



**Figure: Caspase-8 plays a role in LPS-induced gene expression.**

(A) Heatmap of all differentially expressed genes between LPS-treated B6, *Ripk3<sup>-/-</sup>* and *Ripk3<sup>-/-</sup>Casp8<sup>-/-</sup>* BMDMs. (B) Subset of heatmap in A, numbers on the right indicate fold-change. (C) GO enrichment showing Biological Process terms enriched in group 1 from (A). Genes in group 2 were not significantly enriched. (D) GSEA showing enriched pathways from the MSigDb canonical pathways 2 collection comparing B6 or *Ripk3<sup>-/-</sup>* and *Ripk3<sup>-/-</sup>Casp8<sup>-/-</sup>* LPS-treated BMDMs. Columns represent genotype and rows represent individual genes.  $p < 0.01$  and a 1.5-fold cut-off.  $R3^{-/-} = Ripk3^{-/-}$ ;  $R3^{-/-}C8^{-/-} = Ripk3^{-/-}Casp8^{-/-}$ ; GO, gene ontology; GSEA, gene set enrichment analysis; KEGG, Kyoto Encyclopedia of Genes and Genome.