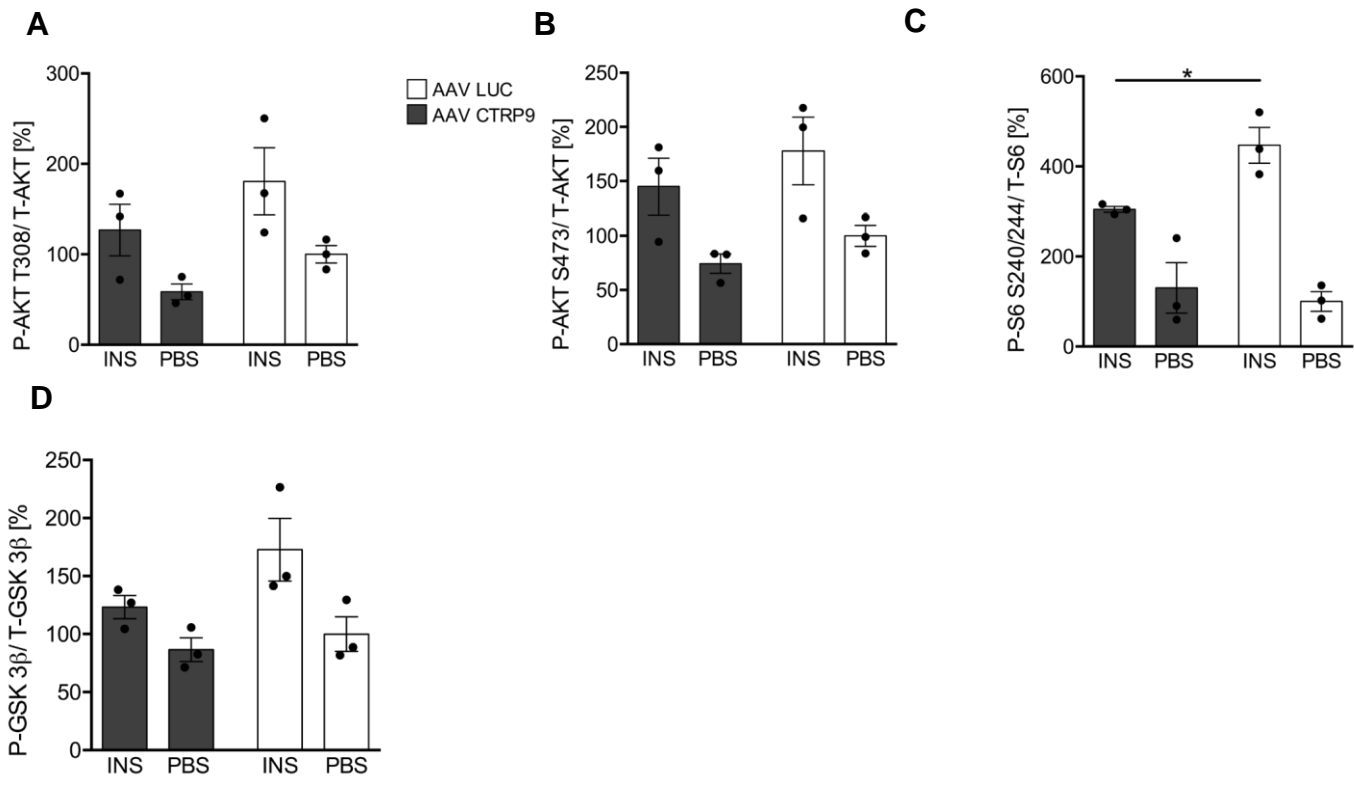
