Supporting Information

Stienstra et al. 10.1073/pnas.1100255108

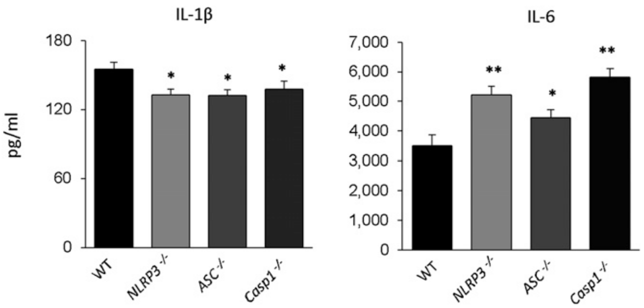

Fig. S1. Cytokine analysis in WAT from HFD-fed wild-type, Nlrp3$^{-/-}$, ASC$^{-/-}$, and Casp1$^{-/-}$ mice. Total adipose of HFD-fed animals (16 wk of diet intervention) was used to analyze concentrations of IL-1β and IL-6. **P* < 0.05 vs. WT; ***P* < 0.01 vs. WT.

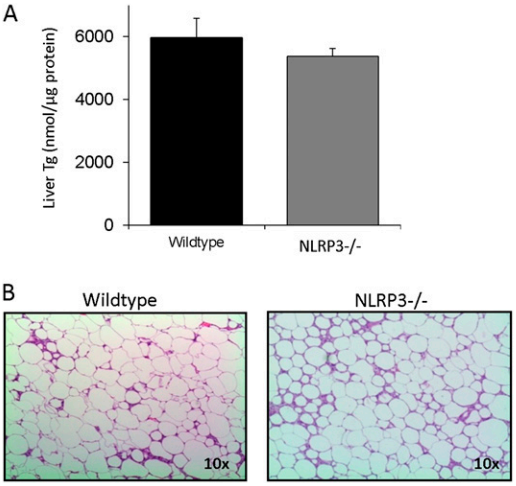

Fig. S2. Liver triglyceride content (*A*) and H&E staining of white adipose tissue (*B*) in HFD-fed wild-type and Nlrp3$^{-/-}$ animals.

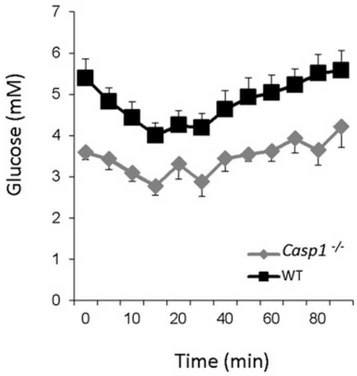

Fig. S3. Glucose levels during euglycemic hyperinsulinemic clamp analysis of HFD-fed wild-type and Casp1$^{-/-}$ animals.

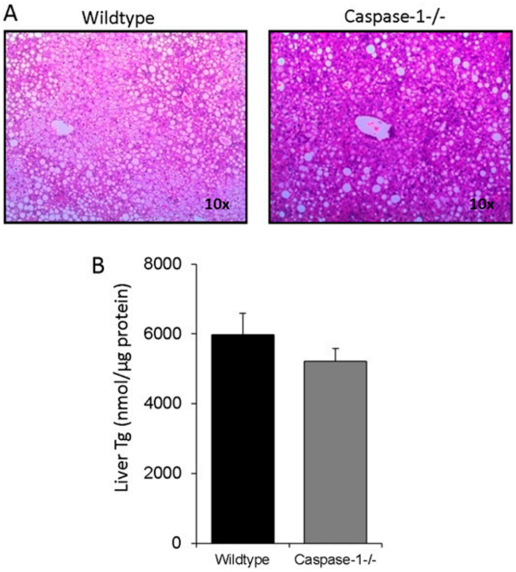

Fig. S4. Liver histology as determined by H&E staining (*A*) and liver triglyceride content (*B*) in HFD-fed wild-type and Casp1$^{-/-}$ animals.

