

Supplementary information

Exercise and high-fat feeding remodel transcript-metabolite interactive networks in mouse skeletal muscle

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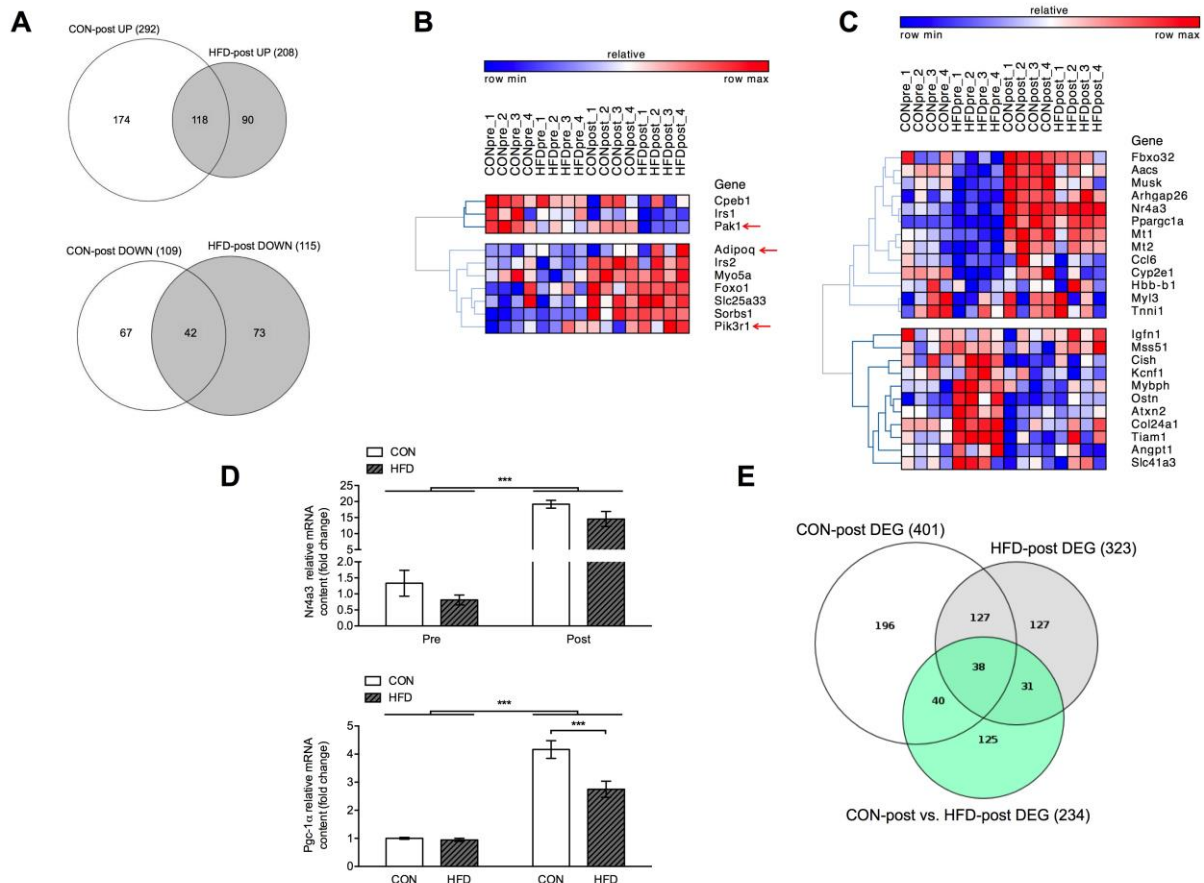
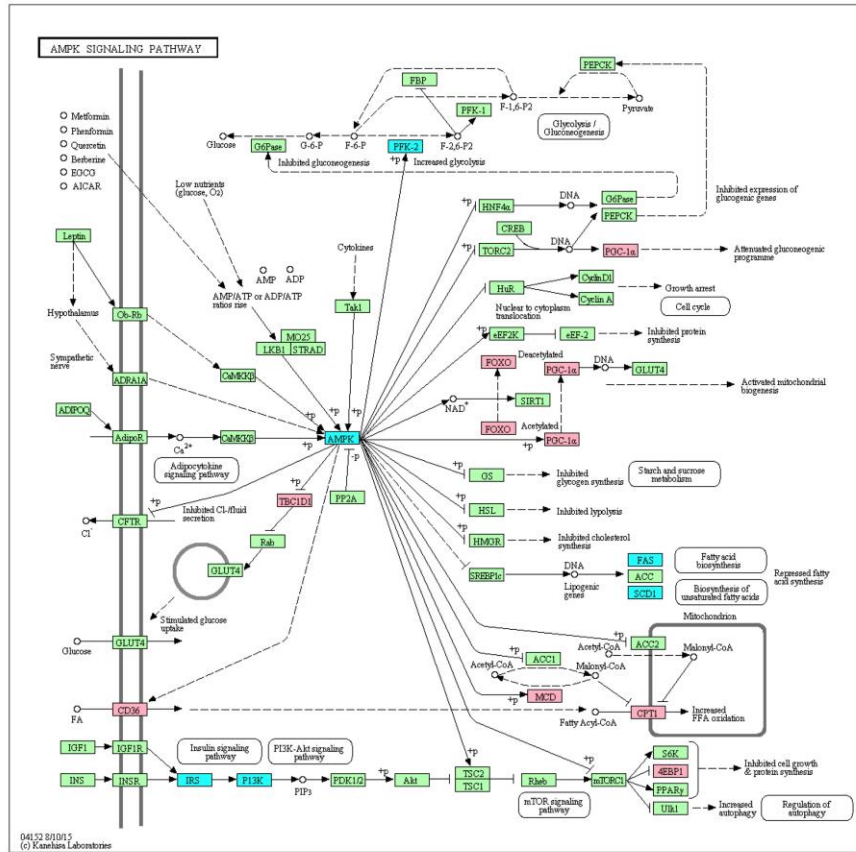


