SUPPLEMENTARY FIGURE LEGENDS

Supplementary Fig. 1: Autoradiogram of a Northern blot analysis of total RNA isolated from noninfected HepG2 cells or cells infected at a multiplicity of infection of 5 with a control adenovirus expressing GFP or an adenovirus expressing the dn-c-Jun. The position of apoE and the GAPDH mRNAs are indicated.

Supplementary Fig. 2: Western Blotting analysis of cytoplasmic or nuclear extracts of HepG2 cells infected at a multiplicity of infection of 5 with a control adenovirus expressing the Green Fluorescence Protein (GFP) or adenoviruses expressing the dn-c-Jun. The position of wild type c-Jun and dominant negative c-Jun is indicated.

Supplementary Fig. 3. Effect of the WT c-Jun on the hepatic expression of apoE and the plasma lipid levels in C57BL/6 mice infected with an adenovirus expressing the dn-c-Jun. **Panels A and B:** Autoradiograms of Northern blotting analysis of total RNA isolated from the liver of mice 4 days post infection with **2x10⁹ pfu** of either a control adenovirus expressing GFP or an adenovirus expressing the WT c-Jun. Blot shown in Panel A was hybridized with a probe that detects c-Jun and GAPDH and Panel B was hybridized with a probe that detects apoE and GAPDH as indicated.

Supplementary Fig. 4: Hepatic VLDL-triglyceride secretion of C57BL/6 mice infected with **2x10⁹ pfu** of either a control adenovirus expressing GFP or adenovirus expressing the dn-c-Jun. Four days post infection three mice per group were fasted for four hours and injected with Triton WR1339. Serum was collected 20, 40, 60 and 90 minutes after administration of the Triton and was analyzed for triglyceride levels.

Supplementary Fig. 5: Molecular pathways presenting with the majority of gene expression changes. The classification was done based on Gene Ontology level 5 categories, for significantly (2% FDR) and highly (>2-fold) changed transcripts.

Supplementary Fig. 6. Autoradiogram of a Northern blot analysis of total RNA isolated from apoE^{-/-} mice infected with **2x10⁹ pfu of** either a control adenovirus expressing GFP or an adenovirus expressing the c-Jundn-c-Jun or an adenovirus expressing WT c-Jun. The positions of Scd-1 and the GAPDH mRNAs are indicated. Quantitation by phosphorimaging showed that the Scd-1 mRNA levels were reduced by 81% and 67% C57BL/6 and apoE^{-/-} mice respectively following treatment with dn-c-Jun. Treatment with WT c-Jun did not affect significantly the Scd-1 mRNA levels in either the C57BL/7 or apoE^{-/-} mice.

Supplementary Fig. 7: Western Blotting analysis of total cell extracts of HepG2 cells infected at a multiplicity of infection of 5 with either a control adenovirus expressing the GFP or increasing amounts of adenoviruses expressing Scd-1.

Supplementary Fig. 8. Cholesterol and triglyceride levels of C57BL/6 mice (**Panels A&B respectively**) and apoE^{-/-} mice (**Panels C&D respectively**). The mice were infected with $2x10^9$ pfu of either control adenoviruses expressing GFP or adenovirus expressing the Scd-1. Three groups of mice containing 3-4 mice per group were infected with $2x10^9$ pfu of the adenoviruses as indicated in the figure and plasma was collected on the fourth day and analyzed for cholesterol and triglyceride levels.

SUPPLEMENTARY TABLE NOT TO BE INCLUDED IN THE PUBLICATION

Supplementary Table 1: Probe sets significantly and highly changed between dn-c-Jun infected and control apoE^{-/-} mice, as identified by SAM using 2-fold and $\leq 2\%$ median FDR thresholds.

Affymetrix ID	Gene Name	Symbol	Fold
1432466_a_at	apolipoprotein E	Apoe	40.39
1424470_a_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	3.19
1419152_at	RIKEN cDNA 2810417H13 gene	2810417H13Rik	-2.00
1449134_s_at	Spi-C transcription factor (Spi-1/PU.1 related)	Spic	-2.00
1439764_s_at	RIKEN cDNA C330012H03 gene	C330012H03Rik	-2.01
1448735_at	ceruloplasmin	Ср	-2.01
1426645_at	heat shock protein 1, alpha	Hspca	-2.02
1423062_at	insulin-like growth factor binding protein 3	Igfbp3	-2.02
1460589_at	zinc finger protein 597	Zfp597	-2.04
1425212_a_at	tumor necrosis factor receptor superfamily, member 19	Tnfrsf19	-2.04
1430633_s_at	RIKEN cDNA C430045118 gene	C430045I18Rik	-2.04
1456700_x_at	Myristoylated alanine rich protein kinase C substrate	Marcks	-2.05
1437456_x_at	YTH domain family 1	Ythdf1	-2.05
1420847_a_at	fibroblast growth factor receptor 2	Fgfr2	-2.05
1444607_at	Similar to corneodesmosin precursor; S protein; differentiated keratinocyte S protein precursor	Cdsn	-2.05
1420697_at	solute carrier family 15, member 3	Slc15a3	-2.06
1445626_at	Lectin, galactose binding, soluble 3	Lgals3	-2.06
1443626_at	Transcribed locus		-2.06
1457035_at	expressed sequence AI607873	AI607873	-2.06

