SUPPORTING INFORMATION

Figure S1. $CpG_{O/E}$ distributions for 123 insect species. Gaussian mixture modeling was performed in R v2.3.4 to estimate uni- and bimodality. The dashed line represents the mean of each distribution, and the shaded area is the 95% confidence interval around the mean.

Figure S2. Character state transition matrices from Pagel's test for evolutionary dependence between two binary traits. Transition rates between states are given for independent and dependent models of evolution. Greyed rates represent a rate of zero (0) between states.

Figure S3. Genomic levels of DNA methylation are a good predictor of genic levels of DNA methylation. Linear regression between genomic and genic levels of DNA methylation for 22 species of insects with sequenced genomes.

Table S1. Species and accompanying behavior, genomic, DNA methylation and sequencing information used in this study.

Table S2. Species and DNA methyltransferase (DNMT) accession id's used in Figure 3.

Table S3. A list of proteins used to estimate multilocus coalescent trees and the best BLAST hit to *Apis mellifera* or *Drosophila melanogaster*.

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