

## Supplementary Materials for Time-restricted feeding promotes skeletal muscle function in diet- and genetic-induced obesity through shared and unique pathways

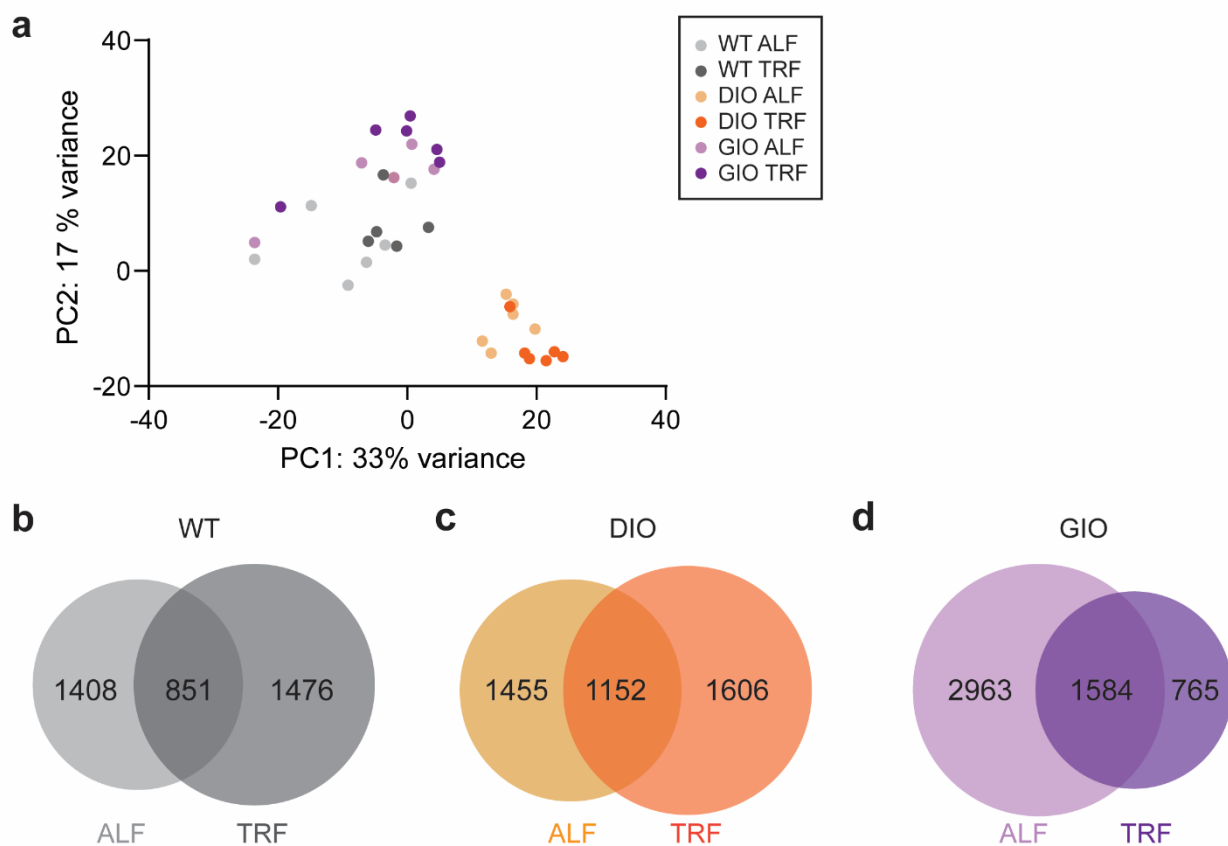
Melkani et al., Correspondence and requests for materials should be addressed to G.C.M. (email: [girishmelkani@uabmc.edu](mailto:girishmelkani@uabmc.edu)).

