

Supporting Information

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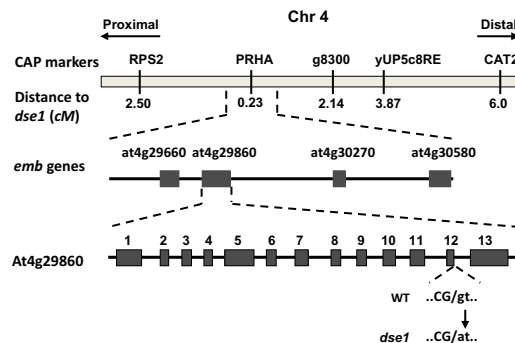


Fig. S1. Molecular cloning of *decreased size exclusion limit 1* (*dse1*). (Top) Molecular mapping of the *DSE1* gene. To map *DSE1*, heterozygous *dse1* plants were crossed to WT Col-0. Homozygous WT F_2 plants derived from F_1 plants heterozygous for *dse1* were screened with Simple sequence length polymorphism and cleaved amplified polymorphism (CAPS) markers from the Arabidopsis Information Resource (<http://www.arabidopsis.org>). *dse1* is closely linked to CAPS marker PHRA on chromosome 4 (chr 4). CAPS markers are shown above the chromosome (gray bar), and their distance relative to *dse1* is shown below. (Middle) Embryo-lethal genes (*emb*) within 300 kb of PHRA. (Lower) Diagram of *At4g29860*. Exons are dark gray boxes and are labeled numerically. The sequences of the junction between exon 12 and intron 12 in WT and *dse1* are displayed below. Exon and intron nucleotides at the junction are in capital letters and lowercase letters, respectively, separated by a slash.

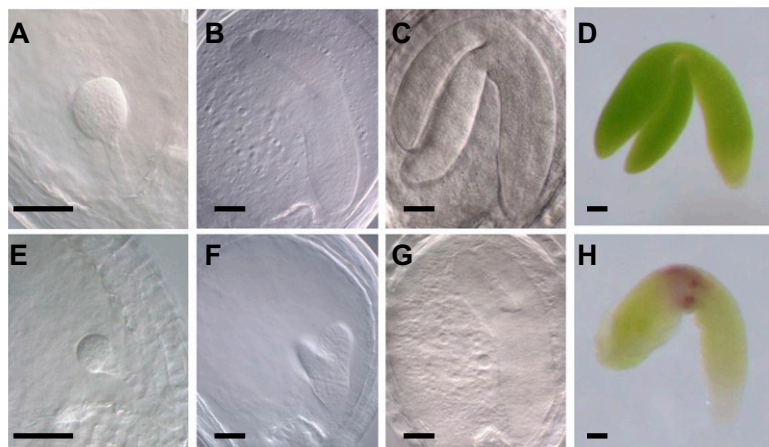


Fig. S2. Development of *dse1* embryos is retarded. (A–C) WT embryos at late globular (A), torpedo (B), cotyledon (C), and mature (D) stages. (E–H) *dse1* embryos from siliques containing the staged sibling WT embryos. (Scale bars: A–H, 100 μ m; J–Q, 50 μ m.) Embryos in A–C, E, and F were cleared in chloral hydrate solution (80 g of chloral hydrate, 8 mL of glycerol, and 30 mL of H_2O) for 1 h at room temperature and observed with a Zeiss Axio Imager M1 microscope using differential interference contrast optics. (Scale bar: 50 nm.)

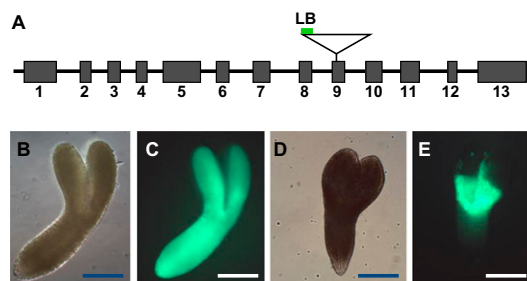


Fig. S3. Characterization of *tan-2* mutant (Salk 097510). (A) Schematic diagram of the *tan-2* allele of *At4g29860*. *At4g29860* consists of 13 exons (gray boxes), labeled 1–13. T-DNA (triangle) was inserted in exon 9. The left border was marked as a green block. (B–D) The 8-hydroxypyrene-1, 3, 6-trisulfonic acid loading assay. Intercellular movement was reduced in *tan-2* embryos (E) compared with WT embryos (C). (B and D) Corresponding bright-field images of C and E. (Scale bar: 100 nm.)

