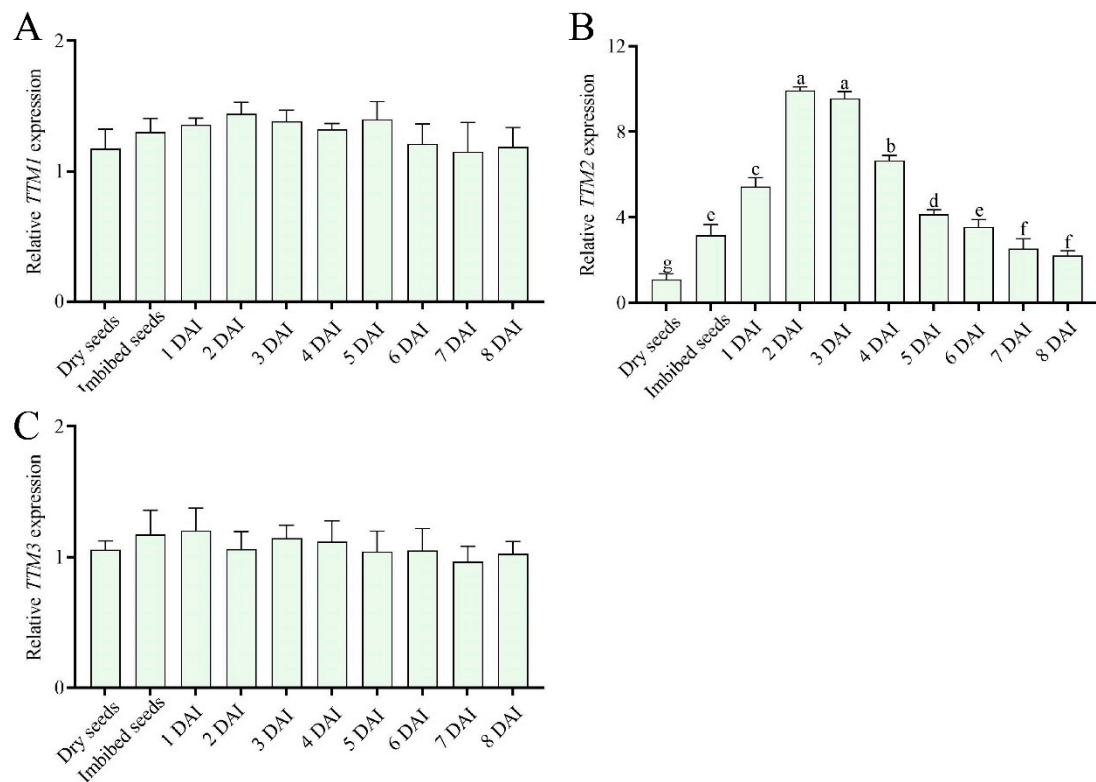
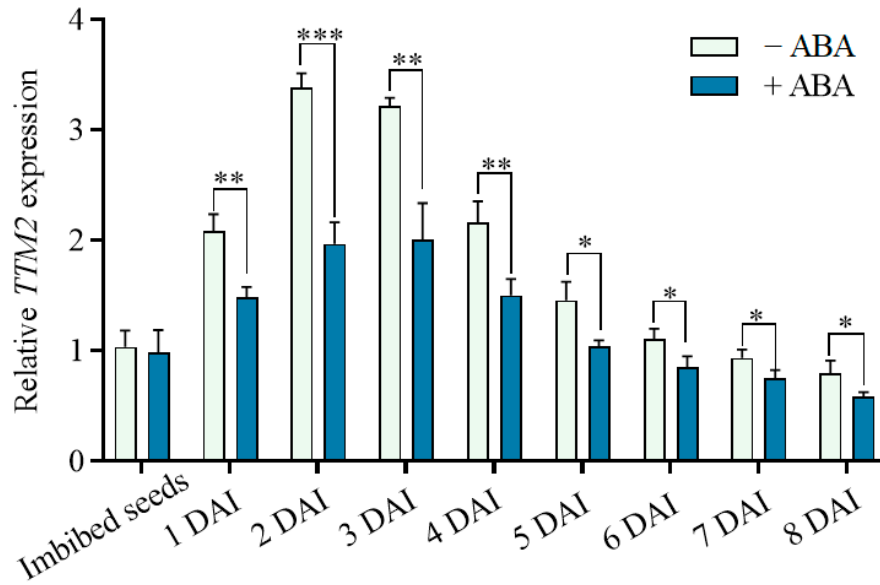