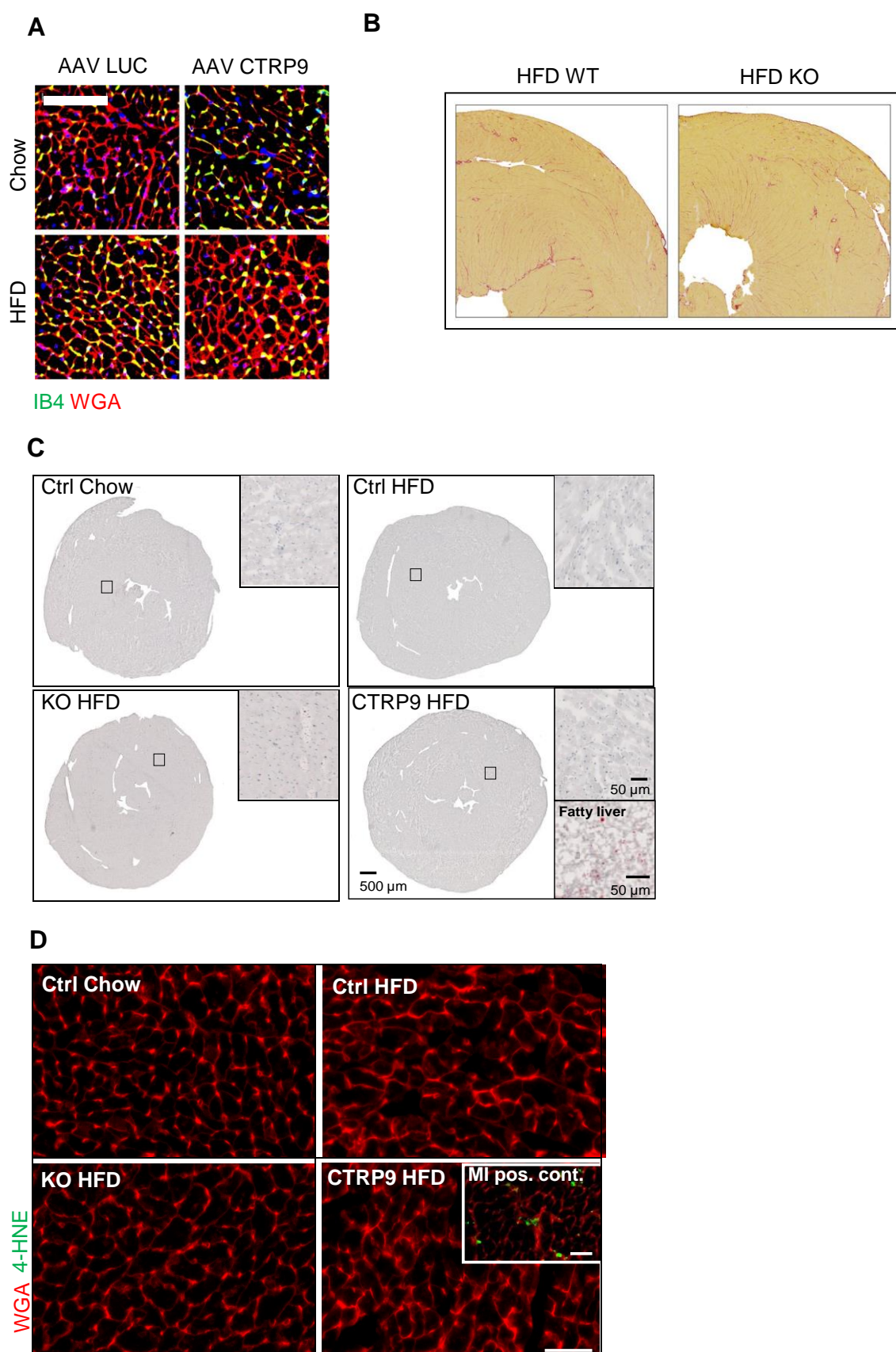


