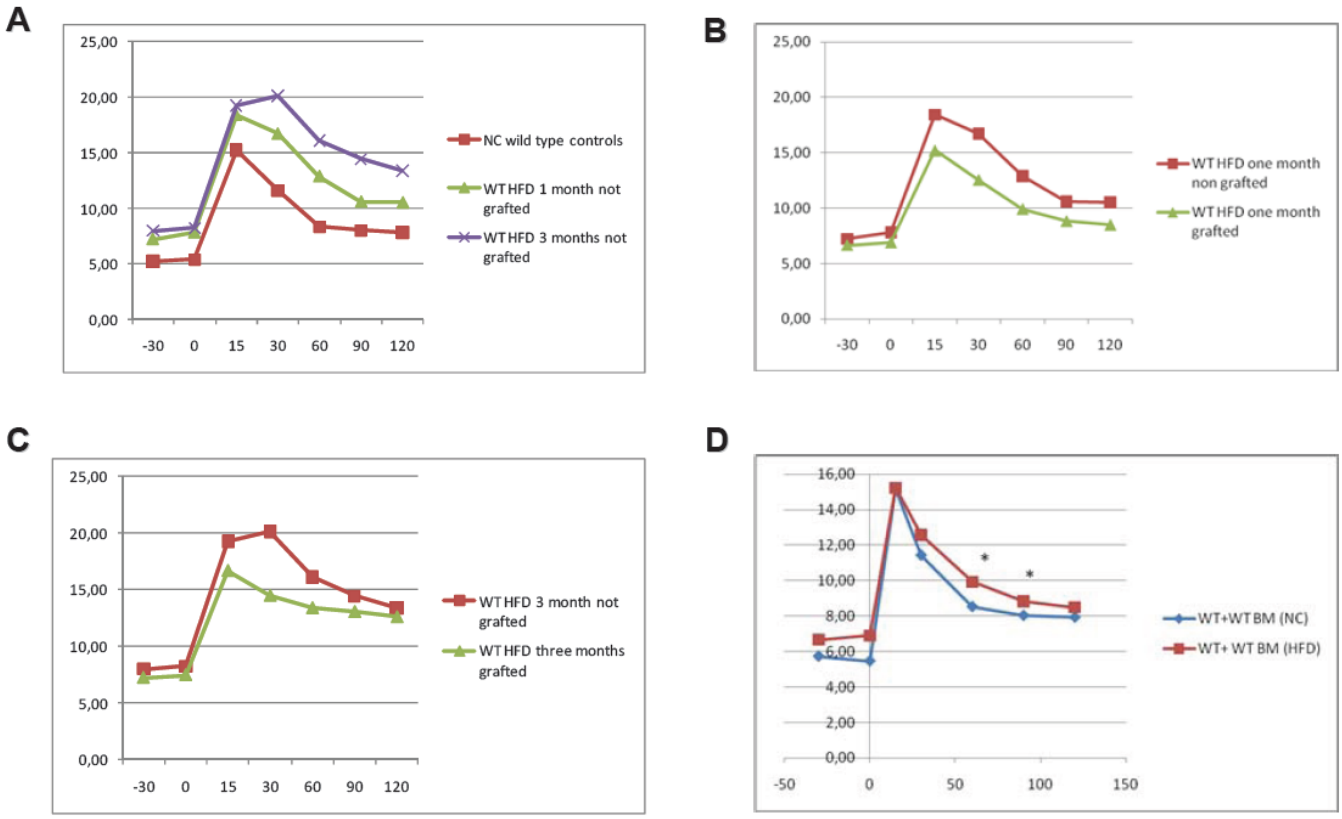
SUPPLEMENTARY DATA

Supplementary Table 1: List of genes up and down regulated in adipose tissue of mice after sCD14 treatment.

