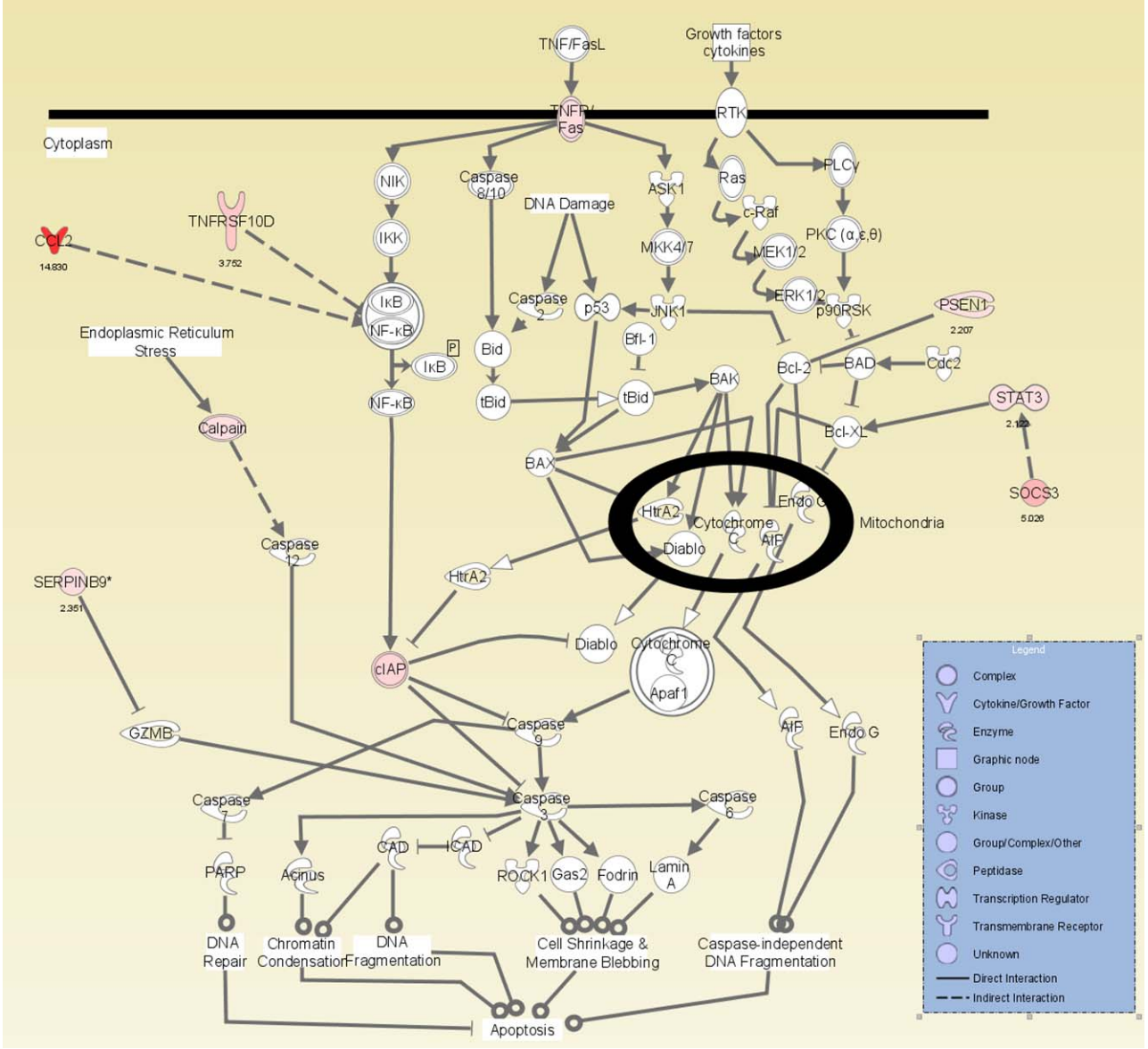
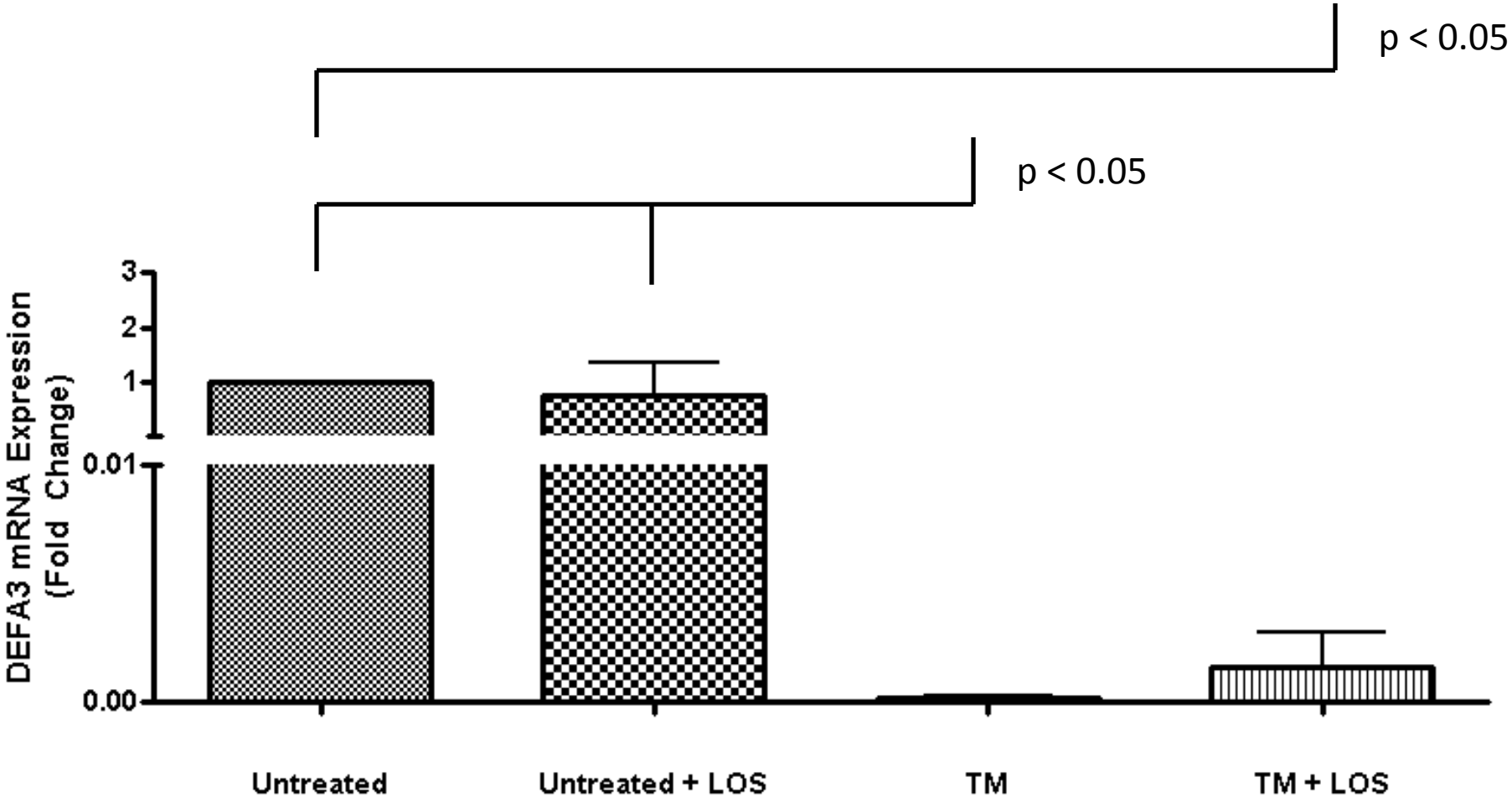
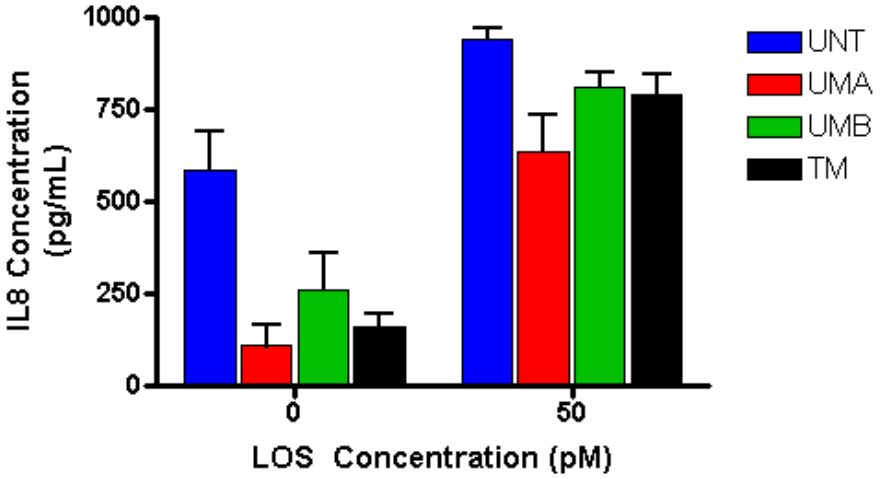
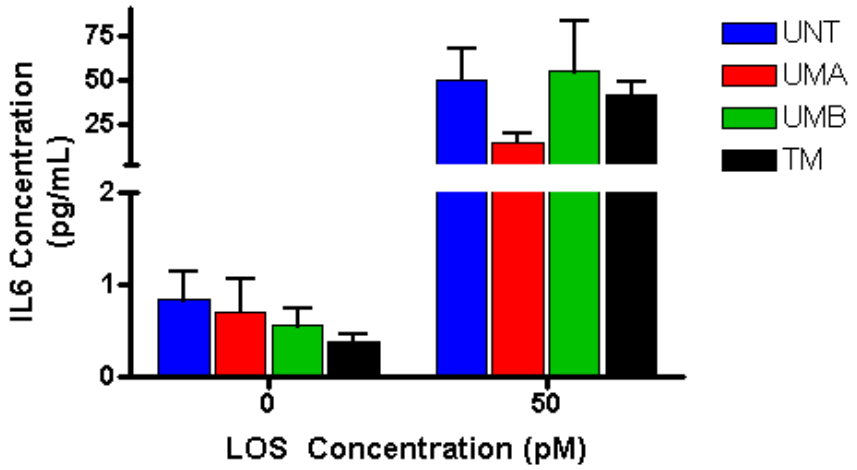


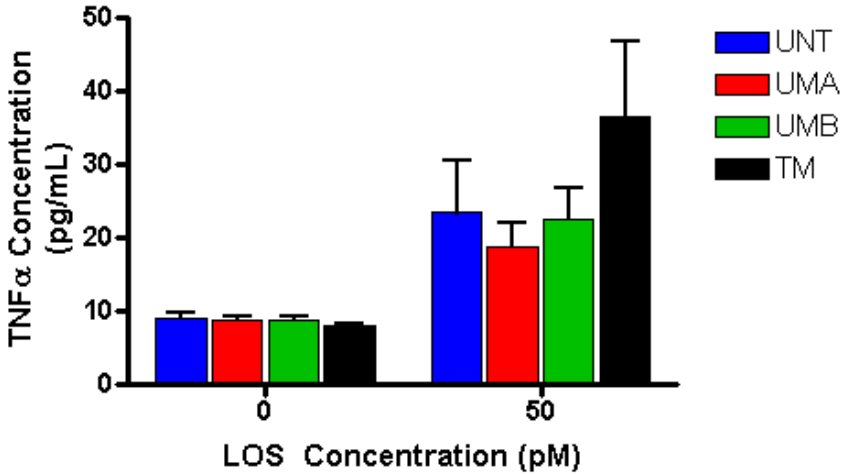
Supplemental Figure 1: Apoptosis pathway generated with Ingenuity Pathways Analysis. Differentially expressed genes within this pathway are shown in shades of red with the darkest shades indicating the largest fold change in transmigrated monocytes as compared to untreated monocytes. Genes that were not found in Ingenuity's apoptosis pathway but belong to the negative regulationof apoptosis functional group according to DAVID were added to the pathway based on