Time-restricted feeding prevents obesity and metabolic syndrome in mice lacking a circadian clock.

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Supplemental figures and tables - Titles and legends

Figure S1 – related to figure 1 and figure 2: Time-restricted feeding does not affect activity and food patterns.

A-B-C. Day/night repartition in % of total activity from metabolic cages recordings in (A) *Bmal1*^{LKO} (n=4/group), (B) *Rev-erbα/β*^{LDKO} (n=4/group), (C) CDKO (n=4/group) during the 3 days on TRF (see figure 2C-2G-2K).
D-E-F. Daily repartition of calorie consumption from metabolic cages recordings in (D) *Bmal1*^{LKO} (n=4/group), (E) *Rev-erbα/β*^{LDKO} (n=4/group), (F) CDKO (n=4/group) during the 3 days on TRF (see figure 2D-2H-2L).

Figure S2 – related to figure 3 and figure 4: Mice on TRF have more lean mass and *Bmal1*^{LKO} mice are insulin sensitive.

A-B-C. Relative lean mass as a percent of body weight in (A) *Bmal1*^{LKO} and littermate controls (n=4-5/group), (B) *Rev-erbα/β*^{LDKO} and littermate controls (n=8-11/group), (C) CDKO and littermate controls (n=8-9/group). Unpaired t-test, * $p<0.05$, ** $p<0.01$, *** $p<0.001$.
D. Insulin tolerance test (ITT) in *Bmal1*^{LKO} and littermate controls (n=6-10/group).

Figure S3 – related to figure 5: selected metabolites levels.

A. Folate levels in *Bmal1*^{LKO}, *Rev-erbα/β*^{LDKO} and CDKO on FA and FT.

B. Three-dimensional PCA plot of metabolomics data from all samples (generated by MetaboAnalyst).

C. Metabolites level and gene expression profiles relevant to the NAD+ salvage pathway.

Figure S4 – related to figure 5: Heatmap of rhythmic metabolites levels.

Heatmap representation showing diurnal levels of rhythmic metabolites identified by MetaCycle and aligned by phase in WT, *Bmal1*^{LKO}, *Rev-erbα/β*^{LDKO} and CDKO.

Figure S5 – related to figure 6 and figure 7: selected gene expression profiles.

A. Expression profile of Pten, Apoe, Fabp1, Scl25a1 in WT, *Bmal1*^{LKO}, *Rev-erbα/β*^{LDKO} and CDKO on FA.

B. Expression profile of Nnt and Dnaja4 in WT, *Bmal1*^{LKO}, *Rev-erbα/β*^{LDKO} and CDKO on FA.

C- Heatmap representation of 141 lipid metabolism and 73 cholesterol metabolism genes that are different between *Bmal1*^{LKO} and versus WT respectively.

D. Expression profile of Sik1 in WT and *Bmal1*^{LKO}, Hsd17b2 in WT and *Rev-erbα/β*^{LDKO} and Poli in WT and CDKO.

E. Expression level of genes represented in figure 6E in *Rev-erbα/β*^{LDKO} versus *Rev-erbα/β*^{LWT} littermates controls from Cho et al, 2012.

Figure S6 – related to figure 6: pathway enrichment analysis.

Results of pathway enrichment analysis from differentially expressed genes between (A) *Bmal1*^{LKO}-FA vs WT-FA, (B) *Rev-erbα/β*^{LDKO}-FA vs WT-FA, (C) CDKO-FA vs WT-FA as indicated.

Figure S7 – related to figure 6 and figure 7: expression profile of clock and clock output genes.

Expression profile (normalized counts from RNA-seq) of (A) Bmal1, (B) Dbp, (C) Per2, (D) Cry1, (E) Rev-erbβ, (F) Nampt, (G) Lpl, (H) Por, and (I) Insig2 in *Bmal1*^{LKO}, *Rev-erbα/β*^{LDKO}, CDKO and control.

