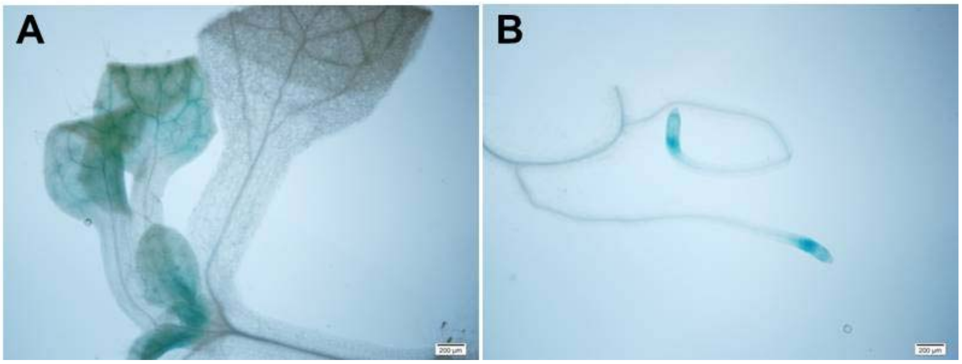
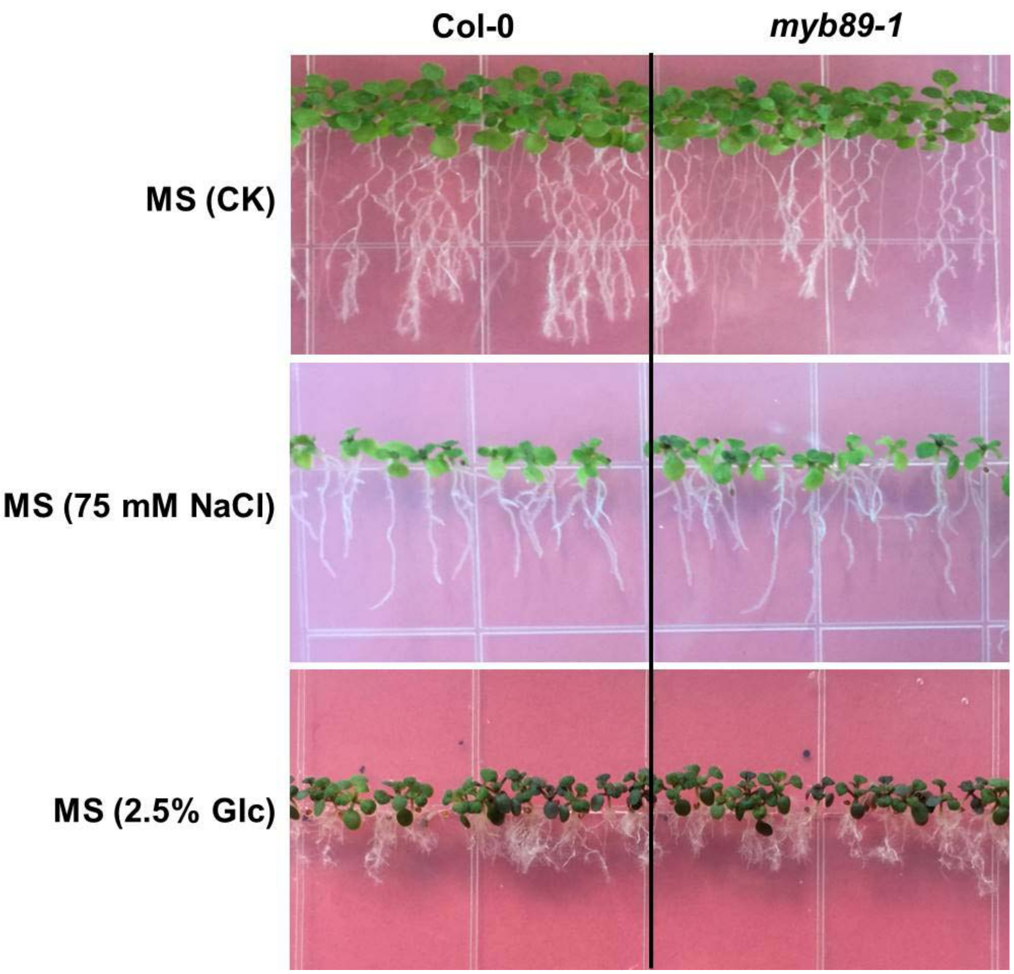
