Supplementary Table S1. *t*-test and mean ± s.e.m. analysis of global CpG methylation percentages in the *LEP*, *PPARG2*, *FABP4* and *LPL* promoter regions examined.

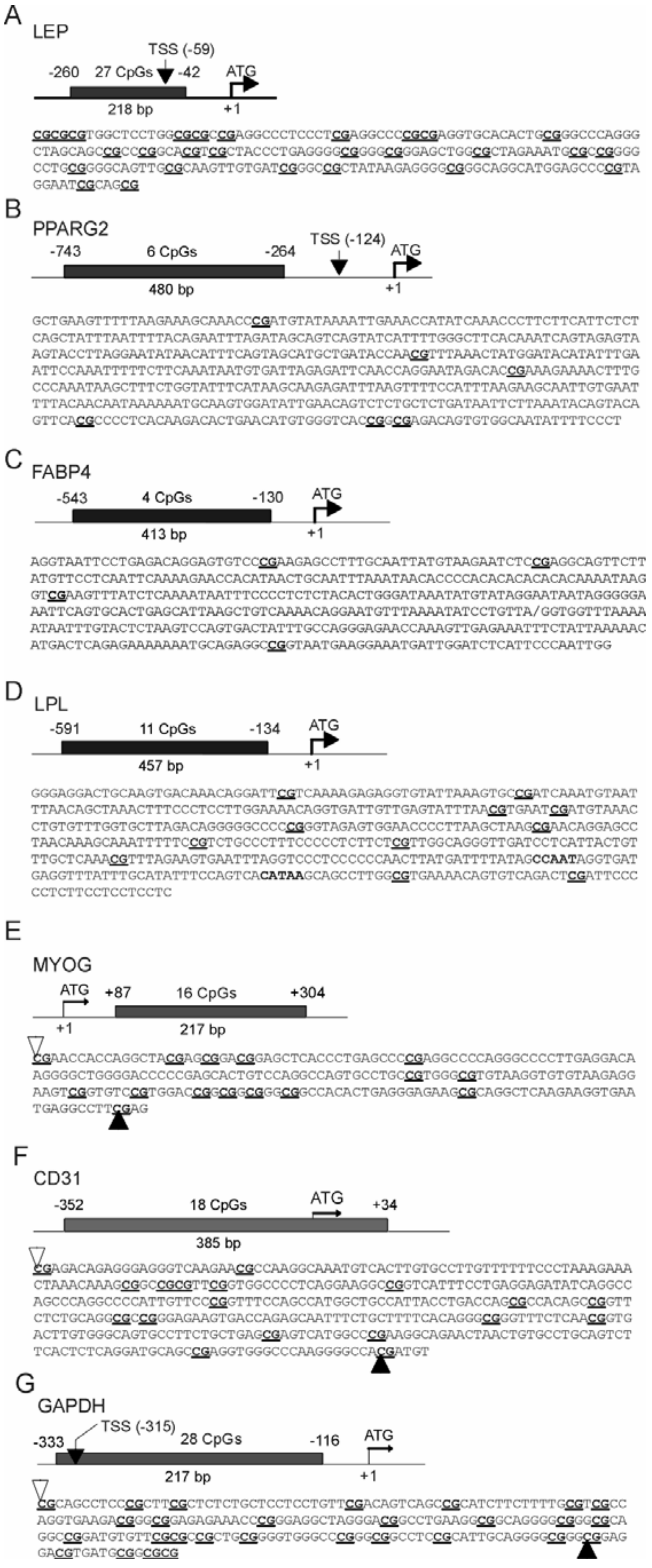
Undifferentiated vs. differentiated ASCs			
		Mean ± s.e.m.	
	P value	*Undifferentiated*	*Differentiated*
LEP	0.165	14.0 ± 1.9	10.1 ± 2.0
PPARG2	0.111	18.3 ± 2.5	11.0 ± 3.3
FABP4	0.838	27.0 ± 8.7	30.5 ± 13.9
LPL	0.968	16.9 ± 5.4	16.6 ± 5.6
Between-donor comparison			
		Mean ± s.e.m.	
D1 vs. D2	*P* value	*Donor 1*	*Donor 2*
LEP	0.507	8.5 ± 2.7	6.3 ± 1.9
PPARG2	0.02	8.3 ± 3.7	31.3 ± 7.9
FABP4	0.127	17.3 ± 8.7	7.5 ± 4.3
LPL	0.007	20.0 ± 5.1	3.6 ± 2.0
D2 vs. D3		*Donor 2*	*Donor 3*
LEP	0.06	6.3 ± 1.9	15.9 ± 2.7
PPARG2	0.425	31.3 ± 7.9	23.3 ± 6.1
FABP4	0.594	7.5 ± 4.3	12.5 ± 7.5
LPL	0.069	3.6 ± 2.0	12.7 ± 4.3
D1 vs. D3		*Donor 1*	*Donor 3*
LEP	0.006	8.5 ± 2.7	15.9 ± 2.8
PPARG2	0.054	8.3 ± 3.1	23.3 ± 6.1
FABP4	0.594	17.3 ± 8.7	12.5 ± 7.5
LPL	0.285	20.0 ± 5.0	12.7 ± 4.3
Uncultured vs. cultured undifferentiated ASCs			
		Mean ± s.e.m.	
	P value	*Uncultured (all donors)*	*Cultured (all clones)*
LEP	0.166	10.3 ± 2.1	14.4 ± 1.9
PPARG2	0.497	21.2 ± 5.6	17.0 ± 1.9
FABP4	0.291	15.0 ± 6.4	31.7 ± 12.9
LPL	0.462	13.3 ± 3.8	18.6 ± 5.9

Supplementary Figure S1. CpG dinucleotide-containing regions examined in this study in the human (A) *LEP*, (B) *PPARG2*, (C) *FABP4*, (D) *LPL*, (E) *MYOG*, (F) *CD31* and (G) *GAPDH* loci. ATG, translational start site. TSS, transcriptional start site. Numbers refer to nucleotide number in relation to the ATG start (+1). Arrows shown for *MYOG*, *CD31* and *GAPDH* indicate the first (5') and last (3') CpG examined by direct sequencing of PCR products (see Supplementary Figure S3).