FIGURE S1 - related to figure 1 and figure 2

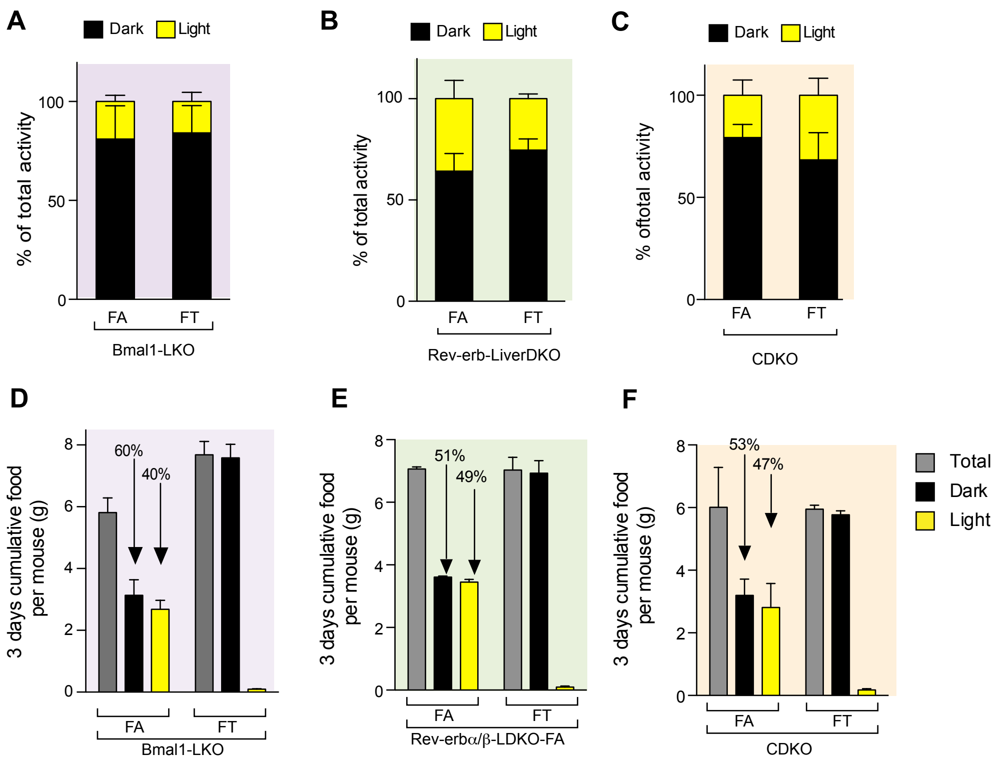


