

Supplemental Table S1. GO analysis of induced, repressed and transiently induced gene groups during 3T3-L1 differentiation. Genes were grouped based on RNA Pol II ChIP-seq tags throughout 3T3-L1 differentiation as described in Fig. 2 (429 induced genes, 640 repressed genes and 104 transiently induced genes). The gene groups were assigned to biological function based on GO using the Database for Annotation, Visualization, and Integrated Discovery (DAVID; <http://david.abcc.ncifcrf.gov>) (Dennis *et al.*, 2003). The *p*-value for each category is indicated.

Supplemental Table S2. GO analysis of early induced and repressed gene groups. Genes were grouped based on RNA Pol II ChIP-seq tags for day 0 and 4 hour time points as described in Fig. 6 (795 induced genes and 776 repressed genes). The gene groups were assigned to biological function based on GO using the Database for Annotation, Visualization, and Integrated Discovery (DAVID; <http://david.abcc.ncifcrf.gov>) (Dennis *et al.*, 2003). The *p*-value for each category is indicated.

Supplemental_TableS1

Gene group	GO category	p-value
Induced genes	Fat cell differentiation	6.4E-15
	Glucose metabolic process	2.2E-12
	Triglyceride metabolic process	2.8E-9
	Mitochondrion	1.8E-9
	Lipid binding	3.0E-4
Repressed genes	G-protein coupled receptor	1.6E-8
	Transmembrane	6.5E-4
	Cell membrane	3.8E-3
Transiently induced genes	DNA packaging	2.3E-14
	Ribosome	9.9E-5
	Cell cycle	2.3E-3
	Translation	3.3E-3

Supplemental_TableS2

Gene group	GO category	p-value
Induced genes	Ribosome	3.1E-29
	Translation	1.2E-24
	Mitochondrion	1.1E-14
	Glucose catabolic process	1.1E-6
Repressed genes	Lysosome	9.1E-9
	Zinc finger, C2H2-like	5.4E-5
	Skeletal system development	1.7E-3
	Apoptosis	4.5E-3