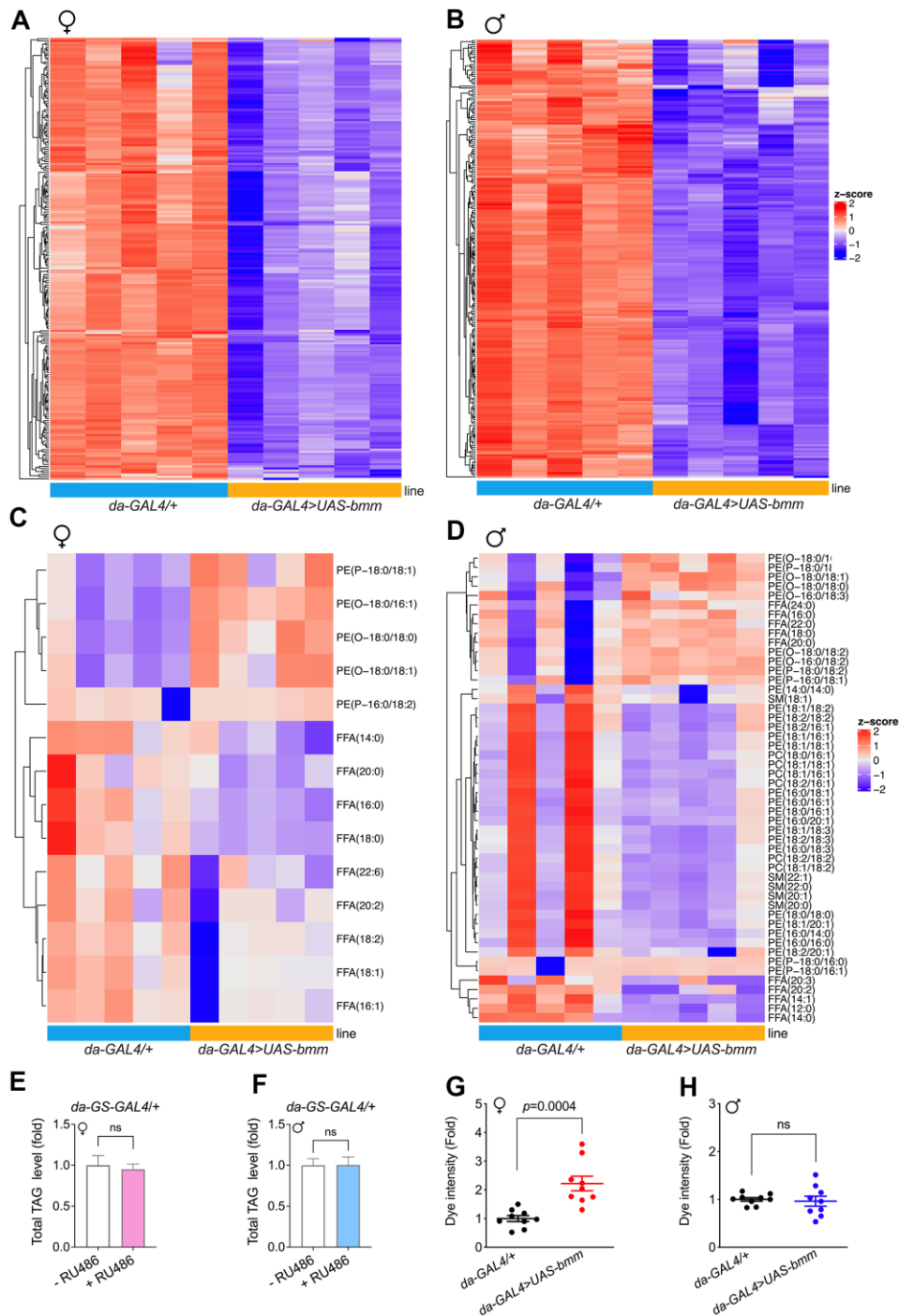
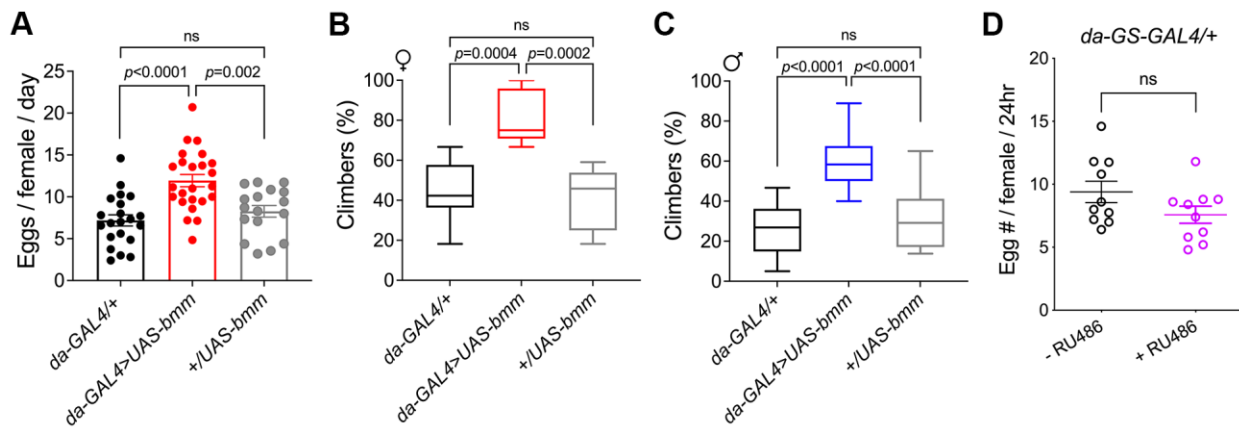


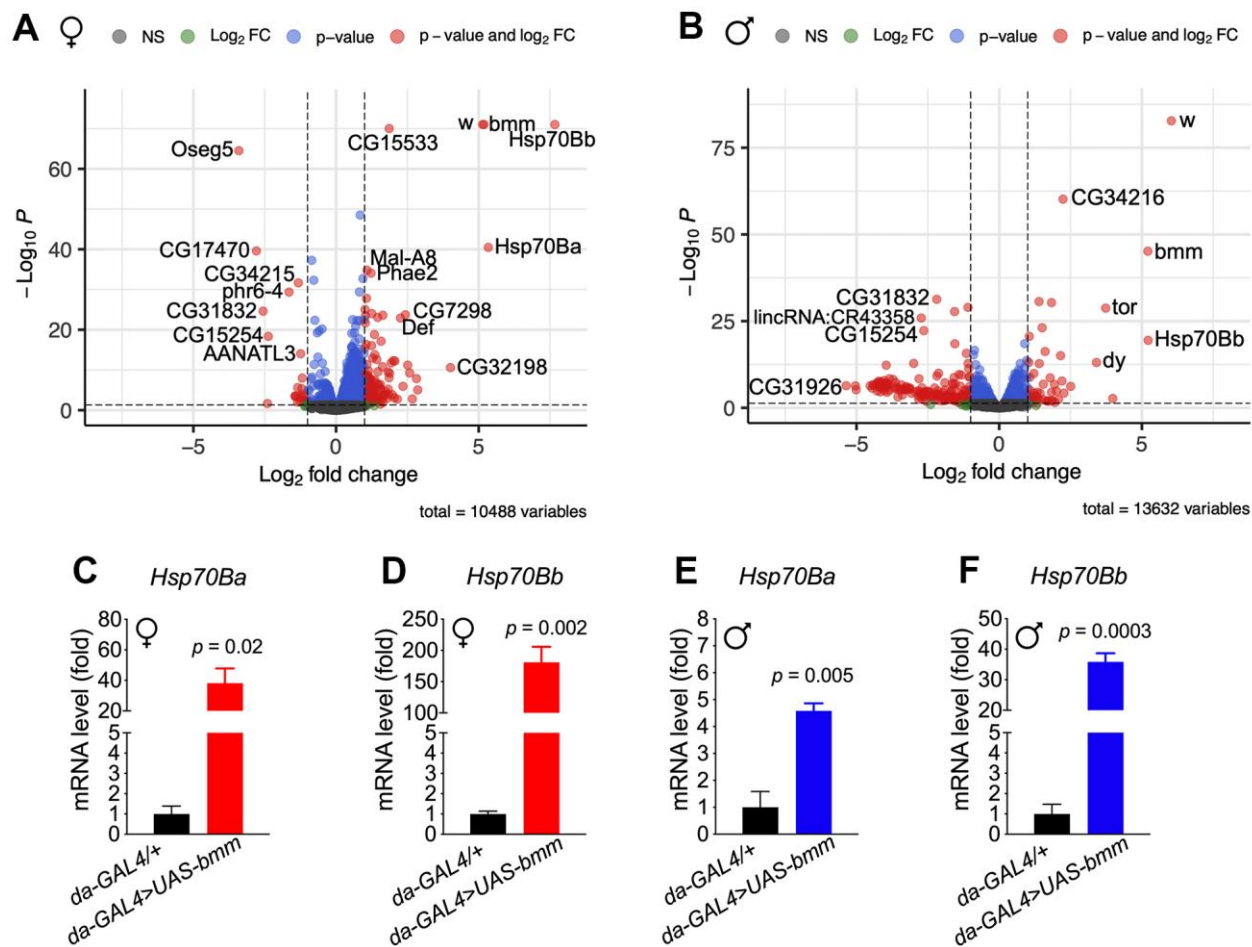
SUPPLEMENTARY FIGURES



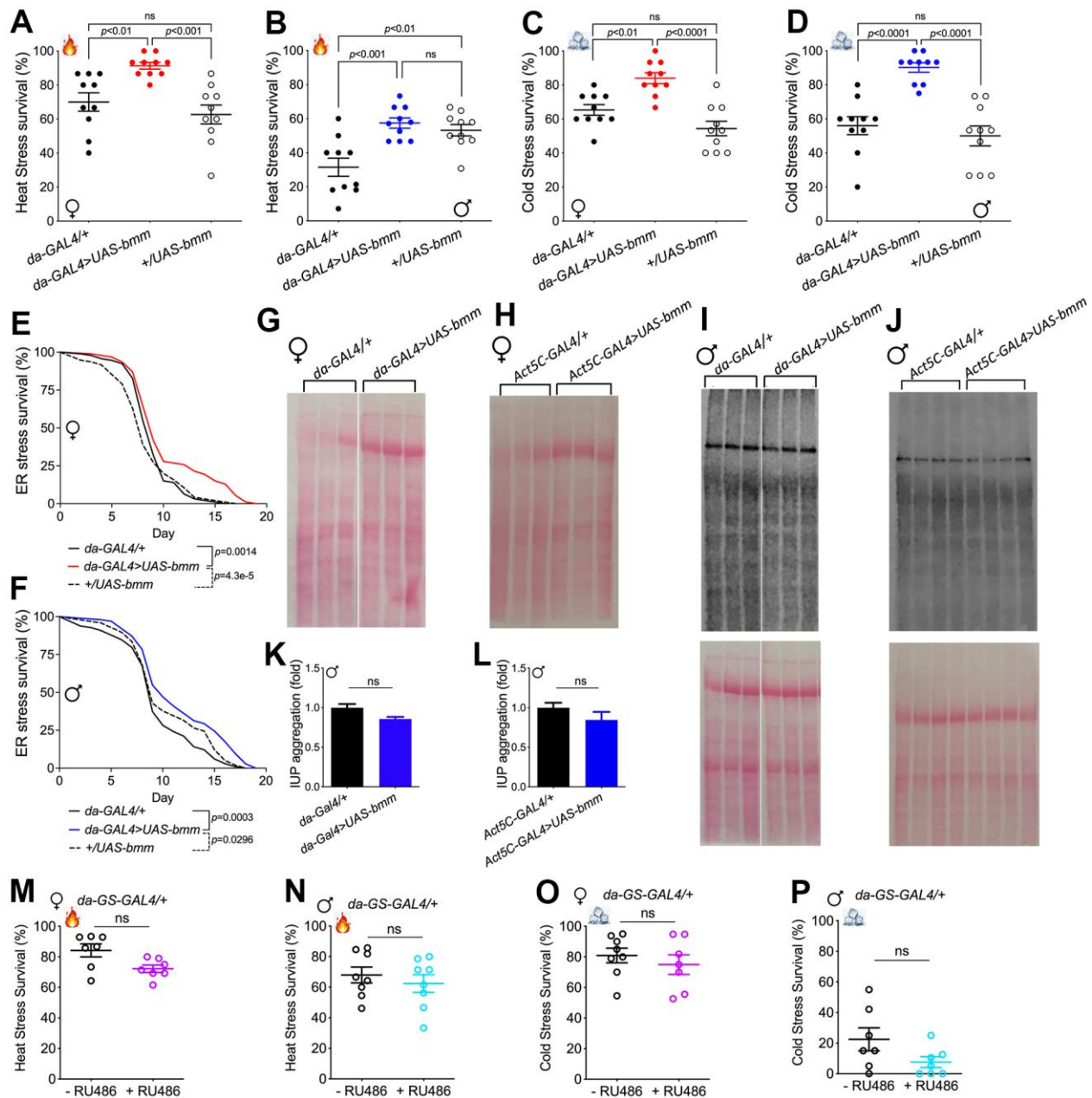
**Supplementary Figure 1. Additional data related to global *bmm* overexpression effectively promotes lipolysis in *Drosophila*, related to Figure 1. (A, B) Heatmap of significantly different TAG lipids identified between *da-GAL4*<sup>+/+</sup> and *da-GAL4*<sup>>UAS-*bmm*</sup> flies. (C, D) Heatmap