FIGURE S2 - related to figure 3 and figure 4

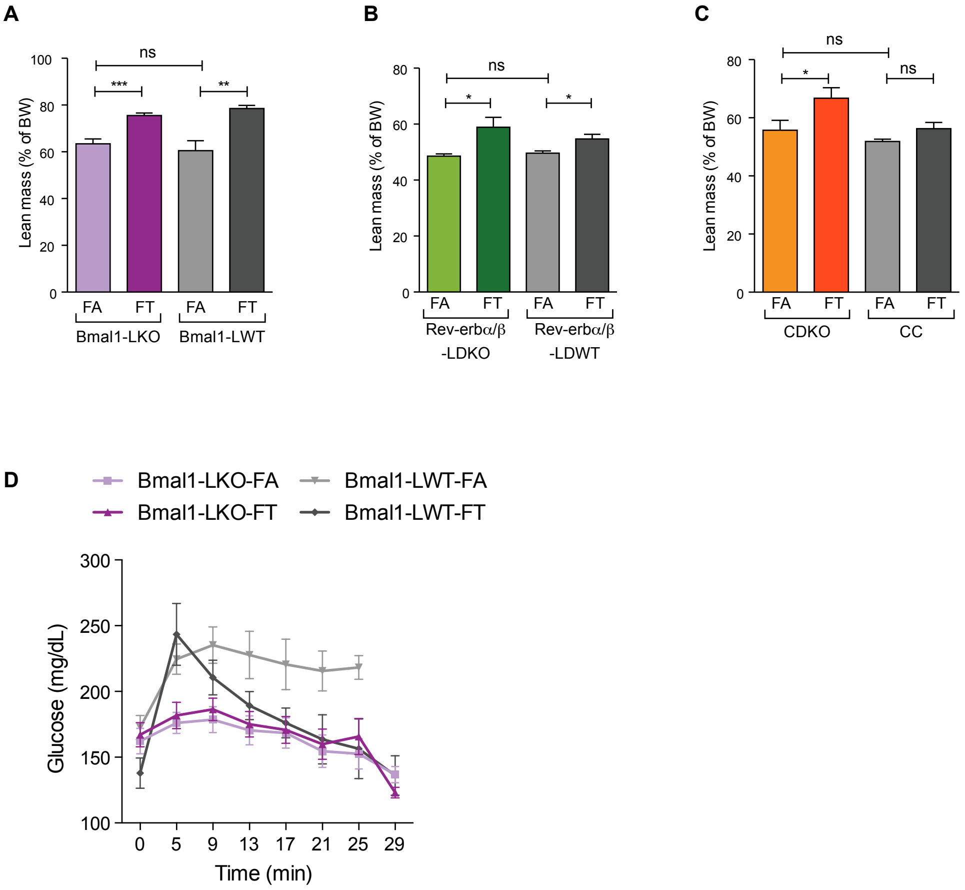


FIGURE S3 - related to figure 5