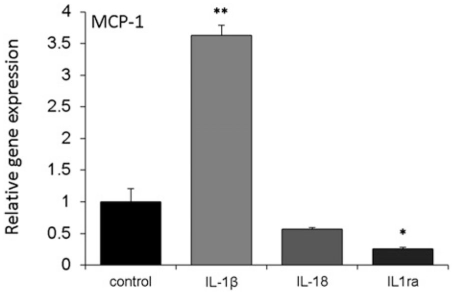

Fig. S5. Monocyte chemotactic protein 1 (MCP-1) gene expression results in human SGBS adipocytes treated with IL-1β, IL-18, or IL-1 receptor antagonist during differentiation. MCP-1 gene expression results were analyzed in SGBS cells after 10 d of differentiation in the absence or presence of recombinant IL-1β (5 ng/mL), IL-18 (25 ng/mL), or IL-1ra (5 μg/mL). **$P < 0.001$; *$P < 0.05$ vs. control.

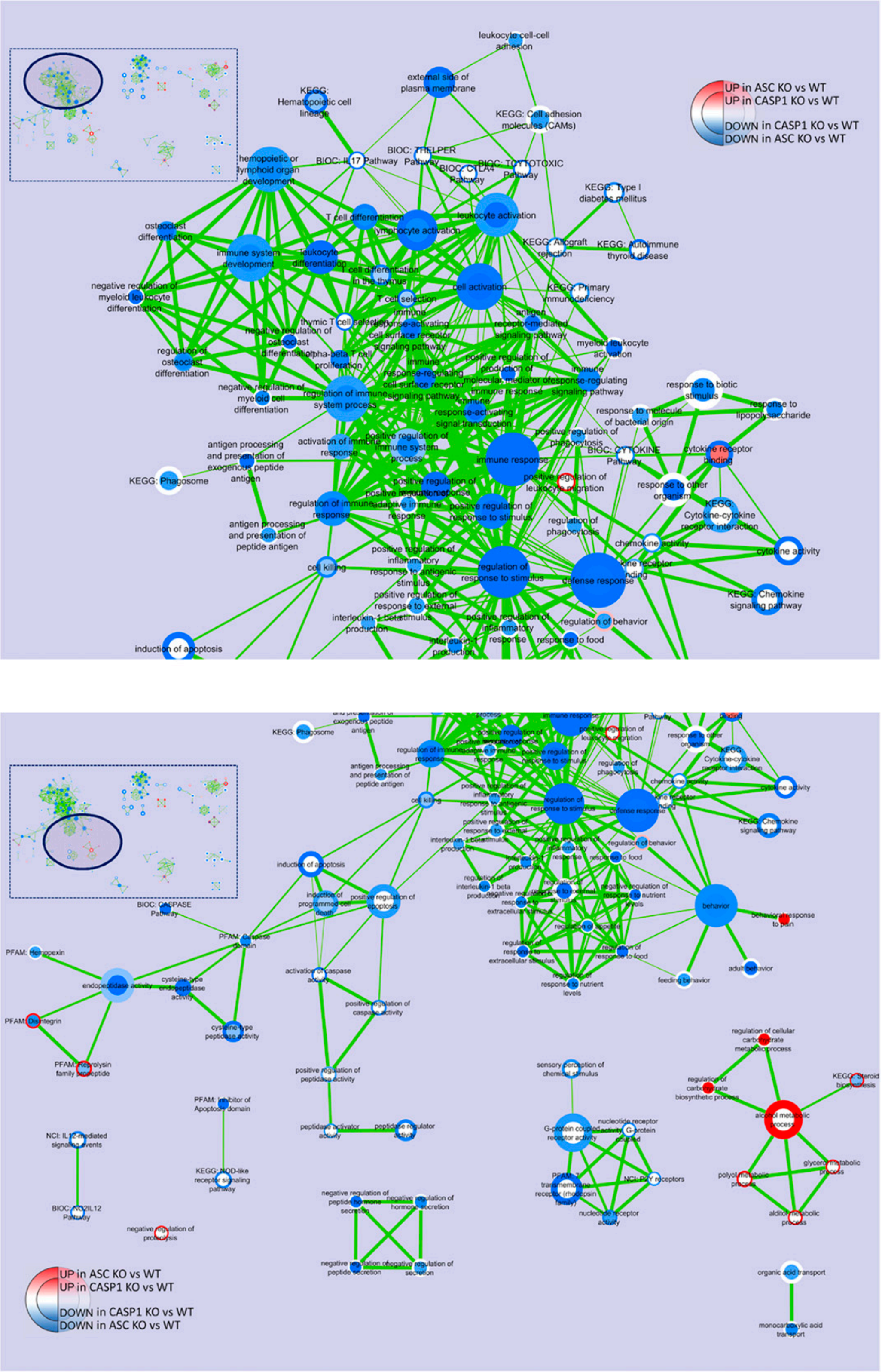

Fig. S6. Detailed pathway analysis of the microarray data obtained from the adipose tissue of HFD-fed wild-type, *ASC*$^{-/-}$ and *Casp-1*$^{-/-}$ animals. Enrichment map for gene expression in WAT of *Casp-1*$^{-/-}$ (inner node area) and *ASC*$^{-/-}$ (node borders) compared to WT at 16 wk after HFD intervention. Nodes represent functional gene sets, and edges between nodes their similarity. Color intensity of node area resp. border is proportional to enrichment significance in *Casp1*$^{-/-}$ resp. *ASC*$^{-/-}$ mice compared to WT. Red indicates increased gene sets and blue indicates suppressed gene sets in null mice compared to WT. Node size represents the gene set size, and edge thickness represent degree of overlap between two connected gene sets.