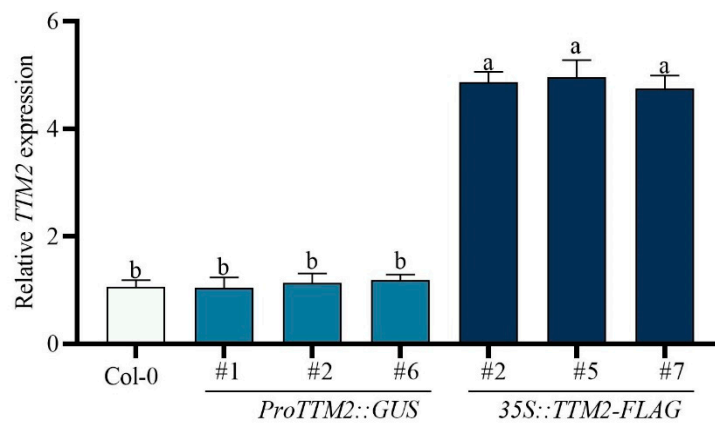
## Supplementary Materials



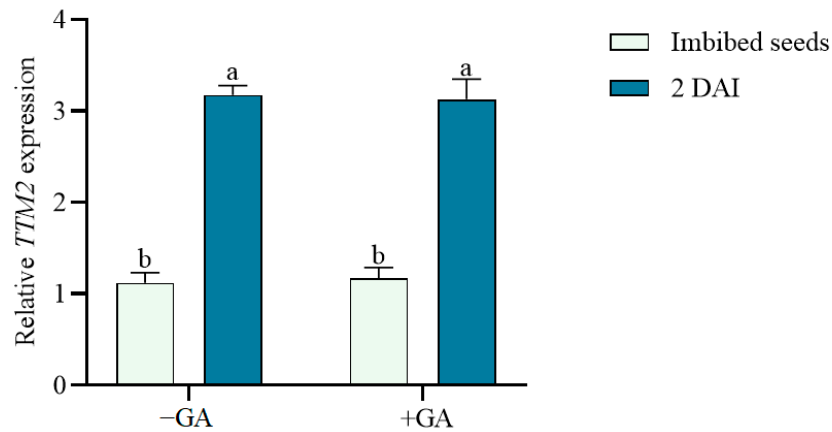
**Figure S1.** Analysis of *TTM1*, *TTM2*, and *TTM3* transcription levels by qRT-PCR. (A-C) The transcription levels of *TTM1*(A), *TTM2* (B), and *TTM3* (C) during seed germination. The wild-type (WT) seeds were soaked at 4°C for 3 days in water and grown on 1/2 Murashige & Skoog (MS) medium for 1-8 days. DAI, days after imbibition. The *ACT2* gene was applied as an internal control. Expression levels were normalized to dry seeds, which was set at 1. Data are shown as mean  $\pm$  SD ( $n = 3$ ). Various letters represent significant differences at  $P < 0.05$  by one-way ANOVA and Tukey's multiple comparison test.



