

Figure S1: DNA glycosylases transcript levels during seed development. Gene expression levels informed based on public transcriptome data (Klepikova et al. 2015; <u>https://bar.utoronto.ca/eFP-Seq_Browser/</u>) using RPKM values. *PP2A-A3* was used as internal standard. Seeds and pods of siliques were separately taken when the first silique was green and 1-1.5 cm long (abscission of the 8th flower) or yellow and ready to open (senescent silique). Color dots not observed in the figure correspond to mean values below 0,0001232.



Figure S2: Abundance of *MBD4L.3* and *MBDL.4* transcripts in 35S:MBD4L.3/mbd4l-1 and 35S:MBD4L.4/mbd4l-1 lines. Transcripts content was determined in dry seeds 1-month post-harvesting. Values were normalized using the geometric mean of two reference genes (*PP2A-A3* and *EF1* α). The average ± standard error of 3 replicates is shown. Circles represent individual replicates.



Figure S3: Germination of independent 35S:MBD4L.3/mbd4l-1 and 35S:MBD4L.4/mbd4l-1 lines. Germination was analyzed along 4 days (a) or after 24 hours of exposing seeds to the light and 22°C (b). Lines denoted as #1 in (b) are those represented in Figure 1. All analyzed transgenic lines are homozygous for the *mbd4l-1* T-DNA insertion and MBD4L.3/MBD4L.4 transgene. The average ± standard error of 3-4 biological replicates is shown. Circles represent individual replicates. Asterisks indicate significant differences compared to the *mbd4l-1* mutant (***p<0.001, ANOVA followed by Bonferroni's Test).



Figure S4: Response of *mbd4l* **mutants to exogenous ABA.** Germination in response to exogenous ABA (a-b). Seeds were germinated in 0.5x MS with the indicated ABA concentrations. Germination percent is shown after 7 (a) and 0-4 (b) days of exposure of seeds to the light and 22°C. Expression of *LEC1* and *DOG1* during early seed development (3DPA siliques) and in dry seeds of *mbd4l-1* (c). Expression values are relative to WT plants. Seedling development in response to exogenous ABA (d). Seedlings were grown in 0.5x MS 1% w/v agar plates for 4 days and then transferred to 0.5x MS 1% w/v agar plates with 0, 5 and 10 μ M ABA for 10 days. Fresh weight values (d) and representative images (bottom; scale bar = 1cm) of WT, *mbd4l-1* and *mbd4l-2* seedlings are shown. The average ± standard error of 3 (b-c) or 4-11 (d) biological replicates is shown. Circles represent individual replicates. Asterisks indicate significant differences compared to the WT by ANOVA followed by Bonferroni's Test (a-b, d) or Kruskal Wallis followed by Dunn's Test (c), ***p<0.001.



Figure S5: Germination of independent 35S:MBD4L.3/mbd4l-1 and 35S:MBD4L.4/mbd4l-1 lines after artificial ageing. WT, *mbd4l-1*, 35S:MBD4L.3/*mbd4l-1_#2* and 35S:MBD4L.4/*mbd4l-1_#2* seeds were exposed to a saturated KCI solution at 37°C for 1 week (a) or 45°C for 4 days (b). Then, seeds were sown in 0.5x MS 1% w/v agar plates and stratified for 3 days at 4°C in the dark. The germination capacity was scored between 0 and 96 hours of transferring the plates to the growth room under light and at 22°C. The average ± standard error of 3 biological replicates is shown. Asterisks indicate significant differences compared to the WT (**p<0.002, ***p<0.001, ANOVA followed by Bonferroni's Test).



Figure S6: Germination of 35S:MBD4L.3/mbd4l-1 and 35S:MBD4L.4/mbd4l-1 lines after 1 year storage under CC. WT, *mbd4l-1*, 35S:MBD4L.3/*mbd4l-1* and 35S:MBD4L.4/*mbd4l-1* seeds were stored for 1 year at 22°C and 42% RH. Then, seeds were sown on 0.5x MS 1% w/v agar plates and stratified for 3 days at 4°C in the dark. The germination capacity was scored between 0 and 96 hours of transferring the plates to the growth room under light and at 22°C. The average ± standard error of 3 biological replicates is shown. Asterisks indicate significant differences compared to the WT (*p<0.033, ***p<0.001, ANOVA followed by Bonferroni's Test).



Figure S7: Imbibition induces higher *MBD4L* **expression in aged seeds.** Seeds were stored at 22°C (control) or incubated in a saturated KCl solution at 37°C for 1 week. Then, seeds were imbibed in water and stratified at 4°C for 24 hours in the dark. The *MDB4L.3* and *MBD4L.4* transcript content determined by RT-qPCR is relative to the control condition. The average ± standard error of 3 replicates is shown. Circles represent individual replicates. Asterisks indicate significant differences compared to the WT (*p<0.033, Kruskal Wallis followed by Dunn's test).