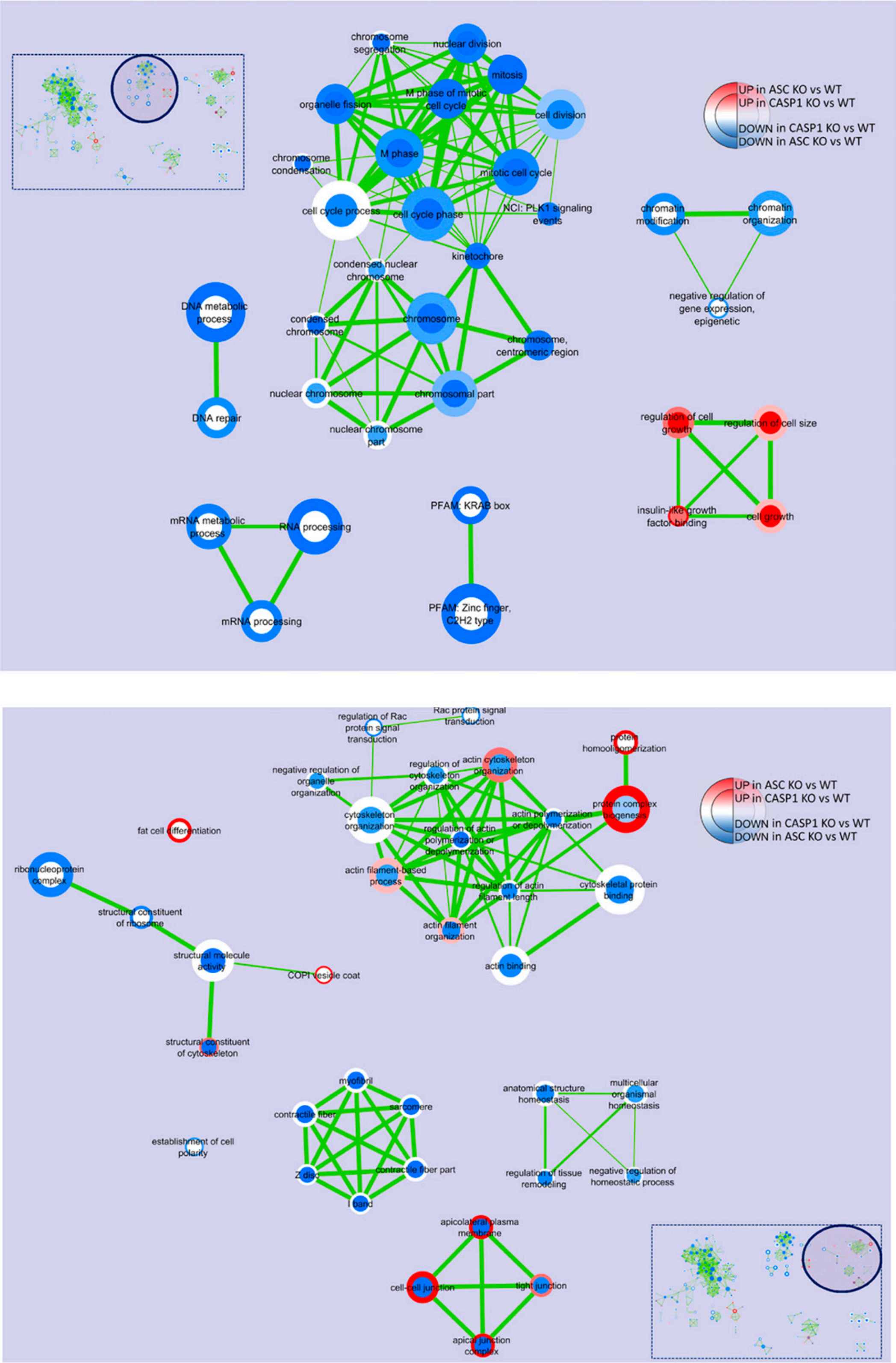

Fig. S7. Detailed pathway analysis of the microarray data obtained from the adipose tissue of HFD-fed wild-type, *ASC*$^{-/-}$ and *Casp-1*$^{-/-}$ animals. Enrichment map for gene expression in WAT of *Casp-1*$^{-/-}$ (inner node area) and *ASC*$^{-/-}$ (node borders) compared to WT at 16 wk after HFD intervention. Nodes represent functional gene sets, and edges between nodes their similarity. Color intensity of node area resp. border is proportional to enrichment significance in *Casp1*$^{-/-}$ resp. *ASC*$^{-/-}$ mice compared to WT. Red indicates increased gene sets and blue indicates suppressed gene sets in null mice compared to WT. Node size represents the gene set size, and edge thickness represent degree of overlap between two connected gene sets.