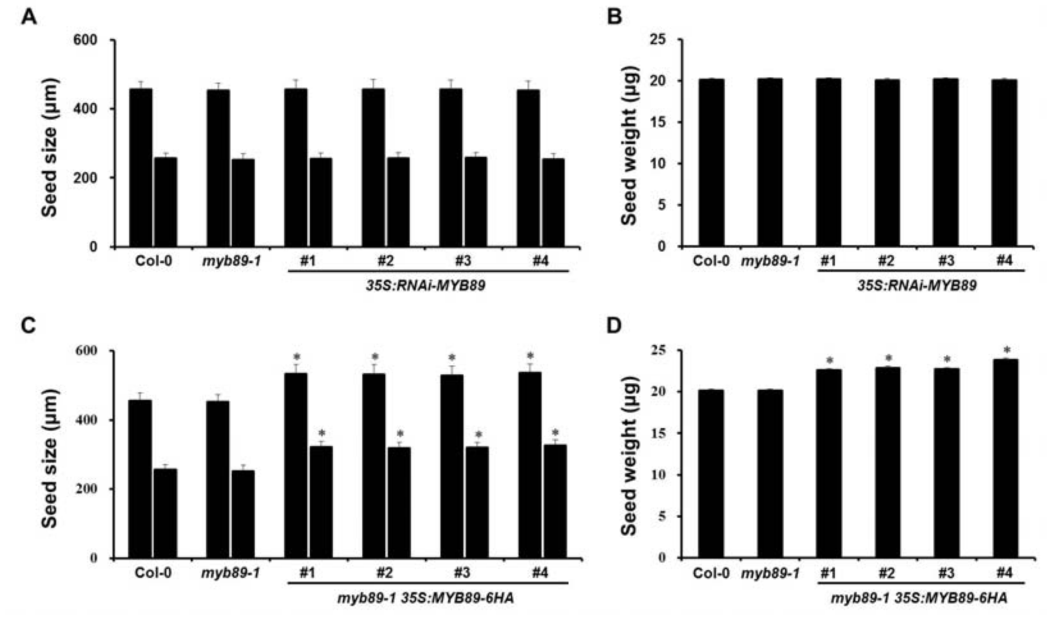