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### Figure S1

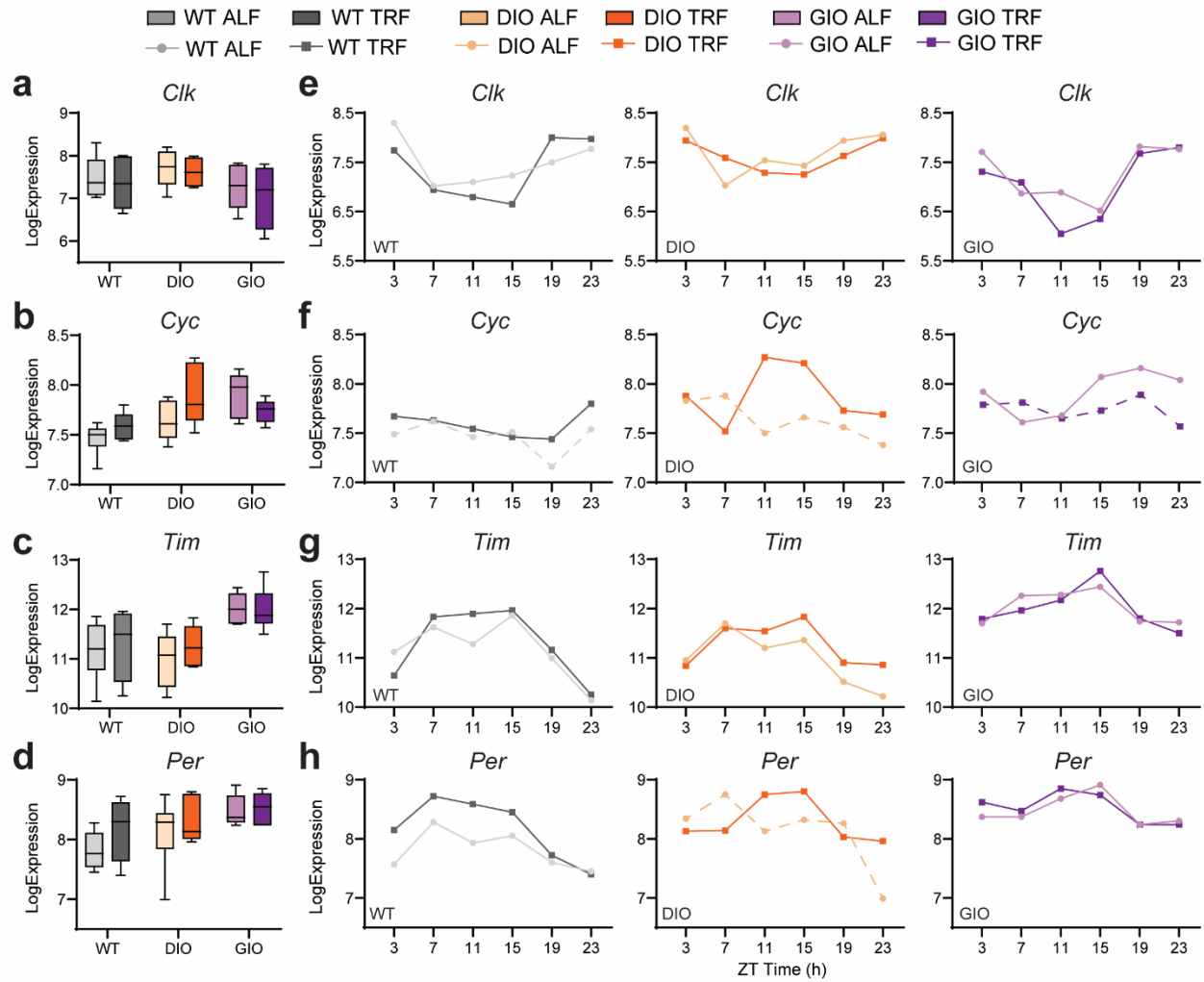


### Figure S1: Overview of transcriptome data in WT, DIO and GIO models

(a) PCA plot of skeletal muscle transcriptome data.

(b-d) Periodic skeletal muscle transcripts identified under ALF and TRF in WT (b), DIO (c) and GIO (d).