1439255_s_at	transmembrane 7 superfamily member 1	Tm7sf1	-2.06
1426262_at	cDNA sequence BC024969	BC024969	-2.06
1427595_at			-2.07
1435281_at	carnitine palmitoyltransferase 1c	Cpt1c	-2.07
1425294_at	SLAM family member 8	Slamf8	-2.07
1418969_at	S-phase kinase-associated protein 2 (p45)	Skp2	-2.07
1438535_at	pleckstrin homology domain interacting protein	Phip	-2.08
1435627_x_at	MARCKS-like protein	Mlp	-2.08
1436643_x_at	hepcidin antimicrobial peptide 2	Hamp2	-2.10
1418571_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	-2.11
1439567_at	T-box 3	Tbx3	-2.11
1452656_at	zinc finger, DHHC domain containing 2	Zdhhc2	-2.11
1432362_at	RIKEN cDNA 1700022C02 gene	1700022C02Rik	-2.12
1445708_x_at	RIKEN cDNA 3110021A11 gene	3110021A11Rik	-2.12
1443981_at			-2.13
1444139_at	DNA-damage-inducible transcript 4-like	Ddit41	-2.13
1437585_x_at	zinc finger protein 161	Zfp161	-2.13
1428903_at	RIKEN cDNA 3110037I16 gene	3110037I16Rik	-2.13
1420438_at	orosomucoid 2	Orm2	-2.13
1459322_at	Synaptic nuclear envelope 2	Syne2	-2.13
1417031_at	RIKEN cDNA 2310028N02 gene	2310028N02Rik	-2.13
1447734_x_at	aldolase 1, A isoform, pseudogene 2	Aldoa-ps2	-2.13
1434401_at	zinc finger, CCHC domain containing 2	Zcchc2	-2.14
1450156_a_at	hyaluronan mediated motility receptor (RHAMM)	Hmmr	-2.14
1437516_at	EST AA407452	AA407452	-2.14

1439301_at	RAD51-like 1 (S. cerevisiae)	Rad5111	-2.14
1460626_at	DNA segment, Chr 5, ERATO Doi 606, expressed	D5Ertd606e	-2.15
1445882_at	Transcribed locus		-2.15
1434255_at	phosphofurin acidic cluster sorting protein 1-like	Pacs11	-2.17
1419943_s_at	cyclin B1	Ccnb1	-2.17
1450050_at	histone cell cycle regulation defective homolog A (S. cerevisiae)	Hira	-2.18
1427347_s_at			-2.18
1429557_at	minichromosome maintenance deficient 8 (S. cerevisiae)	Mcm8	-2.18
1447894_x_at	vacuolar protein sorting 52 (yeast)	Vps52	-2.18
1417019_a_at	cell division cycle 6 homolog (S. cerevisiae)	Cdc6	-2.19
1438751_at	RIKEN cDNA 130106K10 gene	E130106K10Rik	-2.19
1431203_at	serologically defined colon cancer antigen 8	Sdccag8	-2.19
1416412_at	neutral sphingomyelinase (N-SMase) activation associated factor	Nsmaf	-2.19
1449519_at	growth arrest and DNA-damage-inducible 45 alpha	Gadd45a	-2.19
1439377_x_at	cell division cycle 20 homolog (S. cerevisiae)	Cdc20	-2.22
1454903_at			-2.22
1455804_x_at	3-oxoacid CoA transferase 1	Oxct1	-2.22
1453769_at	RIKEN cDNA 2610318C08 gene	2610318C08Rik	-2.22
1439426_x_at	P lysozyme structural	Lzp-s	-2.24
1439376_x_at			-2.24
1424229_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3	-2.25
1426063_a_at	GTP binding protein (gene overexpressed in skeletal muscle)	Gem	-2.26

