

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: **Related to Figure 1. RNA-seq pairwise comparisons.** The full dataset for each of the three pairwise comparisons involving *Pngl*<sup>-/-</sup> midguts is provided as an Excel file (*Pngl*<sup>-/-</sup> vs y w, *Pngl*<sup>-/-</sup> vs *Pngl*<sup>+/-</sup>, and *Pngl*<sup>-/-</sup> vs *Pngl*<sup>-/-</sup>; *Pngl* Dp/+). FC, fold change; CPM, counts per million; LR, likelihood ratio; FDR, false discovery rate.

File Name: Supplementary Data 2

Description: **Related to Figure 1. List of downregulated and upregulated genes in all categories shown in the Venn diagrams in Figure 1b.** Provided as an Excel file.

File Name: Supplementary Data 3

Description: **Related to Figure 1. List of the genes differentially expressed in *Pngl*<sup>-/-</sup> midguts that exhibited >1.5 fold-change in all three pair-wise comparisons based on RNA-seq.** Provided as an Excel file.

File Name: Supplementary Data 4

Description: **Related to Figure 1. List of the top 15 biological processes identified upon GO analysis of the upregulated and downregulated gene categories based on DAVID analysis.** Analysis of differentially expressed genes is based on the *P* value and false discovery rate (FDR) calculations embedded in the DAVID website. The gene count, *P* value, fold enrichment, FDR, and the gene list for each category is provided as an Excel file.