Table S1

Pearson correlation

	eWAT	iWAT	BAT
iWAT	0.60		
BAT	0.47	0.48	
3T3-L1	0.25	-0.05	0.02

Spearman correlation

	eWAT	iWAT	BAT
iWAT	0.62		
BAT	0.53	0.55	
3T3-L1	0.33	0.05	0.13

Table S1. Pearson and Spearman correlation

Pearson and Spearman correlation coefficients of the log2 transformed normalized tag counts for binding sites from eWAT-, iWAT-, and BAT-derived adipocytes, as well as 3T3-L1 adipocytes.

Table S2

GO term (Wiki)	p-value (BAT)	p-value (eWAT)
Squamous cell	1.41E-5	0.0017
Muscle cell	0.00073	5.96E-10
Adipocyte	0.0044	0.0125
Epithelium	0.0063	1.45E-5
Signaling by EGFR	0.007	0.0091
Lymphocyte	0.0078	2.09E-5

GO term (KEGG)	p-value (BAT)	p-value (eWAT)
ECM-receptor interaction	3.39E-5	6.99E-27
PPAR signaling pathway	0.0004	0.0077
Pantothenate and CoA biosynthesis	0.0007	0.0029
Endocytosis	0.0013	0.0058
Insulin signaling pathway	0.011	4.05E-05
Vascular smooth muscle contraction	0.013	0.0108
Focal adhesion	0.014	7.34E-07
Citrate cycle (TCA cycle)	0.014	0.0058
Adipocytokine signaling pathway	0.015	9.55E-05
Glioma	0.017	0.0009

Table S2. Functional enrichment analysis

PPARγ sites enriched in eWAT- or BAT-derived adipocytes were assigned to the nearest gene (within 50kb), and the resulting target gene lists were used for functional enrichment analysis using WikiPathways, and KEGG pathways databases. Significantly enriched pathways ($p<0.02$) that are shared between eWAT- and BAT-derived adipocytes are shown in the table. Abbreviations: EGFR= Epidermal growth factor receptor, ECM=Extracellular matrix, PPAR=Peroxisome proliferator-activated receptor, TCA=Tricarboxylic acid cycle

Figure S1

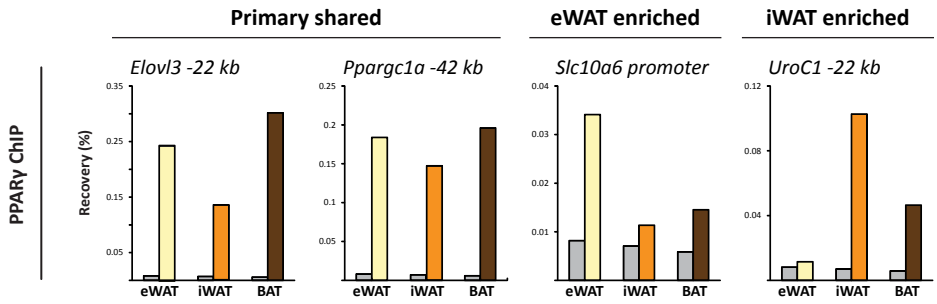

Figure S1. Validation of PPARγ peaks shown in Figure 3

Validation of PPAR*γ* binding by ChIP-qPCR for sites detected in ChIP-seq as shared between eWAT-, iWAT-, and BAT-derived adipocytes (*Elovl3* (-22 kb) and *PGC-1α* (-42 kb)), a site enriched in eWAT-derived adipocytes (*Slc10a6* promoter) and a site enriched in iWAT-derived adipocytes (*UroC1* (-22kb)). PPARγ binding sites enriched in BAT-derived adipocytes are validated in Fig. 5. Data are representative of at least two independent experiments.

Figure S2

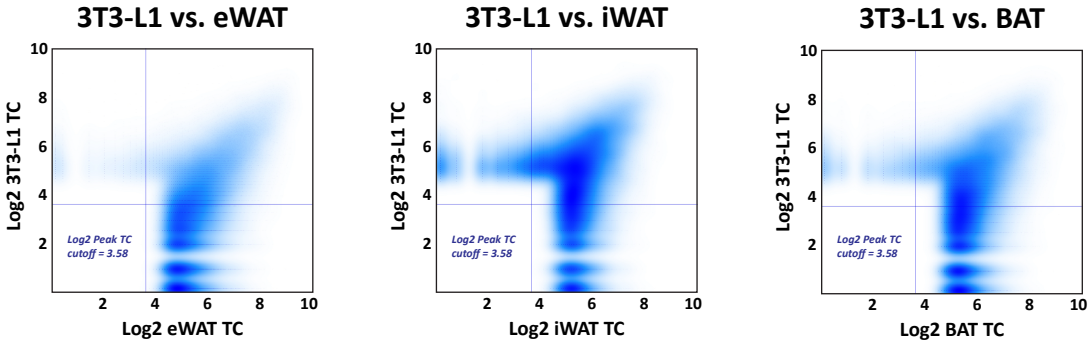

Figure S2. Correlation between PPARγ binding intensities in eWAT-, iWAT-, and BAT-derived adipocytes and 3T3-L1 adipocytes

Density plots showing correlation between log2 transformed normalized tag counts for PPARγ binding in eWAT-, iWAT-, and BAT-derived adipocytes and 3T3-L1 adipocytes. Horizontal and vertical lines indicate log2 normalized tag count cutoff for binding sites at 3.58 (corresponding to 12 tags).

