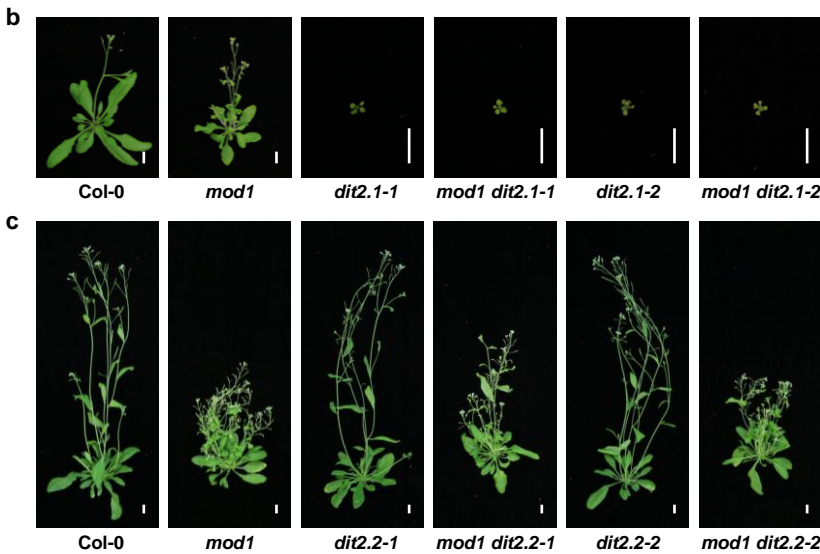


**a**

|                    |   |     |
|--------------------|---|-----|
| At5g12860 (DiT1)   | .....MASLALSGSCSLAFPLKSRSLSLPRPPSSLNLTPLRSLDRSFLSKSPLVSLRRSSSTLVKASSTVASASSS        | 75  |
| At5g64290 (DiT2.1) | MESFALHSLSTTATSTLLSHHHHHHPRLSLLRRTSSRSPSTISLRSLSVQPLSFPLLKPIPRFSTRIAAAPQDNAPP       | 80  |
| At5g64280 (DiT2.2) | .....MESLALRSISLSASYLSLHRSSSKSFALLPSSI SVHTSPTLRSLSSSRPRTLRTATASLPEEQNK             | 66  |
| consensus          |   |     |
| At5g12860 (DiT1)   | PTPEPLVPAFVFWQGAALKPLLASIATGLLILWFVFPVPCVTRNANQLLALFLATIVGITIQPLPLGVALMGLCASVITKT   | 155 |
| At5g64290 (DiT2.1) | PEPSPSFSEFQGAKLIPLLLSISVGLLILRFAMVFPBGVTPQGQQLLSIFLSTIAGLVLSPLPVGAMAFI GLDASIVTKT   | 160 |
| At5g64280 (DiT2.2) | EPPEPSPPEQEGAKLIPLAISVSI GLIVRFLIIRPBCVTSQGWQLLSIFLFTISGLVVLGPLEVGMAMAFI GLDASIVTKT | 146 |
| consensus          | p p p p i p pe vt wql l ifl ti g plp ga a gl as tkt                                 |     |
| At5g12860 (DiT1)   | LTFAAASFAGDPIFNLLIALAFFARGFIKTGLGNRVAYQFVRLFGSSSLGLGYSIVFSEALLAPAI PSVSARAGGFLEP    | 235 |
| At5g64290 (DiT2.1) | LSFSAFSAFTSEVILNLLIVISFFFARGFVKTGLGDRATYFVKWLCKSTLGLSYGLTLSEALLAPAMPSTTARAGGFLEP    | 240 |
| At5g64280 (DiT2.2) | LEFSAFAAFTNELLNLLIALSFFFARGFIKTGLGDRATYFVKWLCKSTLGLSYGLAFCEITMGLIMPSTTARAGGFLEP     | 226 |
| consensus          | l f af af wli fffarf q ktql g r a fv g s lql y l e l ps araqq flp                   |     |
| At5g12860 (DiT1)   | LVKSLCVAAGSNVGDGTEHRLGSWMLLTCFQTSVISSSMFLTAMAAEPLSANLAFNT.IKQTIGWTDMAKAAIVPGLVSL    | 314 |
| At5g64290 (DiT2.1) | IHKSLSLSAGSKENDSSSRRLGSLYLIQSQRCCAGNSALFLTAAACNLCLKLAEEELGVVINSNPVSWKKAASLPATISL    | 320 |
| At5g64280 (DiT2.2) | VHKSLAISAGSYPGDPSSRRLGSEFLIQTLQCCSGASGAILLTSAAACNLCLKLAEEVGVVINSNPITWPKVASVPEAFVSL  | 306 |
| consensus          | k sl gs d lgs l q s lt a n l la w w k a p sl  |     |
| At5g12860 (DiT1)   | LVVPEFLLYLIYPTVWSSPEAPKLAQBKLDKMGEMSKNELIMAATLFLTVGLWIRGAKLGVDAVTAAILGLSVLLVTGVV    | 394 |
| At5g64290 (DiT2.1) | LCTPLLLYKLYPEETRDTEPABGTAATKLRQMGVPTKNEWIMVGTMLLAVTLWICGETLIGIPSWVAAMTGLSLLLVGL     | 400 |
| At5g64280 (DiT2.2) | LCTPLLLYKLYPEELRHTPEAPAAAARKLERLGEITKNEWIMLGAMAFVSLWVPEBATGIASVVSAMTGLSLLLVGLV      | 386 |
| consensus          | p y ypp k p ap a kl gp kne im v lw g g v a gls ll gv                                |     |
| At5g12860 (DiT1)   | TKKECLAE SVAWDTLWFAALIAMAGLNLKYGLTEWFSQTVVRFVGGGLGSLWQLSEGLLVLLYFYTHYEFASGAAHIGAM   | 474 |
| At5g64290 (DiT2.1) | NDDCLSEKSAWDTLWFAVLCMAGQLTNLGVVWMSDCVAKVLQSLSLSWPAEGLLQAAFFTHYLFASQTGHVGCAL         | 480 |
| At5g64280 (DiT2.2) | NDDCLSDKSAWDTLWFAVLLCMAGQLTNLGVVAMSDCVAKLLQSLSLWPAEGLLQACVLLHYLHYFASQTGHACAL        | 466 |
| consensus          | w cl awd l wfa l mag l g w s v k l l w f l y hy fas h ga                            |     |
| At5g12860 (DiT1)   | ETAFISVSTALCTPPYFAADVLAFLSNLMGGLTHYIGSAPIFYGANVYPLAKWNGYGLLISIVNILLWLGCGGANWKF      | 554 |
| At5g64290 (DiT2.1) | ESAFIAMHTAAGVPGILAAALAYNTNLFCAALTHYSSGQAAVYVYAGYVDLEDVFKIGFVMATINAILNGVVTFNWKF      | 560 |
| At5g64280 (DiT2.2) | YPPFLAMQIAAGVPGVLAALCLAFNNNLSGALAHYSGGPAALYVYAGYVDLEDVFKIGFVVMALVQAILNGGCGSPFNWKF   | 546 |
| consensus          | fl a g p aal la nl g l hy g a yga yv l gf iw vg wwkf                                |     |
| At5g12860 (DiT1)   | GLV   | 557 |
| At5g64290 (DiT2.1) | GLY   | 563 |
| At5g64280 (DiT2.2) | GLY   | 549 |
| consensus          | gl  |     |



**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.