of significantly different non-TAG lipid species identified between *da-GAL4*<sup>+/+</sup> and *da-GAL4*<sup>>UAS-*bmm*</sup> flies. n=5 replicates, and each replicate contained 20 flies. (E, F) TAG content measurement in inducible *da-GS-GAL4*<sup>+/+</sup> control flies with or without RU486 induction. n=6 replicates, and each replicate contained 7-10 flies. (G, H) Feeding rate was determined by adding brilliant blue dye into food and dye intensity was measured after 6 hours of feeding. n=9 replicates, and each replicate contained 5 flies for female group, and 8 flies for male group. Data are shown as mean±SEM. Statistical analysis was carried out by two-tailed Student *t*-test.**



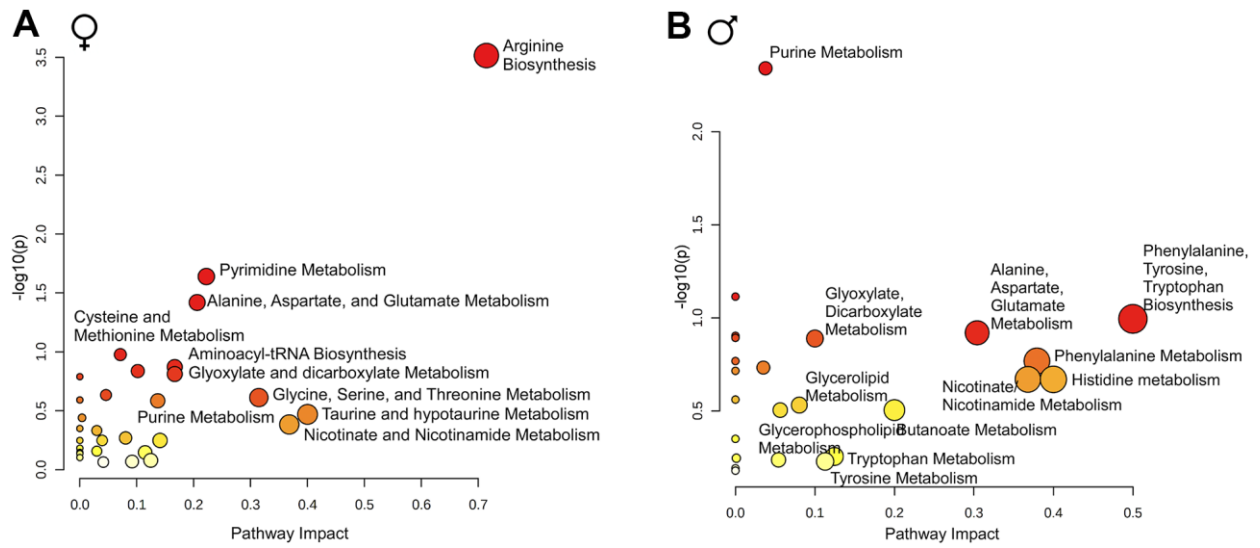
**Supplementary Figure 2. Additional data related to *bmm* overexpression promotes physiological fitness in both female and male *Drosophila*, related to Figure 2.** (A) Fecundity of 2-week-old *da-GAL4*>*UAS-bmm* vs. control *da-GAL4*<sup>+/+</sup> and *+/UAS-bmm* flies. Data are shown as mean±SEM and analyzed by one-way ANOVA. (B, C) Locomotion analysis of *da-GAL4*>*UAS-bmm* vs. control *da-GAL4*<sup>+/+</sup> and *+/UAS-bmm* flies at 30 days of age. Data are shown as box and whisker plot and analyzed by one-way ANOVA. (D) Fecundity of 2-week-old inducible *da-GS-GAL4*<sup>+/+</sup> female flies with or without RU486 induction. n=50 for each group. Data are shown as mean±SEM and analyzed by two-tailed Student *t*-test.



