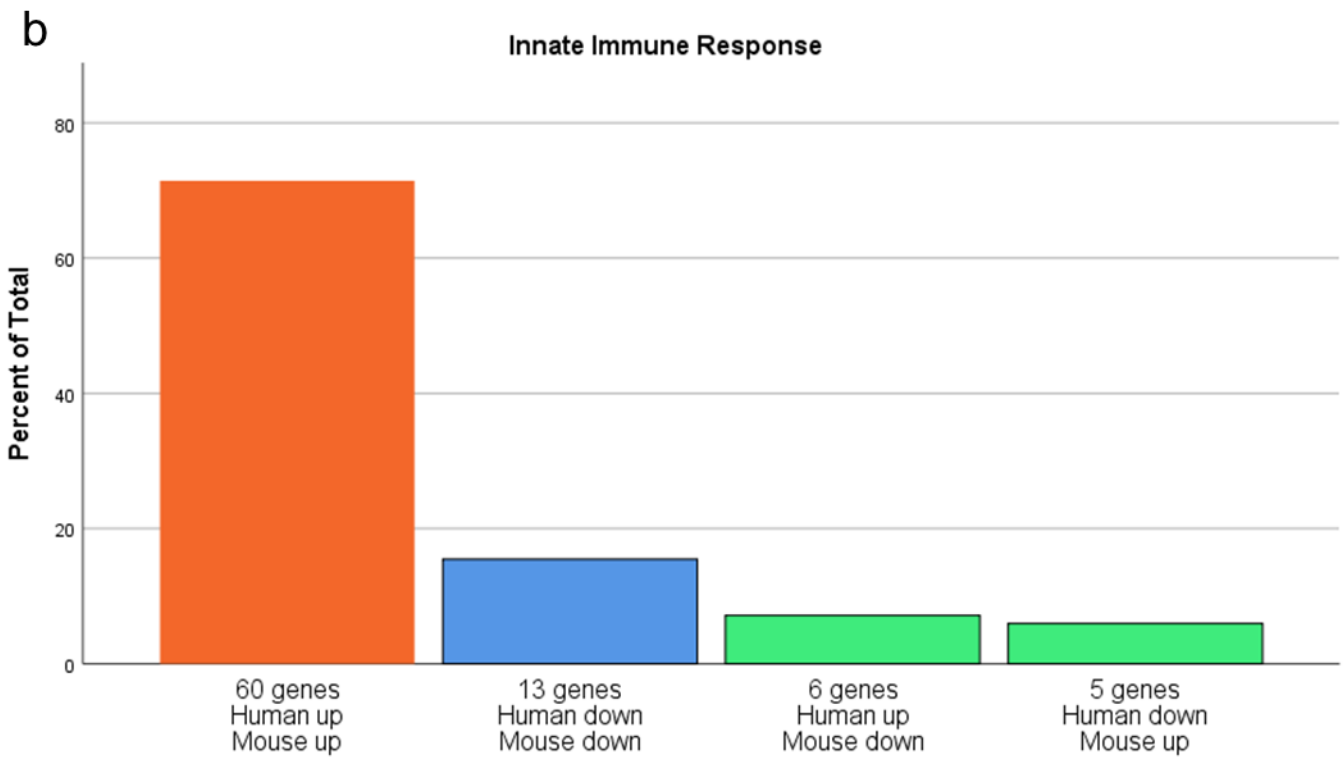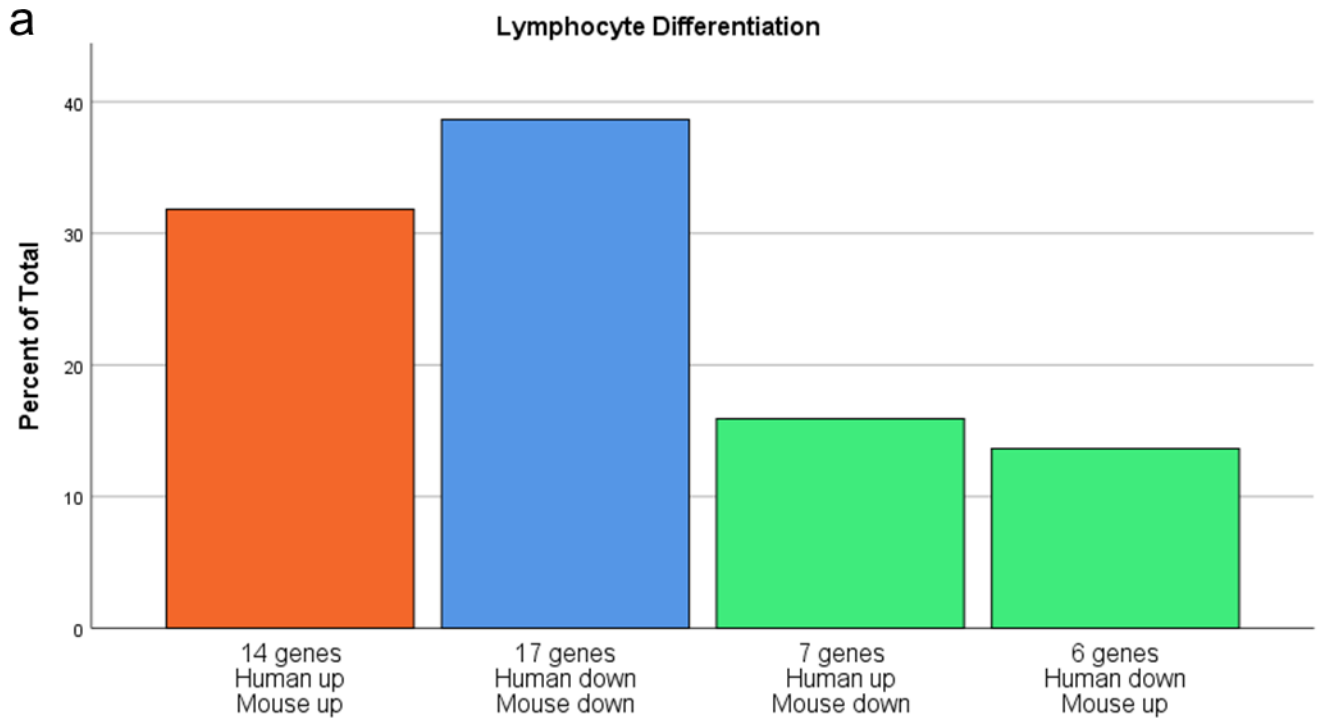**Supplementary Figure 1.** Ingenuity Pathway Analysis illustrating differences in regulation of many genes in the hematological system development and function pathways in (A) post-sepsis day 14 patients versus healthy subjects and (B) day 14 mice in our novel surgical sepsis murine model versus control mice. Orange = upregulation, blue = downregulation.

Supplementary Figure 2. Ingenuity Gene Ontology pathways shared by post-sepsis day 14 patients and day 14 mice in our novel surgical sepsis murine model. Bars represent percentage of total genes in each pathway for (A) Lymphocyte Differentiation and (B) Innate Immune Response.

Supplementary Dataset 1 (separate file). Correlations between ortholog fold changes of human sepsis/healthy subjects and CLP+DCS Mice/ Naïve with different gene selection criteria in separate excel tabs.

Supplementary Dataset 2 (separate file). Correlations between ortholog fold changes in our CLP+DCS Mice/Naïve (UF Mice), the traditional mouse model of CLP (GSE5663), human sepsis/healthy subjects (UF Human) and community acquired sepsis (GSE28750) after coconut normalization.

Supplementary Dataset 3 (separate file). Molecule Activity Predictor tool output in canonical pathway analysis from Ingenuity Pathway Analysis conducted on gene expression post-sepsis day 14 patients and murine CLP+DCS at day 14 that was significantly different (Q < 0.001 and FC ≥ 1.25 for humans).