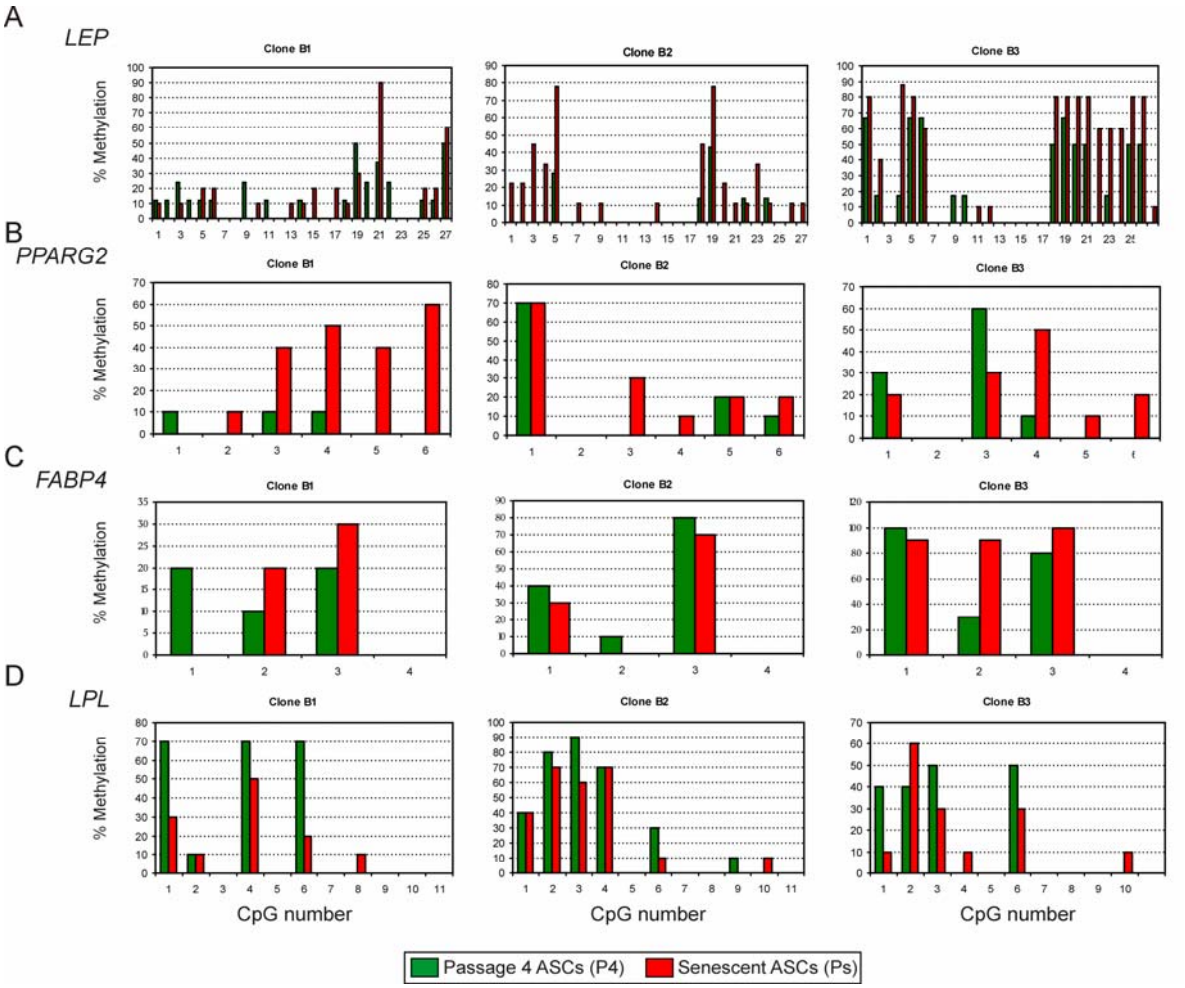
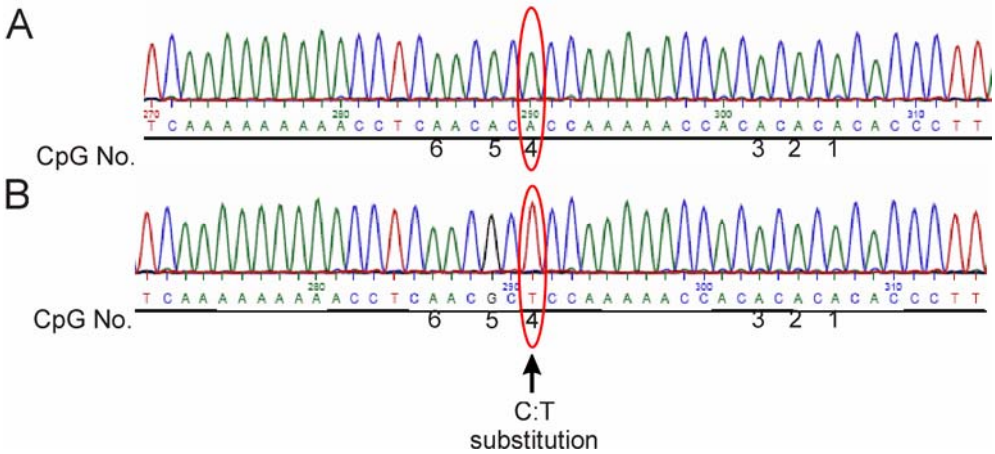
Supplementary Figure 1

DNA methylation of the *LEP*, *PPARG2*, *FABP4* and *LPL* promoters in undifferentiated P4 and senescent (Ps) ASC clones. CpG methylation was analyzed by bisulfite sequencing (Fig. 4A) and data are shown here as percentage of individual methylated CpGs in the (A) *LEP*, (B) *PPARG2*, (C) *FAPB4* and (D) *LPL* promoters for each cell clone.



Supplementary Figure 2

DNA methylation of the *LEP*, *PPARG2*, *FABP4* and *LPL* promoters in ASC clones after three weeks of adipogenic stimulation *in vitro*. CpG methylation was determined by bisulfite sequencing (Fig. 4C) and data are shown here as percentage of individual methylated CpGs in the (A) *LEP*, (B) *PPARG2*, (C) *FAPB4* and (D) *LPL* promoters for each cell clone.



Supplementary Figure 3

Illustration of a C:T substitution detected through bisulfite sequencing. (A) Excerpt of a *LEP* promoter sequence containing 6 potentially methylated cytosines (numbered 1-6), which in this sequence are unmethylated; all read as adenines, or As. (B) In this *LEP* promoter sequence, the cytosine in CpG No. 4 has been substituted for a thymidine (T). Note that the cytosine in CpG. No. 5 is methylated and as such is read as a guanine (G).