**Figure S2**

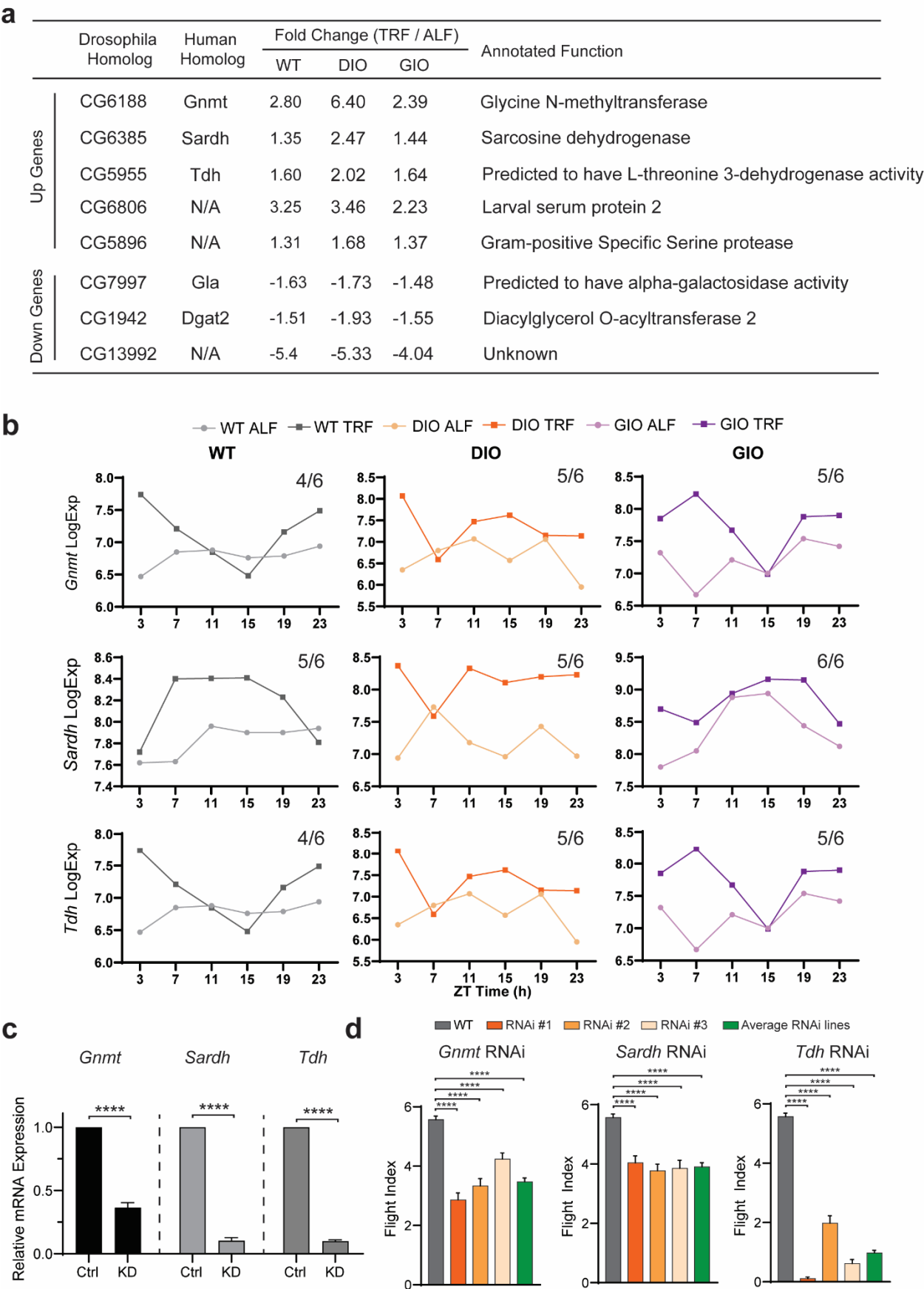


**Figure S2: Periodicity of clock genes**

(a-d) Expression level (normalized read count, log2) of *Clk* (a), *Cyc* (b), *Tim* (c) and *Per* (d) under ALF and TRF in WT, DIO and GIO.

(e-h) Temporal expressions of *Clk* (e), *Cyc* (f), *Tim* (g) and *Per* (h) under ALF and TRF in WT, DIO and GIO. Empirical\_JTK periodicity detection was presented as a solid line (Corrected P-value  $\leq 0.05$ ) or dash line (Corrected P-value  $> 0.05$ ).

