

Supplementary figures

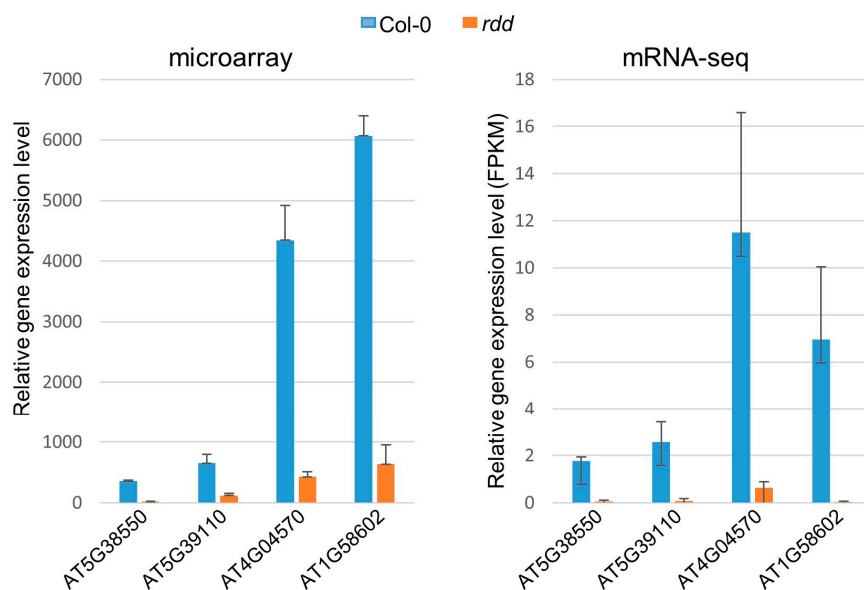


Figure S1. The four genes selected for promoter study in this paper show strong down regulation in *rdd* based on both microarray (left; [1]) and mRNA deep sequencing (right; three biological replicates for each genotype) analyses of three-week old plants.



Figure S2. A typical trace file of bisulfite sequencing analysis of the chloroplast genome-encoded *psaA* gene, showing efficient bisulfite conversion. The original nucleotide sequence is shown above, with cytosines highlighted in blue. Note that all cytosines appear as thymines (red peak) in the sequencing trace of the PCR product. All bisulfite-treated samples used in this study showed a similar trace file, indicating efficient bisulfite conversion