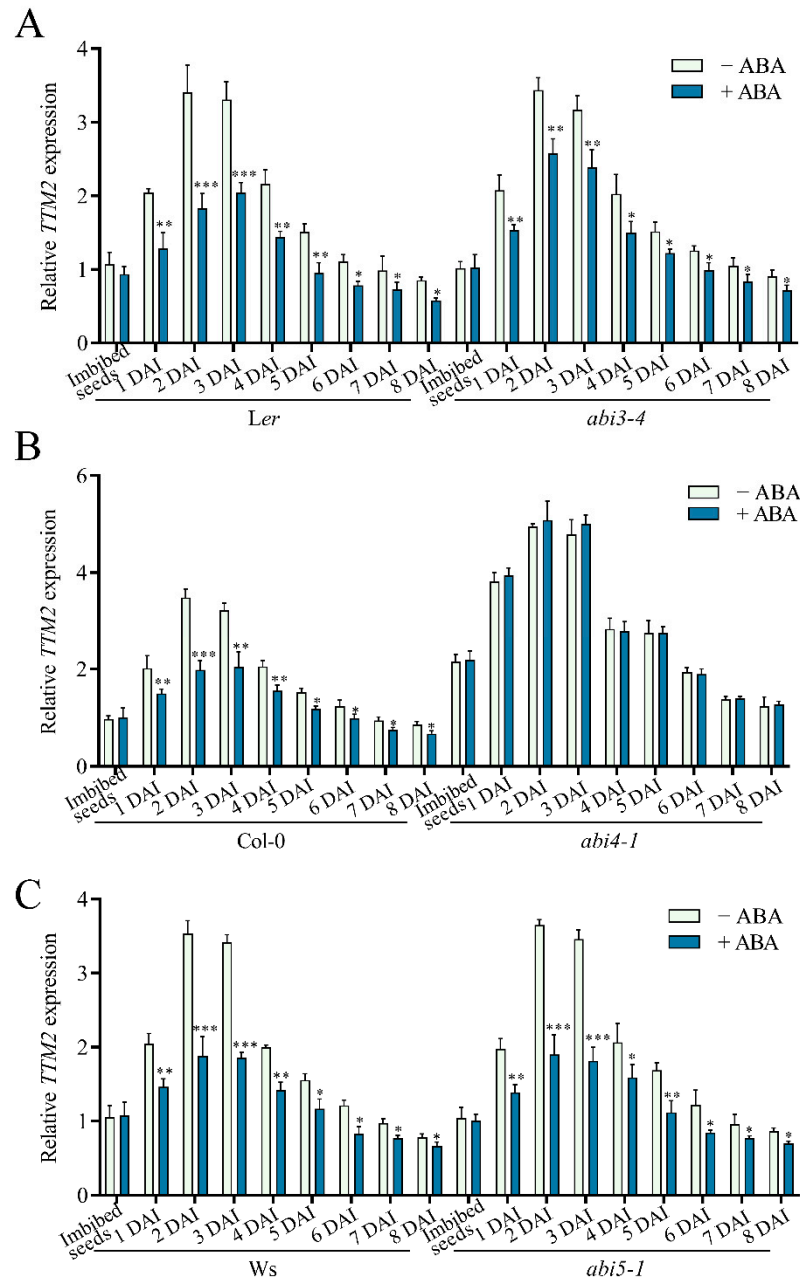
**Figure S2.** The qRT-PCR to determine the expression of *TTM2*. Imbibed seeds of the wild type were planted in 1/2 MS medium (–ABA) or 1/2 MS medium containing 0.5  $\mu$ M ABA (+ABA) for 1–8 days, followed by RNA extraction. The *ACT2* gene was applied as an internal control. Expression levels were normalized to those of untreated (–ABA) imbibed seeds, which was set at 1. Data are shown as mean  $\pm$  SD ( $n = 3$ ). Asterisk denotes a statistically significant difference compared with their –ABA at indicated times. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$  (Student’s *t*-test).