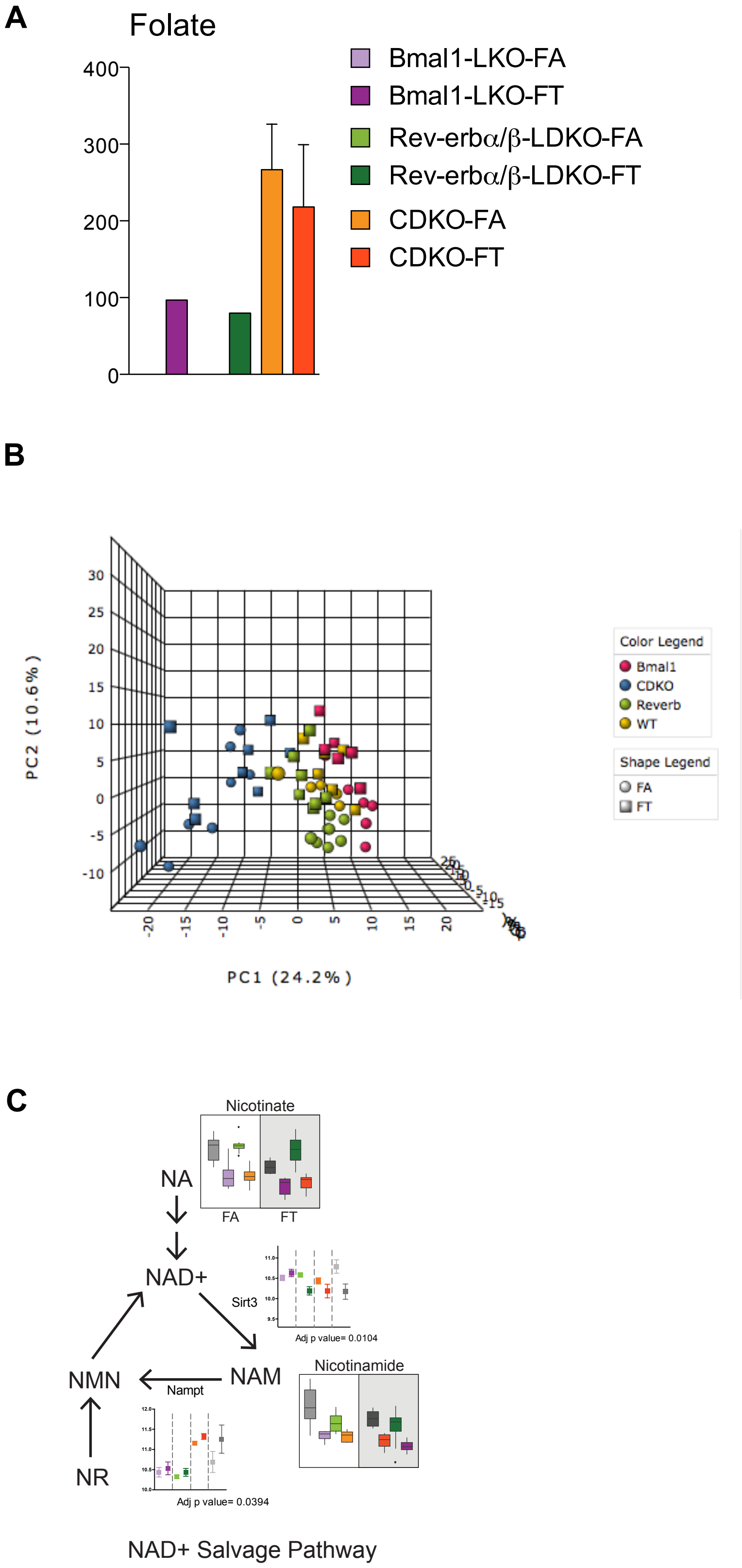


FIGURE S4 - related to figure 5