probe_id	gene_id	symbol	FoldChange (absolut)	logFC	t	P.Value
1419127_at	109648	Npy	3,638	-1,863	-3,253	0,0034238
1422153_a_a	68854	Asb11	3,406	-1,768	-3,832	0,0008217
1450346_at	14765	Gpr50	3,125	1,644	2,970	0,0067392
1452124_at	11735	Ank3	2,989	-1,580	-3,296	0,0030819
1457435_x_a	17930	Myom2	2,741	-1,455	-3,120	0,0047147
1434909_at	52187	Rragd	2,603	-1,380	-5,295	0,0000207
1439036_a_a	11931	Atp1b1	2,563	-1,358	-3,006	0,0061923
1454752_at	666794	Rbm24	2,548	-1,350	-4,275	0,0002705
1449398_at	66211	Rpl3l	2,541	-1,346	-4,621	0,0001129
1418095_at	66106	Smpx	2,414	-1,271	-3,200	0,0038902
1418373_at	56012	Pgam2	2,310	-1,208	-2,911	0,0077279
1426615_s_a	234593	Ndrg4	2,279	-1,189	-2,953	0,0070028
1448182_a_a	12484	Cd24a	2,269	-1,182	-2,857	0,0087778
1450826_a_a	20210	Saa3	2,262	1,177	2,971	0,0067260
1422644_at	50795	Sh3bgr	2,189	-1,130	-4,200	0,0003265
1451152_a_a	11931	Atp1b1	2,185	-1,128	-2,997	0,0063207
1438175_x_a	17930	Myom2	2,180	-1,125	-4,188	0,0003369
1423890_x_a	11931	Atp1b1	2,142	-1,099	-3,031	0,0058273
1424616_s_a	233575	Pgap2	2,115	-1,081	-2,903	0,0078806
1450917_at	17930	Myom2	2,095	-1,067	-2,989	0,0064458
1417889_at	11811	Apobec2	2,082	-1,058	-2,983	0,0065285
1418589_a_a	17349	Mlf1	2,078	-1,055	-3,394	0,0024302
1460318_at	13009	Csrp3	2,058	-1,041	-2,847	0,0089935
1417951_at	13808	Eno3	2,053	-1,038	-2,993	0,0063831
1418453_a_a	11931	Atp1b1	2,053	-1,038	-3,073	0,0052715
1438399_at	58869	Pex5l	2,040	1,028	3,173	0,0041560
1457275_at	233335	Synm	2,002	-1,002	-3,889	0,0007133
1417715_a_a	14719	Got2	1,995	-0,996	-3,023	0,0059438
1419762_at	24108	Ubd	1,979	0,984	2,859	0,0087444
1419606_a_a	21955	Tnnt1	1,967	-0,976	-3,948	0,0006160
1417634_at	20657	Sod3	1,965	0,975	3,817	0,0008545
1451721_a_a	14961	H2-Ab1	1,941	0,957	3,681	0,0011979
1449308_at	12274	C6	1,928	0,947	3,228	0,0036375
1449178_at	53318	Pdlim3	1,912	-0,935	-3,873	0,0007427
1456180_at	666794	Rbm24	1,906	-0,930	-3,497	0,0018899
1418849_x_a	11832	Aqp7	1,880	0,911	3,059	0,0054578
1425341_at	16527	Kcnk3	1,853	0,890	3,461	0,0020618
1453355_at	75607	Wnk2	1,810	-0,856	-3,175	0,0041344
1417633_at	20657	Sod3	1,777	0,830	3,732	0,0010543
1459860_x_a	80890	Trim2	1,763	-0,818	-3,152	0,0043715
1447657_s_a	68760	Synpo2l	1,755	-0,811	-3,072	0,0052825

