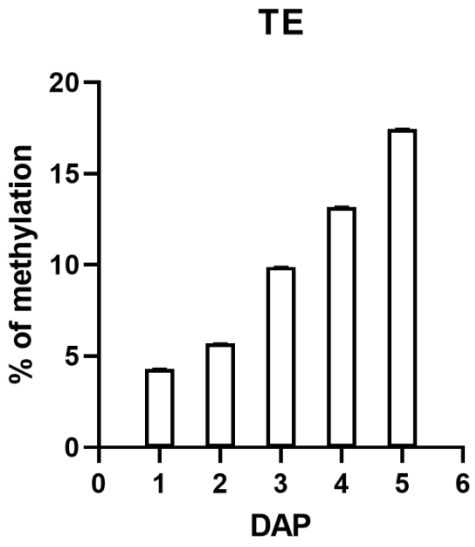
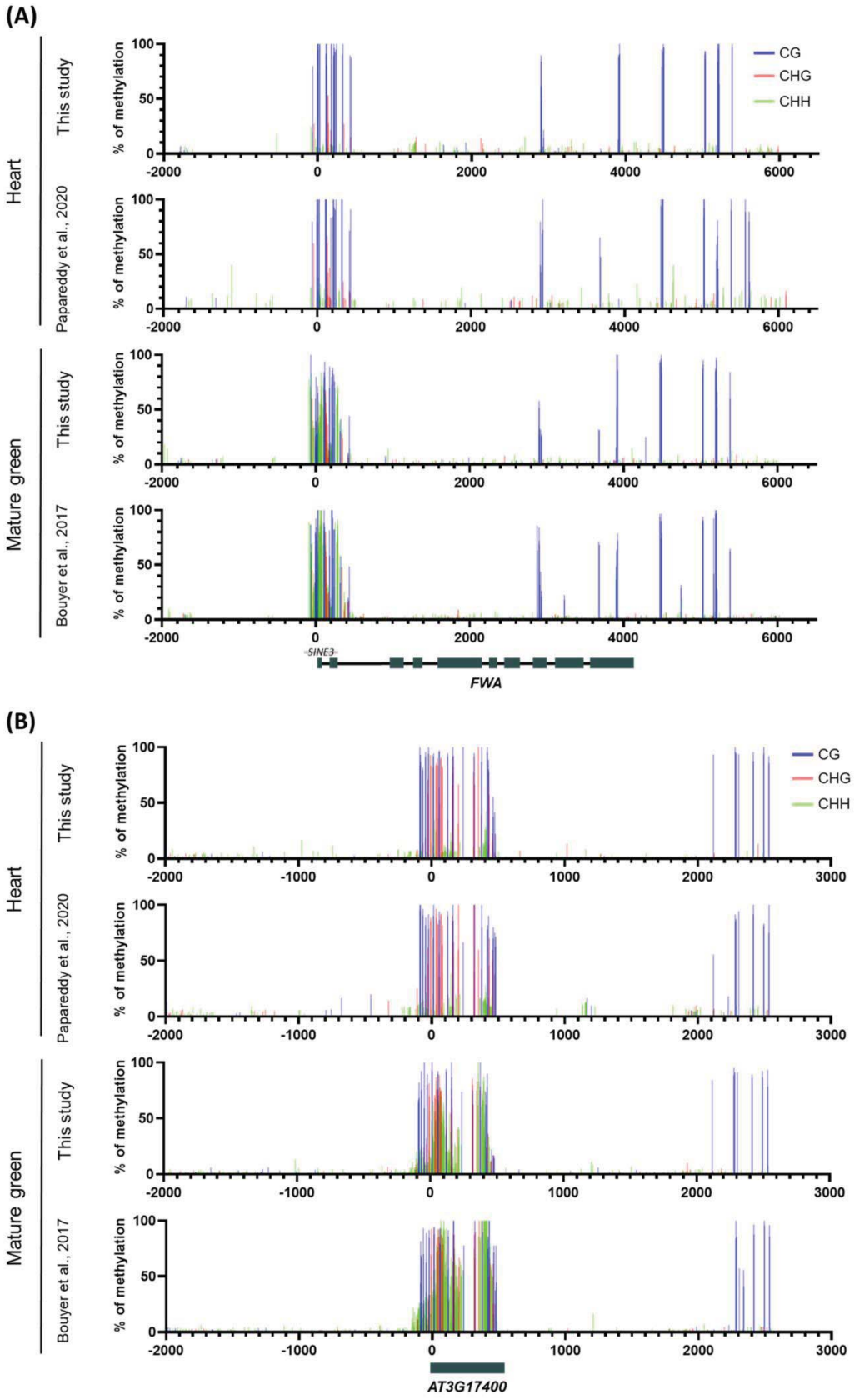
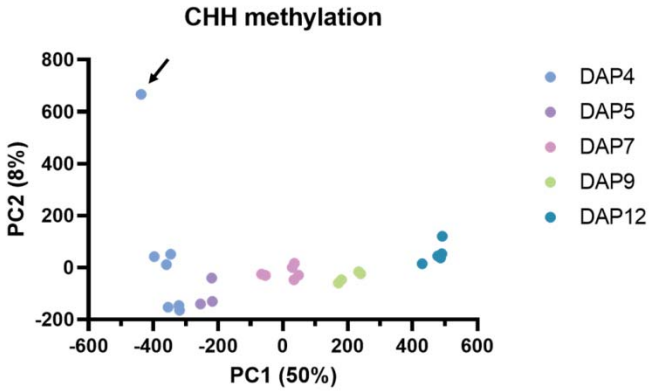
Supplementary Fig. S1. PCR tube lid with a manual cut. When moving embryos to PCR tube lids using glass micropipettes, the lid must be cut due to the shape of the glass micropipette.



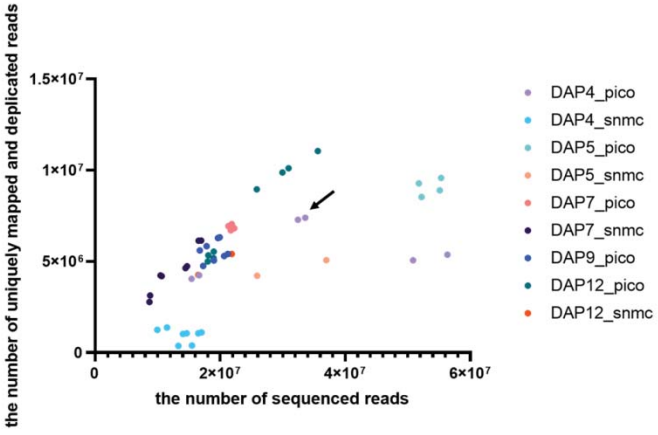
Supplementary Fig. S2. The dynamics of DNA methylation levels of the transposable elements. Total DNA methylation levels are increased in TE regions during embryo development.



Supplementary Fig. S3. Comparison of the DNA methylation levels in the specific gene locus between our and other groups' libraries.
Similar methylation levels of all cytosine contexts in the *FWA* (A) and *AT3G17400* (B) loci were shown in both libraries.



Supplementary Fig. S4. Similarity between BS-seq library replicates. PCA plot was generated at the % of CHH methylation of genes and TEs. Each library was represented by a single dot. One library from DAP 4 looks different from other DAP 4 libraries (black arrow). This might be due to the low coverage from that specific library. However, PC2 is just 8%.



Supplementary Fig. S5. The ratio of practically usable reads. Each library was represented by two single dots with paired ends. Most of libraries were clustered. However, one of the DAP4 data made by Pico kit had high levels of unique reads (black arrow). It could be from the large amounts of sample input.