



Figure S4 Up-regulation of genes spanning the repertoire of *Drosophila* innate immune response. Dashed lines indicate thermal stress at 38.5^o, solid lines indicate recovery up to 48 hours post stress at 25^o. Exon profiles from the microarray analyses (constitutive exon set) are shown as average normalized expression relative to time zero on the Y-axis (log₂). A) Expression profiles of the PGRPs that activate the immune pathways to regulate the expression of antimicrobial peptides; PGRP-LC and LF (black circles) are required to activate the IMD pathway, PGRP-SD (dark grey squares) is required to activate the Toll pathway, other non-activating PGRPs SB1 and SC2 (light grey triangles). B) IMD (grey) and Toll (black) signaling components. C) Bacterial (gram -ve (IMD) and +ve (Toll)) and D) fungal (Toll) AMPs activated by the humoral immune pathways. E) AMPs and other genes regulated by the JAK/STAT pathway (IMD).