**Supplemental Table S11.** Functional enrichment analysis of DE genes, which distinguish subpopulation one from two

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| --- | --- | --- | --- | --- | --- |
| Reactome Pathway | Total genes in pathway | Genes in geneset | P-value | FDR | HitGenes |
| POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation | 13 | 2 | 1.1 x 10-4 | 0.16 | *NR6A1, SALL4* |
| Signal transduction by L1 | 21 | 2 | 2.7 x 10-3 | 0.16 | *FGFR1, ITGB1* |
| G2/M Transition | 109 | 3 | 7.2 x 10-3 | 0.16 | *PKMYT1, AKAP9, PPP1R12A* |
| Transcriptional regulation of pluripotent stem cells | 35 | 2 | 7.3 x 10-3 | 0.16 | *NR6A1, SALL4* |
| Cell Cycle, Mitotic | 399 | 5 | 0.01 | 0.16 | *PKMYT1, ANKLE2, RCC2, AKAP9, PPP1R12A* |
| Repression of WNT target genes | 8 | 1 | 0.02 | 0.16 | *TLE1* |
| Signaling by Wnt | 229 | 3 | 0.05 | 0.16 | *TLE1, USP8, USP34* |
| VEGFA-VEGFR2 Pathway | 266 | 3 | 0.07 | 0.16 | *WASF2, FGFR1, AKAP9* |