

Figure S1. Alignments of PbeMTase family proteins. Sequences in the red box indicate the DNA methylase domain.

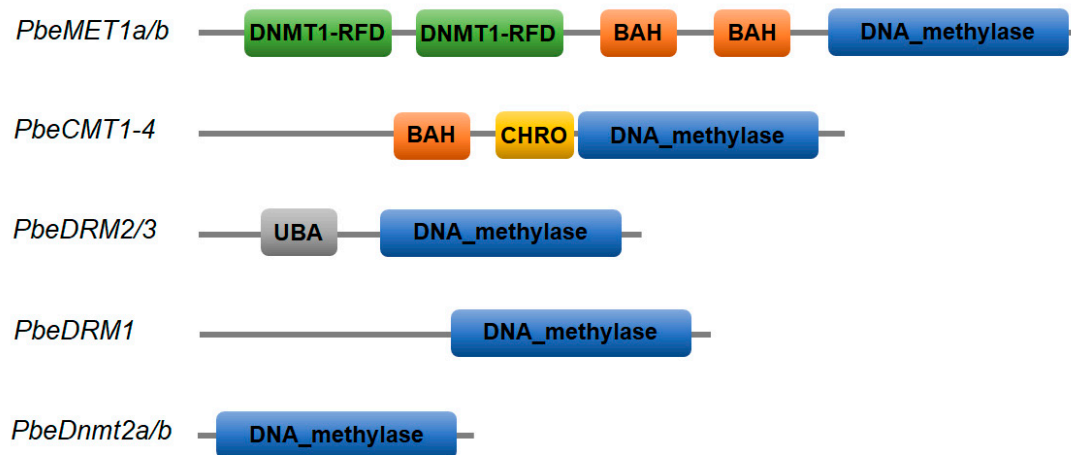


Figure S2. Various domains present in PbeMTase proteins.

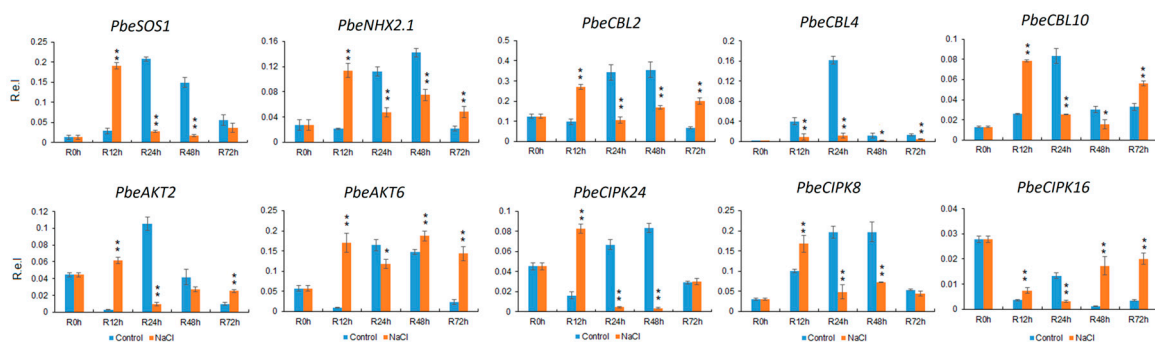


Figure S3. Expression patterns of salt-responsive genes under salt stress in *Pyrus betulaefolia*. Young *P. betulaefolia* plants at the eight leaves stage were subjected to 200 mM NaCl stress by watering them with a salt solution. At 0, 12, 24, 48 and 72 h, samples of roots were collected. RT-qPCR analysis was performed to determine the relative expression levels. The $2^{-\Delta\Delta CT}$ method was used to calculate the relative expression. Significance levels of 0.05 and 0.01 were denoted by an asterisk and double asterisks, respectively. R.e.l. represented the relative expression level.