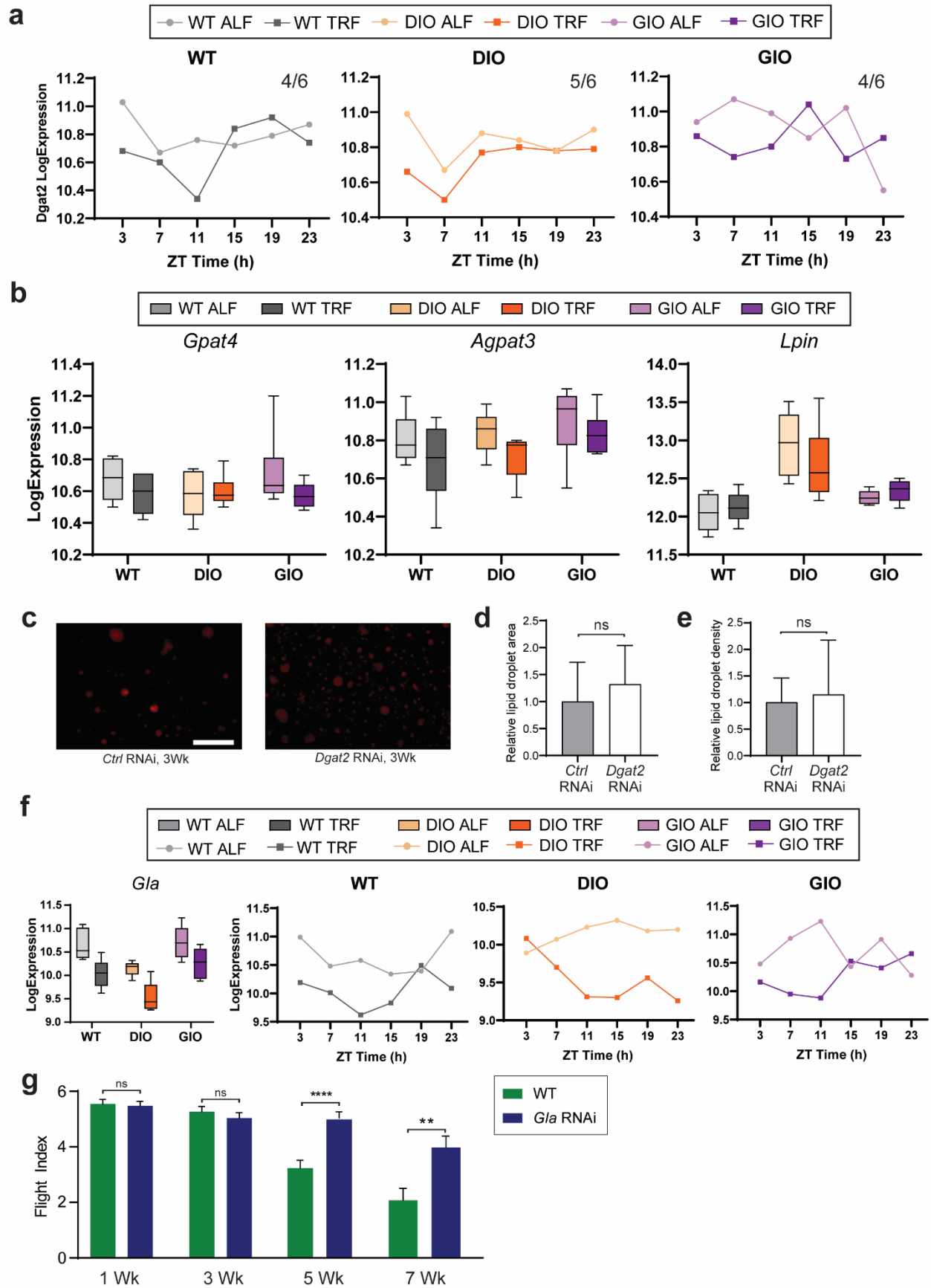
Figure S3



**Figure S3: Profiles of the significantly upregulated genes across WT, DIO and GIO models**

- (a) A table of differentially expressed genes shared across WT, DIO and GIO models.
- (b) Temporal expressions of *Gnmt*, *Sardh* and *CG5955* under ALF and TRF in WT, DIO and GIO.
- (c) Quantification of RNA levels from thoraces of 3-week-old flies following *Gnmt*, *Sardh* and *CG5955* IFM-specific *KD*.
- (d) Flight performance of WT male flies with *Gnmt*, *Sardh* or *CG5955* IFM-specific *KD* at 1 week of age. Three independent RNAi lines per gene were tested. Combined average data were shown in green. N# = 30-50 females for each independent fly line per time point (N# = 100-150 combined). Bar graphs represent mean and SEM, with significance presented as <sup>ns</sup> $p > 0.05$ , \* $p \leq 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .