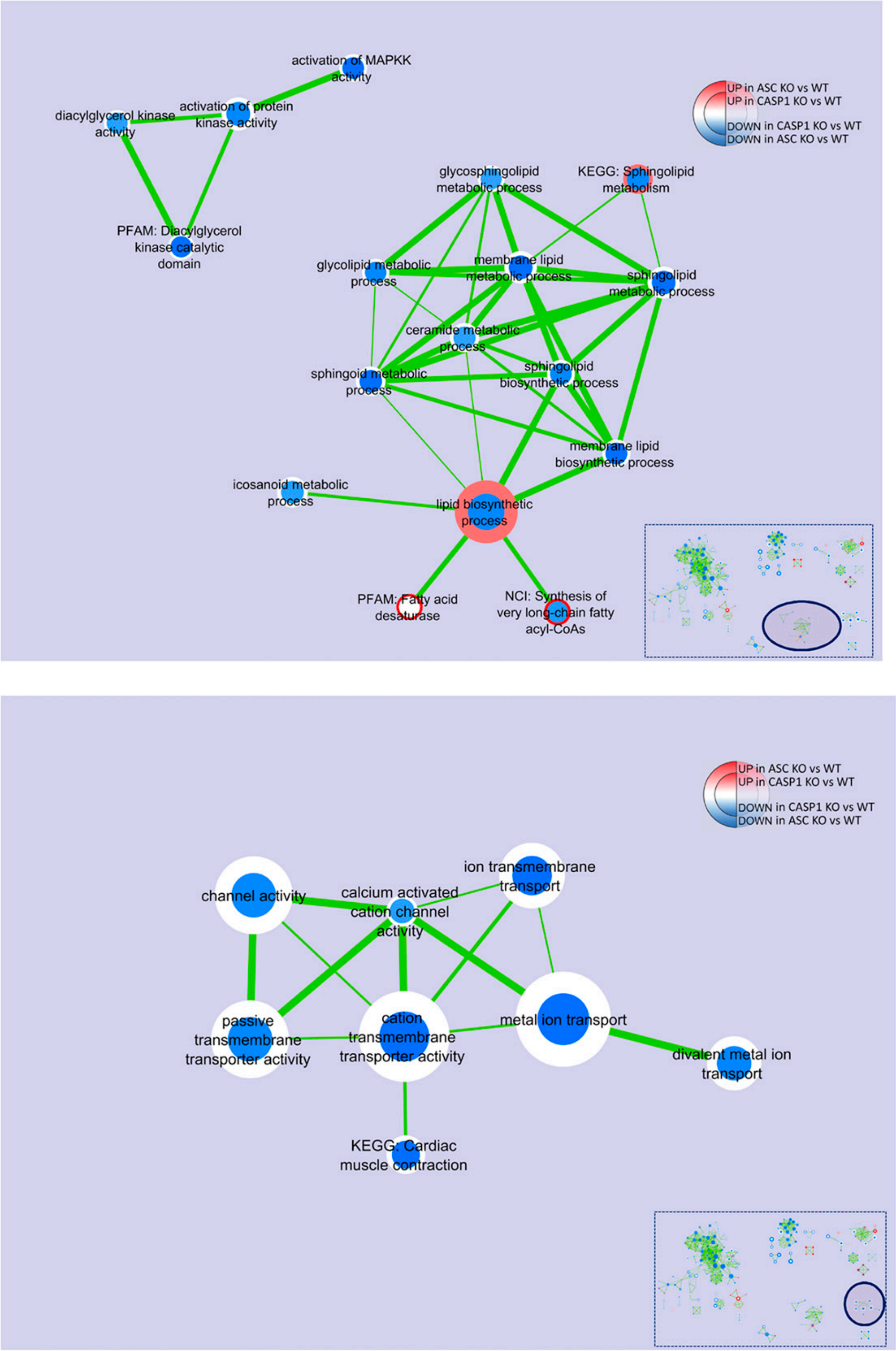

Fig. S8. Detailed pathway analysis of the microarray data obtained from the adipose tissue of HFD-fed wild-type, *ASC*$^{-/-}$ and *Casp-1*$^{-/-}$ animals. Enrichment map for gene expression in WAT of *Casp-1*$^{-/-}$ (inner node area) and *ASC*$^{-/-}$ (node borders) compared to WT at 16 wk after HFD intervention. Nodes represent functional gene sets, and edges between nodes their similarity. Color intensity of node area resp. border is proportional to enrichment significance in *Casp1*$^{-/-}$ resp. *ASC*$^{-/-}$ mice compared to WT. Red indicates increased gene sets and blue indicates suppressed gene sets in null mice compared to WT. Node