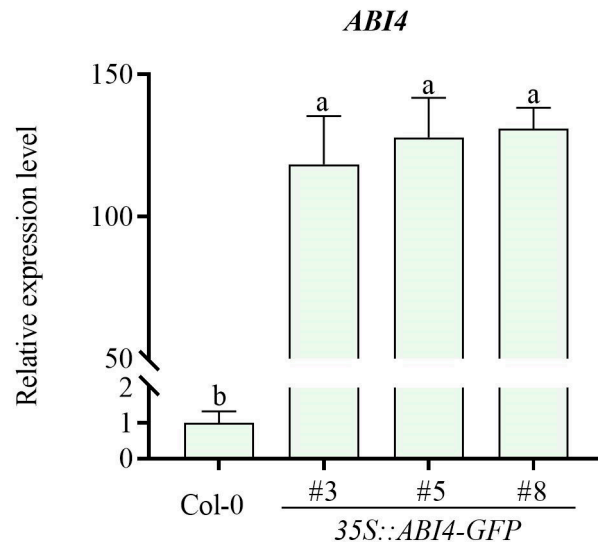
**Figure S3.** Validation of *ProTTM2::GUS* and *35S::TTM2-FLAG* transgenic lines. The qRT-PCR to determine the expression of *TTM2*. The *ACT2* gene was applied as an internal control. Expression levels were normalized to Col-0 plants, which was set at 1. Data are means  $\pm$  SD ( $n = 3$ ). Various letters represent significant differences at  $P < 0.05$  by one-way ANOVA with Tukey’s multiple comparison test.



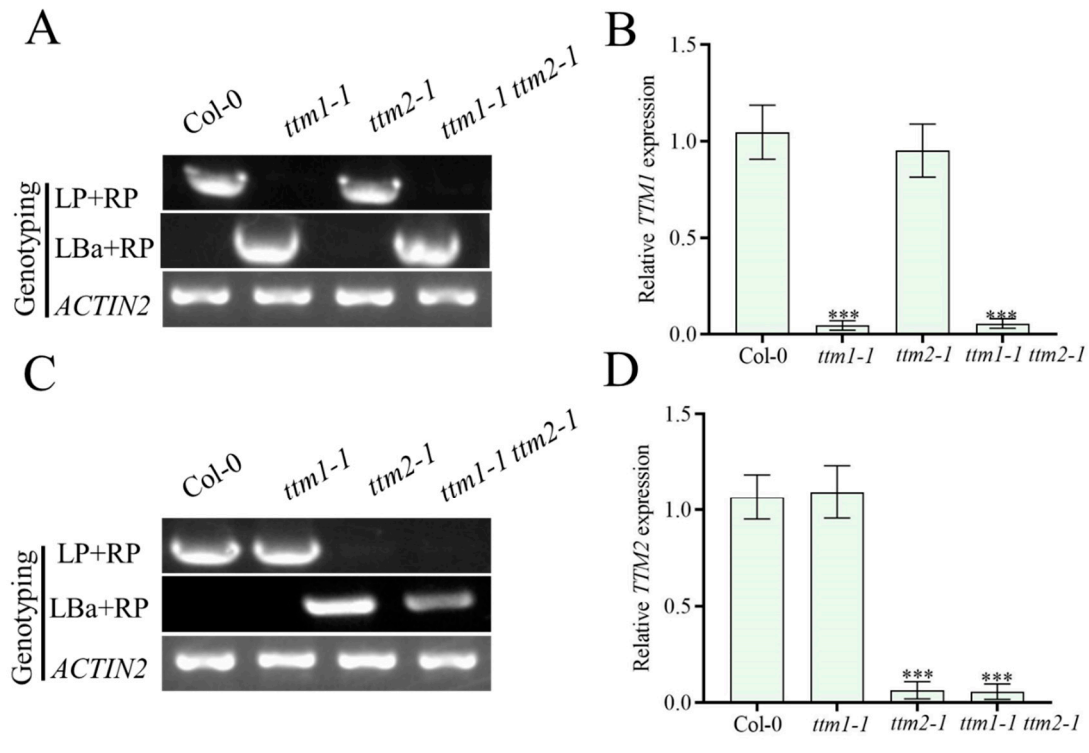
**Figure S4.** The exogenous GA treatment did not affect the *TTM2* expression. The qRT-PCR to determine the expression of *TTM2*. Imbibed wild-type seeds were planted on 1/2 MS medium (-GA) or 1/2 MS medium containing 10 $\mu$ M GA<sub>3</sub> (+GA) for 2 days, followed by RNA extraction. The *ACT2* gene was applied as an internal control. Expression levels were normalized to those of untreated (-GA) imbibed seeds, which was set at 1. Data are shown as mean  $\pm$  SD ( $n = 3$ ). Various letters represent significant differences at  $P < 0.05$  by one-way ANOVA with Tukey's multiple comparison test.