T2 plants, Col-0 background

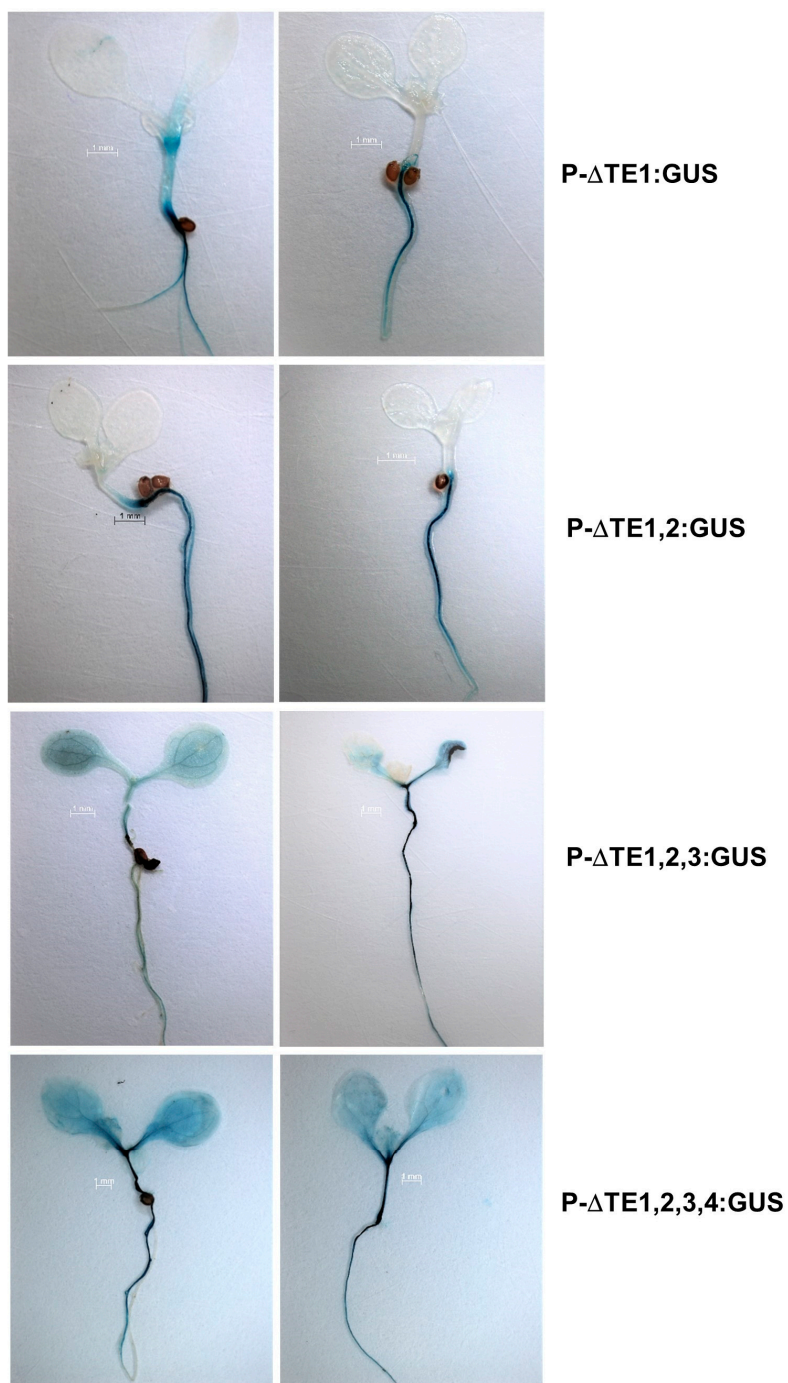


Figure S3. Histochemical analysis of GUS expression in the T2 plants of the truncated At5G38550 promoter:GUS lines. Note that the root specificity of GUS expression is retained when the first two TEs were deleted, but lost after the deletion of the third TE sequence in the promoter fragment.

Sequence of *AT5G38550* promoter :

