Supplementary Table 1: Immunophenotypic profile of undifferentiated human adipose-derived stem cells (ASCs) isolated from control and CD subjects. The values reflect the mean ±SD percentage surface positive staining of ASCs for a part of surface antigens including hematopoietic and stromal markers.

Antibody	Control-ASCs	Active CD-ASCs	Inactive CD-ASCs
CD34	$1.2 \pm 0,8$	$0,1 \pm 0,05$	$0,2 \pm 0,1$
CD45	2 ± 1	$0,1 \pm 0,05$	$0,1 \pm 0,1$
CD73	94 ± 6	$98,3 \pm 0,5$	$96 \pm 0,5$
CD90	94 ± 8	$96,3 \pm 0,9$	$95,9 \pm 1,1$
CD105	99 ± 2	99 ± 1	$98 \pm 0,5$

Supplementary Table 2. TaqMan™ probes used in real-time PCR gene expression analysis.

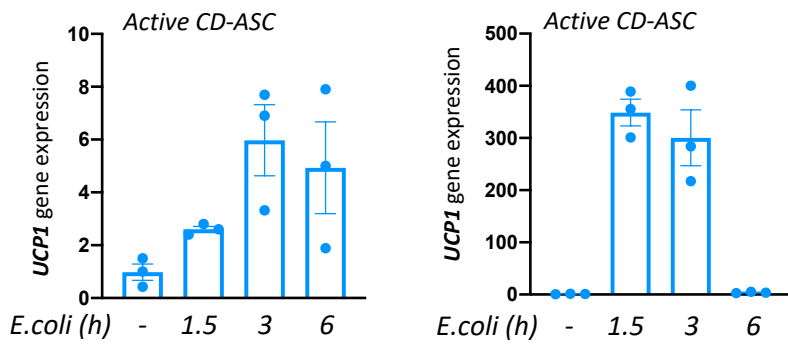|			
TCA cycle	*SUCNR1*	Succinate receptor 1	Hs00263701_m1
Browning markers	*ADRB3*	Adrenergic, Beta-3-, Receptor	Hs00609046_m1
	COX7A1	Cytochrome C Oxidase Subunit 7A1	Hs03045102_g1
	CPT1B	Carnitine Palmitoyltransferase 1B	Hs00189258_m1
	ELOVL3	ELOVL Fatty Acid Elongase 3	Hs00537016_m1
	FOXC2	Forkhead Box C2	Hs00270951_s1
	PPARGC1A	PPARG Coactivator 1 Alpha	Hs00173304_m1
	PPARGC1B	PPARG Coactivator 1 Beta	Hs00993805_m1
	PRDM16	PR/SET Domain 16	Hs00223161_m1
	TBX1	T-Box Transcription Factor 1	Hs00962558_g1
	TMEM26	Transmembrane Protein 26	Hs00415619_m1
	UCP-1	Uncopupling Protein 1	Hs01084772_m1
Inflammation	*IL6*	Interleukin-6	Hs00985639_m1
	TNFA	Tumor Necrosis Factor Alpha	Hs00174128_m1
	ILB1	Interleukin 1 Beta	Hs01555410_m1
Chemokines	*MCP1/CCL2*	Monocyte chemoattractant protein-1	Hs00234140_m1
Phagocytosis marker	*RAB5A*	Ras-related protein Rab-5A	Hs00702360_s1
Housekeeping gene	*18S*	Eukaryotic 18S ribosomal RNA	Hs99999901_s1

Supplementary Table 3. Bio-impedance measurements of the subcohort used for the infrared thermography study.