Supplemental Fig. S1. Representative GUS staining of *pMYB89:GUS* transgenic plants shows MYB89 expression in true leaves **(A)** and a root tip **(B)** of a 15-day-old young seedling. Bar = 200 µm.

Supplemental Fig. S2. Comparison of the plant size between the wild-type (Col-0) and *myb89-1* plants. The photographs were taken 23 days after sowing under the same controlled conditions.



Supplemental Fig. S3. Comparison of the wild-type (Col-0) and *myb89-1* young seedlings under stressed environments. The photographs were taken 20 days after sowing and show the situations on the control medium (without stress, CK), MS agar medium containing 2.5% (w/v) Glucose (Glc), and MS agar medium containing 75 mM NaCl.



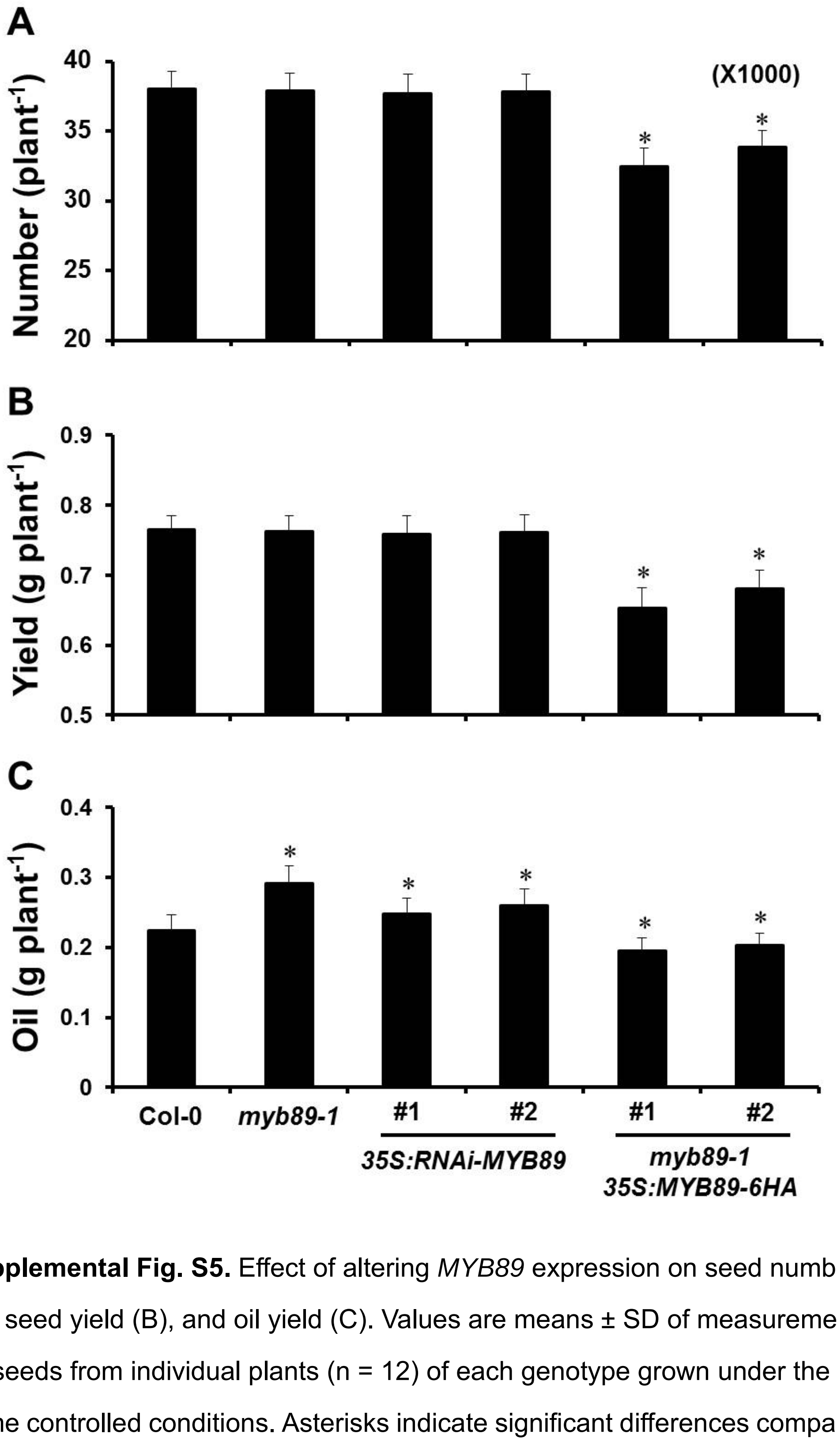
Supplemental Fig. S4. Effect of *MYB89* knockdown in the wild-type (Col-0) background and *MYB89* overexpression in *myb89-1* mutant background on seed size and seed weight. For each construct (*35S:RNAi-MYB89* and *35S:MYB89-6HA*), four independent homozygous T3 transgenic lines with the strongest effect on *MYB89* expression were selected and analysed. Values are means ± SD (n = 5), and each of the three assays for each biological replicate contains 200 seeds from 12 individual plants grown in different pots arranged randomly within one of the three blocks. Asterisks indicate significant differences in the seed total FA content compared to that in the wild-type (ANOVA, Tukey's test, $P \leq 0.05$).

(**A**) Quantitative comparison of seed size [length (Left column) and width (Right column)] between the wild-type (Col-0) and *35S:RNAi-MYB89* transgenic plants.

