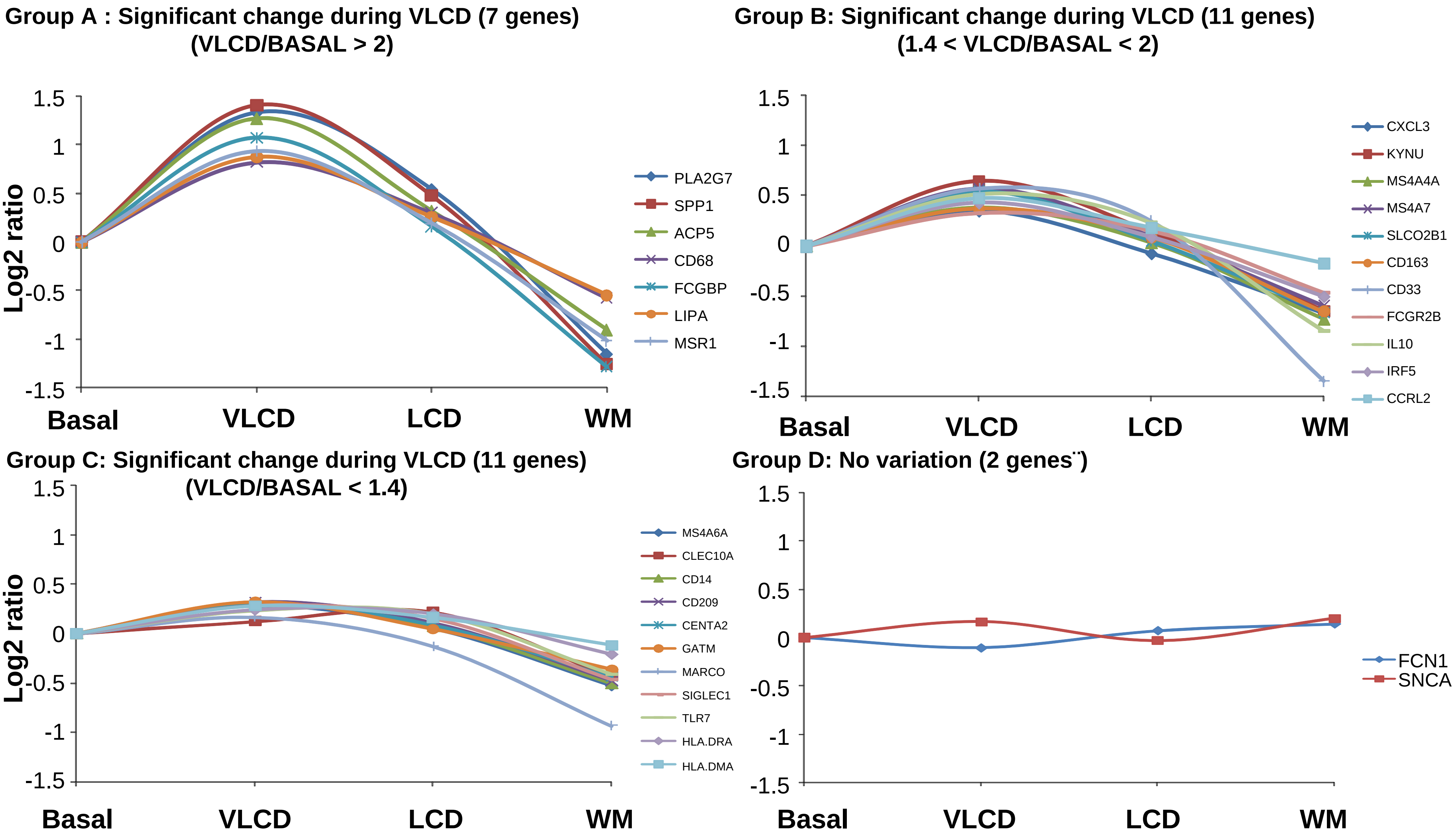
Supplementary Figure 1



Group A : Significant change during VLCD (7 genes) (VLCD/BASAL > 2)