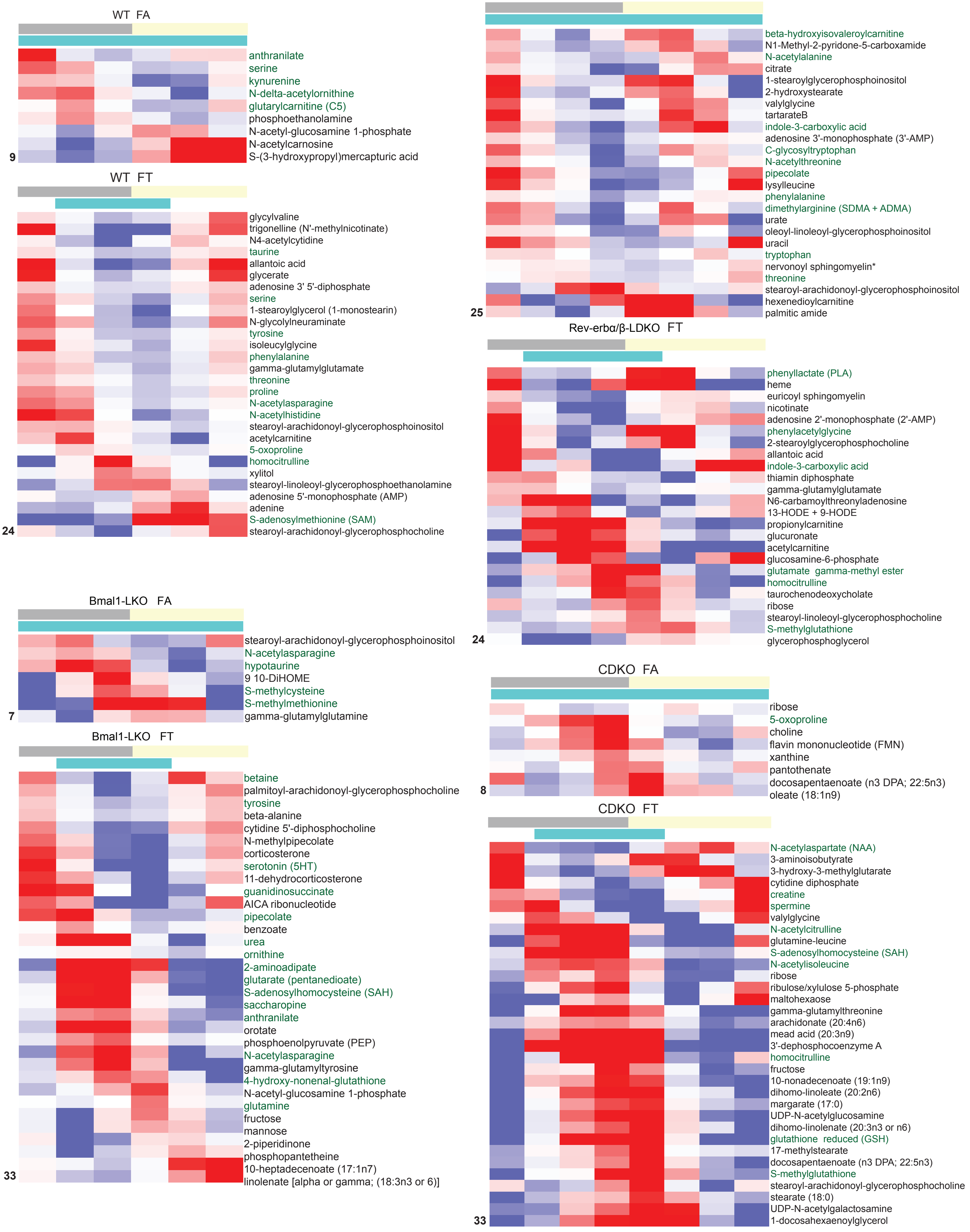


FIGURE S5 - related to figure 6 and figure 7

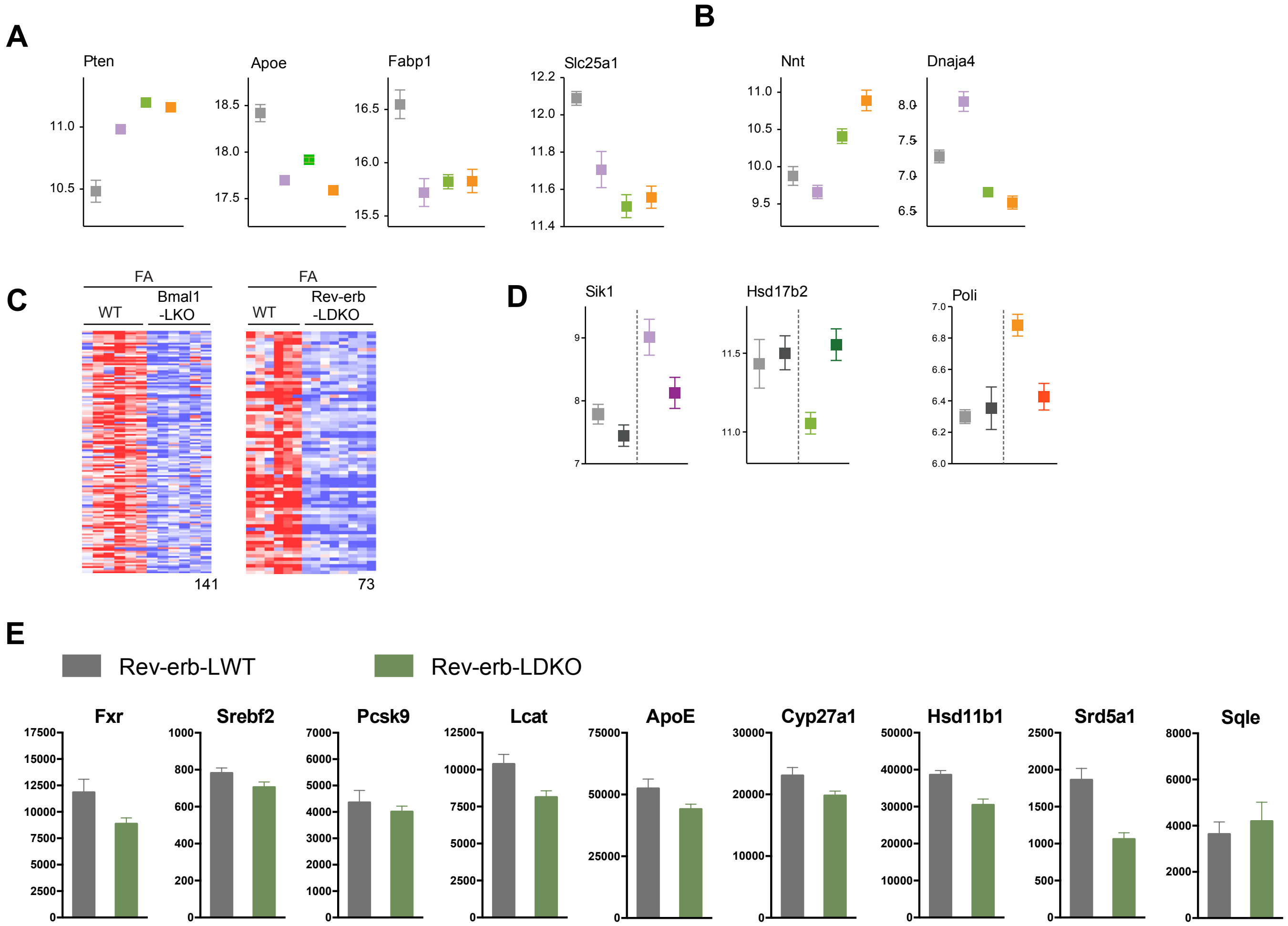