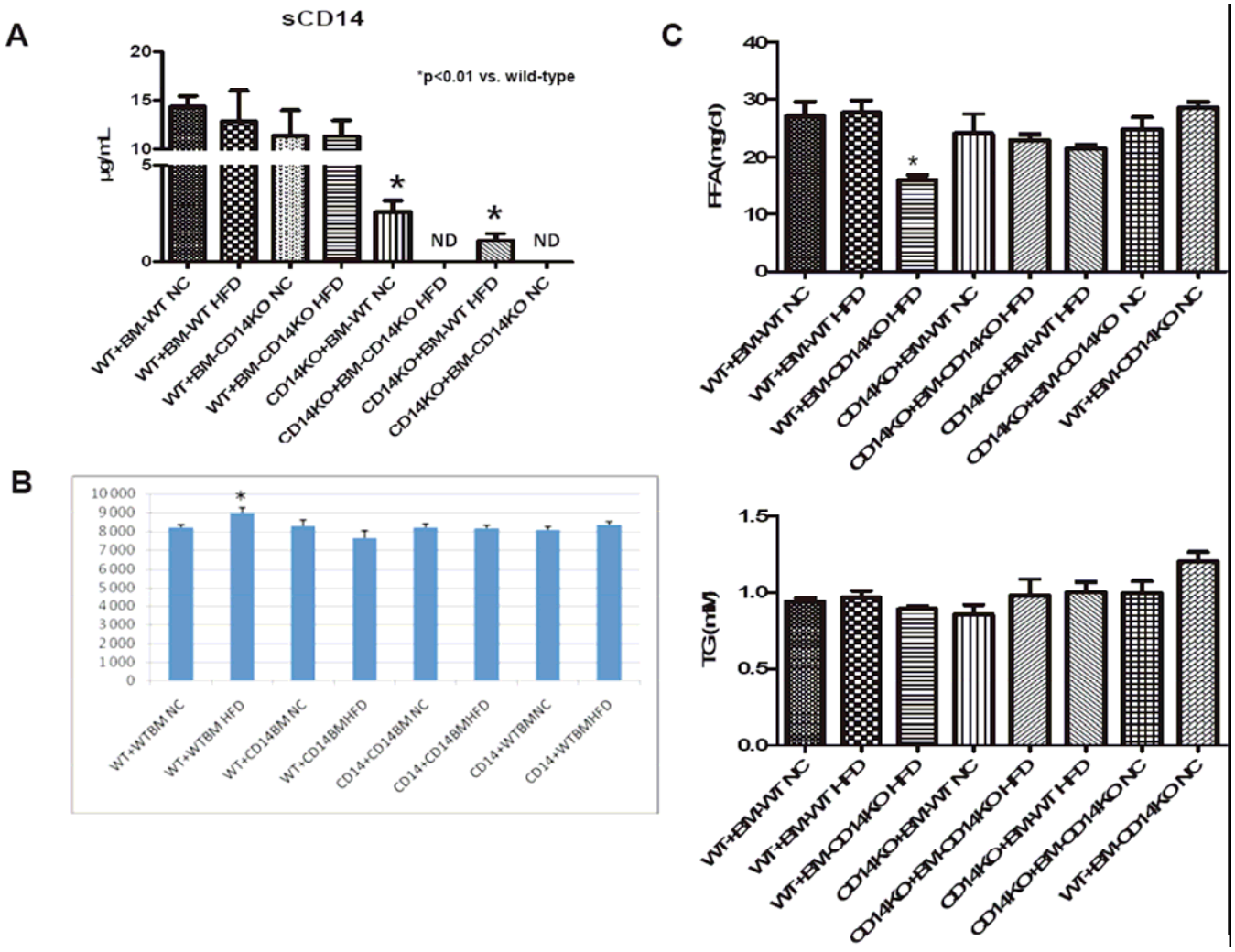
SUPPLEMENTARY DATA

Supplementary Figure 1. A. Effect of high fat diet (HFD) on oral glucose tolerance test in mice after one month (triangles) or 3 months (crosses) versus mice fed a normal chow (NC, squares). Glucose tolerance impairs over time during HFD. **B**. Effect of one month HFD on glucose tolerance test in mice grafted with BM from WT mice (triangles) vs. mice which were not grafted (not irradiated, squares). The irradiation and grafting procedure has impaired the diabetogenic effect of the HFD. **C.** Effect of a 3 month HFD on oral glucose tolerance in mice which were grafted with BM from WT donor (triangles) or not grafted (not irradiated, squares). As for figure B, the impact of HFD on glucose tolerance is reduced. **D.** Impact of a one month HFD (squares) vs. NC (diamonds) on oral glucose tolerance. The data shows that the diabetogenic impact is lower in the grafted mice than in the non grafted mice (Figure A). It requires a longer period of time. The interpretation is that the irradiation has hampered the role of some cells in the development of glucose intolerance.