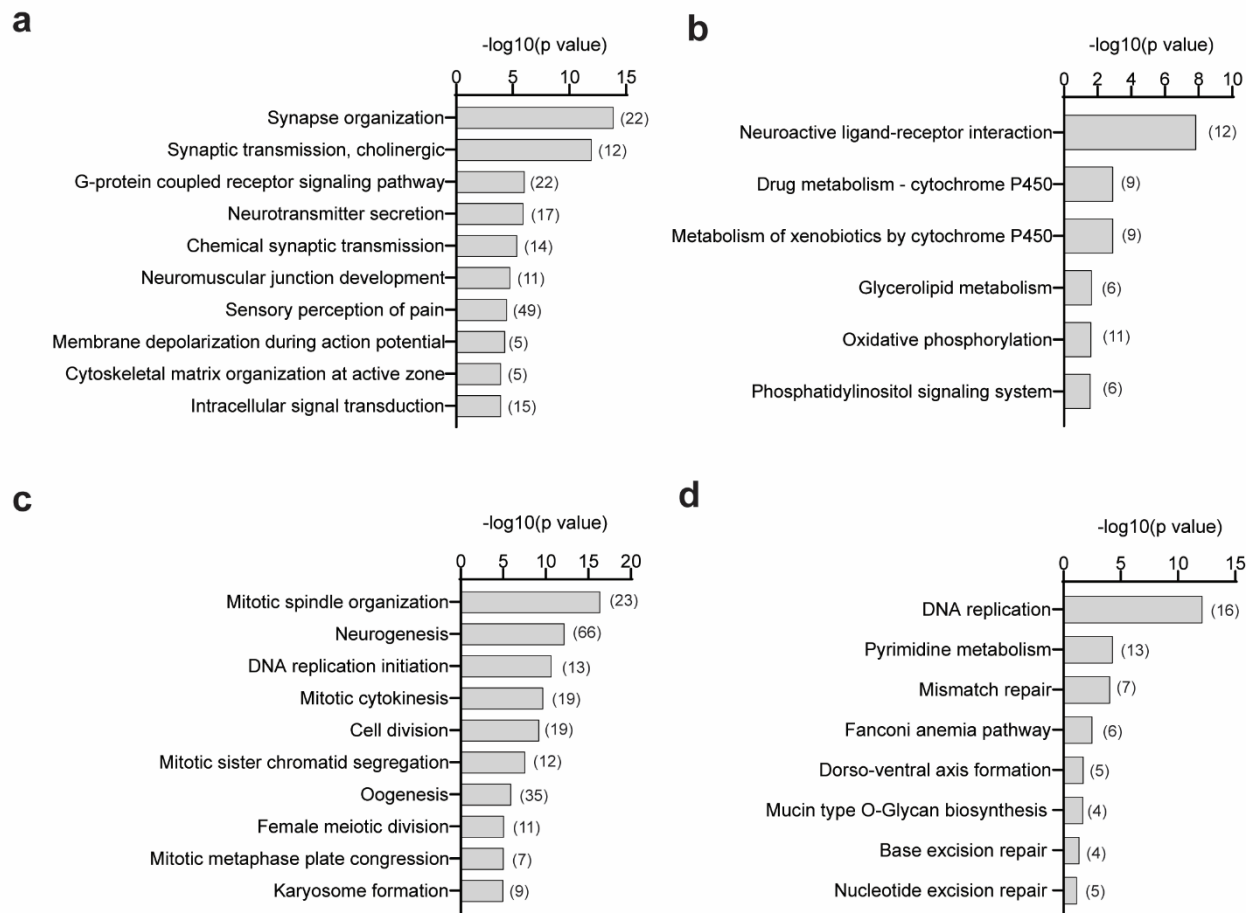
**Figure S4**



## Figure S4: Profiles of the significantly downregulated genes across WT, DIO and GIO models

- (a) Temporal expressions of *Dgat2* under ALF and TRF in WT, DIO and GIO.  
 (b) Expression level (normalized read count, log2) of *Gpat4*, *Agpat3*, and *Lpin* from *de novo* triacylglycerol synthesis under ALF and TRF in WT, DIO and GIO.  
 (c) Fluorescence images of the abdomen from 3-week-old females with IFM-specific *KD* of *Dgat2* upon probing with Nile Red (red puncta). Scale bar is 20  $\mu$ m.  
 (d-e) Lipid quantification (size (d) and density (e)) showed no significant differences in lipid droplet area upon IFM-specific *KD* of *Dgat2* compare to age-matched control. *N*# = 9 from three flies' abdomen per genotype.  
 (f) Expression profiles of *Gla* under ALF and TRF in WT, DIO and GIO.  
 (g) Flight performance of WT male flies with *Gla* IFM-specific *KD* at 1, 3, 5 and 7 weeks of age. *N*# = 67-99 females for each condition per time point. Bar graphs represent mean and SEM, with significance presented as <sup>ns</sup> $p > 0.05$ ,  $*p \leq 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ .

