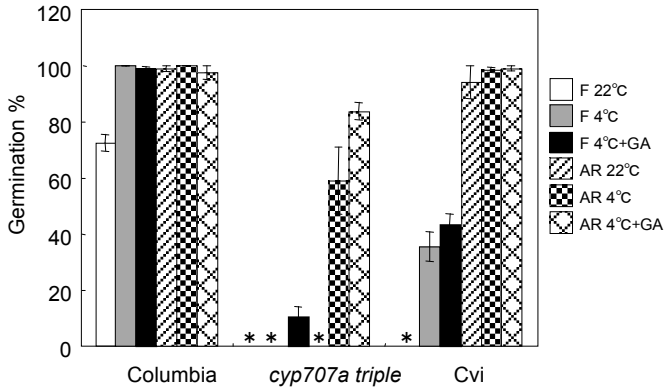

Figure S1. Phenotypic analysis of *cyp707a1a2a3* triple mutant and Cvi accession seeds.
Effects of stratification, GA and after-ripening on *cyp707a1a2a3* triple mutant (Columbia background) and Cvi accession seeds. F and AR represent freshly harvested and after-ripened seeds, respectively. Seeds after-ripened for 6 months were used in this experiment. Stratification was performed for 3 days at 4 °C in the dark. GA_4 (10 μM) was applied during stratification. Asterisk indicates no germination. Seeds were sown on 0.5 % agarose gel and were kept at 22°C under continuous light for 6 days. Germination was scored based on radicle emergence. Experiments were performed five times using independent seed batches. Average values are shown with standard errors.

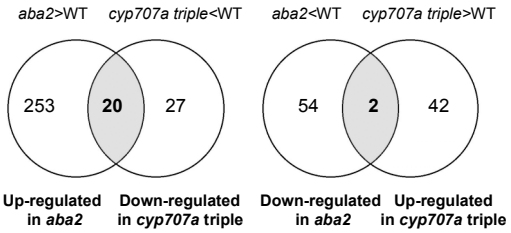

Figure S2. ABA-responsive genes in dry seeds.
ABA-upregulated genes (right) and ABA-downregulated genes (left). Significant differences were judged by Mann-Whitney U-test (FDR α=0.05), and genes with an expression ratio of 2-fold higher or lower were selected for further analysis. Expression ratios and p-values of ABA-responsive genes are shown in Table S3.

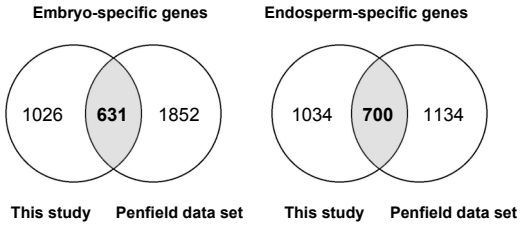

Figure S3. Comparison of embryo- and endosperm-specific genes between this study and Penfield et al. (2006) data set.

Left and right represent embryo- and endosperm-specific genes. A list of embryo and endosperm-specific genes in Penfield data set was referred as reported previously (Penfield et al., 2006) These gene were identified by using 24-h-imbibed seeds (Landsberg *erecta* accession) at 22℃ after stratification for 3 days at 4℃. In this study, the embryo and endosperm-specific genes were identified by using 24-h-imbibed seeds (Columbia accession) at 22℃ without stratification. The gene list is shown in Table S8

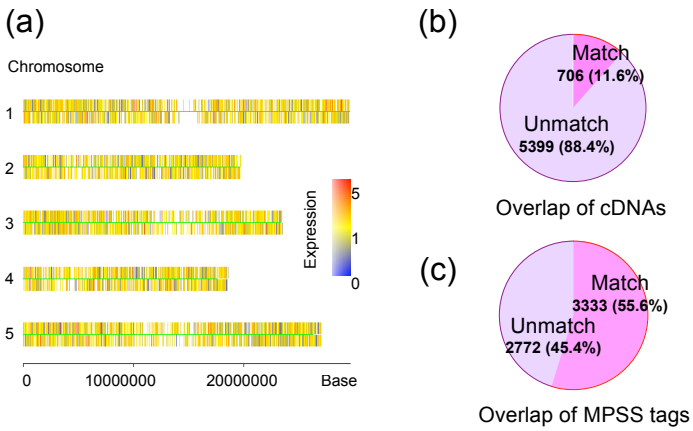

Figure S4. Overview of non-AGI TUs in Arabidopsis seeds.
(a) Distribution of 6,105 non-redundant non-AGI TUs on five chromosomes. Physical position and relative expression levels of non-redundant non-AGI TUs in imbibed wild-type seeds at 24-h imbibition were analyzed using GENESPRING 7.3 software. Colored bars indicate relative expression levels. **(b)** Overlap of non-AGI TUs and full length cDNAs. **(c)** Overlap of non-AGI TUs and MPSS tags.

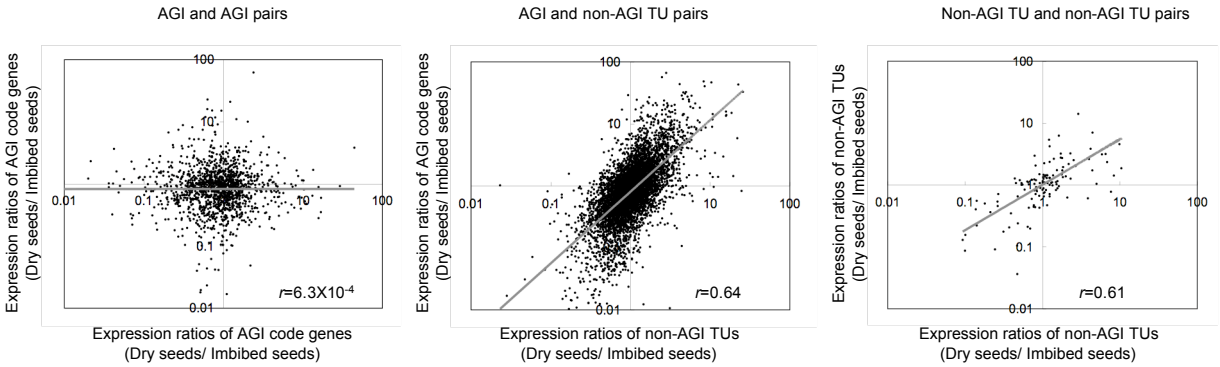

Figure S5. Correlations between expression ratios in AGI/AGI, AGI/non-AGI TU and non-AGI TU/non-AGI TU gene pairs.

Plots of sense and antisense expression ratio (dry seeds/imbibed seeds). Sense/antisense gene pair transcripts are shown in Table S11. Linear correlations were found in the pairs of AGI/non-AGI and non-AGI TU/non-AGI TU, but not in the pairs of AGI/AGI.

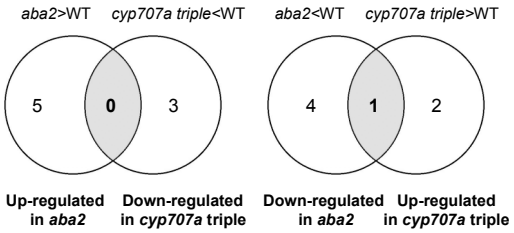

Figure S6. ABA-responsive non-AGI TUs in dry seeds.
ABA-downregulated genes (left), and ABA-upregulated genes (right). Significant differences judged by Mann-Whitney U-test (FDR α=0.05). Genes with expression ratio of 2-fold higher or lower were selected for further analysis. Expression ratios and p-values of ABA-responsive genes are shown in Table S12.