Expanded Experimental Procedures:

Tissue digestion and cell fractionation

Epididymal fat pads were isolated from mice by dissection, washed in sterile PBS, minced, and washed in Krebs-Ringer bicarbonate (KRB) buffer (pH 7.4) containing 4% albumin and 5 mM glucose (25). The tissues were incubated with collagenase (2mg/ml; Sigma) on a shaking platform at 37 ^{0}C for 30 mins. Adipocytes were then separated from other cells by their ability to float upon low speed (200 xg) centrifugation. The medium below the adipocyte layer was centrifuged at 500 x g for 10 min to obtain the stromal vascular fraction, and the resulting pellet was washed three times with KRB buffer. Total RNA was extracted from the two fractions and the amount of KC associated with each determined by real time quantitative PCR.

Immunohistochemistry and *in situ* hybridization

To detect macrophages in mouse tissues, sections were pre-incubated in 2% BSA in PBS, 0.01% Tween 20 and thereafter incubated with the F4/80 primary antibody (CI:A3-1, T-2008, BMA biomedicals, Switzerland) at a dilution of 1/50. The secondary antibody was biotinylated rabbit anti-rat (Vector Laboratories, BA-4001) used at a dilution of 1/50. This step was followed by the Vectastain Elite ABC kit (Vector Laboratories) in combination with 3,3-Diaminobenzidine (Zymed Laboratories, San Francisco, CA) for detection with hematoxylin counterstain.

Bone marrow transplantation

Bone marrow was harvested from 8 week-old CXCR2-deficient or WT (Balb/cJ) mice. Four million cells were injected into lethaly irradiated (10 Gy) recipient male C57BL/6 mice (6 to 8 weeks old) via the tail vein. Mice were allowed 6 weeks to reconstitute their hematopoietic systems with $CXCR2^{-/-}$ or WT bone marrow. Recipient mice were then placed on normal chow or HFD as described above. Genomic DNA was extracted from the circulating blood leukocytes and genotyped by PCR to analyze reconstitution efficiency. Total white blood cell number and differential was assessed by standard techniques (ACP Diagnostic Lab, University of California, San Diego, USA).

Quantification of crown-like structures

Both brightfield (F4/80) and fluorescent photographs (DAPI) were taken of 3 representative fields per slide in a blinded fashion using a fluorescent microscope (10x objective). The total number of nuclei per field were quantified by counting the DAPI-positive nuclei using ImageJ software (NIH freeware). F4/80 positive crown-like structures (CLS) per field were counted manually and the number of CLS per 1000 nuclei per field was used as a measure of AT CLS content.

Metabolic tests

For glucose and insulin tolerance tests, animals were fasted 6 hrs and a basal blood sample was taken. For the insulin tolerance test, animals were injected ip with insulin (0.75 U/kg; Novolin R, Novo-Nordisk, Copenhagen), whereas for the glucose tolerance test 1 g/kg glucose was injected ip. Blood samples were taken at regular intervals for

the determination of blood glucose concentration using a One-Touch glucose-monitoring system (Lifescan). Plasma insulin levels were measured by ELISA (ALPCO).

Additional data and supporting information:

Supplemental Table I: Blood differential in wild type and CXCR2$^{-/-}$ BMT mice fed normal or high fat diet.

Diet	Normal chow		High fat diet	
BM genotype	WT	CXCR2$^{-/-}$	WT	CXCR2$^{-/-}$
White Blood Cells (WBC; 10^9/L)	1.69 ± 0.24	2.17 ± 0.42	2.88 ± 1.15	2.25 ± 0.60
Neutrophils (% of WBC)	49.33 ± 8.11	58.00 ± 3.46	48.00 ± 4.00	56.00 ± 2.00
Lymphocytes (% of WBC)	40.00 ± 5.29	29.00 ± 4.73	28.00 ± 7.50	23.50 ± 4.50
Monocytes (% of WBC)	4.67 ± 2.67	6.67 ± 0.33	9.00 ± 2.00	11.50 ± 6.50
Eosinophils (% of WBC)	6.00 ± 4.16	6.33 ± 1.45	15.00 ± 6.00	9.00 ± 4.30

No significant differences between diets or BM genotypes were observed. n=5. Mean ± SEM.