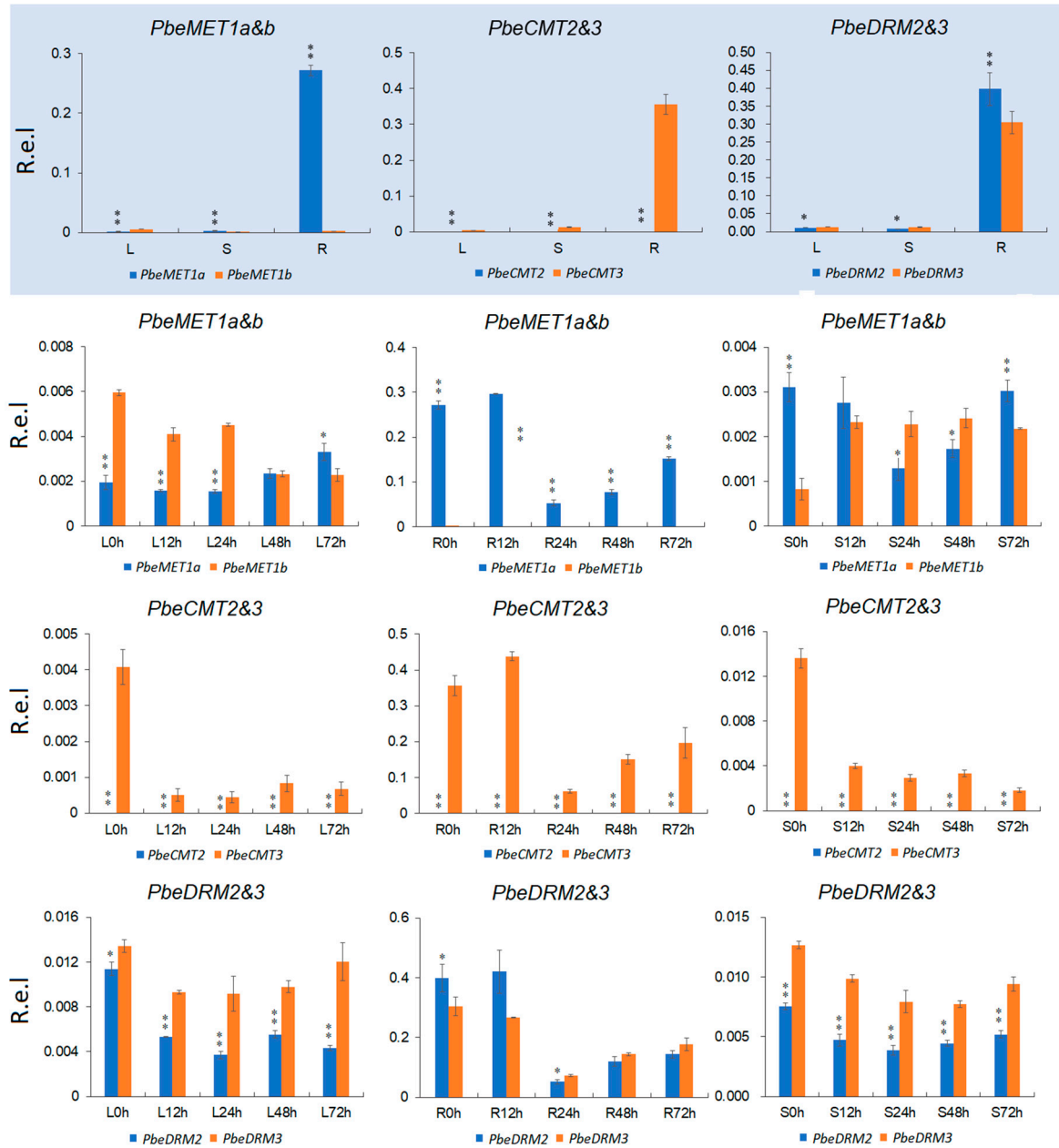


Figure S4. Expression profiles of the *MTase* syntenic gene pairs in response to salt stress treatment. Roots were sampled from *P. betulaefolia* plants growing under normal conditions. At 0, 12, 24, 48 and 72 h, samples were collected. RT-qPCR analysis was performed to determine the relative expression levels. The $2^{-\Delta\Delta CT}$ method was used to calculate the relative expression. Significance levels of 0.05 and 0.01 were denoted by an asterisk and double asterisks, respectively. R.e.l. represented the relative expression level.



Figure S5. The visual picture of a *Pyrus betuleafolia*.