Figure S2. Transcriptional response to exercise in CON and HFD mice. (A) DEG in CON-post and HFD-post skeletal muscles (number of genes is shown in brackets or circle regions). (B) Heat map and clustering of genes comprised in the GO term "cellular response to insulin stimulus" (red arrows show differentially expressed between CON-post vs. HFD-post). (C) Subset of genes deregulated by HFD under basal conditions of which acute maximal exercise normalized their expression levels. (D) qPCR analysis of *Nr4a3* and *Pgc-1α* mRNA levels ($n=6$ muscles per group). (E) Venn diagram with subsets of exercise-sensitive genes of which HFD affected the response to exercise.

A



B

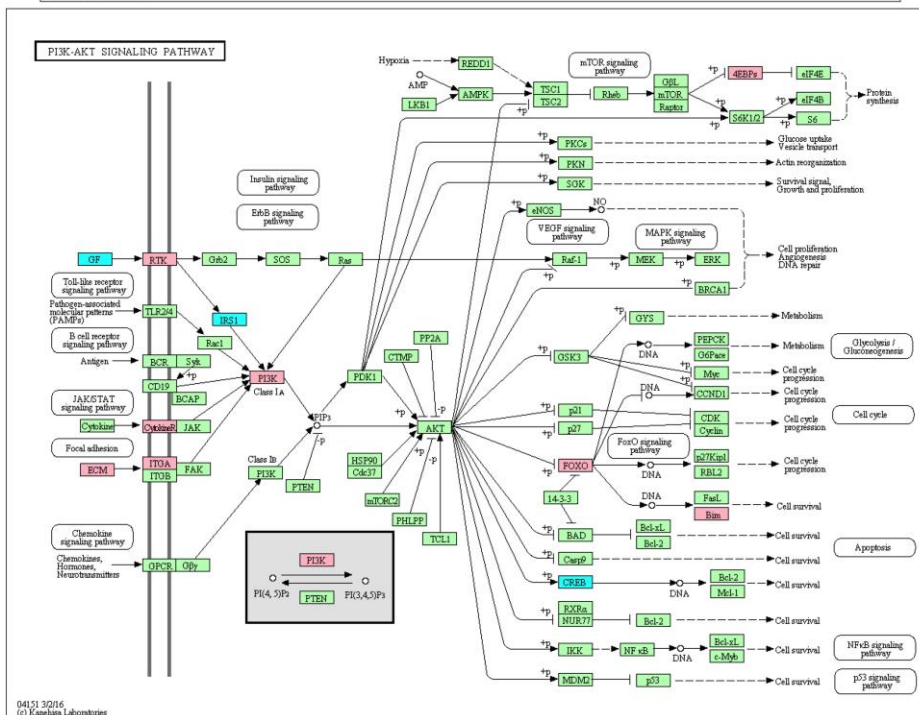


Figure S3. KEGG pathway analysis of CON-post and HFD-post DEG. (A) AMPK and (B) PI3K-Akt signalling pathways showing up- (pink) and down-regulated (cyan) genes in CON-post and HFD-post DEG. $n = 4$ muscles per group. AMPK signaling pathway (map04152) and PI3K-Akt signaling pathway (map04151) maps were obtained with permission from KEGG database (<http://www.kegg.jp/kegg/pathway.html>)¹⁻³.

Supplementary References

- 1 Kanehisa, M., Furumichi, M., Tanabe, M., Sato, Y. & Morishima, K. KEGG: new perspectives on genomes, pathways, diseases and drugs. *Nucleic acids research* **45**, D353-D361, doi:10.1093/nar/gkw1092 (2017).
- 2 Kanehisa, M., Sato, Y., Kawashima, M., Furumichi, M. & Tanabe, M. KEGG as a reference resource for gene and protein annotation. *Nucleic acids research* **44**, D457-462, doi:10.1093/nar/gkv1070 (2016).
- 3 Kanehisa, M. & Goto, S. KEGG: kyoto encyclopedia of genes and genomes. *Nucleic acids research* **28**, 27-30 (2000).