SUPPLEMENTARY DATA

Supplementary Figure 2. **A.** Circulating sCD14 levels in the different models studied. **B.** Glucose intolerance following and oral glucose glucose challenge is significantly impaired (2 way ANOVA, Bonferoni Post hoc test, $p<0.05$) in wildtype mice grafted with bone marrow from the WT donor and fed a HFD when compared to the same group of mice but fed a NC. Conversely, in WT mice grafted with CD14 KO BM donor glucose intolerance was not observed. Similarly, CD14 receiver mice never became glucose intolerant in response to HFD. This suggests that both the hematopoietic cells and the cells from the body require CD14 to become glucose intolerant in response to a HFD. **C.** Fasting triglycerides and free fatty acids in the different models (* $p<0.05$).

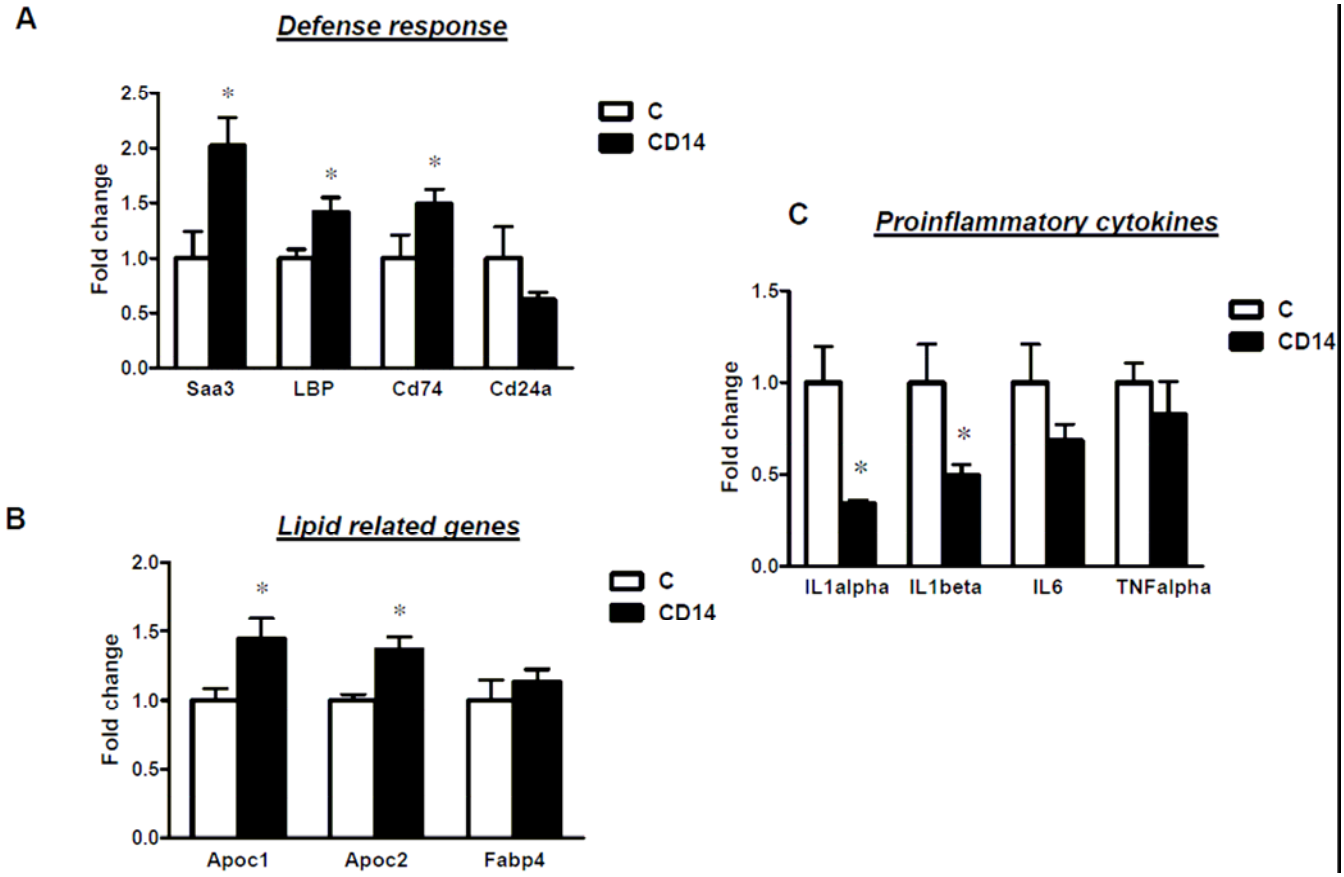


SUPPLEMENTARY DATA

Supplementary Figure 3. Confirmation by real-time PCR of the effect of CD14 treatment on gene expression in epididimal adipose tissue from control and CD14 treated *ob/ob* mice. Gene expression of defense response (A) lipid related (B) and proinflammatory (C) proteins in control (C, white bars) and CD14 treated ob/ob mice (CD14, black bars) are shown. Results are expressed as mean ± SEM relative to the control value set as 1.0 (n=6). Statistical analyses comparing gene expression in control vs. CD14 treated ob/ob mice were performed by paired t test. Saa3, p=0.017; LBP, p=0.023; Cd74, p=0.018; Apoc1, p=0.027; Apoc2, p=0.0046; IL-1-alpha, p=0.01; IL-1-beta, p=0.05.

