**Online Table 6.** Top 10 upregulated and downregulated GO Biological Processes for each MI day ranked by combined score.

| Day 1 | | | Day 3 | | | Day 7 | | |
|---|---|---|---|---|---|---|---|---|
| **Pathway** | **Score** | **p value** | **Pathway** | **Score** | **p value** | **Pathway** | **Score** | **p value** |
| **Upregulated** | | | | | | | | |
| Regulation of T-helper 17 cell lineage commitment | 17.14 | 0.007 | Regulation of alcohol biosynthetic process | 73.18 | 7.00E-18 | Regulation of monocyte chemotaxis | 25.26 | 7.00E-06 |
| Gland morphogenesis | 16.04 | 0.007 | Regulation of steroid biosynthetic process | 61.69 | 3.00E-14 | Ear morphogenesis | 23.71 | 1.00E-05 |
| Positive regulation of janus kinase activity | 15.64 | 0.007 | Cholesterol biosynthetic process | 61.23 | 4.00E-16 | Positive regulation of bone mineralization | 21.69 | 6.00E-06 |
| Positive regulation of memory T cell differentiation | 15.5 | 0.007 | Sterol biosynthetic process | 57.46 | 5.00E-15 | Regulation of endothelial cell chemotaxis | 19.05 | 0.001 |
| Chondroitin sulfate metabolic process | 15.3 | 0.0003 | Isoprenoid biosynthetic process | 33.45 | 2.00E-06 | Negative regulation of mononuclear cell migration | 18.98 | 0.001 |
| Negative regulation of interleukin-10 production | 15.04 | 0.002 | Cell migration involved in sprouting angiogenesis | 23.73 | 4.00E-05 | Positive regulation of collagen metabolic process | 18.87 | 0.0001 |
| Positive regulation of metanephros development | 14.77 | 0.01 | Blood vessel endothelial cell migration | 21.86 | 9.00E-06 | Bleb assembly | 18.74 | 0.002 |
| Positive regulation of macrophage chemotaxis | 14.76 | 0.01 | Bleb assembly | 20.47 | 0.001 | Phospholipid scrambling | 17.65 | 0.003 |
| Negative regulation of cholesterol storage | 14.59 | 0.007 | Cellular response to laminar fluid shear stress | 20.05 | 0.0003 | Positive regulation of wound healing | 17.38 | 0.0002 |
| Amino acid transmembrane transport | 14.49 | 0.003 | Extracellular matrix organization | 19.48 | 7.00E-06 | Protein localization to basolateral plasma membrane | 17.35 | 0.002 |
| **Downregulated** | | | | | | | | |
| Secondary alcohol biosynthetic process | 60.37 | 1.60E-13 | NADH metabolic process | 23.26 | 0.003 | glutathione derivative metabolic process | 28.95 | 3.00E-06 |
| Cholesterol biosynthetic process | 57.47 | 3.70E-15 | Glutathione derivative metabolic process | 16.95 | 0.0006 | glutathione derivative biosynthetic process | 21.8 | 3.00E-06 |
| Sterol biosynthetic process | 52.41 | 3.70E-14 | Regulation of epithelial to mesenchymal transition involved in endocardial cushion formation | 16.88 | 0.003 | Xenobiotic catabolic process | 20.49 | 8.00E-06 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Regulation of steroid biosynthetic process | 46.63 | 6.00E-11 | Regulation of MyD88-independent toll-like receptor signaling | 15.91 | 0.008 | regulation of epithelial to mesenchymal transition involved in endocardial cushion formation | 17.76 | 0.003 |
| Acetyl CoA metabolic process | 27.78 | 0.00002 | Regulation of transcription from RNA pol II promoter involved in heart development | 14.85 | 0.005 | Positive regulation of apoptotic cell clearance | 15.46 | 0.004 |
| Choline catabolic process | 20.99 | 0.0005 | Ventricular trabecula myocardium morphogenesis | 14.31 | 0.008 | Response to iron ion | 14.88 | 0.002 |
| Positive regulation of osteoblast proliferation | 20.91 | 0.0005 | Xenobiotic catabolic process | 14 | 0.0003 | Positive regulation of interleukin-2 biosynthetic process | 14.12 | 0.006 |
| Cellular biogenic amine catabolic process | 19.05 | 0.001 | Membrane lipid metabolic process | 13.99 | 0.002 | Endocardial cushion development | 14.03 | 0.001 |
| Outflow tract septum morphogenesis | 18.97 | 0.0002 | Positive regulation of interleukin-2 biosynthetic process | 13.33 | 0.0006 | Glutathione metabolic process | 12.82 | 0.0003 |
| Regulation of Wnt signaling pathway, planar cell polarity pathway | 18.69 | 0.0008 | Glutathione derivative biosynthetic process | 12.77 | 0.0006 | Drug transmembrane transport | 12.65 | 0.01 |