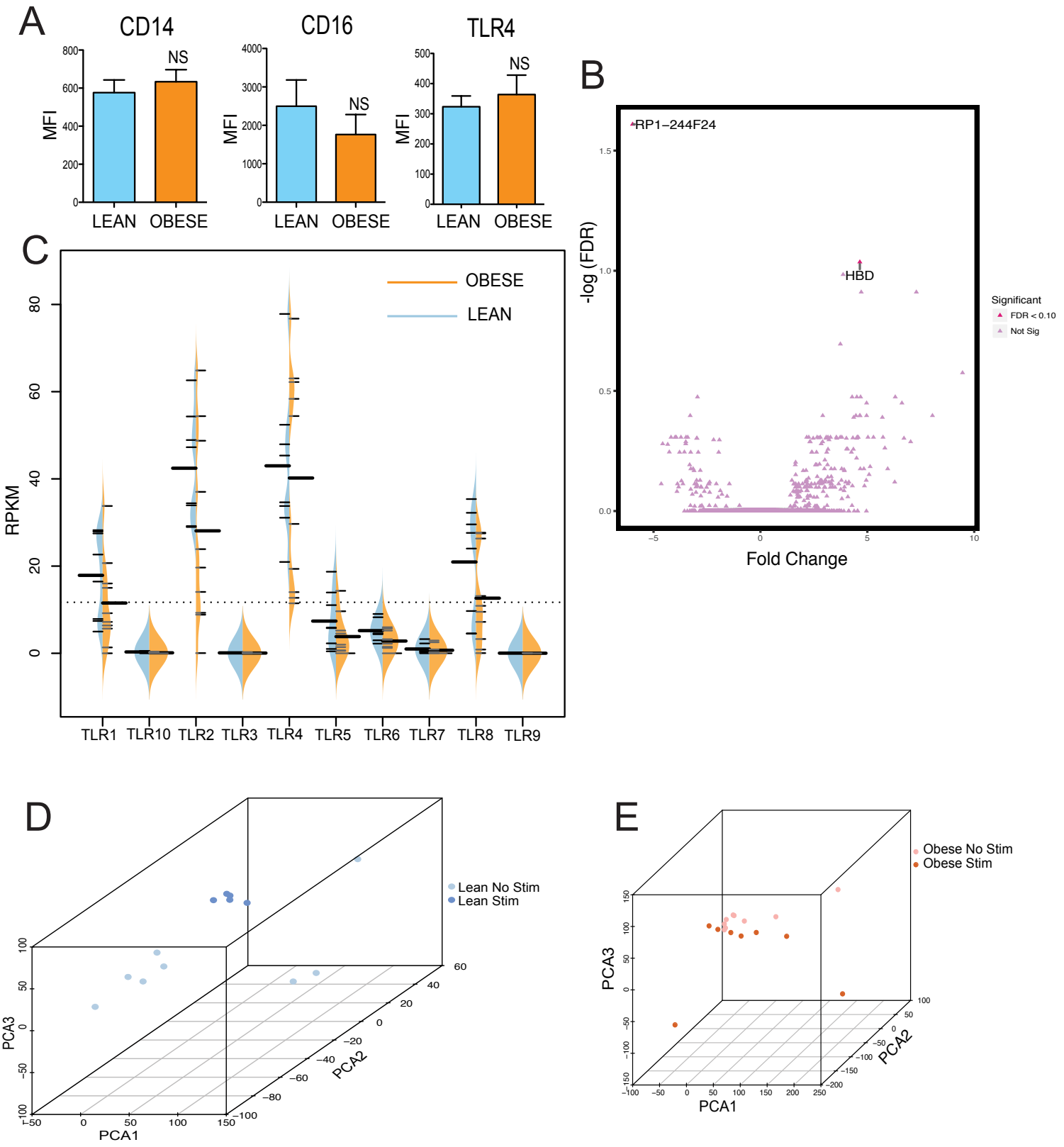
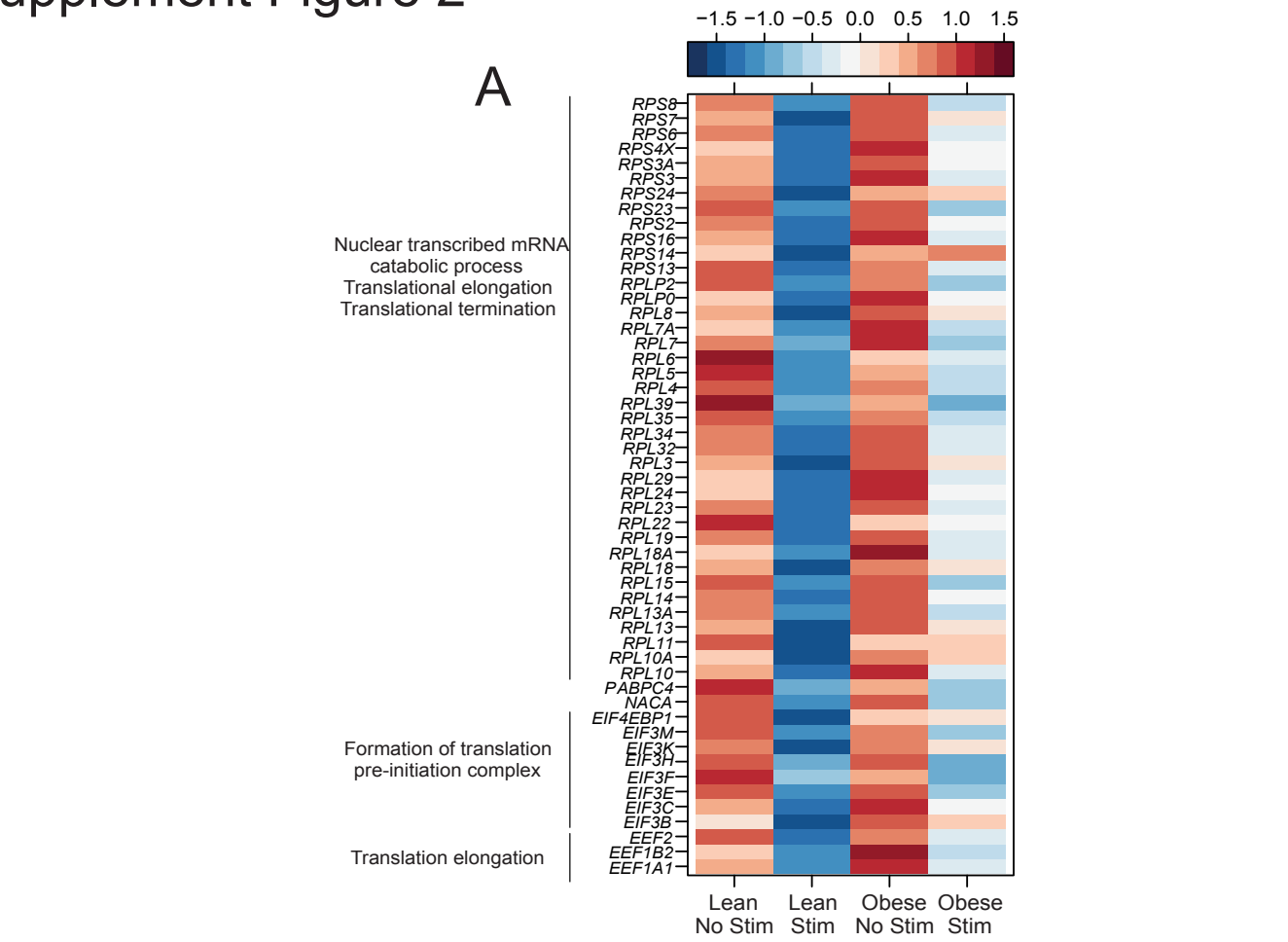
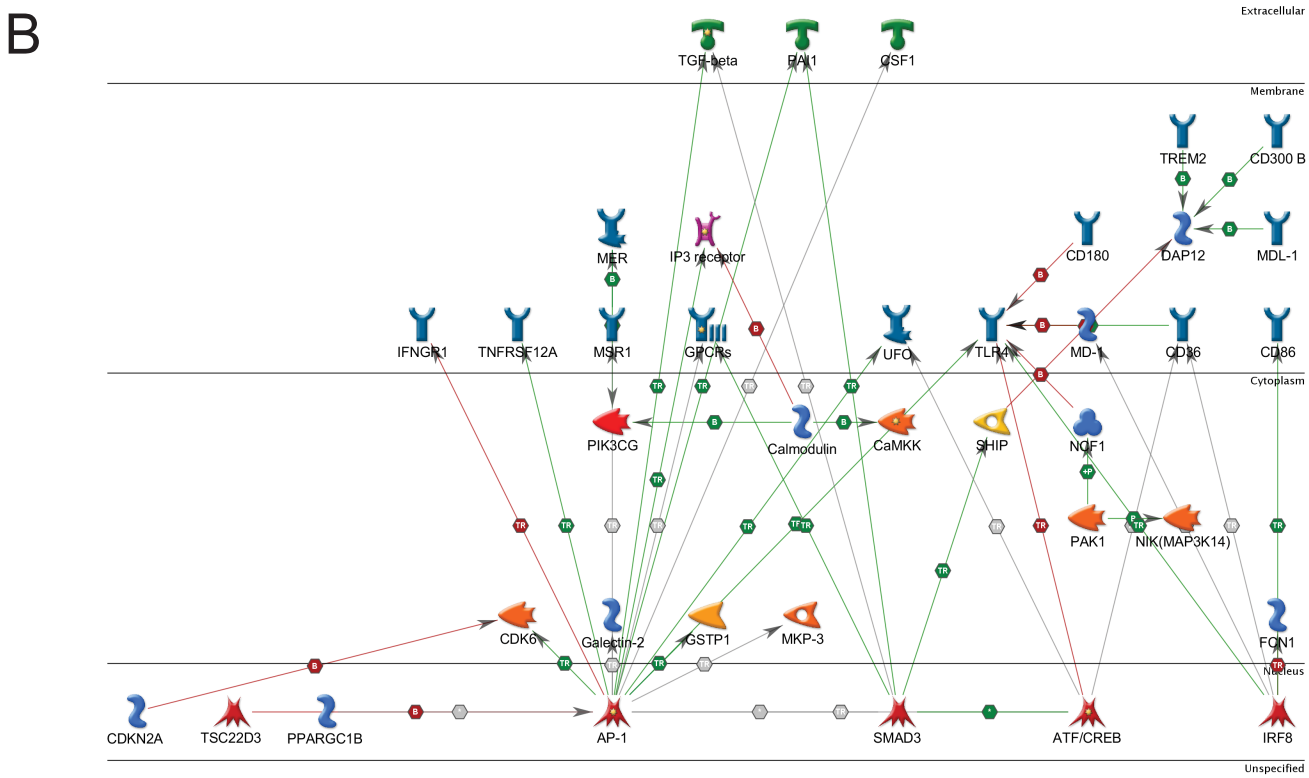
Supplement Figure 1



Supplement Figure 1: Resting UCB monocytes from lean and obese group are transcriptionally similar, but exhibit distinct transcriptional profiles following LPS stimulation.
(A) Surface expression of CD14, CD16, and TLR4 markers in UCB monocytes measured using flow cytometry.
(B) Volcano plot representing overall gene expression changes observed in between unstimulated UCB monocytes from lean and obese groups.
(C) Bean plot representing expression of TLRs in resting UCB monocytes in lean and obese groups.
(D, E) Principal component analysis of transcriptional profiles of lean (C) and (D) obese group following LPS stimulation.