## Figure S5



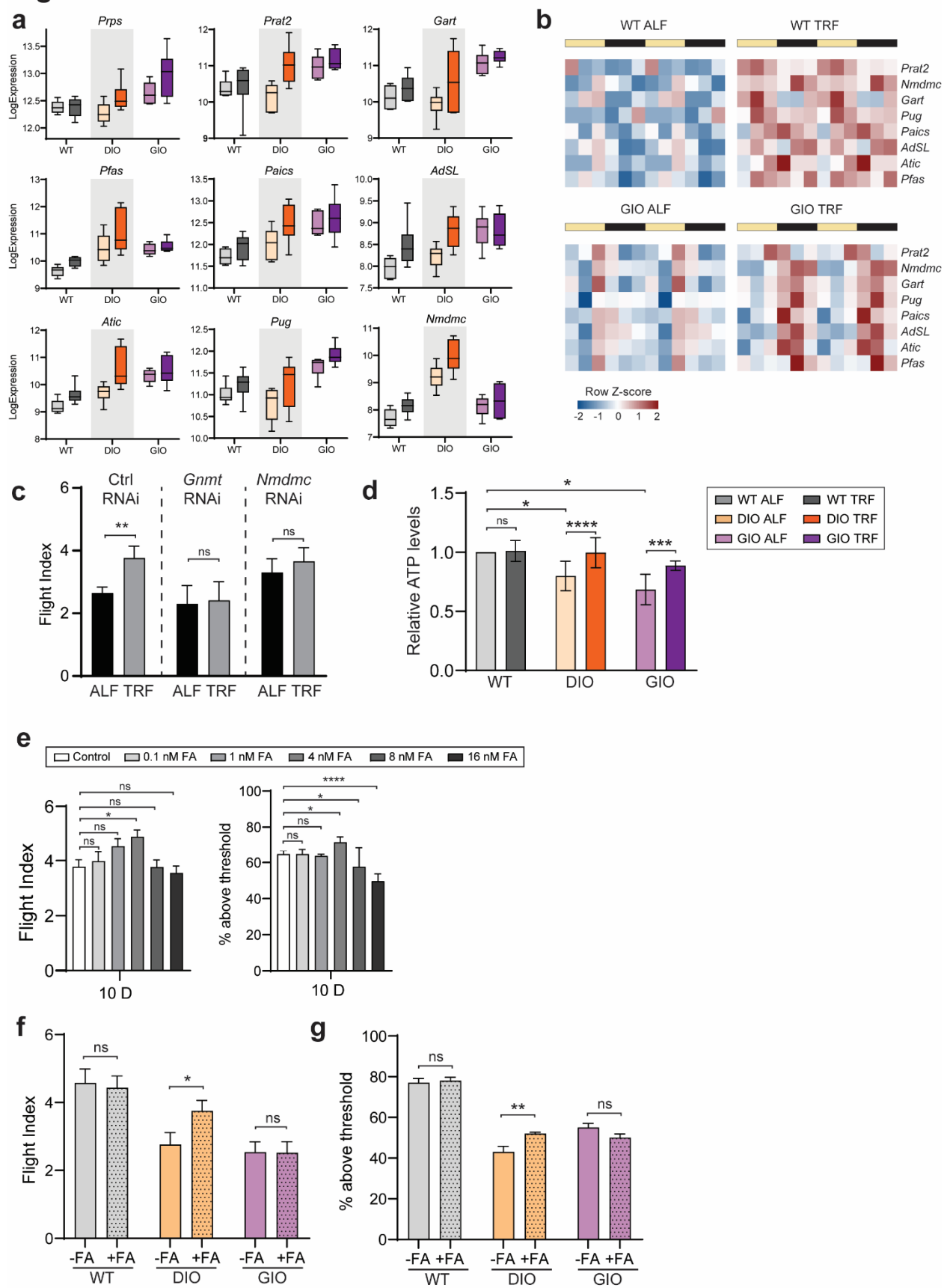
## Figure S5: GO and Reactome analyses of significantly downregulated genes under TRF versus ALF in obesity models.

- (a) GO analysis and (b) Reactome pathway analysis of 636 genes that were significantly downregulated under TRF in the DIO model. Bar charts represent the - Log10 (*p* value) of each

enriched GO term and pathway. The number of genes identified in each GO term and pathway is shown in parenthesis.

(c) GO analysis and (d) Reactome pathway analysis of 579 genes that were significantly downregulated under TRF in the GIO model. Bar charts represent the  $-\text{Log}_{10}(p \text{ value})$  of each enriched GO term and pathway. The number of genes identified in each GO term and pathway is shown in parenthesis.

