

1 **Supplementary information**

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3 **Supplementary Table 1 Output from edgeR v3.20.1⁵³ with gene expression**
4 **(Fragments Per Kilobase of transcript per Million mapped reads [FPKM]) for *O.***
5 ***fasciatus* ovaries ds-*dnmt1* and control biological and technical replicates.**

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7 **Supplementary Table 2 Output from edgeR v3.20.1⁵³ with gene expression (FPKM)**
8 **for *O. fasciatus* gut, head, and thorax ds-*dnmt1* and control biological replicates.**

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10 **Supplementary Table 3 Gene expression FPKM for *A. mellifera* queen and drone**
11 **brains.**

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13 **Supplementary Table 4 Gene expression (FPKM) for *Z. nevadensis* female worker at**
14 **the final instar larva.**

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16 **Supplementary Table 5 DNA methylation summary statistics for all species**
17 **investigated in this study.**

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19 **Supplementary Table 6 Output General Features File (GFF) from RepeatMasker**
20 **v4.0.5 (<http://www.repeatmasker.org>).**

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22 **Supplementary Table 7 Gene Ontology (GO) terms for *O. fasciatus* v1.1 reference**
23 **genome assembly²⁶ annotated genes.**

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25 **Supplementary Table 8 Significantly enriched GO terms for the intersections**
26 **between Differentially Methylated Genes (DMG), Similarly Methylated Genes**
27 **(SMG), Differentially Expressed Genes (DEG), and non-Differentially Expressed**
28 **Genes (non-DEG).**

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