

**Supplementary Table 4** – Pathway analysis associated with microRNAs that were differentially regulated when comparing neonatal and adult CPCs

| Pathway                                   | $-\ln(\text{pvalue})^*$ |
|---|-------------------------|
| MAPK signaling pathway                    | 26.14                   |
| Ribosome                                  | 25.29                   |
| Regulation of actin cytoskeleton          | 23.61                   |
| Wnt signaling pathway                     | 21.31                   |
| Adherens junction                         | 21.23                   |
| Focal adhesion                            | 20.5                    |
| Oxidative phosphorylation                 | 17.34                   |
| TGF-beta signaling pathway                | 16.81                   |
| ErbB signaling pathway                    | 12.21                   |
| Tight junction                            | 10.14                   |
| Long-term potentiation                    | 10.13                   |
| Ubiquitin mediated proteolysis            | 10.04                   |
| Arachidonic acid metabolism               | 9.77                    |
| Insulin signaling pathway                 | 9.47                    |
| mTOR signaling pathway                    | 8.59                    |
| p53 signaling pathway                     | 8.52                    |
| Glycolysis / Gluconeogenesis              | 7.46                    |
| Androgen and estrogen metabolism          | 7.36                    |
| Pyruvate metabolism                       | 7.31                    |
| GnRH signaling pathway                    | 7.23                    |
| SNARE interactions in vesicular transport | 6.99                    |
| Circadian rhythm                          | 6.37                    |
| Complement and coagulation cascades       | 6.04                    |

|  |      |
|--|------|
| Tryptophan metabolism                      | 5.73 |
| Polyunsaturated fatty acid biosynthesis    | 5.53 |
| Gap junction                               | 5.38 |
| Neuroactive ligand-receptor interaction    | 5.35 |
| ECM-receptor interaction                   | 5.33 |
| Glycine, serine and threonine metabolism   | 5.3  |
| Linoleic acid metabolism                   | 5.14 |
| Proteasome                                 | 4.74 |
| Calcium signaling pathway                  | 4.5  |
| VEGF signaling pathway                     | 4.32 |
| Glycan structures – degradation            | 4.24 |
| Methionine metabolism                      | 4.24 |
| Starch and sucrose metabolism              | 4.2  |
| Glutathione metabolism                     | 4.08 |
| Phosphatidylinositol signaling system      | 4.01 |
| Notch signaling pathway                    | 3.88 |
| Base excision repair                       | 3.65 |
| Adipocytokine signaling pathway            | 3.65 |
| Valine, leucine and isoleucine degradation | 3.64 |
| Histidine metabolism                       | 3.39 |
| D-Glutamine and D-glutamate metabolism     | 3.12 |
| Butanoate metabolism                       | 3.1  |
| Propanoate metabolism                      | 3.04 |

\*Only pathways found to be significantly different ( $p < 0.05$ ) are displayed and are listed from most significant to least significant.