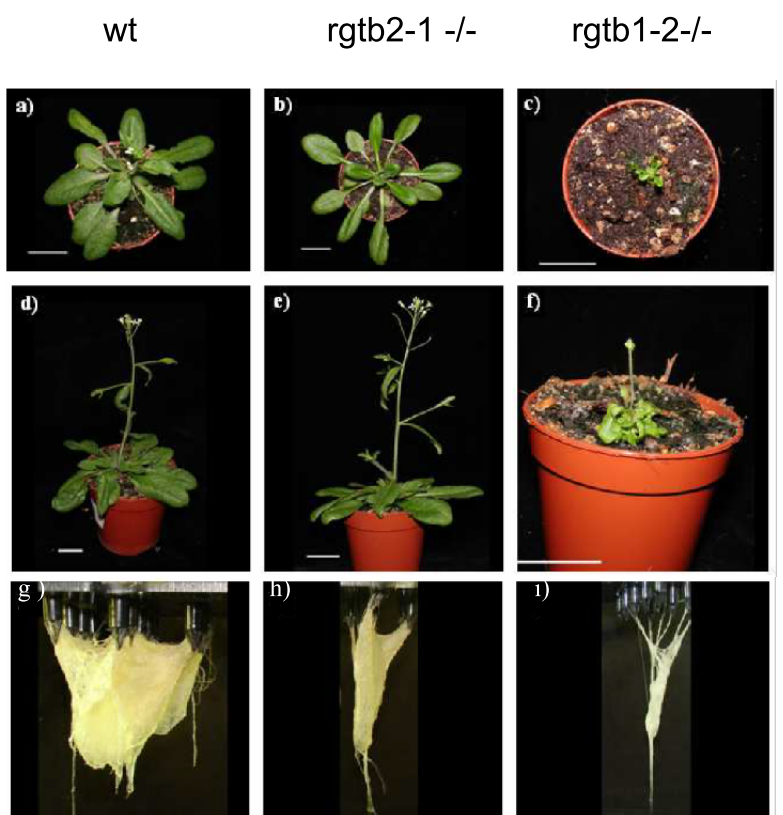


Comparison of AtRGTB subunits. A) chromosomal location of AtRGTB genes, B) gene structure and location of inserts in corresponding SALK lines, C) comparison of nucleotide and D) aminoacid sequences of AtRGTB. Homology regions are shaded.

Amino acid and nucleotide sequence analysis and insert positioning

AtRGTB1 and AtRGTB2 nucleotide sequences, NM_121259 and NM_180236, respectively, were derived from the EMBL server. Corresponding amino acid sequences, NP_568259 and NP_850567, respectively, were derived from the PDB server. Alignments were performed with the T-coffee (http://www.ebi.ac.uk/Tools/msa/tcoffee) and visualized with Jalview. DNA obtained from genotyping PCR reaction of each mutant line was sequenced from the Lbb1.3 primer (http://oligo.ibb.waw.pl). Results of the sequencing were aligned with genomic sequence of the AtRGTB1 and AtRGTB2 genes with the EMBOSS program (http://emboss.bioinformatics.nl).

Fig. S2



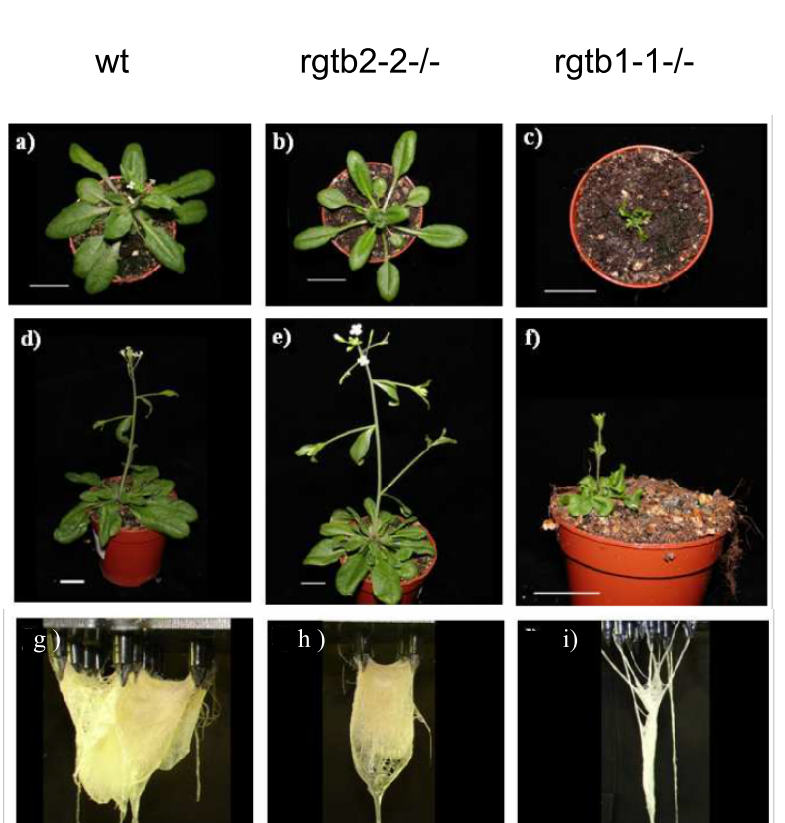


Fig. S2 Morphology of rgtb homozygous mutants. a-c) 4-week old rosette, d-f) 5-week old flowering stem,
g-i) 5-week old root system grown in hydroponics.