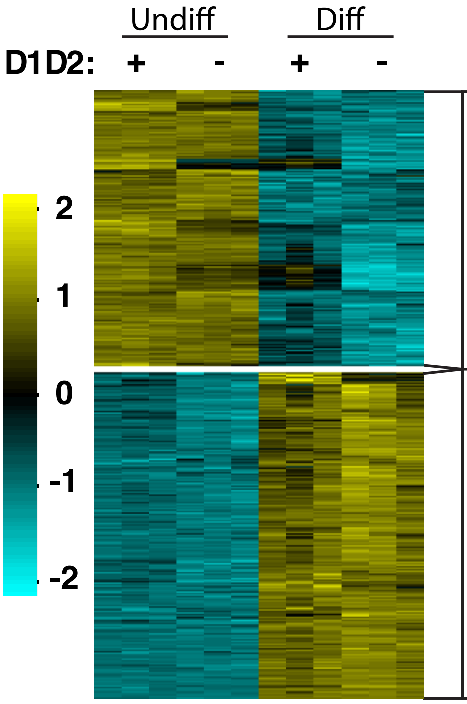
Harris_SupFig1



Enriched GO Terms

Repressed Genes	GO:22610 Biological adhesion
	GO:48856 Anatomical structure development
	GO:31032 Actomyosin structure development
	GO:43062 Extracellular structure organization
	GO:40011 Locomotion
Induced Genes	GO:06091 Generation of precursor metabolites and energy
	GO:55114 Oxidation reduction
	GO:06006 Glucose metabolic process
	GO:50873 Brown fat cell differentiation
	GO:19216 Regulation of lipid metabolic process
	GO:06732 Coenzyme metabolic process

Supplementary Figure Legend

Supplementary Figure 1. D1D2KO adipocytes have a transcriptional profile similar to WT adipocytes. (A) Heatmap of unbiased HOPACH clustering of samples from undifferentiated and differentiated MEFs from WT and D1D2KO using criteria of greather than two-fold change and nominal $p < 0.0001$. Shown at right are GO pathways for each cluster of the heat map.

Supplementary Table 1. Gene Set Enrichment Analysis comparing the effects of the differentiation protocol in WT and D1D2 KO cells.

KEGG Pathway Name (Number)	WT				D1D2 KO			
	ES	NES	P-value	Rank	ES	NES	P-value	Rank
Val, Leu and Ile degradation (HSA00280)	0.859	2.593	<0.001	1	0.860	2.582	<0.001	2
Oxidative phosphorylation (HSA00190)	0.716	2.567	<0.001	2	0.807	2.875	<0.001	1
PPAR signaling pathway (HSA03320)	0.798	2.566	<0.001	3	0.807	2.552	<0.001	3
Fatty acid metabolism (HSA00071)	0.814	2.439	<0.001	4	0.807	2.379	<0.001	6
Propanoate metabolism (HSA00640)	0.816	2.427	<0.001	5	0.843	2.386	<0.001	5
Pyruvate metabolism (HSA00620)	0.796	2.423	<0.001	6	0.818	2.377	<0.001	7
Citrate cycle (HAS00020)	0.855	2.364	<0.001	7	0.904	2.447	<0.001	4
Metabolism of xenobiotics and CYP450 (HSA00980)	0.787	2.342	<0.001	8	0.749	2.171	<0.001	10
Glycolysis and gluconeogenesis (HSA00010)	0.667	2.164	<0.001	9	0.747	2.364	<0.001	8
Butanoate metabolism (HSA0050)	0.680	2.084	<0.001	10	NA	NA	NA	NA
Gly, Ser and Thr metabolism (HSA00260)	NA	NA	NA	NA	0.722	2.213	<0.001	9

D1D2KO adipocytes show similar gene set enrichment as WT adipocytes with differentiation. ES, Enrichment Score, NES, Normalized Enrichment Score. P-value and False Discovery Rate (FDR) are calculated as described (1).

Supplementary Table 2. Quantitative PCR analysis of markers of adipocyte differentiation.

		Relative Expression*	
Class	Gene	D1D2KO-Diff	WT-Diff
Pan-adipocyte	Adipoq	435.3	284.8
White adipocyte specific	Retn	1562.3	828.1
	Retnla	9.6	4.5
	Serpina3k	2.3	3.6
	Psat1	2.8	1.7
	Hmgn3	1.1	1.0
Brown adipocyte specific	Cox8b	375.6	111.0
	Ucp1	347.6	120.5
	Otop1	66.5	24.5
	Cidea	7.5	4.0
	Cycs	8.6	5.0
	Cpn2	10.3	3.2
	Acaa2	6.5	5.4
	Cox5b	5.4	3.6
	Cox4i1	5.8	3.5
	Mt-co3	4.7	2.8
	Prdm16	3.7	2.0
Transcription Factor	Srebf1	1.5	2.1
	Ppard	2.9	2.2
	Pparg	61.1	57.6
	Ppara	16.5	7.7
	Cebpb	2.1	2.2
	Cebpa	20.7	11.7
	Cebpd	2.8	2.7
Lipolysis	Plin1	65.5	236.1
	Prkar2b	77.9	30.3
	Lipe	106.3	71.6

*Values are mean for n = 3 samples for each class and represent relative expression as compared with that for WT undifferentiated.

Analysis of induction of adipogenic genes in WT and D1D2KO adipocytes by qRTPCR. Induction ratios were calculated by normalization to cyclophilin.

Supplementary Reference

1. Subramanian, A., P. Tamayo, V. K. Mootha, S. Mukherjee, B. L. Ebert, M. A. Gillette, A. Paulovich, S. L. Pomeroy, T. R. Golub, E. S. Lander, and J. P. Mesirov. 2005. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* **102**: 15545-15550.