

Figure S1. Expression levels for corresponding full-length coding regions for various *OTU* T-DNA insertion mutants. Expression levels of full-length transcripts were examined by RT-PCR in various *OTU* T-DNA insertion mutants and Col-0 (control). The corresponding primer pairs for cloning His-tagged or GST-tagged (for *OTLD1a*) recombinant constructs were used as previously described [9]. The amplification of the *UBQ10*-specific fragment was used as a control with the primer pair UBQ10-5'/UBQ10-3' (Table S4).

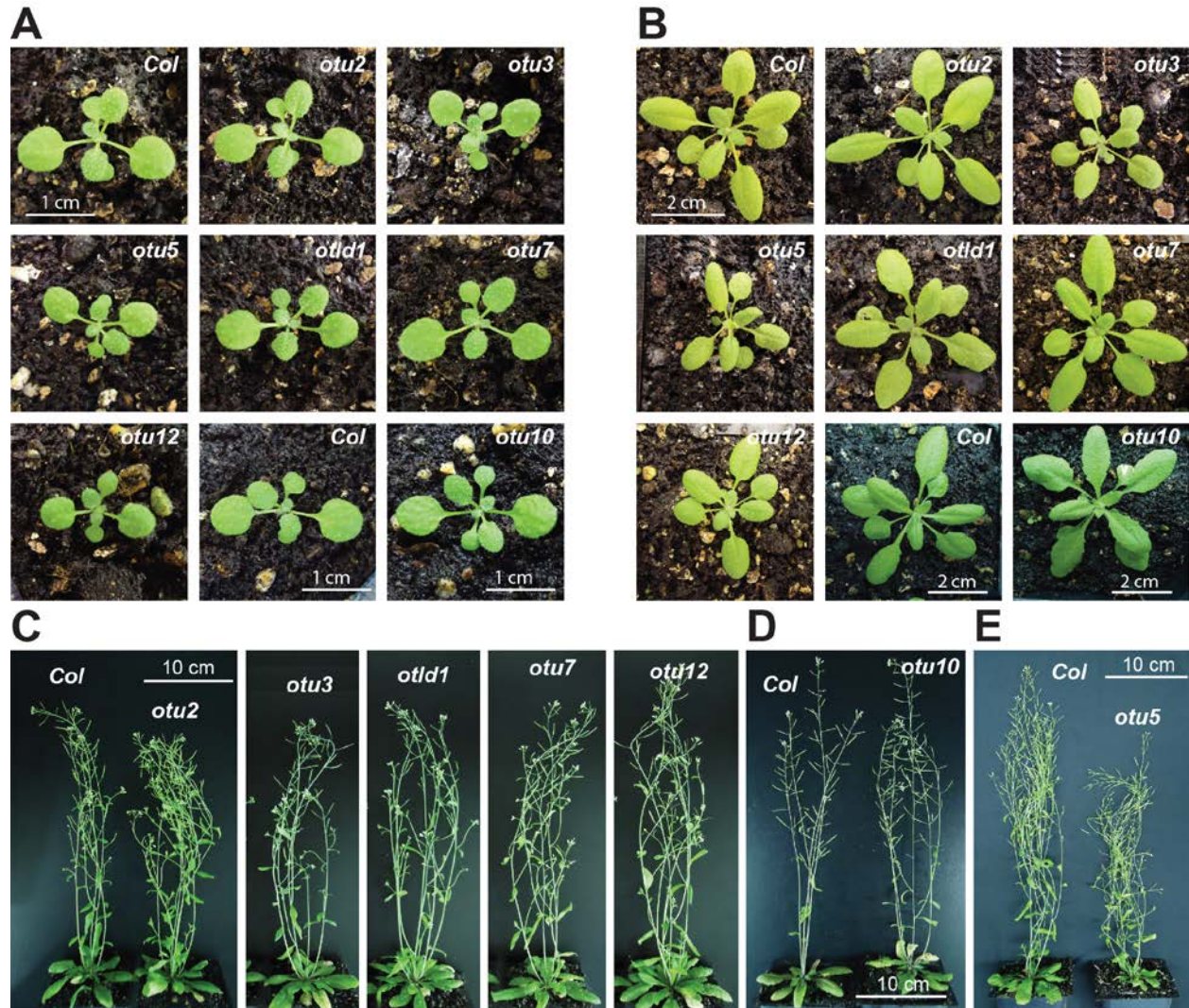


Figure S2. Growth phenotypes at different developmental stages for various *A. thaliana* OTU T-DNA insertion mutants. (A) and (B) Representative plants at 14 (A) and 21 DAS (B) for Col-0 and various OTU mutants: *otu2-1*, *otu3-1*, *otu5-1*, *otld1-1*, *otu7-1*, *otu10-1*, and *otu12-1*. The *otu10-1* and Col-0 plants were from different growth batches (bottom, middle and right panels). (C) to (E) Representative plants at 45 DAS for various OTU mutants: the *otu2-1*, *otu3-1*, *otld1-1*, *otu7-1*, *otu12-1* (C), *otu10-1* (D), and *otu5-1* (E) plants were grown together with Col-0 plants.