**Supplemental Figure S1. CTRP9 knock-out mice (KO) do not activate Akt/Protein Kinase B dependent signaling in response to insulin.** A-E Densitometric quantification of the Western blots of the indicated proteins that are shown in Figure 3D.

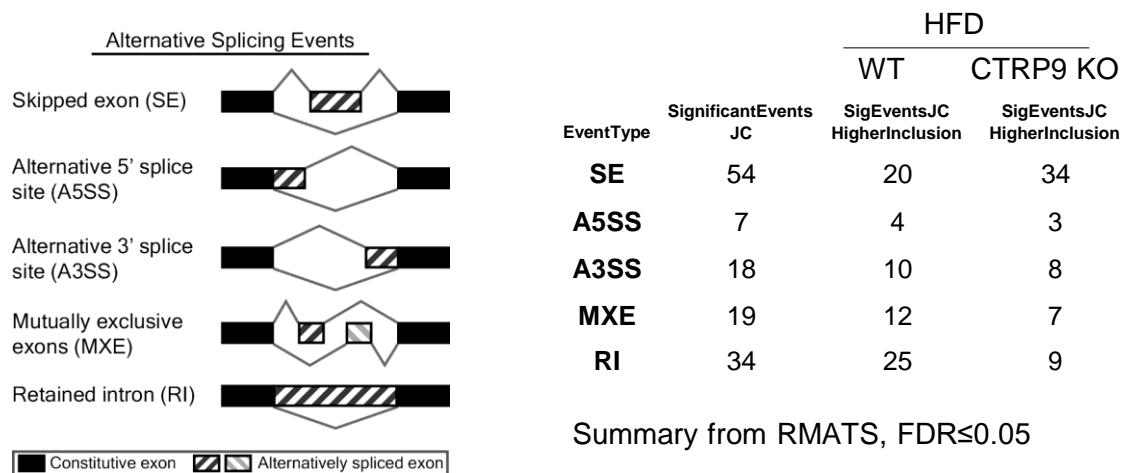


**Supplemental Figure S2. Cardiac CTRP9 overexpression in mice does not change signaling in response to insulin.** A-E Densitometric quantification of the Western blots of the indicated proteins that are shown in Figure 6C.

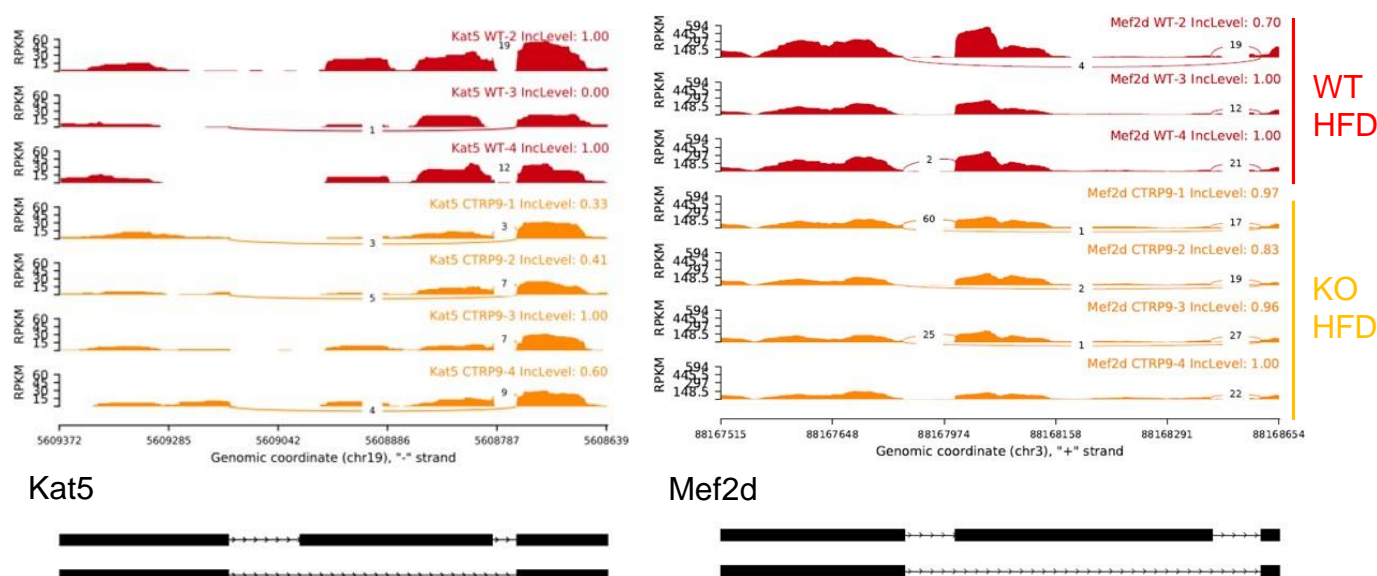


**Supplemental Figure S3. Histological examinations in CTRP9 knock-out mice and in mice with cardiac CTRP9 overexpression.** (A) Immunofluorescence staining for Isolectin B4 (IB4) and wheat-germ agglutinin (WGA) to measure cardiomyocyte cross-sectional area and myocardial capillary density in the indicated mice. Scale bar: 100 μm. (B) Sirius red staining of myocardial sections of the indicated mice after high fat diet (HFD) exposure to analyze fibrosis. (C) Oil red O staining to analyze lipid deposition in heart sections from mice as indicated. Control mice (Ctrl) were wild-type mice with and without AAV-Luc administration. Fatty liver tissue served as positive control. (D) Immunofluorescence staining of heart sections of mice as indicated for WGA and 4-hydroxynonenal (4-HNE) to analyze oxidative damage. Heart tissue from mice after myocardial infarction (MI) served as positive control. Scale bar: 50 μm.