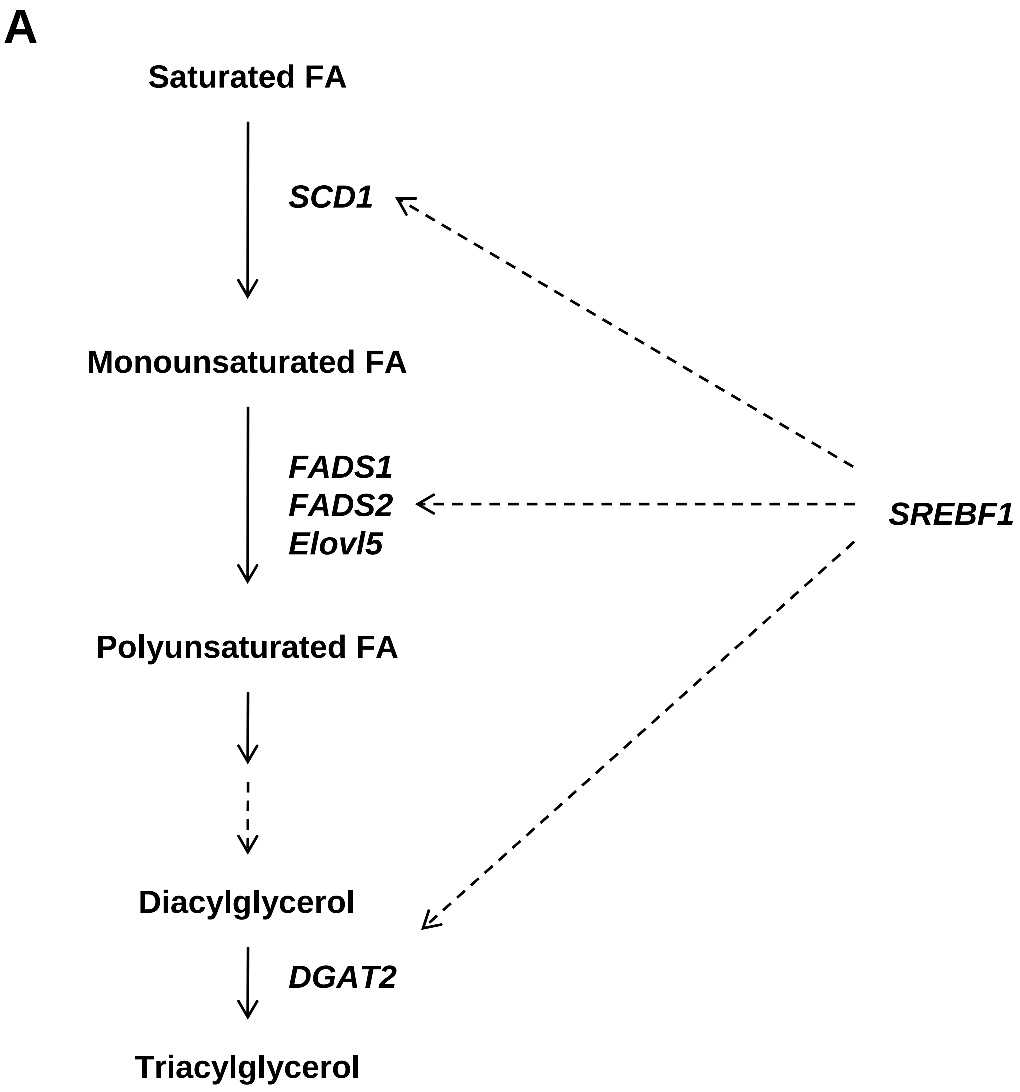
Group B: Significant change during VLCD (11 genes) (1.4 < VLCD/BASAL < 2)

Group C: Significant change during VLCD (11 genes) (VLCD/BASAL < 1.4)

Group D: No variation (2 genes¨)

Gene expression of macrophage-specific markers determined by reverse transcription-quantitative PCR at each time point of the dietary weight loss program. ANOVA revealed four groups of genes (A, B, C, D) according to profiles of changes.

Supplementary Figure 2



PLS-R model of insulin sensitivity during the energy restriction phase. Enzymes of fatty acid and triacylglycerol synthesis regulated by the transcription factor SREBF1 are part of the model. The names of genes in the PLS-R models are provided on Supplementary Table 5.

