**Table 2.** Table showing Gene Ontology pathways in complicated patients that were significantly up or down regulated on day 7 after admission. Direction of regulation was determined by heatmap evaluation and DFRs were calculated from robust microarray analysis (RMAs) generated from each pathway and compared between groups and controls. The following pathways listed were also found to have significant differences between their means greater than expected by chance in the two compared to control, p < 0.001 by ANOVA.

|  |  |
| --- | --- |
| **Pathway Analysis Day 7 in Complicated Patients** | |
| **Pathway** | **Direction of Regulation** |
| Negative regulation of myeloid Cell differentiation | Up regulated |
| Regulation of INF gamma production\* | Up regulated |
| CXCR4 signaling | Up regulated |
| T-cell activation involved in the immune response\*\* | Up regulated |
| B-cell activation involved in the immune response | Up regulated |
| Negative regulation of myeloid cell, mononuclear cell and lymphocyte proliferation | Up regulated |
| Regulation of Th-1 immune response\* | Up regulated |
| Cytokine production in the immune response | Up regulated |
| Regulation of B-cell differentiation | Up regulated |
| Regulation of CD4/CD25 alpha-beta regulation of T-cell differentiation\*\* | Up regulated |
| IL-22 signaling\*\* | Down regulated |
| Th-2 regulation | Down regulated |
| Alpha-beta differentiation of T-cells | Down regulated |

\*Multiple comparisons analysis by Dunn’s Method, p < 0.05 \*\* Multiple

Comparisons Analysis by Student-Newman-Keuls Method, p < 0.05