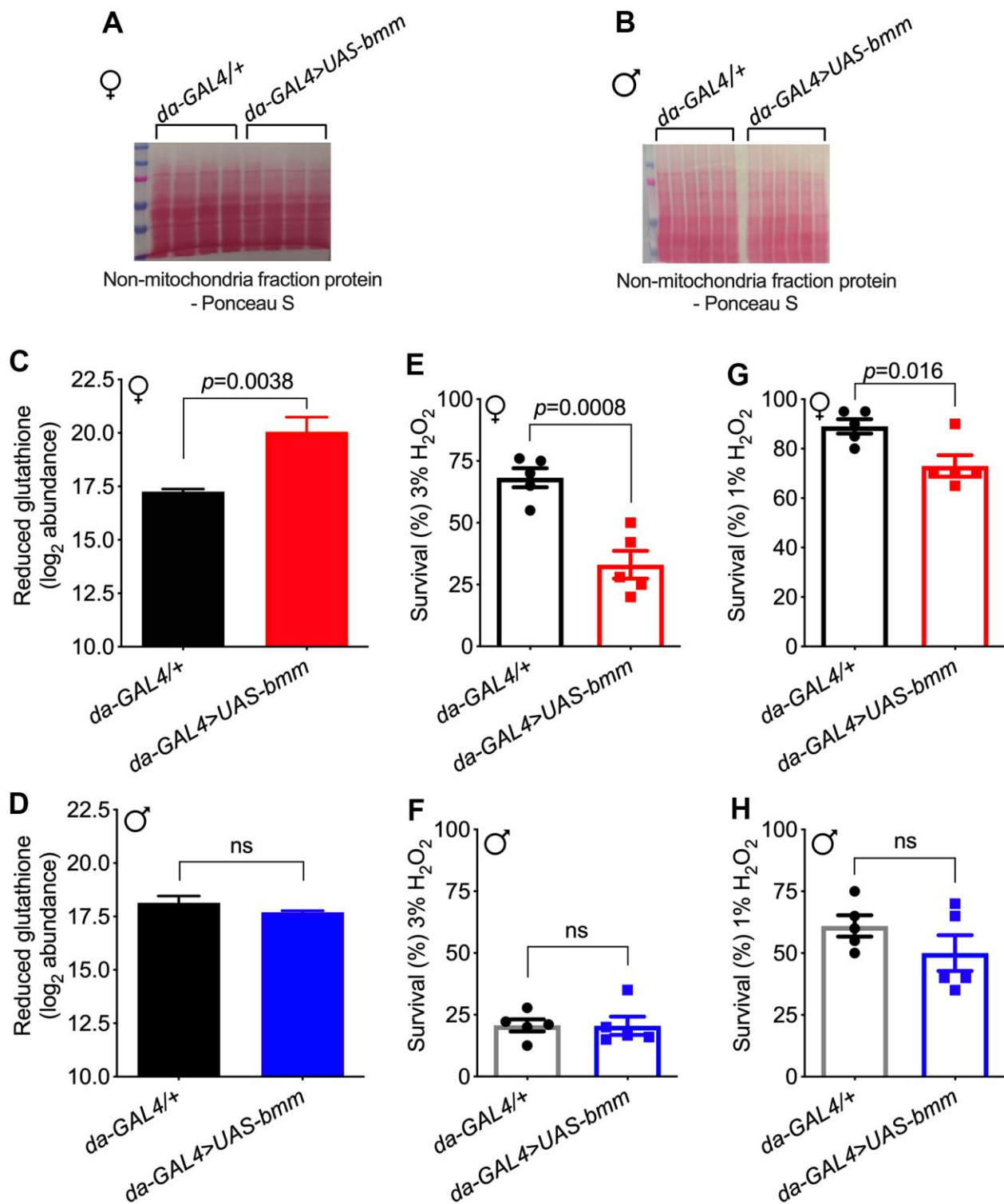
**Supplementary Figure 3. Additional data related to *bmm* overexpression enhances stress resistance and improves protein homeostasis, related to Figure 3.** (A, B) “Volcano plot” of genes by RNA-seq analysis with statistical significance against Log<sub>2</sub> fold change between *da-GAL4/+* and *da-GAL4>UAS-bmm* flies ( $p$ -value < 0.05, horizontal dotted line). Gene names for some of the most significantly differentially expressed genes (DEGs) are highlighted. NS=not significant. (C–F) *Hsp70Ba* and *Hsp70Bb* mRNA level measured by RNA-seq analysis in *da-GAL4/+* vs. *da-GAL4>UAS-bmm* flies. Data are shown as mean±SEM and analyzed by two-tailed Student *t*-test.



