



**Supplemental Fig S11. Overview of how to use the Silkworm Mutant database.** The database provide photographs displaying the phenotypes of the mutants, assisting researchers in their selection of genes and materials of interest. By retrieving the Sample ID, users can access the photographs. By retrieving the silkworm gene ID, users can gain access to functional annotations, such as KO, GO, KOG, Pfam and KEGG enzyme, as well as related PubMed links. Moreover, exons, untranslated regions (UTR), and introns are displayed to provide a viewer with the genomic architecture of the chosen gene. To explore more information about a specific gene, users can simply click on the eFP module, which shows the expression values of selected genes in various tissues during distinct growth phases, represented by different color shades.