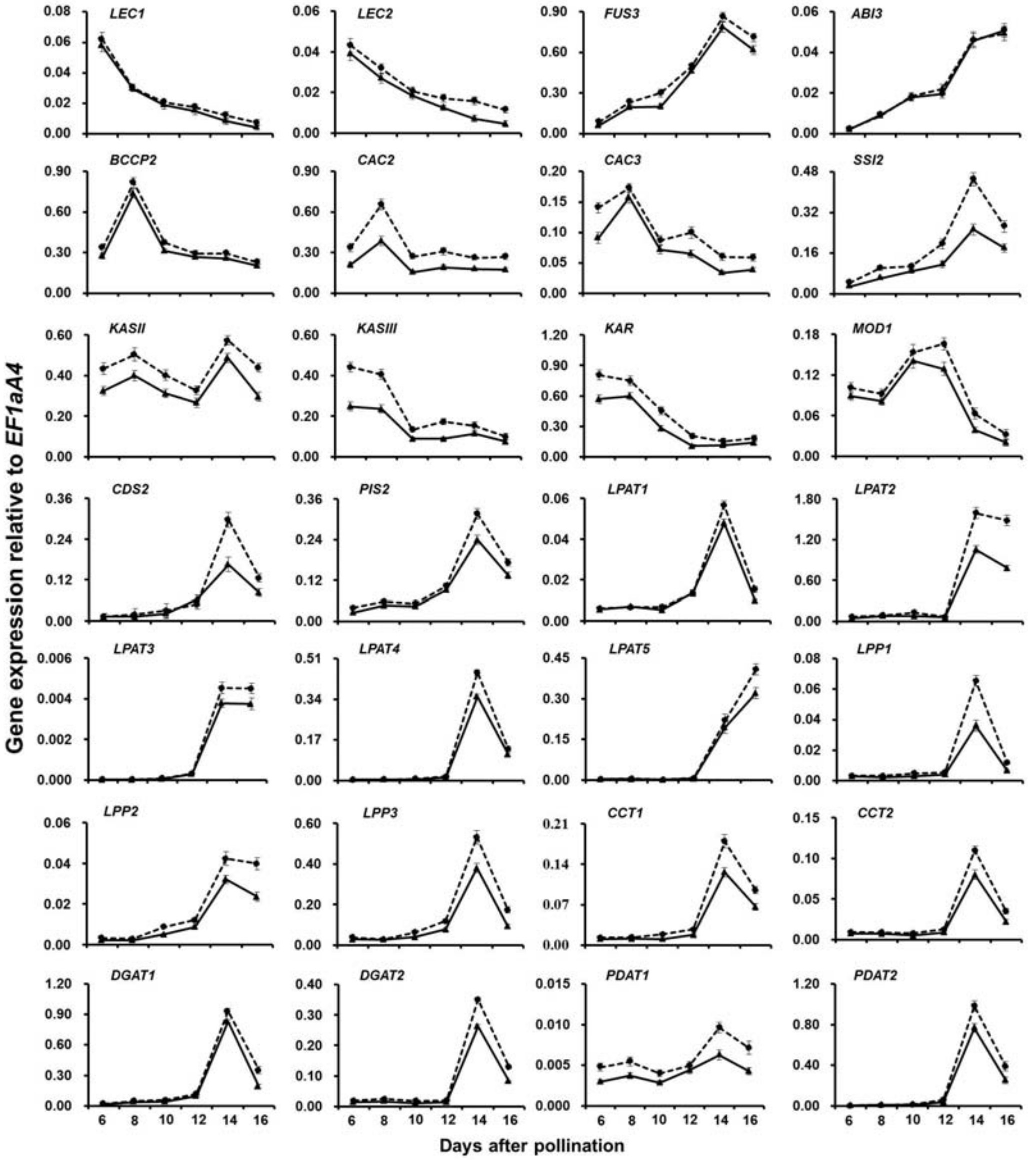
(**B**) Quantitative comparisons of seed dry weight between the wild-type (Col-0) and *35S:RNAi-MYB89* transgenic plants.

(**C**) Quantitative comparison of seed size [length (Left column) and width (Right column)] between the wild-type (Col-0) and *myb89-1 35S:MYB89-6HA* transgenic plants.

