**Supplemental Table S14.** Expression (counts per million) of genes in the enriched Reactome pathway: ‘Transcriptional regulation of pluripotent stem cell’

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene Symbol | Subpopulation 1 | Subpopulation 2 | Subpopulation 3 | Subpopulation 4 |
| *EPAS1* | 1.7 | 2.0 | 0.0 | 0.0 |
| *FGFR1* | 164.1 | 204.6 | 59.6 | 34.2 |
| *HIF3A* | 7.0 | 7.7 | 4.0 | 5.7 |
| *ITGB1* | 36.6 | 38.2 | 18.7 | 9.8 |
| *KLF4* | 6.0 | 7.0 | 5.8 | 0.0 |
| *LIN28A* | 169.9 | 189.9 | 111.5 | 113.2 |
| *NANOG* | 42.5 | 46.8 | 25.1 | 22.9 |
| *NODAL* | 210.4 | 211.8 | 129.1 | 36.1 |
| *NR6A1a* | 119.0 | 148.8 | 48.2 | 46.6 |
| *PBX1* | 83.2 | 91.6 | 62.5 | 86.5 |
| *PRDM14* | 4.8 | 4.6 | 3.6 | 0.0 |
| *SALL4* | 42.7 | 47.8 | 38.8 | 26.5 |
| *SMAD2* | 33.3 | 35.1 | 34.7 | 23.2 |
| *SMAD4* | 19.6 | 23.8 | 5.9 | 4.3 |
| *SOX2* | 280.8 | 299.6 | 235.1 | 219.1 |
| *STAT3* | 58.5 | 67.4 | 39.8 | 38.0 |
| *UTF1* | 178.2 | 201.1 | 64.3 | 44.1 |
| *ZIC1* | 31.5 | 37.8 | 12.3 | 10.2 |
| *ZIC3* | 15.1 | 17.4 | 20.3 | 18.2 |
| *ZSCAN1* | 1.7 | 1.6 | 0.6 | 0.0 |
| *ZSCAN10* | 99.8 | 114.3 | 97.5 | 55.2 |

aGene symbols highlighted in bold indicate genes that were significantly differentially expressed between subpopulations one and two.