**Figure S5.** *TTM2* expression in response to ABA in *abi3-4*, *abi4-1*, and *abi5-1*. **(A)** *TTM2* expression in Landsberg erecta (*Ler*) and *abi3-4*. **(B)** *TTM2* expression in Columbia (*Col-0*) and *abi4-1*. **(C)** *TTM2* expression in Wassilewskija (*Ws*) and *abi5-1*. Imbibed seeds of different genotypes were germinated on 1/2 MS medium (–ABA) or 1/2 MS medium with 0.5  $\mu$ M ABA (+ABA) for 1–8 days. Harvested plants were subjected to RNA extraction and qRT-PCR analysis. The *ACT2* gene was applied as an internal control. Expression levels were normalized to those of untreated (–ABA) imbibed seeds, which was set at 1. Data are shown as mean  $\pm$  SD ( $n = 3$ ). Asterisk denotes a statistically significant difference compared with their –ABA at indicated times. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$  (Student’s *t*-test).



**Figure S6.** Validation of *35S::ABI4-GFP* transgenic lines. The qRT-PCR to determine the *ABI4* expression. The *ACT2* gene was applied as a control. Expression levels were normalized to Col-0 plants, which was set at 1. Data are means  $\pm$  SD ( $n=3$ ). Various letters represent significant differences at  $P < 0.05$  by one-way ANOVA with Tukey's multiple comparison test.



**Figure S7.** The verification of plant genotype in Col-0, *ttm1-1*, *ttm2-1*, and *ttm1-1 ttm2-1*. (A) The T-DNA insertion of *ttm1-1* was determined by genotyping in Col-0, *ttm1-1*, *ttm2-1*, and *ttm1-1 ttm2-1*. (B) The determination of *TTM1* expression by qRT-PCR in Col-0, *ttm1-1*, *ttm2-1*, and *ttm1-1 ttm2-1*. (C) The T-DNA insertion of *ttm2-1* was determined by genotyping in Col-0, *ttm1-1*, *ttm2-1*, and *ttm1-1 ttm2-1*. (D) The determination of *TTM2* expression by qRT-PCR in Col-0, *ttm1-1*, *ttm2-1*, and *ttm1-1 ttm2-1*. Expression levels were normalized to Col-0, which was set at 1. Data are shown as mean  $\pm$  SD ( $n = 3$ ). Asterisk denotes a statistically significant difference compared with Col-0. \*\*\*,  $P < 0.001$  (Student's *t*-test).