ATCAGAGAGTTTTCCCTATCGTTTTCCCTCGTTTATAATTGCATTTTTTCATCGTTACTATT
 CGTTAAATATTTTAAATTTTTTAAATTTAAATATCTTTGCAGTTATGTCTTCTTACAAAGT
 GTCTTTTCTCCATATTTATTTGTATTTTCTTATCACAATTATTTCTTTCTAAAAATTA
 ATATTTTACAAATATTTGTGTCAATTTAATTGTTTATATCTTCTGAACTCTATATACTTTT **At5TE55860**
 GTTTACCAATATTCAATCTTCTGACAATTGTTTTTTTAAAGATGATTGATGGTCCAAGA
 TTAAACCCGACCCGGACAGTGAACCCGACTACCTTCTCGATTATTGGGTCATCGGGTTAA
 CCAGGTTGGACCATAAGTCAATTAATTTAAATTTTATTTAATAAAATTTAATATTAATAAGA
 TTTTAGAGTTCTTTATAAATTTAAAAATAAAAATAATCATGTTTATAAAATATAAAATCAG
 ATTTATGTTTAAATAAAATATAAAATCATTATACCAAAAAATAATAAAAAAAATAAAT
 AATATATATATATATAATCAACAATAATAATAAAGTGATTAAATTTTTTAAATCCAAC
 AAACGTCTAATACCATAACAAATATAGTAGTAGATCACCAATGACGGAATAAACTAGTA
 AAACATCGTGAATTTACACAATAATATCGGGTGTCTCACTCACCATTTCGTTTCATTTTT
 AAGGCGGCATTGTAAAGTCTTCGTCAAATGTAAACCATAAAATGAGTTTACGAACGTAA
 AAGATTTCTAAAAATGATTGAATAAAGTCTAAAATCTCATATTATATTTCCAAAAATAAGA
 GAATATTTTAAACCCACACCCGACCGGTTCCACGGATCATAGGTTAATAGTGAGTTTTT
 GTGGGTTTTTTTGAATTTGAACTTGTCTGGGTTTTAGCACTAAACCTAAATCAGAAAAATG
 TTTGGGTCACGGTTCAACCGGTCGGACCGAGTGTGAAAACTGACCAC TGGGTTTTTCT **At5TE55855**
 ATTTAAAAATAAGTTGAGAGTTTTTAAATGGATAAGTCTAAACTTGAGGGTTTTTTCATT
 AAAATTTATTTTCTAAAAATAACAACAACAATTTATAATATTCATCATTTTGAGTTTGAT
 TTATTTGTTGAGAAATATTGTATAAACAATTTTAAATATTTTCTTCATGAAATCGCGA
 GAAAAGATATGTTTGAGTTTATTAATAATAAAAAATAATCAGATCATGTTTAAACAAAATA
 TAAAGTCTAACAATAATAAGAAAGTGATTAAAAATTTATAAATCTAACTAAAAACACGGTAA
 AAAATACTAAGATAGTAGGATAGTGAATACGAAGAATTTAAAAAGTTTTGAAATAATT
 CAATAATGAACAGTGAATACACTAAAACTCTATCTTTTTTGTCCAAAATCAAATATATATA **At5TE55850**
 TTTTAAACGAATACCCGACAGTTTACCAGATCACAAGTTAGTGCCAAATTTTTGTGGA
 TTTTGTGCGCTTTTTAAATTTGTCTGGATATTAACAGTAACTCAAACCCGATAAATATCTGT
 AACACTGGTTAACCAGTAAGGATTGGACGTGCAGATTTTTTTTTTCTTTTTTGAATGAAT
 GACCAATGTCTGAAGCTTTACGGTTTGGTTGCAAACAGAGTTGCAGTCCATCTCTCATGG
 AGGTTGAACCCATTGAGATATATATAGAAGCGATTCCGAAGTGTCCGGTCAATCACT **At5TE55845**
 TGAATTATTACCGATGCAGAGATGGGAAGCTCACCATTGTCTTCTCGATTCTTTCCGTC
 CAAATTGAATGGACTGTCTGCTTTAAATATACGTAGCGTAAAAATGAATTGATGCGTCTTCG
 AGAACTGAGAAGTGGAGACAATACTTAGCAAAGCAGAGTAATCCAAAGTAAAAATCTTGCA
 TGAGAATTGCGCTTGGCAAGATGTTCCAGATTTGAGCCGAGAATGTGCAGCTGAAAAACA
 AATGATCCCTTGTCTCAAAATGGAACCTGACAAAACACACATGTTGGATTGAGATTTCGATG
 ACCAAGAGCACATTTGATCACATGTACGTTGAAGTTGGTTTTATGTTTCTAAAAATAAT
 GCCAAACAATAAATGCTCGAACTGAAGTCCACCTACAAGTTTACGAGTAGGTTTGTCA
 TATCATAAAAAACAAAATCTACGCTGTGATGAGATGCAATCATGCAAGGTCGTTTTAAA
 ATAATCGTTTTGTTTGTGAAGACGTACTTTAGGTAGTCTTTGAATAATTATTTTCACAACT
 AGTTTATATTTTACAAAATTTAATATTTAATCTTGCAACCAGCAGCCTCATATATAACAA
 TATAAATATACATTTTAGAAAAATGGCCAAAACCTGTATATATGAAAAAGCCAAAGTCCA
 TCGCTAAACTTACTGATCAGCATAGCAGTCTGTTCACTTCAGAGGTCAGCTCTTTTCTC **At5G38550 gene**
 TTTCCCTCATAAGCATGCTTACTTCTTATTTCGCACCAATGTTTTAACCTTAAATAAGATC
 TTATCGAAATCTATTATTTATGTGAACGTAATGAGCATAGTTTTAGATATCCTCTTACAG
 TAGTTCCGTT

Figure S4. The hAT TE sequence (At5TE55850) contains potential binding sites for AHL20 (AAAT) and ARR11 (GGATT)-binding motifs.

Reference

1. Le, T.N.; Schumann, U.; Smith, N.A.; Tiwari, S.; Au, P.C.; Zhu, Q.H.; Taylor, J.M.; Kazan, K.; Llewellyn, D.J.; Zhang, R.; et al. DNA demethylases target promoter transposable elements to positively regulate stress responsive genes in Arabidopsis. *Genome Biol.* **2014**, *15*, 458.