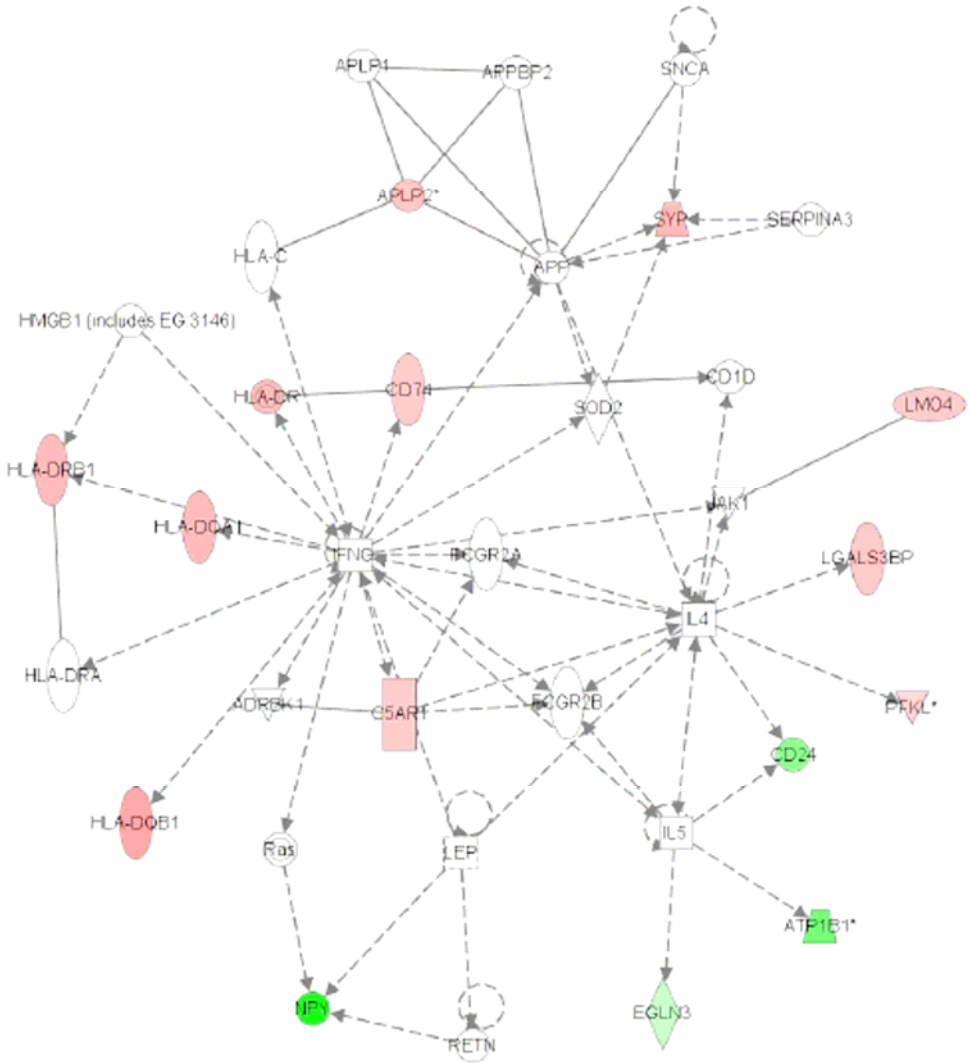
RNA from epididimal adipose tissue was extracted using a kit (RNeasy; Qiagen, Valencia, CA, USA). RNA (2 μg) was reverse-transcribed to cDNA using SuperscriptII enzyme (Invitrogen, USA). Real-time PCR was used to measure specific mRNAs (ABI-PRISM 7700 Sequence Detector; Perkin-Elmer Applied Biosystems, Foster City, CA, USA). All reactions were performed in 384-well optical plates (MicroAmp; Applied Biosystems, Foster City, CA, USA). Amplification mixes (10 μl) contained the diluted cDNA sample, 2X TaqMan Universal PCR Mastermix (Applied Biosystems) or Sybr green PCR Mastermix (Applied Biosystems), forward and reverse primers, and probe for the specific mRNAs. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as endogenous control. Thermal cycling conditions included 10 min at 203,00°F before the onset of the PCR cycles, which consisted of 40 cycles at 95°C for 15 s and 65°C for 1 min. The oligonucleotide sequences for the primer pairs used for *GAPDH* was 5'-catggccttccgtgttccta -3' and 5'-gcggcacgtcagatcca -3'. The primers and probes for Saa3, Cd74, Cd24a, LBP, Apoc1, Apoc2, IL-1 alpha, IL-1 beta, IL-6 and TNF-alpha were supplied as a kit (TaqMan Reagents Mm00441203_m1, Mm00658576_m1, Mm00782538_sH, LBP, Mm00431816_m1, Mm00431816_m1, Mm00439620_m1 