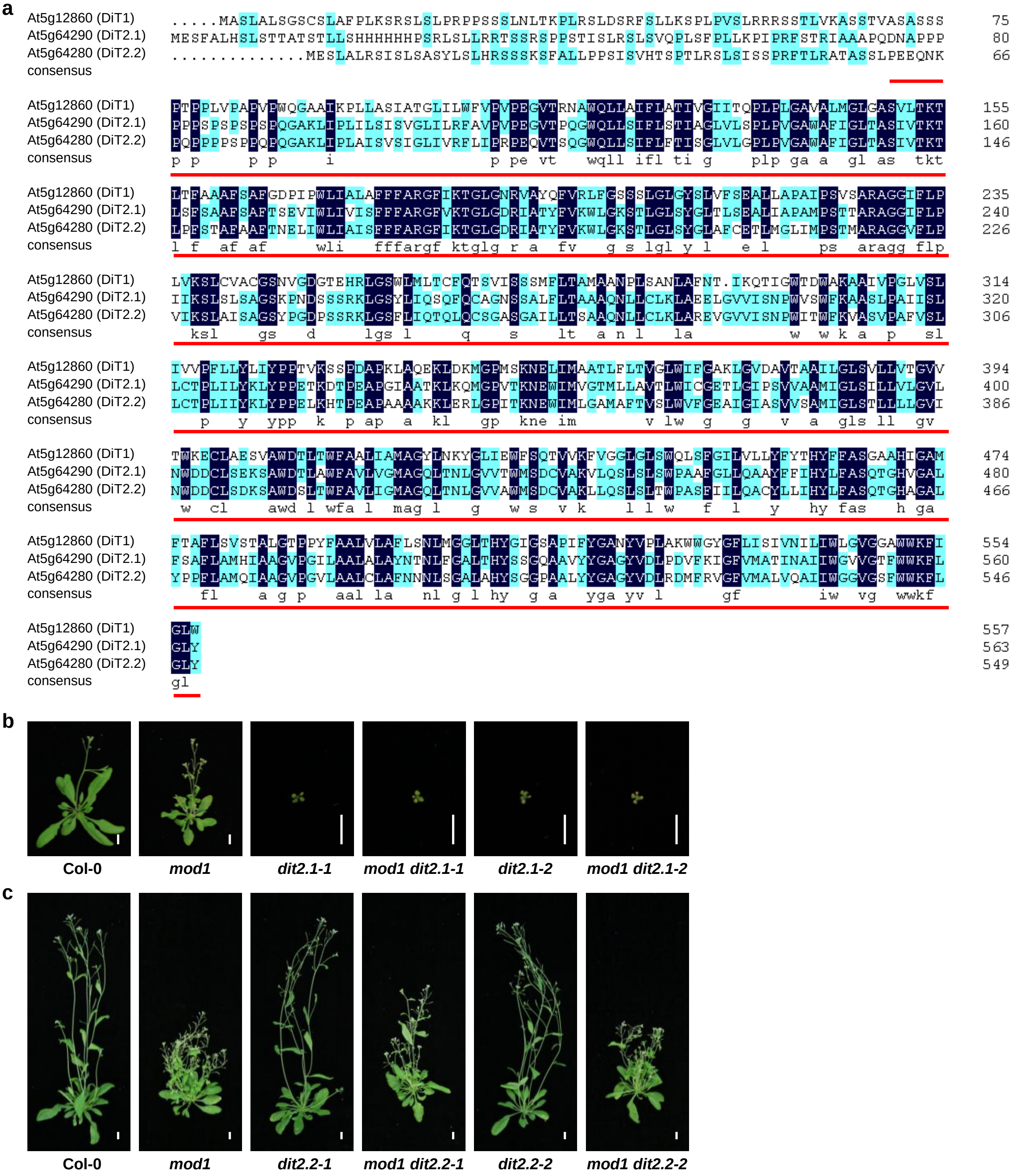

Supplementary information, Figure S7 *dit2.1* and *dit2.2* fail to suppress *mod1* phenotypes.

(a) Amino acid sequence alignments of DiT proteins in *Arabidopsis*. The red line indicates the dicarboxylate transporter domain. Dark blue and cyan shading indicate 100% and 67% conserved amino acid residues, respectively. DiT1, At5g12860; DiT2.1, At5g64290; DiT2.2, At5g64280.

(b) Phenotypes of Col-0, *mod1*, *dit2.1-1*, *mod1 dit2.1-1*. *dit2.1-2*, and *mod1 dit2.1-2* at 26 DAG. N663245; *dit2.1-2*, N669411. Scale bars, 1 cm.

(c) Phenotypes of Col-0, *mod1*, *dit2.2-1*, *mod1 dit2.2-1*. *dit2.2-2*, and *mod1 dit2.2-2* at 35 DAG. *dit2.2-1*, N661169; *dit2.2-2*, N655976. Scale bars, 1 cm.