1424190_at	phosphatidylinositol glycan, classC	Pigc	-2.26
1418572_x_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	-2.26
1422954_at	zinc finger protein 60	Zfp60	-2.27
1425642_at	cDNA sequence BC004690	BC004690	-2.29
1450063_at	formin 2	Fmn2	-2.29
1435802_at	gene model 157, (NCBI)	Gm157	-2.32
1416021_a_at	fatty acid binding protein 5, epidermal	Fabp5	-2.32
1420444_at	solute carrier family 22 (organic cation transporter), member 3	Slc22a3	-2.32
1444706_at	Neuron navigator 2	Nav2	-2.33
1452338_s_at	intersectin 1 (SH3 domain protein 1A)	Itsn1	-2.33
1426092_a_at	tripartite motif protein 34	Trim34	-2.34
1458374_at	expressed sequence C79407	C79407	-2.35
1428069_at	cell division cycle associated 7	Cdca7	-2.36
1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	-2.37
1440184_at	similar to p47 protein isoform a	LOC434492	-2.37
1436905_x_at	lysosomal-associated protein transmembrane 5	Laptm5	-2.37
1443669_at	Zinc finger, FYVE domain containing 28	Zfyve28	-2.37
1420570_x_at	T-cell leukemia/lymphoma 1B, 3	Tcl1b3	-2.38
1420380_at	chemokine (C-C motif) ligand 2	Ccl2	-2.39
1443911_at	Exportin 1, CRM1 homolog (yeast)	Xpo1	-2.40
1447679_s_at	BMS1-like, ribosome assembly protein (yeast)	Bms11	-2.40
1450381_a_at	B-cell leukemia/lymphoma 6	Bcl6	-2.43
1442531_at	DNA segment, Chr 12, ERATO Doi 123, expressed	D12Ertd123e	-2.43
1418872_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	-2.44

1433888_at	ATPase, Ca++ transporting, plasma membrane 2	Atp2b2	-2.45
1451798_at	interleukin 1 receptor antagonist	Il1rn	-2.45
1454617_at	arrestin domain containing 3	Arrdc3	-2.46
1416022_at	fatty acid binding protein 5, epidermal	Fabp5	-2.47
1422016_a_at	centromere autoantigen H	Cenph	-2.48
1437611_x_at	kinesin family member 2C	Kif2c	-2.49
1421228_at	chemokine (C-C motif) ligand 7	Ccl7	-2.51
1449984_at	chemokine (C-X-C motif) ligand 2	Cxcl2	-2.57
1458287_at	Transcribed locus		-2.65
1447877_x_at	DNA methyltransferase (cytosine-5) 1	Dnmt1	-2.75
1422642_at	CDC42 effector protein (Rho GTPase binding) 3	Cdc42ep3	-2.80
1432059_x_at	RIKEN cDNA 5031425E22 gene	5031425E22Rik	-2.82
1450992_a_at	myeloid ecotropic viral integration site 1	Meis1	-2.85
1426464_at	nuclear receptor subfamily 1, group D, member 1	Nr1d1	-2.86
1426541_a_at			-2.87
1419004_s_at	B-cell leukemia/lymphoma 2 related protein A1a /// B-cell leukemia/lymphoma 2 related protein A1b /// B-cell leukemia/lymphoma 2 related protein A1d	Bcl2a1a /// Bcl2a1b /// Bcl2a1d	-2.88
1442771_at	RAD51-like 1 (S. cerevisiae)	Rad5111	-2.88
1440304_at	RIKEN cDNA E030004N02 gene	E030004N02Rik	-2.89
1449153_at	matrix metalloproteinase 12	Mmp12	-2.94
1458163_at	cDNA sequence BC066028	BC066028	-3.06
1416111_at	CD83 antigen	Cd83	-3.11
1427729_at	EH-domain containing 2	Ehd2	-3.11
1425271_at	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	Psmc3ip	-3.17
1447837_x_at			-3.21

1415965_at	stearoyl-Coenzyme A desaturase 1	Scd1	-3.27
1435122_x_at	DNA methyltransferase (cytosine-5) 1	Dnmt1	-3.27
1417256_at	matrix metalloproteinase 13	Mmp13	-3.32
1437712_x_at	exosome component 4	Exosc4	-3.43
1420330_at	C-type lectin domain family 4, member e	Clec4e	-3.51
1427381_at			-3.53
1422155_at	histone 2, H3c2	Hist2h3c2	-3.63
1416290_a_at	proteasome (prosome, macropain) 26S subunit, ATPase, 4	Psmc4	-4.67
1442547_at	Ataxia telangiectasia and rad3 related	Atr	-5.68

SUPPLEMENTARY FIGURE NOT TO BE INCLUDED IN THE PUBLICATION









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SUPPLEMENTARY FIGURE NOT TO BE INCLUDED IN THE PUBLICATION



Supplementary Figure 8