

SUPPLEMENTARY FIGURES

Figure S1

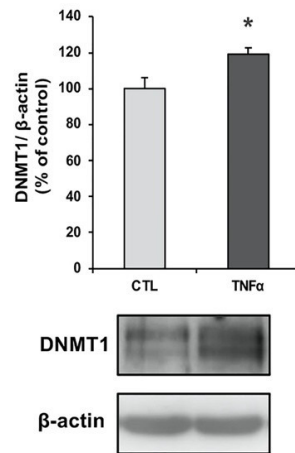


Fig. S1. TNF α effect on DNMT1 protein expression in hfNBMs. Immunoblotting of DNMT1 expression in untreated (CTL) and TNF α -treated (10 ng/ml, 24 hours) hfNBMs by western blot analysis. Bands intensity are normalized over β -actin signal, expressed as percentage of CTL and displayed as mean $\pm$ SEM of three separate experiments performed in duplicate (unpaired Student's t-test; *p<0.05 vs CTL; n=6).

Figure S2

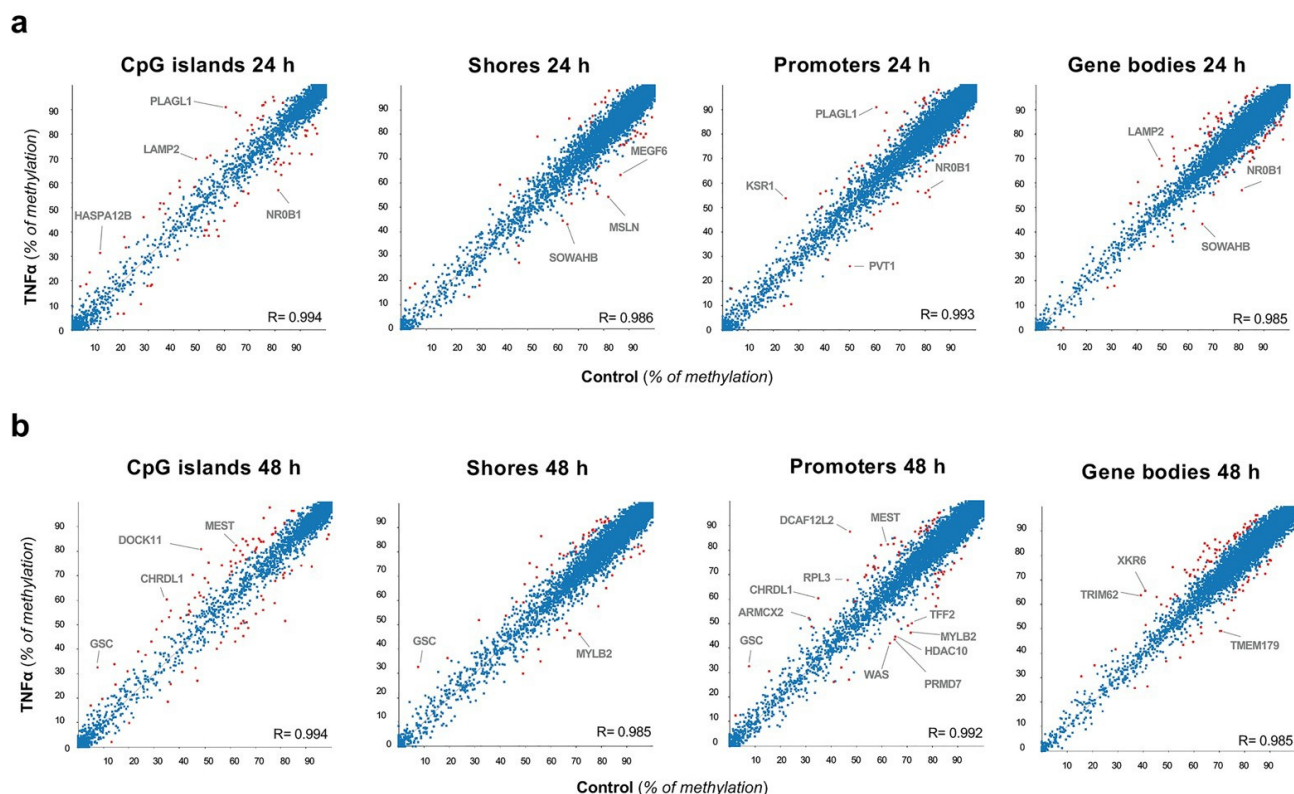


Fig. S2. DNA-methylation changes in hfNBMs under inflammatory condition. a, b Scatterplots showing correlation of methylation levels of CpG island, shore, promoter and gene body regions between untreated (CTL) and TNFα-treated (10 ng/ml) RRBS libraries of hfNBMs at **(a)** 24 hours and **(b)** 48 h of stimulation. Red dots indicate differentially methylated regions (DMRs) with a minimum difference of 10% by logistic regression after multiple testing correction using Benjamini-Hochberg method (FDR<0.05). Significant DMRs with a minimum difference of 20% by logistic regression after multiple testing correction using Benjamini-Hochberg method (FDR<0.05) are highlighted with the official symbol of the closest associated gene. The Pearson's correlation coefficient (R) is indicated into the corresponding plots (n=3).

Figure S3

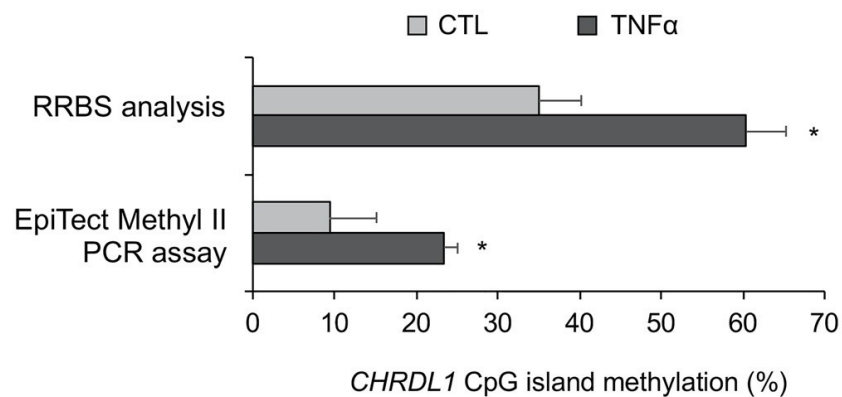


Fig. S3. Validation of the methylation status for *CHRD1* CpG island in hfNBMs. Percentage of DNA methylation in untreated (CTL) and TNF α -treated (10 ng/ml, 48 hours) hfNBMs by (upper bars) RRBS and (lower bars) EpiTect Methyl II PCR technique of *CHRD1* CpG island (115193-GRch37, UCSC genome). Data are expressed as percentage of methylated cytosines in the interested region and displayed as mean $\pm$ SEM SEM of three separate experiments performed in duplicate (unpaired Student's t-test; *p<0.05 vs CTL; n=6).