

Description of Additional Supplementary Files

Supplementary Data 1

Description: Gene Ontology analysis based on network of differentially expressed genes (adjusted $p < 0.05$) in unstimulated preterm monocytes compared to the combined groups of term and adult monocytes. Cluster 1 includes upregulated genes, whereas cluster 2 includes downregulated genes (selected for input into the analysis based on >2 -fold differential expression; $FDR < 0.01$). Sorted by decreasing number of genes in cluster 2.

Supplementary Data 2

Description: Gene Ontology analysis based on network of genes significantly differentially expressed (adjusted $p < 0.05$) between LPS stimulated and unstimulated preterm monocytes, compared to the combined groups of term and adult monocytes. Cluster 1 includes genes upregulated and cluster 2 included genes downregulated upon LPS (selected for input into the analysis based on >2 -fold differential expression; $FDR < 0.01$). Sorted by decreasing adjusted significance.

Supplementary Data 3

Description: Normalized expression values (log₂ scale) of manually selected genes involved in the mTOR pathway.