Table S2. Pathway analysis of RNA-Seq expression signature consisting of genes de-regulated upon p53 knockdown

| # | Networks | Total | p-value | FDR | # genes in data | Genes Deregulated |
|---|---|---|---|---|---|---|
| 1 | Proteolysis_ECM remodeling | 85 | 9.426 E-06 | 5.314 E-04 | 7 | MMP-7, MMP-19, MMP-16, SPOCK3, SERPINA3, MMP-2, Lumican |
| 2 | Proteolysis_Connective tissue degradation | 119 | 9.489 E-06 | 5.314 E-04 | 8 | MMP-7, MMP-19, MMP-16, SPOCK3, SERPINA3, MMP-2, Lumican, HABP2 |
| 3 | Cell adhesion_Cell-matrix interactions | 211 | 9.669 E-05 | 3.610 E-03 | 9 | MMP-7, MMP-19, GJA1, MMP-16, MMP-2, THBS1, Lumican, HABP2, SGCZ |
| 4 | Development_Neurogenesis_Synaptogenesis | 180 | 1.059 E-03 | 2.965 E-02 | 5 | RIMS1, GRIK1, THBS1, WNT10B, ACTA2 |
| 5 | Apoptosis_Anti-apoptosis mediated by external signals via NF-κB | 111 | 3.040 E-03 | 6.413 E-02 | 5 | PRKACB, RPS6KA2, p53, TNFRSF1B, ADORA1 |
| 6 | Development_EMT_Regulation of epithelial-to-mesenchymal transition | 225 | 3.774 E-03 | 6.413 E-02 | 6 | KRT14, LOX, RPS6KA2, MMP-2, WNT10B, ACTA2 |
| 7 | Development_Neurogenesis_Axonal guidance | 230 | 4.259 E-03 | 6.413 E-02 | 7 | EPHA4, CCL28, ROBO1, SEMA3A, PRKACB, ACTA2 |
| 8 | Cell adhesion_Attractive and repulsive receptors | 175 | 4.581 E-03 | 6.413 E-02 | 6 | EPHA4, ROBO1, SEMA3A, PRKACB, ACTA2 |
| 9 | Cell adhesion_Cadherins | 180 | 5.252 E-03 | 6.512 E-02 | 6 | PKP1, DSG3, PCDH7, ACTA2, WNT10B |
| 10 | Cytoskeleton_Intermediate filaments | 81 | 5.814 E-03 | 6.512 E-02 | 4 | PKP1, KRT14,KRT6A, ACTA2 |

green text indicates up-regulation in response to p53 knockdown

red text indicates down-regulation in response to p53 knockdown