**Figure S6**

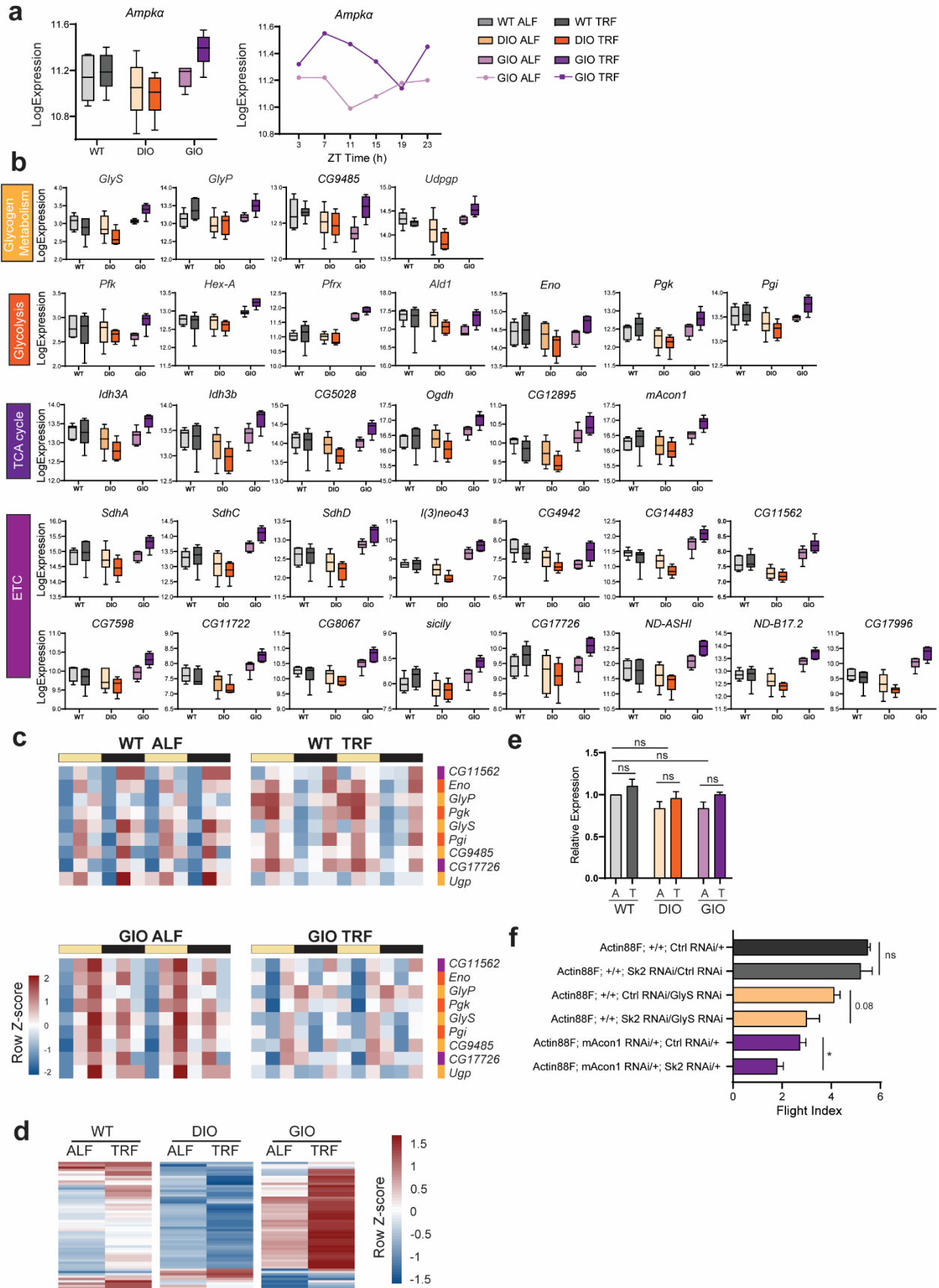




**Figure S6: De novo purine biosynthesis and folate cycle genes under ALF and TRF in WT, DIO and GIO models**

- (a) Expression levels of genes from Fig. 4d in WT, DIO and GIO
- (b) Heatmap representation of genes from Fig. 4e in WT and GIO models.
- (c) Flight performance of 3-week-old female flies with IFM-specific *KD* of *Gnmt* and *Nmdmc*. *N#* = 30-50 females for each condition. Bar graphs represent mean and SEM, with significance presented as <sup>ns</sup> $p > 0.05$ ,  $*p \leq 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ .
- (d) Relative ATP levels of 3-week-old WT, DIO and GIO flies under ALF and TRF with *N#* = 4.
- (e) Flight performance of 10--day-old (left) and climbing performance of 10-day-old (right) DIO-ALF female flies with supplement of 0.1 mM, 1 mM, 4 mM, 8 mM, and 16 mM folic acid.
- (f) Flight performance of 3-week-old WT, DIO and GIO female flies with or without folic acid supplement. *N#* = 64-111. Bar graphs represent mean and SEM, with significance presented as <sup>ns</sup> $p > 0.05$ ,  $*p \leq 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ .
- (g) Climbing performance of 3-week-old WT, DIO and GIO female flies with or without folic acid supplement. *N#* = 60-70. Bar graphs represent mean and SEM, with significance presented as <sup>ns</sup> $p > 0.05$ ,  $*p \leq 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ .