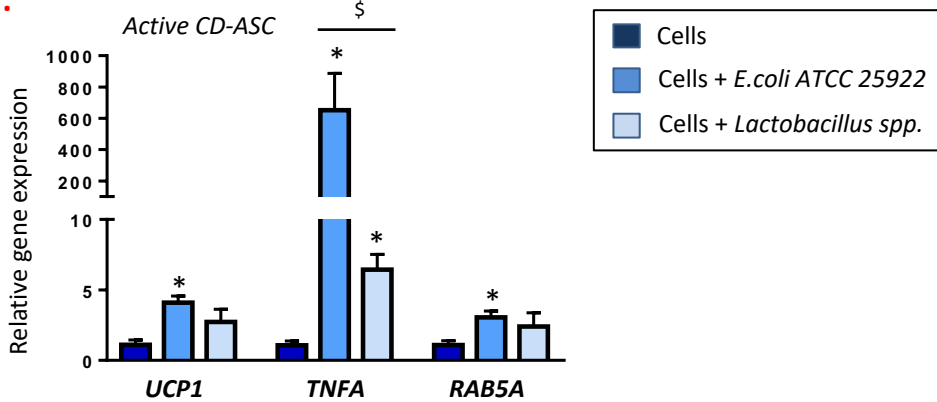|	Healthy Control (n= 12)	Crohn disease (n=11)	
		Active (n=5)	Inactive (n=6)
Sex (male/female)	(3/9)	(1/4)	(3/3)
Age	41.41 ± 13.13	49.8 ± 23.12	33.66 ± 10.03
BMI (kg/m^2)	23.40 ± 2.37	20.61 ± 2.58	25.79 ± 4.78
FFMI (kg/m^2)	15.92 ± 1.88	15.6 ± 2.53	17.45 ± 1.55
FMI (kg/m^2)	7.15 ± 2.02	4.76 ± 2.40	8,18 ± 4.62
VAT (l)	1.42 ± 0.9	0.72 ± 0.65	1.40 ± 0.58
SMM (kg)	21.24 ± 6.65	17.48 ± 4.17[b]	24.76 ± 5.59
Phase angle (º)	6.15 ± 0.77	5,14 ± 1.56[a,b]	6.8 ± 0.61

