

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Genome size estimation by flow cytometry analysis.

File name: Supplementary Data 2

Description: Classification of repetitive sequences of the *D. nigrofasciatus* genome.

File name: Supplementary Data 3

Description: Statistics for the sequencing data of the *D. nigrofasciatus* genome.

File name: Supplementary Data 4

Description: Statistics of the *D. nigrofasciatus* genome assembly.

File name: Supplementary Data 5

Description: Statistics of chromosomes in the *D. nigrofasciatus* genome.

File name: Supplementary Data 6

Description: Chromosome coverages based on DNA-seq from male individual.

File name: Supplementary Data 7

Description: Statistics of the *D. nigrofasciatus* gene annotation.

File name: Supplementary Data 8

Description: Number of differentially expressed genes between long- and short-day eggs during early embryonic development.

File name: Supplementary Data 9

Description: Number of differentially expressed genes between consecutive developmental timepoints in long- and short-day eggs.

File name: Supplementary Data 10

Description: Cosine similarity values and gene overlap statistics for significantly associated cluster pairs between long- and short-day eggs.

File name: Supplementary Data 11

Description: Gene Ontology and KEGG pathway enrichment analysis of representative homochronic cluster pairs.

File name: Supplementary Data 12

Description: Gene Ontology and KEGG pathway enrichment analysis of representative heterochronic cluster pairs.

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44 **File name:** Supplementary Data 13

45 **Description:** Gene Ontology and KEGG pathway enrichment analysis of differentially
46 expressed genes at each developmental time point.

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48 **File name:** Supplementary Data 14

49 **Description:** Chromatin accessibility profiles from ATAC-seq analysis.

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51 **File name:** Supplementary Data 15

52 **Description:** Gene Ontology enrichment analysis of genes associated with decreased
53 chromatin accessibility in short-day egg.

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55 **File name:** Supplementary Data 16

56 **Description:** Number of eggs used for RNA-seq analysis at each developmental timepoint.

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58 **File name:** Supplementary Data 17

59 **Description:** Number of eggs used for ATAC-seq analysis.

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61 **File name:** Supplementary Data 18

62 **Description:** Numerical source data for Fig. 4b, c (TPM values of individual samples).

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