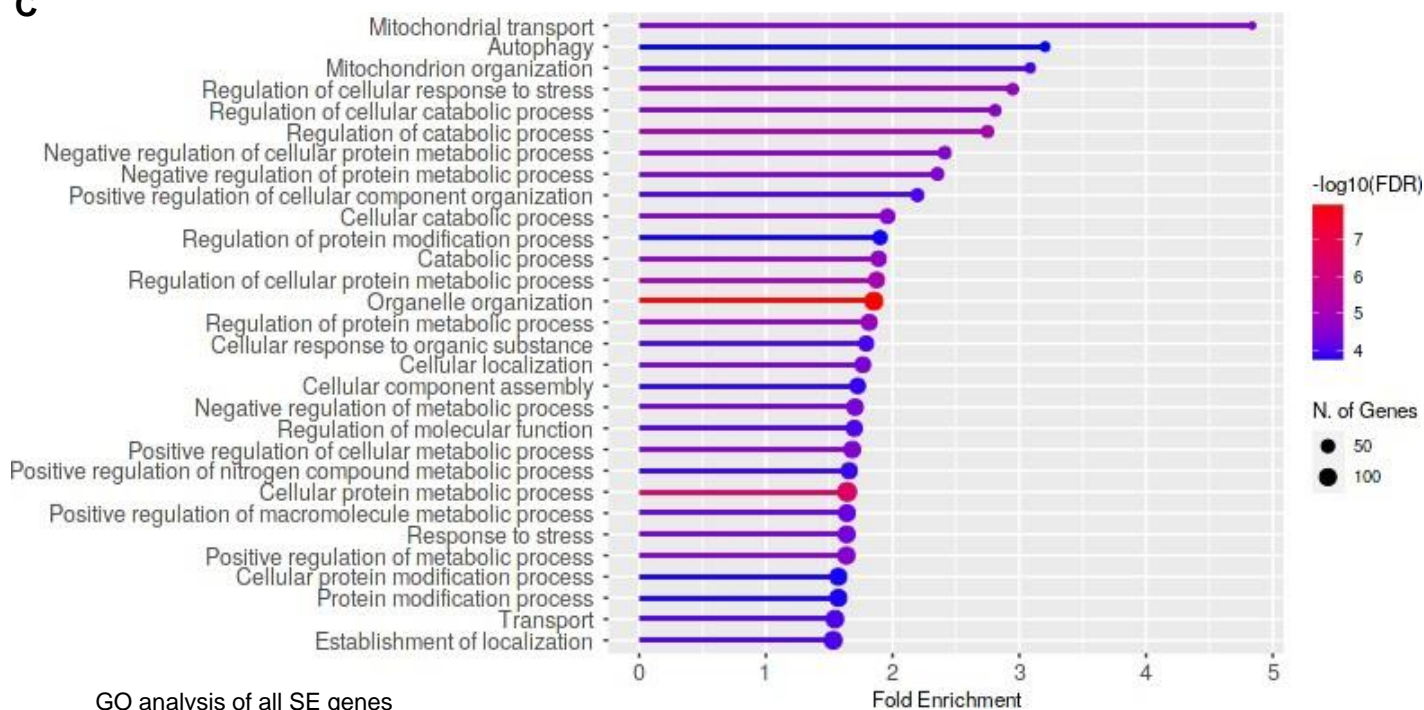
A



B

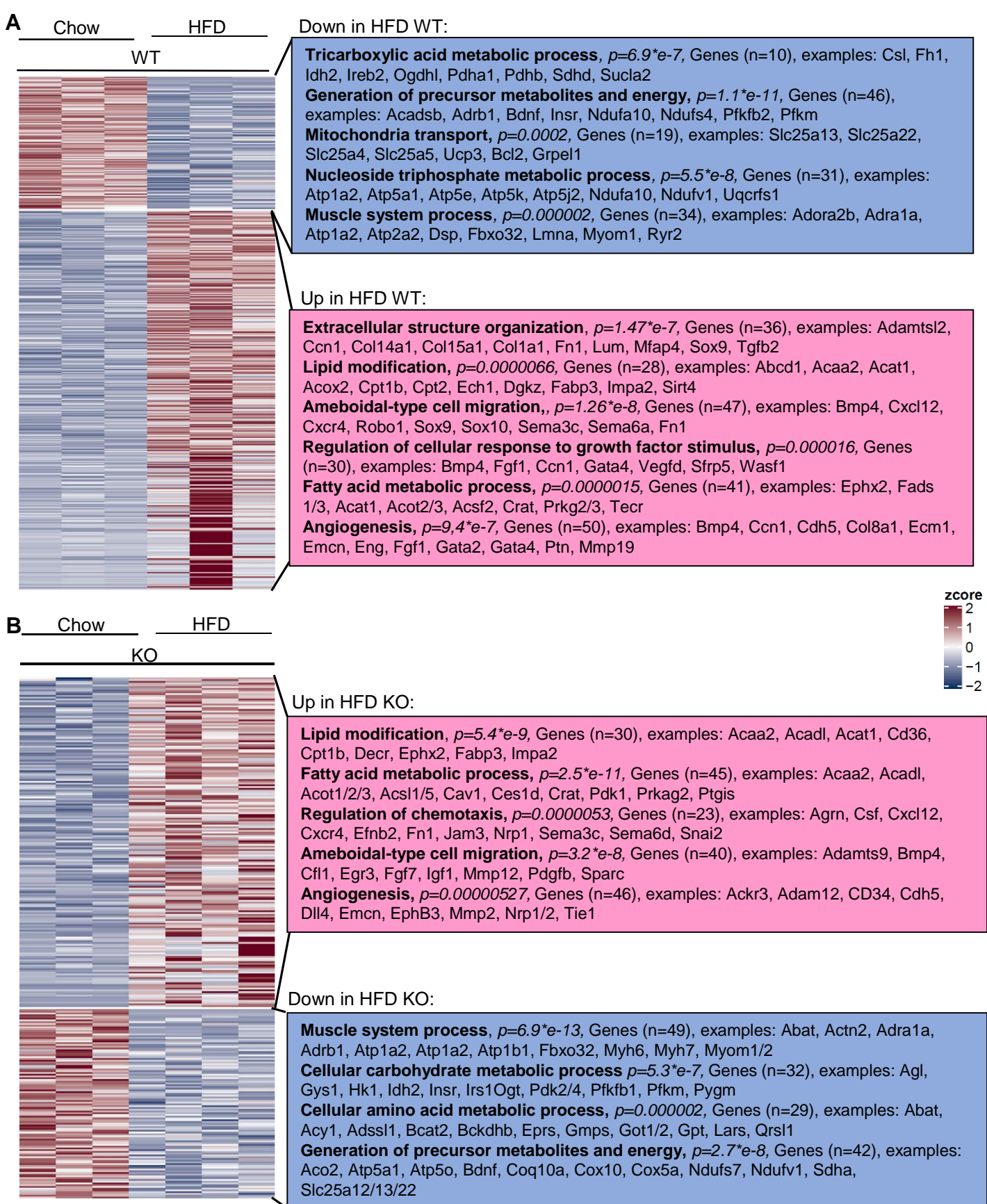


C



**Supplemental Figure S4. Alternative splicing events in CTRP9 knock-out (KO) mice during high fat diet (HFD).** (A) Different alternative splicing events in the indicated mice. (B) Example of alternative splicing in the *Kat5* and *Mef2d* genes in the indicated mice. (C) Functional classes of genes with skipped exons in CTRP9 KO mice.





**Supplemental Figure S5. Different gene-expression patterns in response to HFD (high fat diet) inCTRP9 knock-out (KO) and wild-type (WT) mice.** (A) Transcriptomic profiling in WT mice exposed to 12 weeks of chow or HFD. A heat map of differentially expressed genes is shown. Gene-ontology classes of differentially downregulated and upregulated genes and example genes are shown on the right. (B) Transcriptomic profiling in KO mice exposed to 12 weeks of chow or HFD. A heat map of differentially expressed genes is shown. Gene-ontology classes of differentially downregulated and upregulated genes and example genes are shown on the right.