

Figure S2. Pathway analysis of the effects of HFD on liver gene transcription in C57BL/6J and 129S6 mice. Only KEGG biological pathways identified by GSEA as significantly affected by HFD in at least one of the strains are reported. False discovery rate (FDR) q-values (<0.05) were used to test for statistically significant pathway upregulation (red) or downregulation (green) in response to fat feeding in 129S6 (*) and C57BL/6J (\$) mice.

- Proteasome
- Ubiquitin mediated proteolysis
- Protein export
- Spliceosome
- Aminoacyl trna biosynthesis
- Ppar signaling pathway
- Peroxisome
- Fatty acid metabolism
- Biosynthesis of unsaturated fatty acids
- Steroid hormone biosynthesis
- Primary bile acid biosynthesis
- Valine leucine and isoleucine degradation
- Complement and coagulation cascades
- N glycan biosynthesis
- Adherens junction
- Vibrio cholerae infection
- Pathogenic escherichia coli infection
- Propanoate metabolism
- Basal cell carcinoma
- Neuroactive ligand receptor interaction
- Metabolism of xenobiotics by cytochrome p450
- Type i diabetes mellitus
- Calcium signaling pathway
- Hedgehog signaling pathway
- Glutathione metabolism
- Drug metabolism cytochrome p450
- Cysteine and methionine metabolism
- Arginine and proline metabolism
- Autoimmune thyroid disease
- Intestinal immune network for iga production
- Allograft rejection
- Pentose phosphate pathway
- Hematopoietic cell lineage
- Mapk signaling pathway
- Snare interactions in vesicular transport
- Antigen processing and presentation
- Rna polymerase
- Ribosome
- Amino sugar and nucleotide sugar metabolism
- Purine metabolism
- Pyrimidine metabolism

Normalised enrichment score