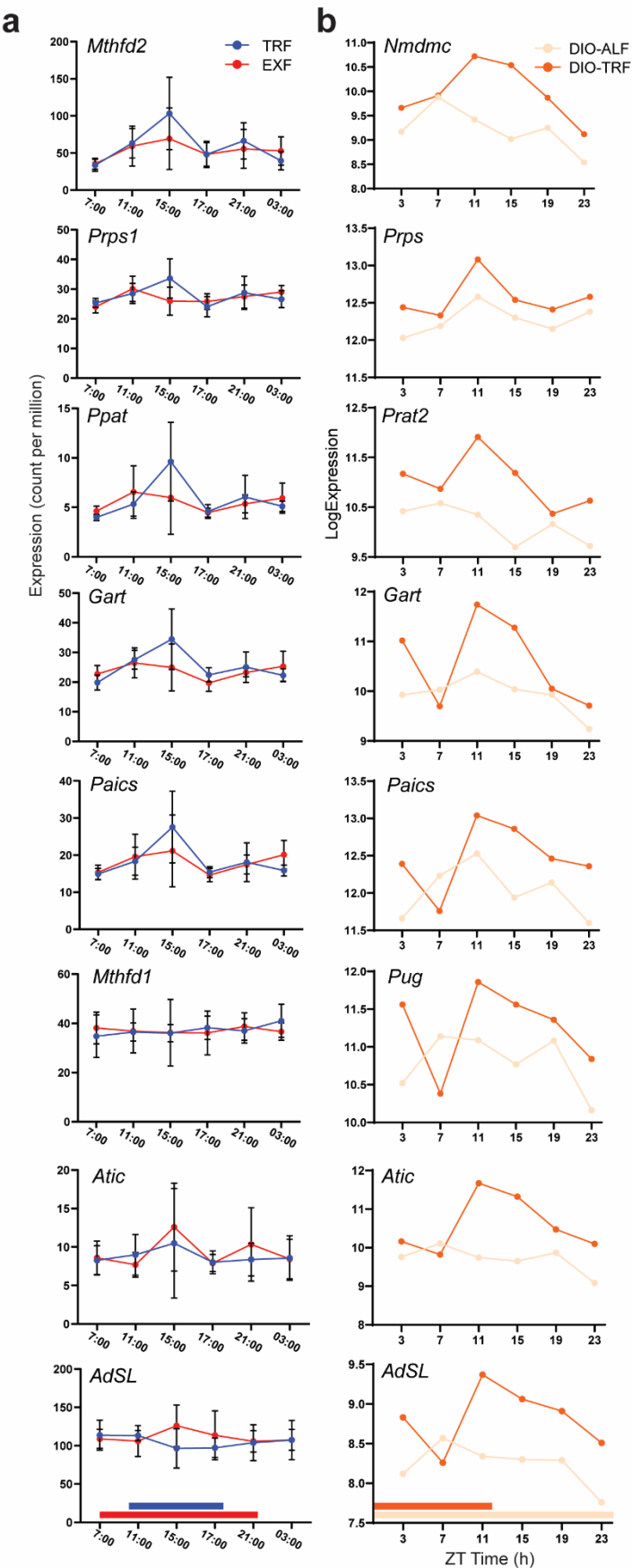
# Figure S7



**Figure S7: Glycolysis, glycogen metabolism, TCA cycle and ETC genes under ALF and TRF in WT, DIO and GIO models**

- (a) Expression of *Ampk $\alpha$*  mRNA levels in WT, DIO and GIO models
- (b) Expression levels of genes from Fig. 5d in WT, DIO and GIO
- (c) Heatmap representation of the expression levels of purine biosynthesis associated genes in ALF and TRF in the WT and GIO model.
- (d) Heatmap representation of the average expression levels of genes related to glycolysis, glycogen metabolism, TCA cycle, and ETC with increased but not significant expression under TRF versus ALF in the GIO model.
- (e) Quantification of relative expression of western blot of AMPK $\alpha$  protein levels of WT, DIO and GIO under ALF and TRF, with  $N\# = 3$ .
- (f) Flight index of 3-week-old flies with indicated genotypes.

Figure S8



**Figure S8: Comparison with skeletal muscle transcriptomic data from obese men under TRF.**

- (a) Expression levels of genes associated with purine synthesis and folate cycle from Lundell et al., 2020 RNA-seq dataset under EXF and TRF.
- (b) Expression levels of the same genes from (a) in our *Drosophila* RNA-seq dataset under ALF and TRF.