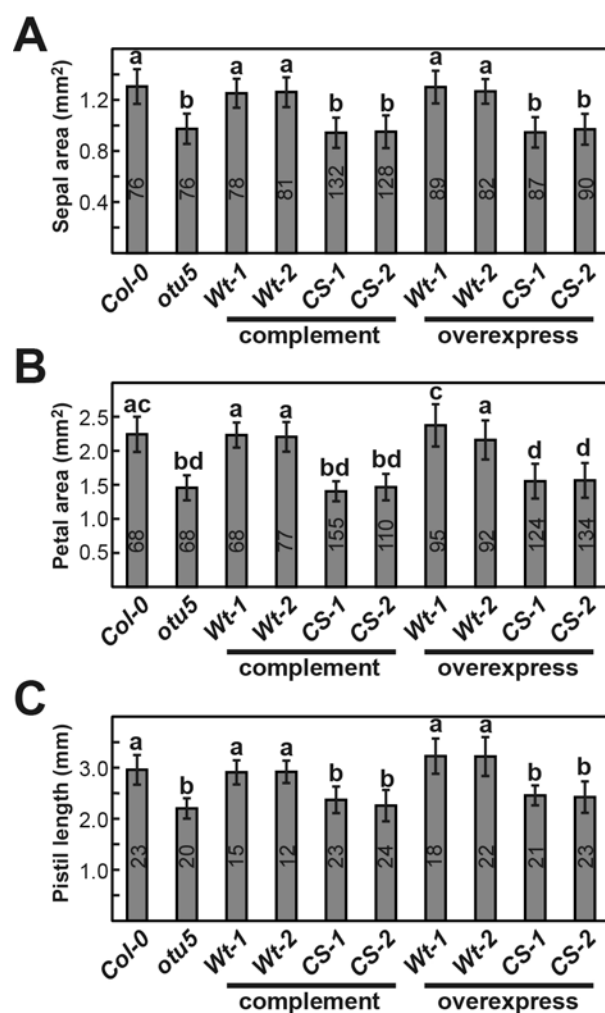


Figure S3. Averaged sepal area, petal area, and pistil length of opened flowers for Col-0, *otu5-1*, and various complemented and overexpressed lines. Averaged sepal area (**A**), petal area (**B**), and pistil length (**C**) for various *Arabidopsis* lines. Numbers of sepals, petals, pistils used for average are indicated. Different letters denote significant difference by pairwise comparison using Student's *t* test.

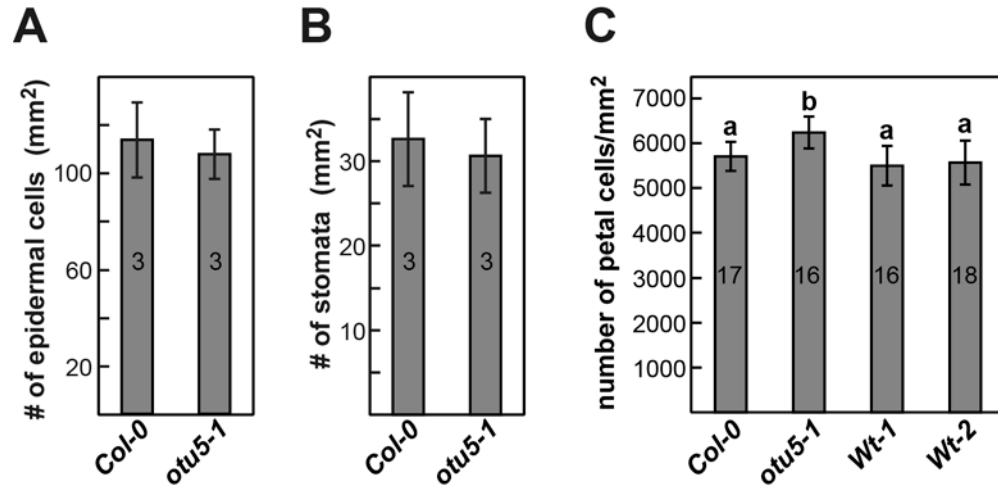


Figure S4. Averaged densities of epidermal cells and stomata for rosette leaves and adaxial epidermal cells of petals in Col-0 and *otu5-1* plants. (A) and (B) Densities of epidermal cells and stomata were averaged from 32 and 39 unit areas from three 5th rosette leaves for Col-0 and *otu5-1*, respectively. (C) Density of adaxial epidermal cells for petals was calculated from 16-18 petals as indicated for Col-0, *otu5-1* and two complemented lines: *Wt-1* and *Wt-2*. Different letters denote significant difference by pairwise comparison using Student's *t* test.

