**Figure 1-source data 2:**

**Enriched pathways in GSEAs of EMT transitioning cells:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **Trans vs Epi** | | **Trans vs Mes** | |
| **PATHWAY NAME** | **SIZE** | **NES** | **NOM p-val** | **NES** | **NOM p-val** |
| GOBP\_CELL\_CELL\_JUNCTION\_ORGANIZATION | 123 | 1.570 | 0.008 | 2.450 | 0.000 |
| GOBP\_SKIN\_DEVELOPMENT | 170 | 1.760 | 0.000 | 2.270 | 0.000 |
| GOBP\_EPIDERMIS\_DEVELOPMENT | 194 | 1.690 | 0.000 | 2.240 | 0.000 |
| GOBP\_KERATINOCYTE\_DIFFERENTIATION | 70 | 1.730 | 0.000 | 2.210 | 0.000 |
| **GOBP\_RIBOSOMAL\_LARGE\_SUBUNIT\_BIOGENESIS** | 68 | 1.730 | 0.008 | 2.190 | 0.000 |
| **GOBP\_RIBOSOME\_BIOGENESIS** | 291 | 1.640 | 0.008 | 2.190 | 0.000 |
| **GOBP\_RIBONUCLEOPROTEIN\_COMPLEX\_BIOGENESIS** | 392 | 1.630 | 0.010 | 2.180 | 0.000 |
| GOBP\_EPIDERMAL\_CELL\_DIFFERENTIATION | 104 | 1.690 | 0.002 | 2.150 | 0.000 |
| **GOBP\_RRNA\_METABOLIC\_PROCESS** | 233 | 1.750 | 0.004 | 2.150 | 0.000 |
| GOBP\_RNA\_PHOSPHODIESTER\_BOND\_HYDROLYSIS\_ENDONUCLEOLYTIC | 26 | 1.830 | 0.000 | 2.040 | 0.002 |
| GOBP\_EPITHELIAL\_CELL\_DIFFERENTIATION | 346 | 1.580 | 0.000 | 2.020 | 0.000 |
| GOBP\_ACTIN\_FILAMENT\_BASED\_MOVEMENT | 57 | 1.770 | 0.000 | 2.000 | 0.000 |
| GOBP\_CELL\_JUNCTION\_ASSEMBLY | 232 | 1.850 | 0.000 | 1.980 | 0.000 |
| GOBP\_CELL\_CELL\_ADHESION | 371 | 1.620 | 0.000 | 1.980 | 0.000 |
| **GOBP\_ENDONUCLEOLYTIC\_CLEAVAGE\_INVOLVED\_IN\_RRNA\_PROCESSING** | 16 | 1.890 | 0.000 | 1.920 | 0.006 |
| GOBP\_RNA\_LOCALIZATION | 143 | 1.690 | 0.006 | 1.900 | 0.000 |
| GOBP\_POSITIVE\_REGULATION\_OF\_MRNA\_PROCESSING | 34 | 1.670 | 0.006 | 1.890 | 0.000 |
| GOBP\_POSITIVE\_REGULATION\_OF\_MRNA\_METABOLIC\_PROCESS | 112 | 1.730 | 0.002 | 1.880 | 0.000 |
| GOBP\_ESTABLISHMENT\_OR\_MAINTENANCE\_OF\_CELL\_POLARITY | 158 | 1.830 | 0.000 | 1.870 | 0.000 |
| GOBP\_ESTABLISHMENT\_OF\_RNA\_LOCALIZATION | 121 | 1.690 | 0.008 | 1.860 | 0.002 |
| GOBP\_NUCLEAR\_TRANSPORT | 281 | 1.700 | 0.000 | 1.850 | 0.000 |
| GOBP\_REGULATION\_OF\_MRNA\_METABOLIC\_PROCESS | 236 | 1.590 | 0.010 | 1.830 | 0.000 |
| GOBP\_TISSUE\_MORPHOGENESIS | 401 | 1.600 | 0.000 | 1.820 | 0.000 |
| GOBP\_ACTIN\_MEDIATED\_CELL\_CONTRACTION | 39 | 1.770 | 0.002 | 1.820 | 0.002 |
| GOBP\_MUSCLE\_CONTRACTION | 118 | 1.610 | 0.008 | 1.820 | 0.002 |