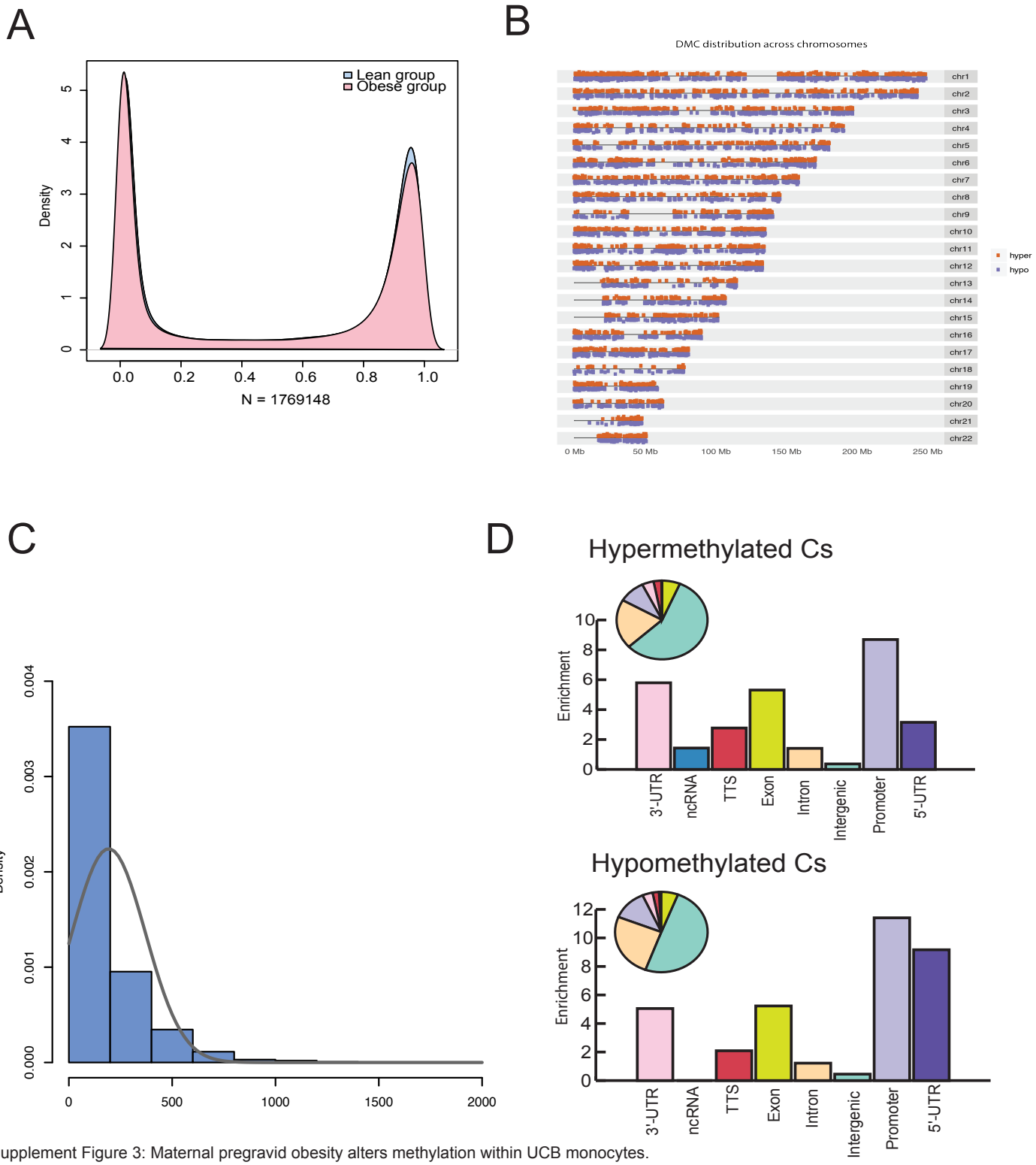
Supplement Figure 2





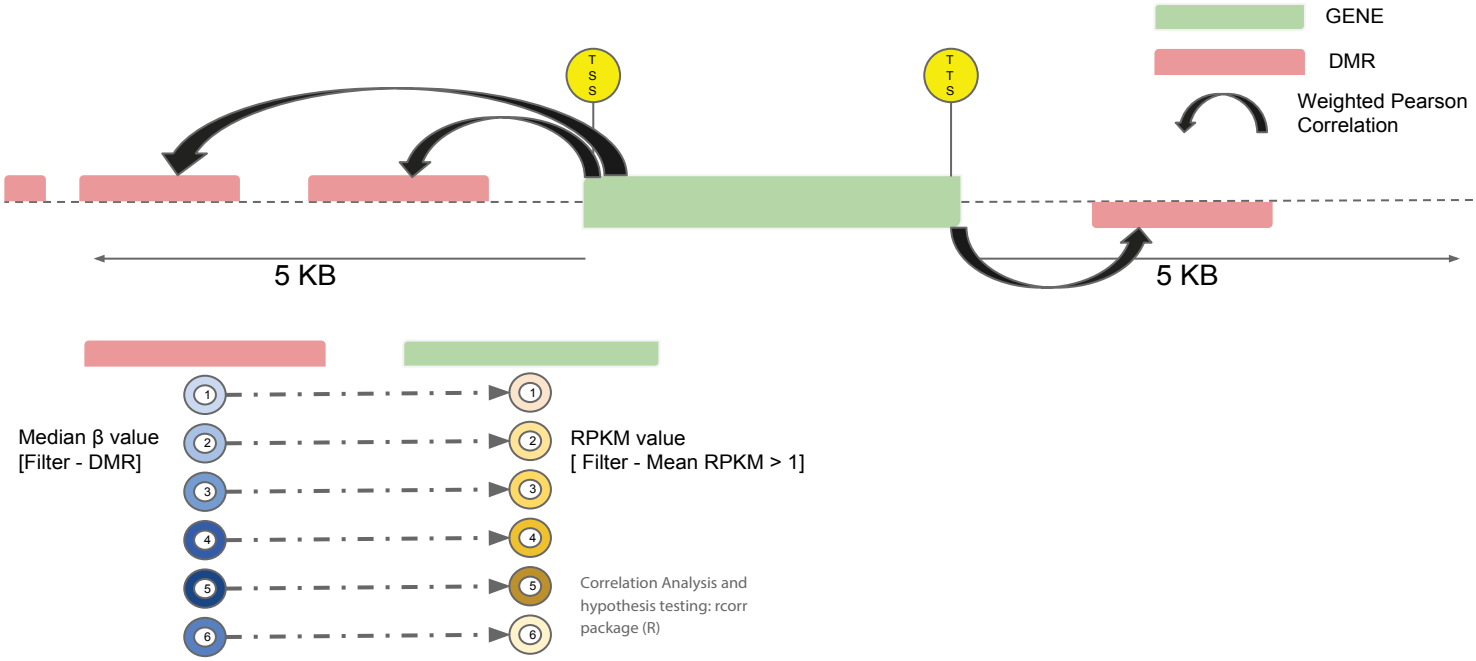
Supplement Figure 2:Genes down-regulated exclusively in UCB monocytes in the lean group enrich to gene ontology (GO) terms related to innate immunity, antigen presentation and inflammation.
(A) Heatmap displaying average expression level (RPKM) of genes involved in mRNA catabolic process (translation, initiation, elongation, and termination) in both lean and obese groups following stimulation.
(B) Network image of genes down-regulated exclusively in UCB monocytes from lean group following LPS stimulation that map to innate immune response and directly interact generated using Metacore™.

Supplement Figure 3



Supplement Figure 3: Maternal pregravid obesity alters methylation within UCB monocytes.
(A) Distribution of beta values in lean and obese group showing hypomethylation in obese group.
(B) Genome wide changes in DNA methylation levels.
(C) Distribution of DMR lengths determined in an unsupervised manner by eDMR.
(D) Context specific methylation changes determined by overlapping DMRs indicate enrichment in 3' and 5' regulatory elements of genes after correction for genomic loci length.(Pie charts pie charts above each bar graph represent the proportion of raw number of hypo- and hyper-methylated cytosines in each context before correction for genomic lengths).

Supplement Figure 4



Supplement Figure 4: Weighted pair-wise correlation analysis provides a robust method for comparing gene expression and methylation levels. Pictorial representation of data integration method utilized in Figure 7:
5 KB upstream of transcription start site (TSS) and 5 KB downstream of transcription termination site (TTS) of every gene with mean RPKM > 1 is scanned for presence of DMRs. For every gene-DMR pair, correlation analysis and hypothesis testing is performed in a sample-wise manner, allowing us to account for changes in intergenic regions as well. For correlation measures, median beta values for methylation are correlated with RPKM and tested using \ rcorr package.