Supplementary Figure 2

B

Leukocyte extravasation signaling

Acute phase response signaling

Cytokines
CCL2
GDF13
CCL13
SPP1

Enzymes
CYPB
RAC2
PLA2G7
LIPA
KYNU
CES1
MMP9

Kinases
TK1
FGR

G-protein-coupled receptors
CXCR4
FPR1

Transmembrane receptors
CD163
FCGR2B
MSR1
MARCO
CD14

Others
ApoC1
ITGAX
TGB2
C1QA
C1QB
C1QC
TYROPBP
CD83
SLA
SPOCD1
HSCT
S100A4
CD68
TGFB1
ARPCB1

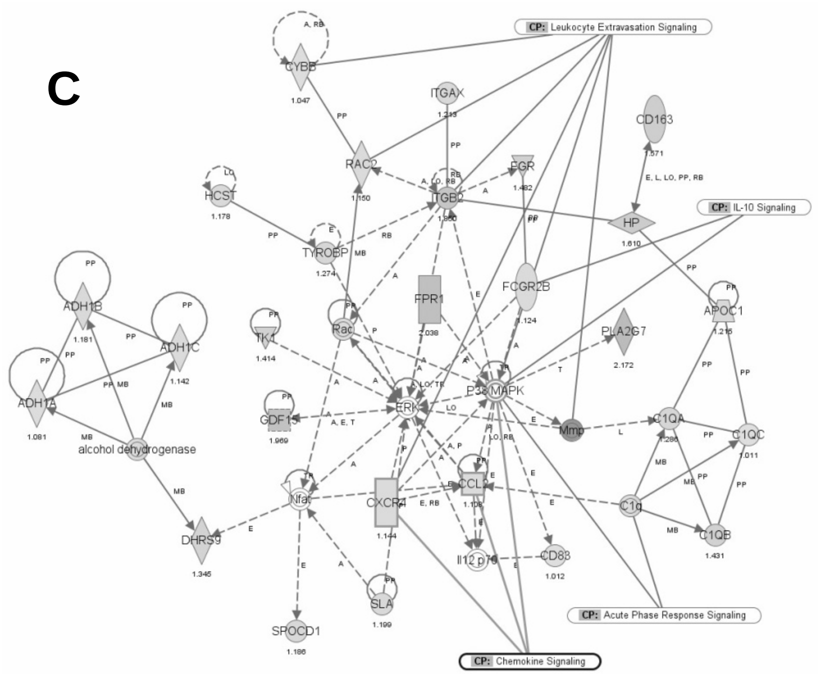
Interleukin 10 signaling

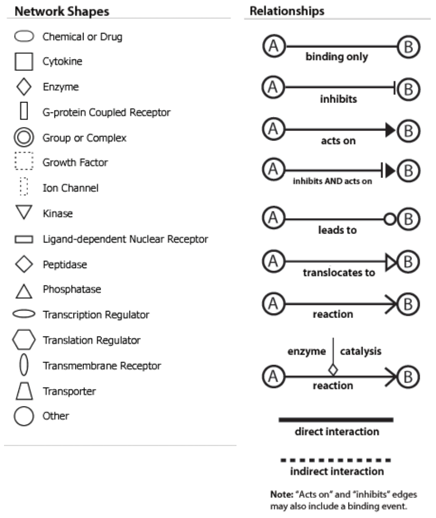
Chemokine signaling

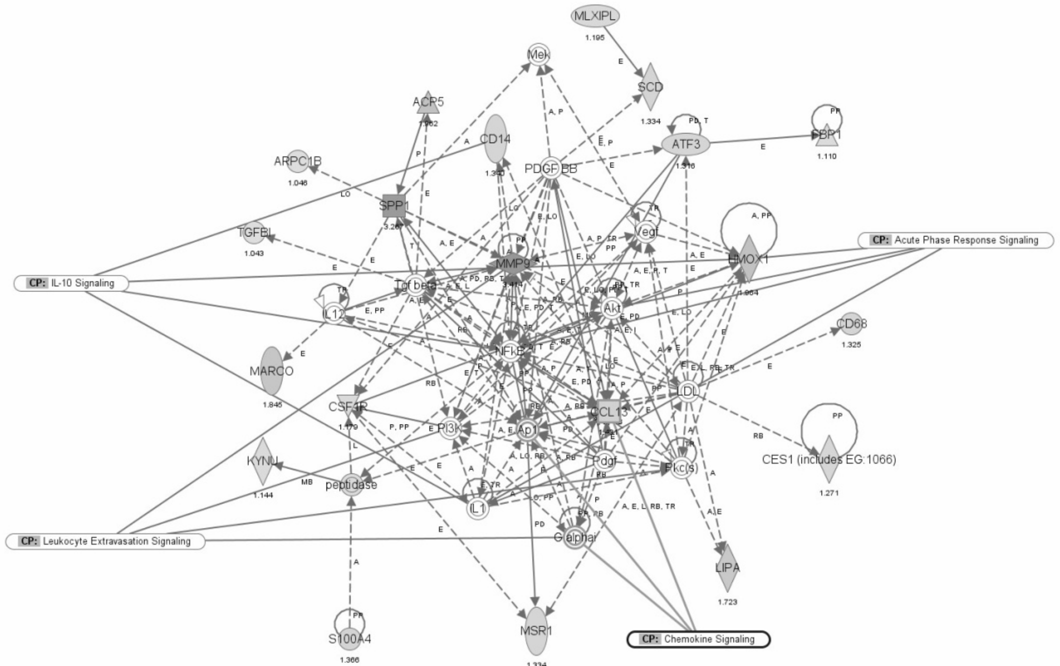
During the entire dietary intervention, Ingenuity Pathway Analysis revealed networks of closely interacting genes. The genes classified by molecular function shown within the rectangle were involved in four canonical pathways shown on each side of the rectangle. The comprehensive graphical representation of the interactions is shown on Supplementary Figure 2C. The names of genes in the PLS-R models are provided on Supplementary Table 5.

Supplementary Figure 2

C







During the entire dietary intervention, Ingenuity Pathway Analysis revealed networks of closely interacting genes involved in several canonical pathways (CP). Below each gene participating in the PLS model (grey shades) is the variable importance for projection which represents the value of each predictor in fitting the PLS model for both predictors and response. Edge labels besides connecting lines are : A Activation, B Binding, C Causes/Leads to CC Chemical-Chemical interaction, CP Chemical-Protein interaction, E Expression (includes metabolism/ synthesis for chemicals), EC Enzyme Catalysis, I Inhibition, L Proteolysis (includes degradation for Chemicals), LO Localization, M Biochemical Modification, MB Group/complex Membership, P Phosphorylation/Dephosphorylation, PD Protein-DNA binding, PP Protein-Protein binding, PR Protein-RNA binding, RB Regulation of Binding, RE Reaction, T Transcription and TR Translocation. The names of genes are provided on Supplementary Table 5.