and Mm01336189_m1, Applied Biosystems) and used according to the manufacturer's instructions. The primers for IL-6 were: 5'-GCCCACCAAGAACGATAGTCA-3' and 5'-CAAGAAGGCAACTGGATGGAA-3'; and for TNFalpha: 5'-CACAAGATGCTGGGACAGTGA-3' and 5'-TCCTTGATGGTGGTGCATGA-3'. mRNA expression was calculated using the ΔC_t method.

SUPPLEMENTARY DATA



SUPPLEMENTARY DATA

Supplementary Figures 4 and 5. Expression profiles of genes listed in Supplementary Table 1 were analyzed using The Ingenuity Pathway Analysis (IPA) methodology to compose a set of interactive networks, taking into consideration canonical pathways and the relevant biological interactions. Focus genes were defined as those with an absolute mean fold-change of at least 1.5. A number of canonical pathways came up as playing an important role, especially those related with Glycolysis and Gluconeogenesis and IL-4 signaling. Next, two significant biological networks were identified by IPA. Further analysis of the highest scored network (score 24, 14 focus genes) identified inflammatory response ($p<0.028$), Genetic Disorder ($p<0.048$) and Inflammatory Disease ($p<0.0375$) as the most significant biological functions linked to these networks.



SUPPLEMENTARY DATA