Abbreviations: BMI. body mass index; FFMI. fat free mass index; FMI. fat mass index; SMM. skeletal muscle mass; VAT. visceral adipose tissue.
[a] *P <0,05 significant differences compared with healthy control ;* [b] *P <0,05 significant differences compared with patients in remission of the disease.*
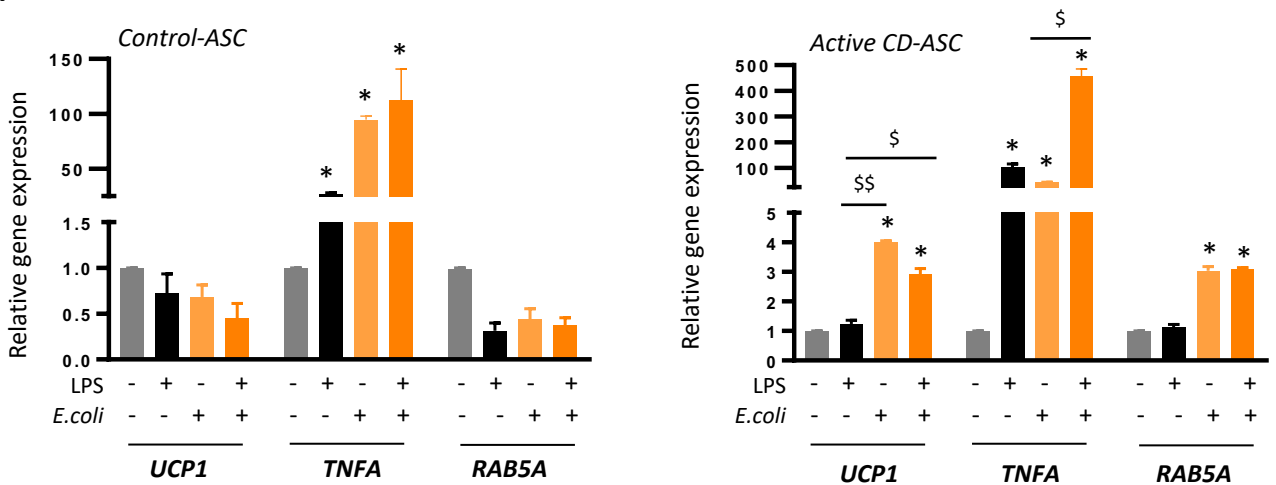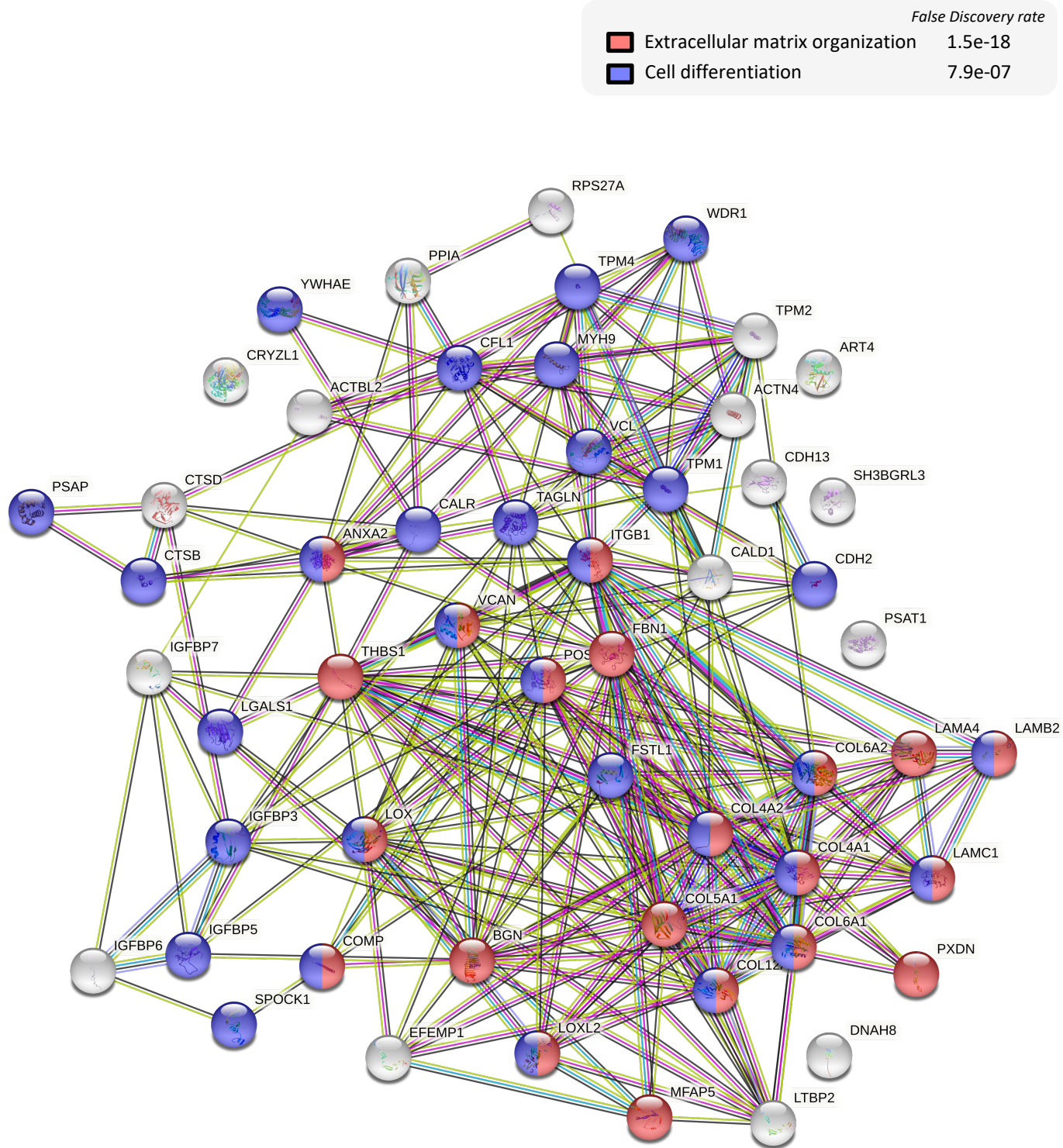
Supplementary Figure 1. Acute inflammatory stimulus is not enough to increase UCP-1 gene expression in adipose-stem cells from healthy individuals. (A) Time-course of *E.coli* infection in adipose-stem cells isolated from CD patients **(B)** Relative gene expression of the browning marker *UCP1*, inflammatory marker *TNFA* and phagocytic marker *RAB5A* in ASC isolated from VAT of active CD patients and co-cultured with *E.coli ATCC 25922* or *Lactobacillus spp.* for 3 hours. **(C)** ASC isolated from healthy individuals (control group) or active CD patients were treated with LPS at 100 ng/ml for 1 hour and then were infected with *E.coli* or not for 3 hours. The gene expression of the *UCP1, TNFA* and *RAB5A* were studied. Bars in graphs represent mean ± SEM. Data are representative of three independent experiments. *P<0.05 versus control; $^{\$}$P<0.05 and $^{\$\$}$P<0.01 as indicated in the figure.

Supplementary Figure 2. Protein-protein interaction network of up-regulated proteins in adipose-stem cells of CD patients. The integrated functional network built from proteins up-regulated in adipose-stem cells of CD patients. The densely connected sub-networks extracted using STRING from the total network are shown in different colours. Number of nodes: 55; number of edges: 268; number of expected edges: 28; PPI enrichment p-value: <1.0e-16.