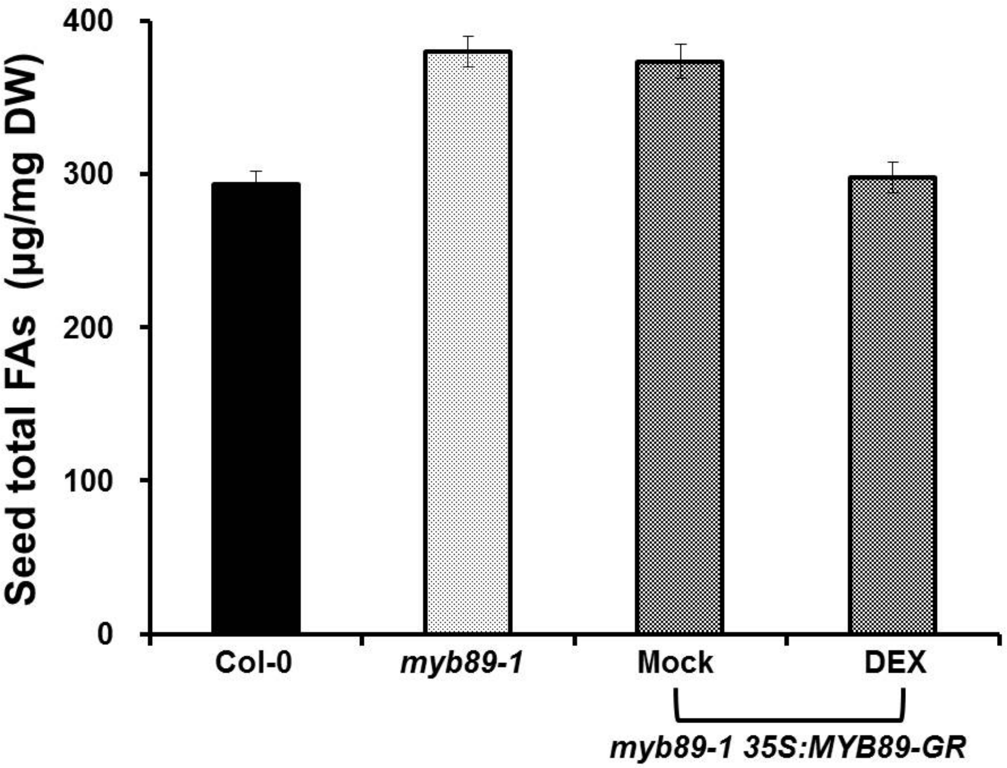
(**D**) Quantitative comparisons of seed dry weight between the wild-type (Col-0) and *myb89-1 35S:MYB89-6HA* transgenic plants.



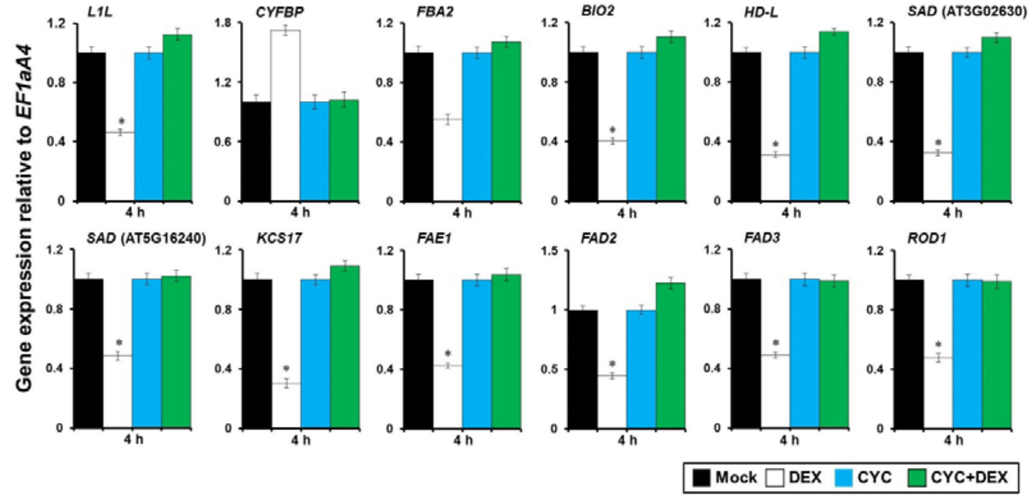
Supplemental Fig. S5. Effect of altering *MYB89* expression on seed number (A), seed yield (B), and oil yield (C). Values are means ± SD of measurements on seeds from individual plants (n = 12) of each genotype grown under the same controlled conditions. Asterisks indicate significant differences compared to the wild-type (two-tailed paired Student's *t* test, $P \leq 0.05$).