**Table S1. List of the primers used in this study**

| <b>Primer name</b>       | <b>Sequence (5' to 3')</b>               |
|--------------------------|--|
| <b>Genomic DNA PCR</b>   |  |
| LBa1                     | ATTTTGCCGATTTCGGAAC                      |
| <i>ttm1-1-LP</i>         | TTCTGCTCATGCTTTGATTG                     |
| <i>ttm1-1-RP</i>         | AGCAAGGGTGATTAATCTGGG                    |
| <i>ttm2-1-LP</i>         | TATGTCCATCAGAAAGGACCG                    |
| <i>ttm2-1-RP</i>         | CTTCTGGTGCTGGAAAGACTG                    |
| <i>ttm2-2-LP</i>         | GTAATGCGTGACGTGATTGTG                    |
| <i>ttm2-2-RP</i>         | GTATCCGTAACCCATTCCTGG                    |
| <i>abi4-1-F</i>          | GCCACCGTAGGAGGAGGATC                     |
| <i>abi4-1-R</i>          | TGTTGGAATTGTCCCATCTGGA                   |
| <i>ACT2F</i>             | TCGATCTAAGTTGACCGATC                     |
| <i>ACT2R</i>             | ACCTCTCTTGGATTGTGCTT                     |
| <b>Molecular Cloning</b> |  |
| 35S                      | CCACGTCTTCAAAGCAAGTGGATTGATGTG           |
| 35S-TTM2-F               | CAAATCTATCTCTCTCGAGATGGGTCAAGACAGCAATGG  |
| 35S-TTM2-R               | TCGTGGTCCTTATAATCTTGCCGCTTGTTAATGTAGC    |
| 1300F                    | TGTGTGGAATTGTGAGCGGATAAC                 |
| TTM2-GUS-F               | TCGGTACCCGGGGATCCTATAAATATAAATTTCTAGT    |
| TTM2-GUS-R               | CCCTCAGATCTACCATTATGAACAATAATCTGCAAA     |
| 35S-ABI4-F               | CCGGGCTCGAGAAGCTTATGGACCCTTTAGCTTCCC     |
| 35S-ABI4-R               | GTCGACTCTAGAGGATCATAGAATTCCCCCAAGATGG    |
| T7                       | TAATACGACTCACTATAGG                      |
| pET28a-ABI4-F            | AGCAAATGGGTCGCGGAATGGACCCTTTAGCTTCCC     |
| pET28a-ABI4-R            | CGGAGCTCGAATTCGGAATAGAATTCCCCCAAGATGG    |
| TTM2-LUC-F               | GGTACCGGGCCCCCCTCGAGTATAAATATAAATTTCTAGT |
| TTM2-LUC-R               | TCGATACCGTCGACCTCGAGTATGAACAATAATCTGCAAA |
| <b>RT-qPCR</b>           |  |
| <i>ACT2-F</i>            | TAACAGGGAGAAGATGACTCAGATCA               |
| <i>ACT2-R</i>            | AAGATCAAGACGAAGGATAGCATGAG               |
| <i>TTM2-F</i>            | GAAATCACGACTCGCCAGCG                     |
| <i>TTM2-R</i>            | GCTCTGCTGTGTTGGAGAGT                     |
| <i>ABI4-F</i>            | CTCGCAATGTCAAGATCCATTGGC                 |
| <i>ABI4-R</i>            | TTACTCGCCGCACTGAAGTCAC                   |
| <i>TTM1-F</i>            | TTCCAAGATCCCGAACAGGA                     |
| <i>TTM1-R</i>            | ACCAGTACGACCTCTTCCAT                     |

|                   |  |
|-------------------|--|
| <i>TTM3-F</i>     | AGTCACCGGCTAAGCTCTCA   |
| <i>TTM3-R</i>     | ACACGCTCTGGTTCCTCTGT   |
| <b>ChIP-qPCR</b>  |  |
| TTM2-P1F          | GTTTTATTATTACCTATGAC   |
| TTM2-P1R          | TTGATGACAGTTTTTGGTTTTTT  |
| TTM2-P2F          | AAAACGTGCATCAATAAAAA   |
| TTM2-P2R          | CTCTCTTCACTTCACGACCC   |
| TTM2-P3F          | GAAGTCAGAGAAAACCAAAA   |
| TTM2-P3R          | CATAGGCTTATGACTTATGA   |
| TTM2-P4F          | TAAATTGGTTCTCATTTCATT  |
| TTM2-P4R          | GGGAGAGCGATTTGTAGAG  |
| UBQ5-F            | AGAAGATCAAGCACAAGCAT   |
| UBQ5-R            | CAGATCAAGCTTCAACTCCT   |
| <b>EMSA Probe</b> |  |
| TTM2-F            | AAAATTGCACTCAAGAACATGTGGATCCTCGTCACATTCA<br>C<br>TCATAAGTCATAA |
| TTM2-R            | TTATGACTTATGAGTGAATGTGACGAGGATCCACATGTTCT<br>TGAGTGCAATTTT     |