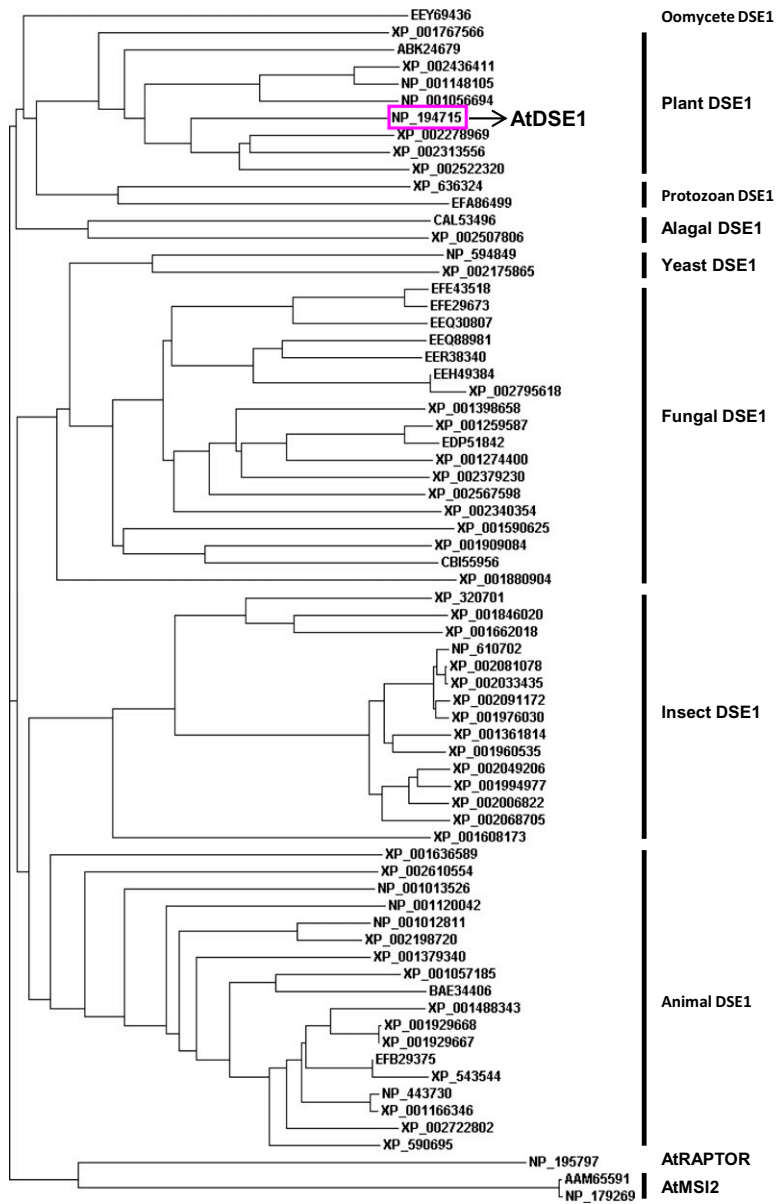


Fig. S4. Phylogenetic analysis of DSE1 homologs from the National Center for Biotechnology Information database. The tree was built with ClusterW2 (*Materials and Methods*).

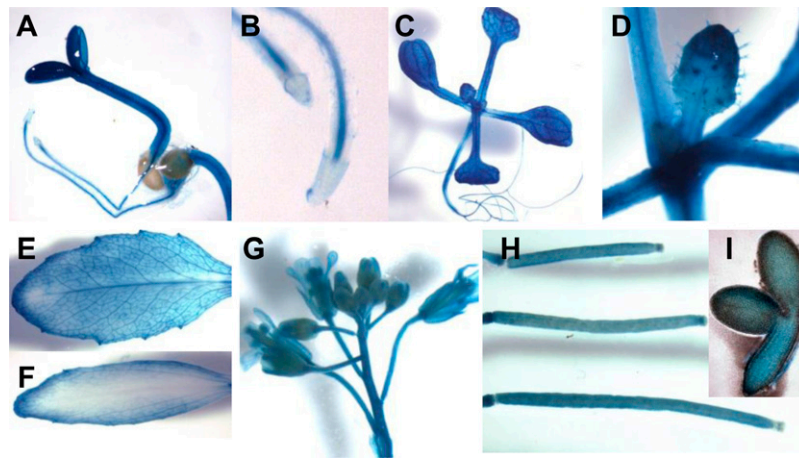


Fig. 55. GUS staining patterns of transgenic *Arabidopsis* carrying the *pDSE1::GUS* gene. (A) Two-d-old seedling. (B) Root tips from A. (C) Ten-d-old seedling. (D) Shoot apical from C. (E) Rosette leaves from 4-wk-old plants. (F) Cauline from 4-wk-old plants. (G) Inflorescence. (H) Siliques. (I) Embryos.

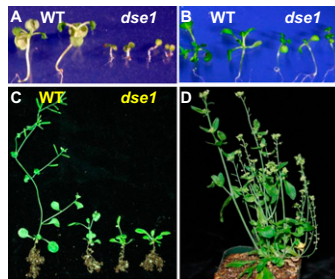


Fig. 56. Development of *dse1* plants is retarded. *Arabidopsis thaliana* Landsberg *erecta* (*Ler*) plants were used as WT control. (A) Fifteen-d-old seedlings on 1/2 Murashige and Skoog medium, showing the arrested development of *dse1* seedlings after germination. (B) Ten-d-old seedlings grown on 1/2 Murashige and Skoog medium with 0.5% sucrose, showing that *dse1* seedlings can develop true leaves, but more slowly than WT. (C) Five-wk-old plants. WT plants flowered 2 wk earlier, whereas *dse1* plants just began to flower. (D) Three-mo-old *dse1* plants. *Ler* plants growing under the same conditions finished setting seeds 1 mo earlier.