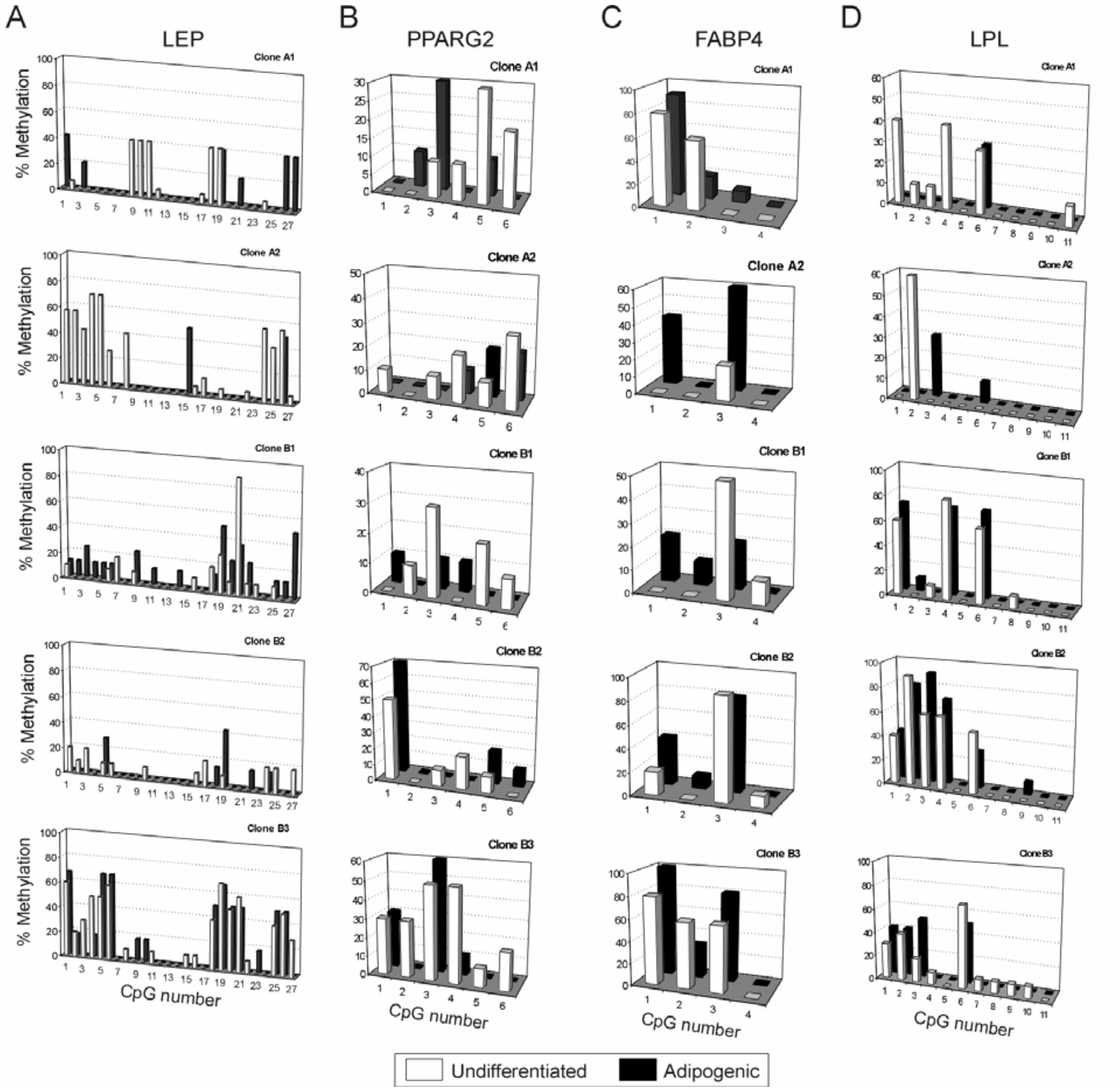
Supplementary Figure S2. DNA methylation analysis of *LEP*, *PPARG2*, *FABP4* and *LPL* promoters in each ASC clone, before differentiation and after three weeks of adipogenic differentiation. Percentage of methylation at each CpG for indicated loci is shown. Note that data shown for *LEP,* clone A2, only rely on 2 bacterial clone sequences (Figure 4A) due to cloning difficulties.

Supplementary Figure S3. Sequences of PCR products from bisulfite-converted DNA (direct sequencing). (A) *MYOG*, (B) *CD31* and (C) *GAPDH*. White and black arrows indicate, respectively, the 5'- and 3'-most CpG sequenced. Matching arrows in each sequence are shown in Supplementary Figures S1A-S1E. Note the reversed position of the 3' and 5' ends in Supplementary Figure S3 compared to Figures S1E-S1G, due to reverse sequencing.

Noer et al.
Supplementary Figure S1



Noer et al.
Supplementary Figure S2



Noer et al.
Supplementary Figure S3