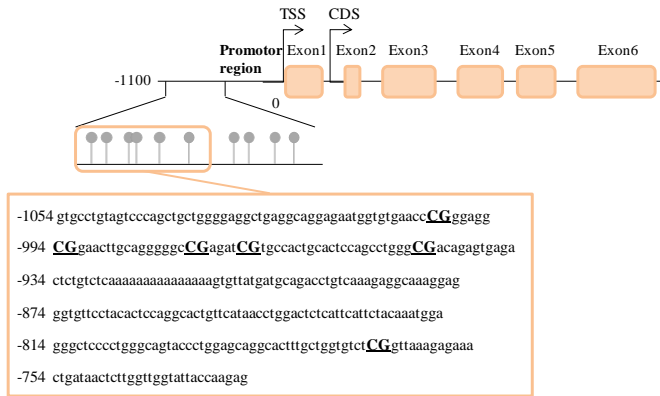


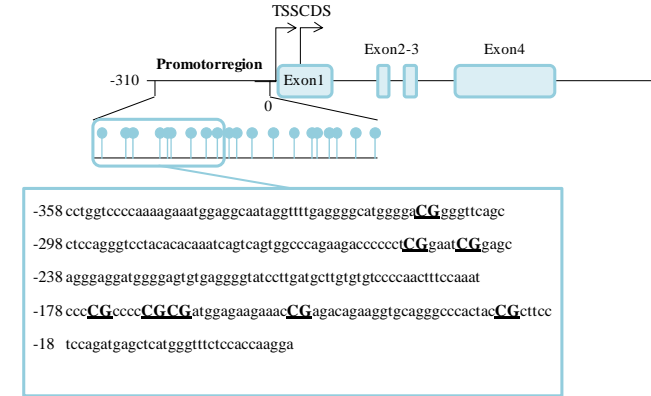
Supplementary table 1. Primer sequences used for MassArray Epityper assay.

Gene	Primer	Sequence	Length (pb)	CpG covered
<i>IL-1β</i>	left	5'-gtgttgtagtttagttggtggg-3'	331	6
	right	3'-tctcttaataataccaacccaaaattatca-5'		
<i>TNF-α</i>	left	5'-tttggttttaaaagaaatggaggt-3'	273	8
	right	3'-tccttaataaaaaaacccataaactca-5'		
<i>SERPINE1</i>	left	5'-tttggtataaaaggaggtagtggtt-3'	343	12
	right	3'-actctcctacaatcacccctaaaac-5'		
<i>IL18</i>	left	5'-ttggtgagtttttgtttttgg-3'	251	6
	right	5'-cctctaattaccataactttcca-3'		

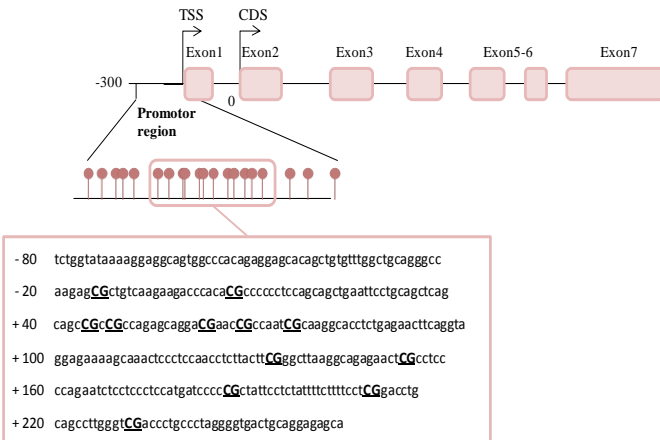
IL-1β (NC_000002.12) chr2:112,837,566-112,837,895



