

Supplementary Table 2. Attributes of mouse strains used for comparative GO analysis

Targeted Gene	Strain	Sex	Number of animals
Scd1 ^a	SV129 backcrossed 5 generations to C57BL/6	Female	5
Ppara ^b	129/Sv	Female/male	12/12
Mdr2 (Abcb4) ^c	FVB.129P2-Pgy2 ^{tm1Bor}	Male	3

- a. Stearoyl-CoA desaturase-1 (Scd1)^{-/-} mice, which develop hypoglycemia, hypercholesterolemia and hepatic dysfunction when fed a very low-fat, high-sucrose diet (Scd1 is essential for de novo synthesis of monounsaturated fatty acids) (1) (see Supplementary Fig. 5 for a description of the genomic locus of Scd1).
- b. Peroxisome proliferator activated receptor alpha (Ppara)^{-/-} (2), which is involved in regulation of hepatic detoxification, energy homeostasis, and inflammatory responses.
- c. Multi-drug resistance 2 (Abcb4 or Mdr2)^{-/-} (3), which have a pronounced liver pathology at three months and develop hepatocellular carcinoma at 12-15 months of age. In all three cases, we compared our DGE data (CerS2 null versus WT) to microarray analyses performed on approximately 3 month-old mice, comparing null to WT (Scd1, Ppara) or heterozygotes (Mdr2) to the DGE data from CerS2 null mice.

1. Flowers, M. T., Keller, M. P., Choi, Y., Lan, H., Kendzierski, C., Ntambi, J. M., and Attie, A. D. (2008) *Physiol Genomics* **33**, 361-372
2. Leuenberger, N., Pradervand, S., and Wahli, W. (2009) *J Clin Invest.* , doi: 10.1172/JCI39019
3. Katzenellenbogen, M., Pappo, O., Barash, H., Klopstock, N., Mizrahi, L., Olam, D., Jacob-Hirsch, J., Amariglio, N., Rechavi, G., Mitchell, L. A., Kohen, R., Domany, E., Galun, E., and Goldenberg, D. (2006) *Cancer Res.* **66**, 4001-4010

Supplementary Table 3. Overlapping GO terms

CerS2 compared to	Enriched in knock-out mice up-regulated genes	Enriched in knock-out mice down-regulated genes
Scd1 (very low fat diet)	<ul style="list-style-type: none"> Cell cycle Intracellular transport Cell division Protein complex assembly Establishment of localization Translation Localization Transport Protein polymerization Establishment of protein localization Endocytosis RNA processing Protein folding DNA replication Biopolymer modification 	<ul style="list-style-type: none"> Generation of precursor metabolites and energy Blood coagulation
PPAR α	-----	<ul style="list-style-type: none"> Oxidation reduction Fatty acid metabolic process Cellular lipid metabolic process Lipid metabolic process Monocarboxylic acid metabolic process Carboxylic acid metabolic process Organic acid metabolic process Steroid biosynthetic process Lipid biosynthetic process Vitamin metabolic process Hormone metabolic process
Mdr2	<ul style="list-style-type: none"> Immune system process Antigen processing and presentation of peptide antigen Antigen processing and presentation Antigen processing and presentation of exogenous peptide antigen Antigen processing and presentation of exogenous antigen DNA replication initiation DNA-dependent DNA replication Cell cycle Protein complex biogenesis 	-----

Protein complex assembly
Antigen processing and
presentation of exogenous peptide
antigen via MHC class I
Anatomical structure formation
Regulation of protein metabolic
process
Regulation of cellular protein
metabolic process
DNA replication
Cellular component organization
Regulation of cellular component
organization
Death
Positive regulation of endocytosis
Actin filament-based process
Regulation of actin
polymerization or
depolymerization
Regulation of actin filament
length
Cellular component assembly
Cell death
Actin cytoskeleton organization
Regulation of cellular component
size
Regulation of anatomical structure
morphogenesis
Programmed cell death
Phagocytosis, recognition
Regulation of cell cycle
Regulation of actin cytoskeleton
organization
Apoptosis
Cell cycle phase
Regulation of actin filament
polymerization
Regulation of actin filament-based
process
Cell cycle process
Mitotic cell cycle
Actin polymerization or
depolymerization
Macromolecular complex
assembly
Actin filament organization
Cell division
Actin filament polymerization

Supplementary Table 4. DGE results for the genes used in the comparative expression analysis

Gene	Accession Number	Fold Change	Corrected P-value
Scd1	NM_009127*	-1.5240	3e-81
	AK142630	-2.2539	3.42e-5
	AK135642	1.12229	0.03633
	BC055453	1.6271	0.00311
Ppar α	NM_011144	**	
	X57638	**	
Mdr2	NM_008830	1.9512	1.33e-21

* major transcript

** under limit of detection

For a discussion, see Supplementary Fig. 5