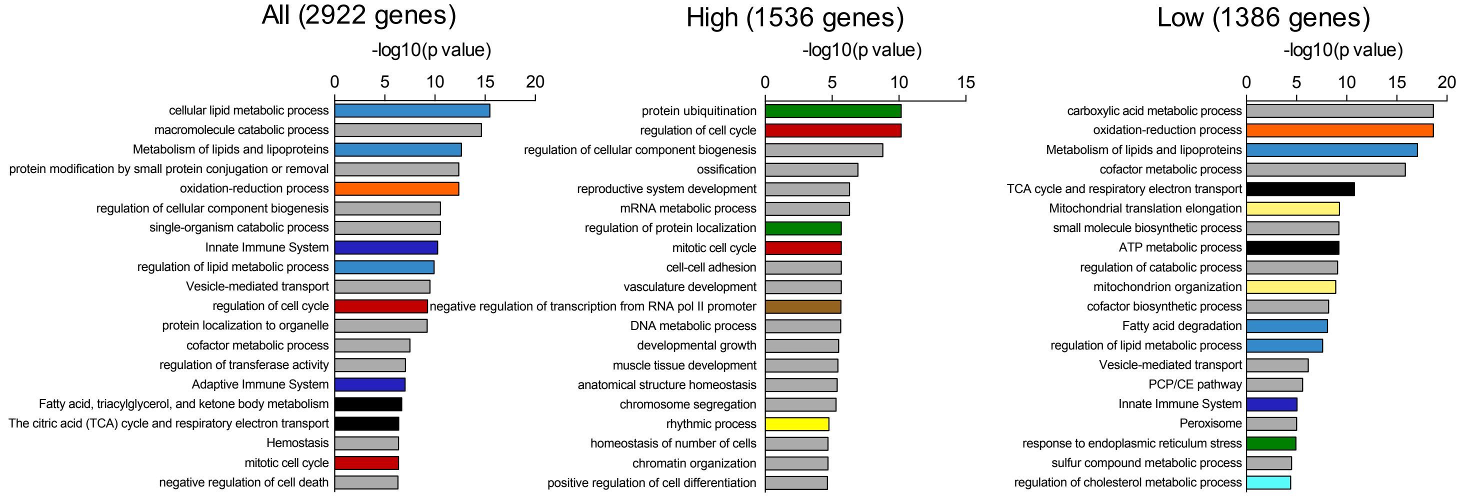
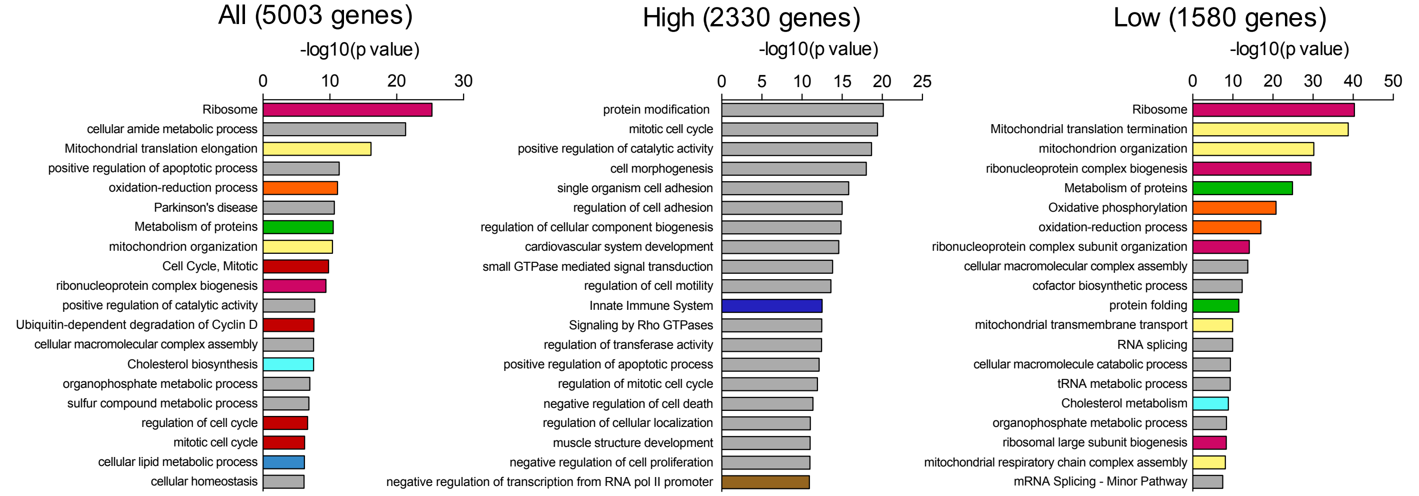