Figure S3

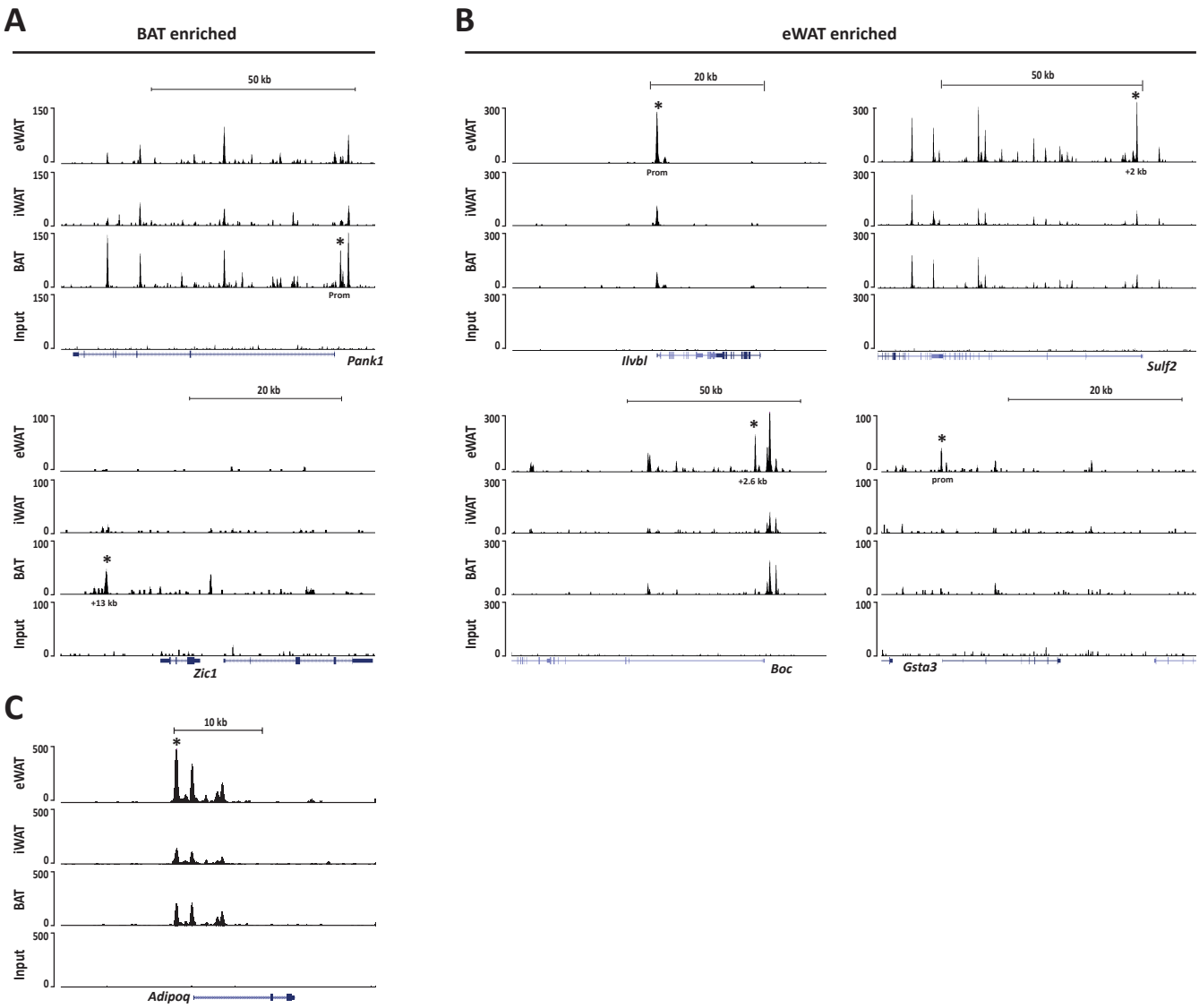

Figure S3. PPARγ binding at selected loci with eWAT- or BAT-selective binding

PPARγ binding to selected loci that display depot-selective binding of PPARγ enriched in BAT- (**A**) and eWAT-derived adipocytes (**B**). **(C)** PPARγ binding in the *Adipoq* locus. UCSC Genome Browser tracks of PPARγ binding in eWAT-, iWAT-, and BAT-derived adipocytes are shown. Sites investigated in Fig. 5 and Fig. 6 are marked by an asterisk (*).