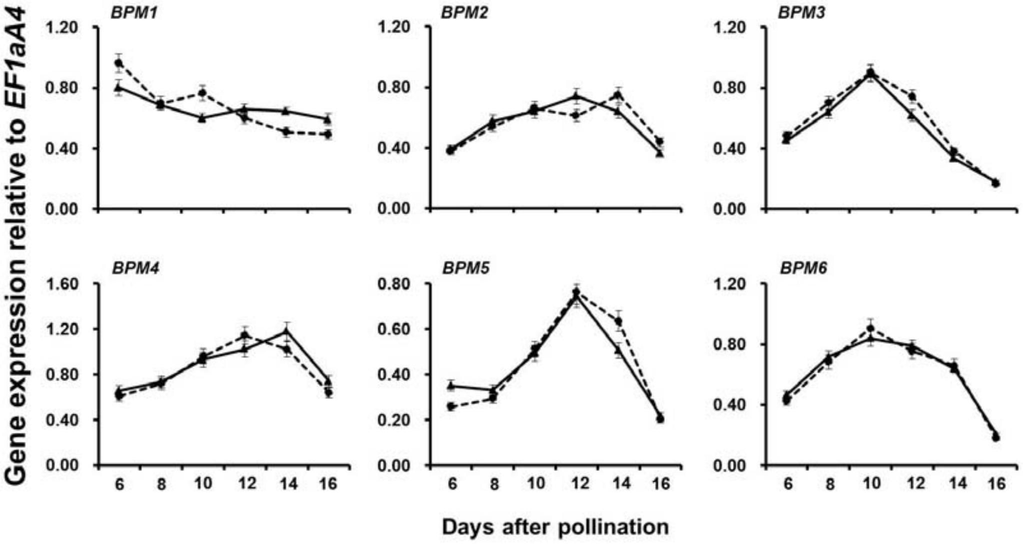
Supplemental Fig. S6. qRT-PCR analysis of the expression of genes involved in FA biosynthesis and TAG deposition in developing seeds of the wild-type (Col-0) and *myb89-1* plants. Solid and dotted lines indicate the dynamic expression of genes in the wild-type and *myb89-1* plants, respectively. Results were normalised against the expression levels of *EF1aA4* as an internal control. Values are means ± SD (n = 3). No significant differences in expression levels of these genes in *myb89-1* compared with those in the wild-type plants were observed (two-tailed paired Student's *t* test, $P \leq 0.05$).



Supplemental Fig. S7. Confirmation of the biologically active MYB89-GR fusion. Seedlings of *myb89-1 35S:MYB89-GR* were mock-treated (Mock) or treated with 10 µM dexamethasone (Dex) every alternate day after germination. The seed FA content of mock-treated plants was similar to that of *myb89-1* plants, whereas dexamethasone treatment rescues this phenotype to the wild-type (Col-0) level. Values are means ± SD (n = 5).



Supplemental Fig. S8. The genes involved in glycolysis, FA biosynthesis and modification, and TAG deposition in developing seeds are not immediate targets of transcriptional regulation by MYB89 in developing seeds. The *myb89-1 35S:MYB89-GR* siliques at 12 DAP were mock-treated (Mock) or treated with 10 µM dexamethasone (DEX), 10 µM cycloheximide (CYC), or 10 µM CYC plus 10 µM DEX (DEX + CYC), and siliques at 14 DAP were used for the transcriptional analysis of *FAD2*, *FAD3*, *FAE1*, and *ROD1*. The expression of these genes was examined after 4 h of treatment by qRT-PCR analyses. Results were normalised against the expression of *EF1aA4* as an internal control. Values are means ± SD (n = 3). Asterisks indicate significant differences in gene expression in dexamethasone-treated samples compared with their respective controls (two-tailed paired Student’s *t* test, P ≤ 0.05).



Supplemental Fig. S9. qRT-PCR analysis of the expression of six *BPM* genes in developing seeds of the wild-type (Col-0) and *myb89-1* plants. Solid and dotted lines indicate the dynamic expression of genes in the wild-type and *myb89-1* plants, respectively. Results were normalised against the expression levels of *EF1aA4* as an internal control. Values are means ± SD (n = 3). No significant differences in expression levels of these genes in *myb89-1* compared with those in the wild-type plants were observed (two-tailed paired Student’s *t* test, P ≤ 0.05).