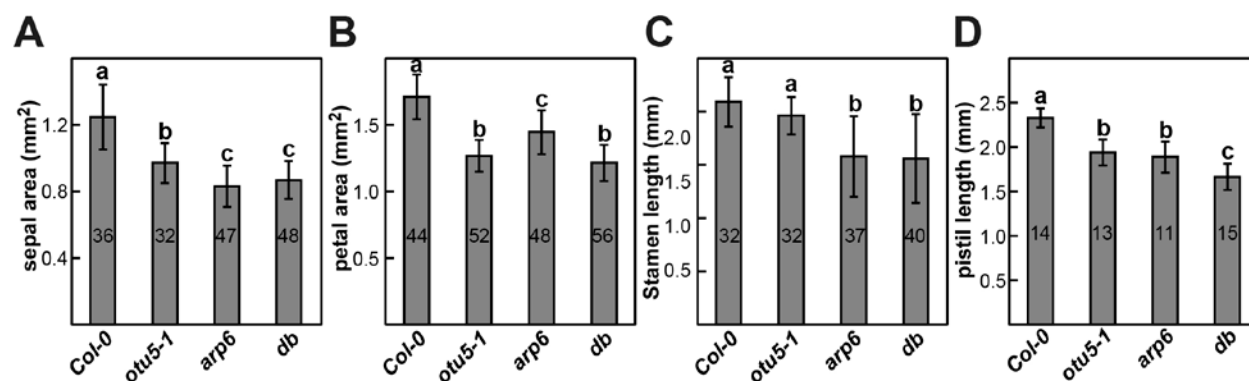


Figure S5. Averaged area or lengths of various floral organs for Col-0, *otu5-1*, *arp6-1*, and the *otu5 arp6* double mutant plants. Averaged sepal area (A), petal area (B), stamen lengths (C), and pistil lengths (D) from Col-0, *otu5-1*, *arp6-1*, and *otu5 arp6* (*db*) flowers. Number of various floral organs used were indicated. Different letters denote significant difference by pairwise comparison using Student's *t* test.

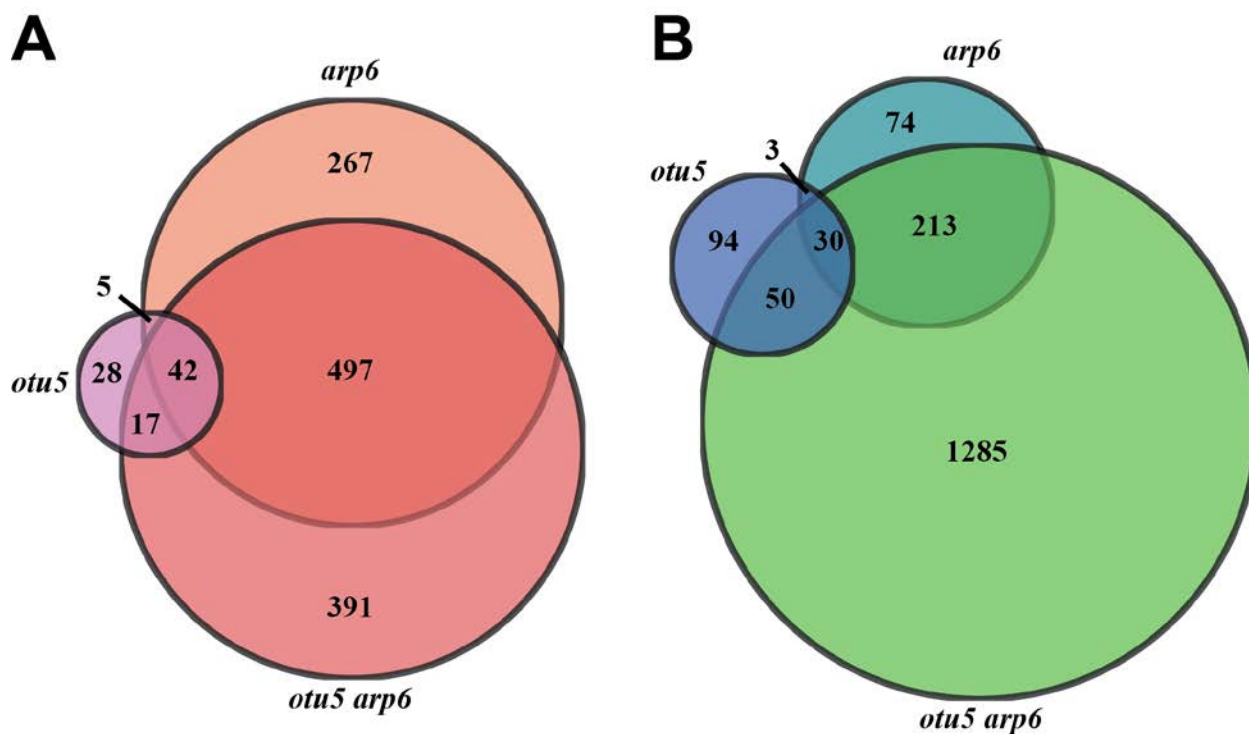


Figure S6. Venn diagrams showing numbers of up- and downregulated DEGs detected from *otu5-1*, *arp6-1* and *otu5 arp6*. **(A)** upregulated and **(B)** downregulated DEG numbers. The numbers not overlapped are unique to specific genotypes and those in overlapped regions are DEG numbers shared between genotypes.