FIGURE S6 - related to figure 6

A Bmal1-LKO FA vs WT-FA



B Reverb α/β-LDKO FA vs WT-FA



C CDKO FA vs WT-FA

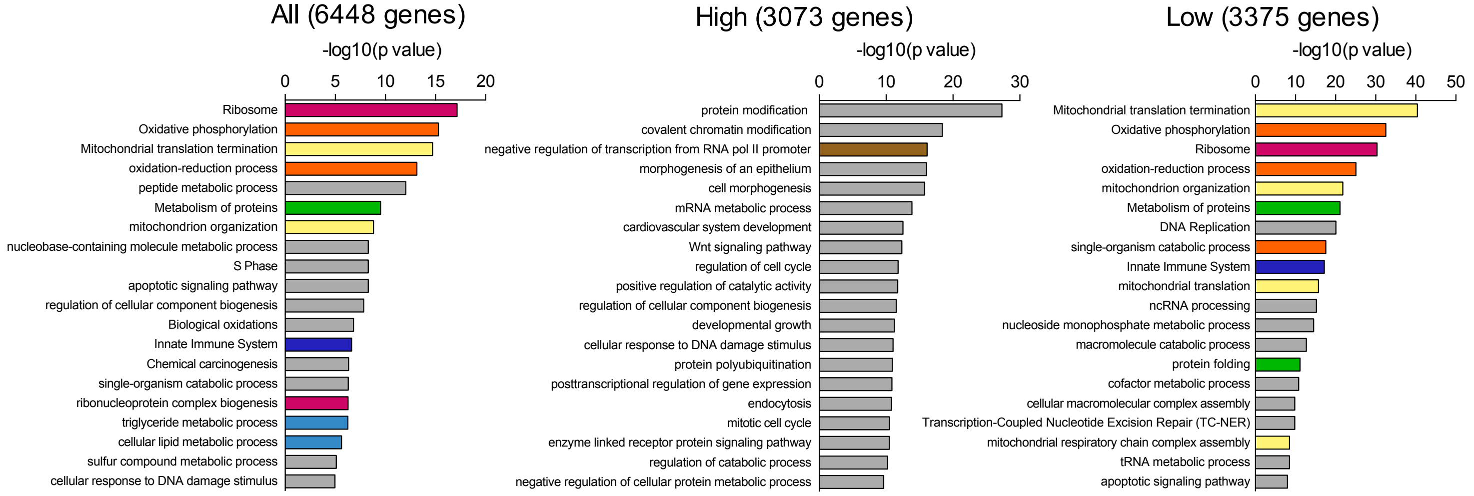


FIGURE S7 - related to figure 6 and figure 7