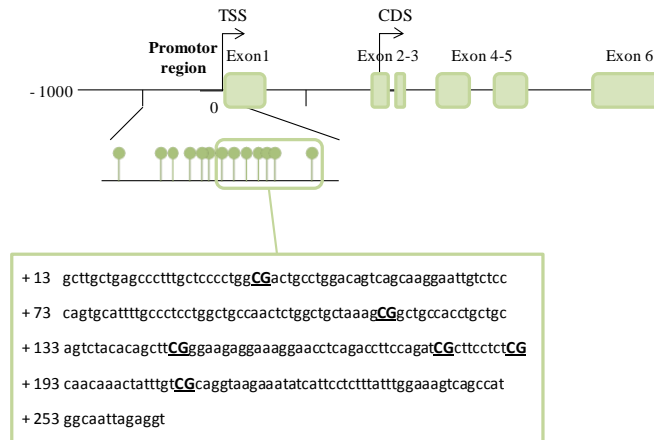
TNF-α (NC_000006.12) chr6:31,575,209-31,575,481



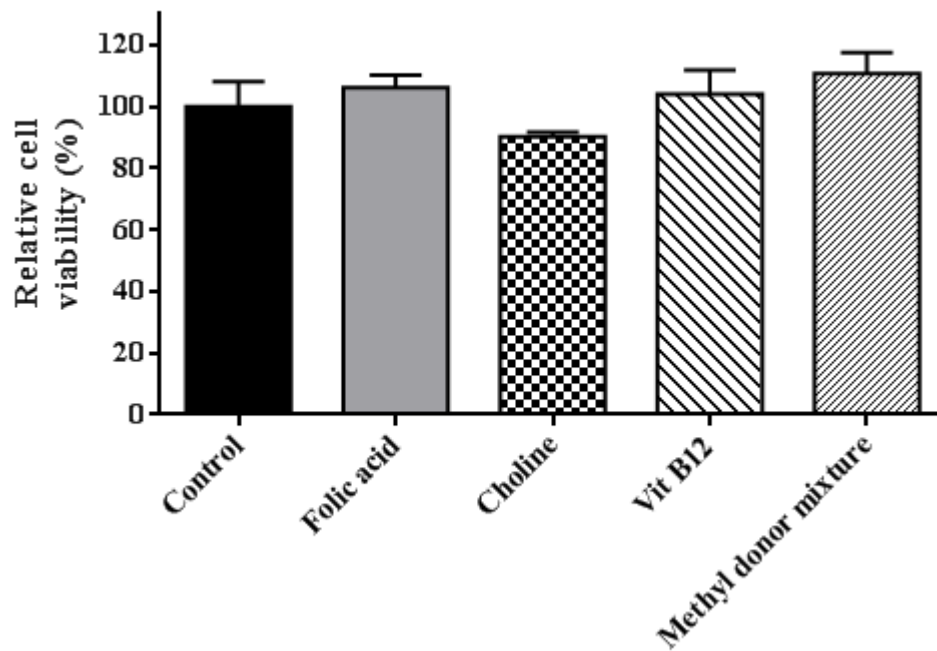
SERPINE1 (NC_000007.14) chr7:101,127,068-101,127,411



IL-18 (NC_000007.14) chr11:112,163,853-112,164,105



Supplementary figure 1. Genomic localization and nucleotide sequences of CpGs sites covered by the MassARRAY EpiTYPER probes for the study of DNA methylation levels of *IL1B*, *TNF*, *SERPINE1* and *IL18* genes. Number of the left of each sequence represents the positions with respect to the start of transcription or TSS. Nucleotides in the box are the sequences selected for each gene. CpGs underlined and highlighted in bold are those that were quantified by MassARRAY EpiTYPER. Transcription Start Site (TSS). Coding DNA Sequence (CDS).



Supplementary Figure 2. Relative cell viability (measured by MTT assay) after THP-1 monocyte incubation with folic acid (11.3 μM), choline (105 μM), vitamin B12 (18.5 nM) and methyl donor mixture. Data are shown as the means \pm SD (n=6). Differences between groups were analyzed by one-way ANOVA.