| GOBP\_NUCLEAR\_EXPORT | 141 | 1.710 | 0.000 | 1.810 | 0.000 |
| GOBP\_GLAND\_MORPHOGENESIS | 95 | 1.560 | 0.000 | 1.810 | 0.000 |
| GOBP\_MRNA\_TRANSPORT | 95 | 1.710 | 0.006 | 1.810 | 0.002 |
| **GOBP\_RIBOSOMAL\_SUBUNIT\_EXPORT\_FROM\_NUCLEUS** | 16 | 1.850 | 0.000 | 1.800 | 0.002 |
| GOBP\_CELL\_JUNCTION\_ORGANIZATION | 428 | 1.700 | 0.000 | 1.800 | 0.000 |
| GOBP\_ESTABLISHMENT\_OF\_CELL\_POLARITY | 118 | 1.740 | 0.004 | 1.790 | 0.002 |
| GOBP\_IMPORT\_INTO\_NUCLEUS | 140 | 1.590 | 0.008 | 1.790 | 0.000 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LOCOMOTION | 366 | 1.660 | 0.000 | 1.760 | 0.000 |
| GOBP\_REGULATION\_OF\_ERBB\_SIGNALING\_PATHWAY | 56 | 1.670 | 0.002 | 1.760 | 0.004 |
| GOBP\_REGULATION\_OF\_CELL\_ADHESION | 419 | 1.590 | 0.000 | 1.750 | 0.000 |
| GOBP\_CELL\_MATRIX\_ADHESION | 127 | 1.820 | 0.002 | 1.750 | 0.002 |
| GOBP\_NUCLEOBASE\_CONTAINING\_COMPOUND\_TRANSPORT | 151 | 1.690 | 0.008 | 1.730 | 0.004 |
| GOBP\_ACTIN\_FILAMENT\_BASED\_PROCESS | 471 | 1.720 | 0.000 | 1.720 | 0.000 |
| GOBP\_REGULATION\_OF\_NUCLEOCYTOPLASMIC\_TRANSPORT | 104 | 1.750 | 0.000 | 1.710 | 0.008 |
| GOBP\_PROTEIN\_LOCALIZATION\_TO\_NUCLEUS | 253 | 1.640 | 0.004 | 1.680 | 0.000 |
| GOBP\_ACTOMYOSIN\_STRUCTURE\_ORGANIZATION | 122 | 1.590 | 0.006 | 1.680 | 0.004 |
| GOBP\_ERBB\_SIGNALING\_PATHWAY | 82 | 1.800 | 0.000 | 1.670 | 0.008 |
| GOBP\_RNA\_DESTABILIZATION | 78 | 1.690 | 0.006 | 1.670 | 0.004 |
| GOBP\_CELL\_SUBSTRATE\_ADHESION | 200 | 1.710 | 0.002 | 1.660 | 0.002 |
| GOBP\_REGULATION\_OF\_PROTEIN\_LOCALIZATION\_TO\_NUCLEUS | 117 | 1.570 | 0.004 | 1.660 | 0.002 |
| GOBP\_RNA\_MEDIATED\_GENE\_SILENCING | 87 | 1.650 | 0.010 | 1.650 | 0.009 |
| GOBP\_NUCLEUS\_ORGANIZATION | 114 | 1.790 | 0.000 | 1.640 | 0.006 |
| GOBP\_HEART\_PROCESS | 108 | 1.690 | 0.000 | 1.600 | 0.004 |
| GOBP\_MUSCLE\_SYSTEM\_PROCESS | 184 | 1.680 | 0.006 | 1.540 | 0.006 |

\* GSEAs of scRNA-seq data were performed with BP subset of GO pathway (3185 gene sets with a filter of 15 – 500 genes/set). Totally, 49 gene sets were overlapped with the significantly enriched gene sets (P < 0.01) in comparisons of Trans vs Epi and Trans vs Mes. Gene set size (number of genes), normalized enrich scores (NES) and nominal P values (NOM p-val) are shown in the table. Pathways related to Ribosome or RRNA processing were highlighted in red.