**Supplementary Figure 4. Additional data related to *bmm* overexpression enhances stress resistance and improves protein homeostasis, related to Figure 3.** (A, B) Heat stress resistance test in *da-GAL4>UAS-bmm* vs. control *da-GAL4*<sup>+/+</sup> and *+UAS-bmm* flies. (C, D) Cold stress tolerance test in *da-GAL4>UAS-bmm* vs. control *da-GAL4*<sup>+/+</sup> and *+UAS-bmm* flies. Data are shown as mean±SEM and analyzed by one-way ANOVA in (A–D). (E, F) The survival curves upon tunicamycin-induced ER stress in *da-GAL4>UAS-bmm* vs. control *da-GAL4*<sup>+/+</sup> and *+UAS-bmm* flies. *n* equaled about 100 flies for each group and *p* value was determined by log-rank test. (G, H) Ponceau S staining for normalization of insoluble ubiquitinated protein (IUP) aggregation intensity study in Figure 3H, 3I. *n*=3–6 replicates for each group, and each replicate protein was extracted from 10 flies. Samples in (G) were run on the same blot with the middle lanes of unrelated treatment groups cropped out. (I, J) IUP measurements by Western blotting and the corresponding Ponceau S staining in old male control vs. *bmm* overexpression flies at 35 to 40 days of age. *n*=3–4 replicates for each group, and each replicate protein was extracted from 10 flies. Samples in (I) were run on the same blot with the middle lanes of unrelated treatment groups cropped out. (K, L) IUP signal intensity quantification for (I, J) by Western blotting analysis. Ponceau S staining was served as loading control and was used for IUP signal quantification. (M, N) Heat stress resistance test in *da-GS-GAL4*<sup>+/+</sup> control flies with or without RU486 induction. *n*=101–116 for each group. (O, P) Cold stress tolerance test in *da-GS-GAL4*<sup>+/+</sup> control flies with or without RU486 induction. *n*=126–146 for each group. Data are shown as mean±SEM and analyzed by two-tailed Student *t*-test.



**Supplementary Figure 5. Additional data related to *bmm* overexpression increases mitochondrial biogenesis and oxidative metabolism, related to Figure 4. (A, B) Enriched analysis of a metabolic pattern of interest in datasets generated by targeted metabolomics analysis on flies overexpressing *bmm*.**



**Supplementary Figure 6. Additional data related to *bmm* overexpression increases mitochondrial biogenesis and oxidative metabolism, related to Figure 5.** (A, B) Ponceau S staining of non-mitochondria fraction protein corresponding to Figure 5I, 5J for mitochondria content quantification.  $n=4$  replicates for female group,  $n=6$  replicates for male group, and each replicate protein was extracted from 50 flies. (C, D) Level of reduced glutathione ( $\log_2$  abundance) in *da-GAL4/+* vs. *da-GAL4>UAS-bmm* flies.  $n=5$  replicates, and each replicate contained 20 flies. The FDR=0.00026 for *bmm* overexpression vs. control female flies. (E, F) Survival rates of female and male flies under 3%  $\text{H}_2\text{O}_2$  treatment.  $n=100$  for each group. (G, H) Survival rates of female and male flies under 1% of  $\text{H}_2\text{O}_2$  treatment.  $n=100$  for each group. Data are shown as mean $\pm$ SEM. Statistical analysis was carried out by two-tailed Student *t*-test in (C–H).