**Supplemental Table S9.** Functional enrichment analysis of differentially expressed (DE) genes for cells in subpopulation one compared to cells in the remaining subpopulations

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Reactome Pathway | Total genes in pathway | Genes in gene set | P-value | FDR | HitGenes |
| mRNA Splicing - Major Pathway | 127 | 8 | 1.5x 10-6 | 1.0 x 10-4 | *YBX1, LSM3, FUS, POLR2L, POLR2I, HNRNPA3, HSPA8, SRSF2* |
| RNA polymerase III transcription initiation from type 2 promoter | 27 | 3 | 7.4 x 10-6 | 0.02 | *POLR2L, GTF3C6, POLR3H* |
| Golgi associated vesicle biogenesis | 27 | 3 | 7.4 x 10-6 | 0.02 | *FTL, FTH1, HSPA8* |
| Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. | 117 | 5 | 9.4 x 10-6 | 0.02 | *ATP5E, UQCR10, UQCRH, COX7C, NDUFA2* |
| RNA polymerase II transcription elongation | 44 | 3 | 3.0 x 10-4 | 0.04 | *POLR2L, POLR2I, SSRP1* |
| Golgi associated vesicle biogenesis | 27 | 3 | 7.4 x 10-4 | 0.02 | *FTL, FTH1, HSPA8* |
| RNA polymerase II transcription | 108 | 4 | 5.2 x 10-3 | 0.06 | *POLR2L, POLR2I, SSRP1, SRSF2* |
| Cellular senescence | 125 | 2 | 0.2 | 0.2 | *HMGA1, ANAPC15* |