size represents the gene set size, and edge thickness represent degree of overlap between two connected gene sets.

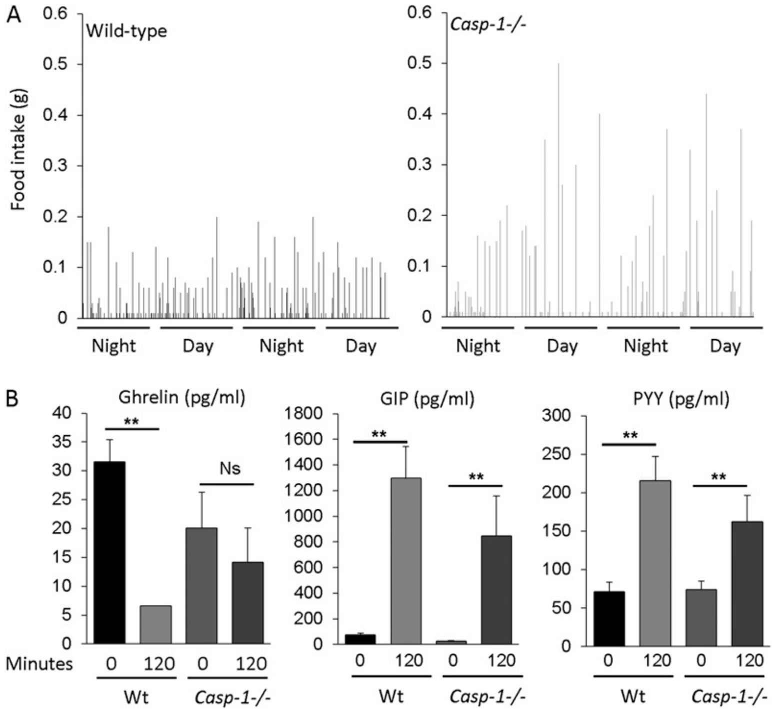

Fig. S9. Feeding behavior (*A*) and gut hormones levels after a postprandial response (*B*) in wild-type and *Casp1*$^{-/-}$ animals.

Table S1. Plasma free fatty acids (FFA) and insulin levels during the euglycemic hyperinsulinemic clamp analysis

	FFA (mM)		Insulin (ng/mL)	
	Basal	Hyperinsulinemic	Basal	Hyperinsulinemic
Wild-type high-fat diet	0.74 ± 0.07	0.58 ± 0.04	1.38 ± 0.40	4.74 ± 0.40
Casp1$^{-/-}$ high-fat diet	0.71 ± 0.04	0.42 ± 0.06*	0.64 ± 0.15	3.30 ± 0.30*

Other Supporting Information Files

Dataset S1 (XLSX)