their interaction with genes within the pathway. These genes include CCL2, TNFRSF10D, PSEN1, STAT3, SOCS3, and SERPINB9. cIAP is a group of proteins including NAIP, XIAP, BIRC2, and BIRC3 which inhibit caspase 3 and caspase 9 activity.



Supplemental Figure 2: Transmigration of monocytes in the presence of LOS does not inhibit down-regulation of DEFA3 mRNA in transmigrated monocytes. Monocytes were allowed to transmigrate in the presence and absence of 50 pM LOS in the dish beneath IL1b stimulated ECs and assayed for DEFA3 mRNA expression. Untreated monocytes exhibited no change in DEFA3 expression in response to LOS. Transmigrated monocytes showed similar levels of DEFA3 down-regulation compared to untreated monocytes in the presence or absence of LOS. (TM vs Untreated and Untreated + LOS, $p<0.05$, TM + LOS vs Untreated, $p<0.05$)







Supplemental Figure 3: UNT, UMA, UMB, and TM all exhibit normal responses to LOS stimulation with increased cytokine production. Monocyte samples were collected, purified, and incubated in the presence or absence of 50 pM LOS for 20 hours. The supernatant was collected and assayed for the presence of (A) IL8, (B) IL6, and (C)TNFα. Monocytes exhibited increased expression of each of these cytokines in response to LOS treatment (n=3, $p<0.05$ for all comparison s of 0 pM LOS to 50 pM LOS).