**Supplementary Table 3.** Top 20 GO gene sets correlate with down-regulated mRNAs by GSEA

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GO Name | SIZE | ES | NES | NOM p-val | FDR q-val |
| GO\_UROGENITAL\_SYSTEM\_DEVELOPMENT | 65 | -0.55 | -2.87 | <0.001 | <0.001 |
| GO\_KIDNEY\_EPITHELIUM\_DEVELOPMENT | 34 | -0.62 | -2.75 | <0.001 | <0.001 |
| GO\_NEPHRON\_DEVELOPMENT | 32 | -0.61 | -2.66 | <0.001 | <0.001 |
| GO\_METANEPHROS\_DEVELOPMENT | 23 | -0.66 | -2.61 | <0.001 | <0.001 |
| GO\_NEPHRON\_EPITHELIUM\_DEVELOPMENT | 27 | -0.62 | -2.56 | <0.001 | <0.001 |
| GO\_CARDIAC\_CHAMBER\_MORPHOGENESIS | 16 | -0.71 | -2.51 | <0.001 | <0.001 |
| GO\_MESONEPHROS\_DEVELOPMENT | 22 | -0.65 | -2.5 | <0.001 | <0.001 |
| GO\_RENAL\_TUBULE\_DEVELOPMENT | 23 | -0.61 | -2.38 | <0.001 | 0.001 |
| GO\_SODIUM\_ION\_HOMEOSTASIS | 11 | -0.75 | -2.37 | <0.001 | 0.001 |
| GO\_CARDIAC\_CHAMBER\_DEVELOPMENT | 20 | -0.62 | -2.36 | <0.001 | 0.001 |
| GO\_KIDNEY\_MORPHOGENESIS | 24 | -0.59 | -2.34 | <0.001 | 0.002 |
| GO\_REGIONALIZATION | 44 | -0.49 | -2.3 | <0.001 | 0.003 |
| GO\_TISSUE\_MORPHOGENESIS | 81 | -0.42 | -2.3 | <0.001 | 0.003 |
| GO\_ACTOMYOSIN\_STRUCTURE\_ORGANIZATION | 10 | -0.76 | -2.26 | <0.001 | 0.004 |
| GO\_ORGANIC\_ACID\_CATABOLIC\_PROCESS | 31 | -0.52 | -2.24 | <0.001 | 0.005 |
| GO\_PATTERN\_SPECIFICATION\_PROCESS | 56 | -0.44 | -2.22 | <0.001 | 0.005 |
| GO\_CELLULAR\_RESPONSE\_TO\_STEROID\_HORMONE\_STIMULUS | 29 | -0.52 | -2.2 | <0.001 | 0.007 |
| GO\_TUBE\_DEVELOPMENT | 93 | -0.39 | -2.19 | <0.001 | 0.008 |
| GO\_MONOCARBOXYLIC\_ACID\_CATABOLIC\_PROCESS | 16 | -0.61 | -2.17 | <0.001 | 0.009 |
| GO\_CARDIAC\_VENTRICLE\_MORPHOGENESIS | 11 | -0.7 | -2.16 | 0.004 | 0.009 |