**Methylome Analysis**

Previously published whole-genome bisulfite sequencing data [1-5] was downloaded from the Short-Read Archive (**Supplementary Table X**) and remapped to each species’ respective genome using methylpy [6]. Custom python scripts and pybedtools [7] were used to map methylation data to the first 150 base pairs of each transcript and call the weighted methylation level [8]. All methylation analysis scripts and tables of methylation levels are available on Github (https://github.com/niederhuth/Bowers-Gene-Duplication-Methylation).

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