**Supplementary Table S3.** Cancer-associated gene fold regulation by *E. coli* strains in the NCM460 cell line, identified using the Human Cancer PathwayFinder™ RT² Profiler™ PCR Array

|  |  |  |  |
| --- | --- | --- | --- |
| **Genes** | **functions** | **≥ 2 fold-upregulation relative to PBS** | **J47 vs Δ*hly*****(≥2 folds)** |
| **MG1655**  | **J47Δ*hly*** | **J47** |
| CCL2 | Angiogenesis |  |  | 4.32 | 3.36 |
| FGF2 | Angiogenesis |  | 2.53 | 2.73 |  |
| BIRC3 | Anti-apoptosis  |  |  | 2.25 |  |
| E2F4 | Cell Cycle  |  |  | 2.39 |  |
| FOXC2 | Epithelial-to-Mesenchymal Transition |  |  | 2.64 | 2.43 |
| SLC2A1 | Glucose transportation |  | 2.23 | 6.32 | 2.83 |
| PFKL | Metabolism |  | 2.85 | 4.23 |  |
| GPD2 | Metabolism |  |  | 2.11 |  |
| ACLY | Metabolism  |  |  | 2.87 |  |
| CPT2 | Metabolism  |  |  | 2.14 |  |
| TINF2 | Telomeres & Telomerase |  | 2.31 | 3.29 |  |
| BCL2L11 | Apoptosis |  |  | 3.2 | 2.23 |
| MAPK14 | Cell Senescence |  |  | 3.01 |  |
| IGFBP5 | Cell Senescence |  | 8.63 |  |  |
| DDB2 | DNA Repair  |  |  | 2.11 |  |
| ADM | Angiogenesis | 5.39 | 8.22 | 12.82 | 　 |
| SERPINF1 | Angiogenesis | 6251.56 | 　 | 5.86 | 　 |
| PGF | Angiogenesis  | 3.84 | 　 | 　 | 　 |
| BMI1 | Anti-cell senescence | 2.45 | 2.79 | 2.5 | 　 |
| APAF1 | Apoptosis | 2.55 | 　 | 4.2 | 　 |
| CASP9 | Apoptosis | 2.85 | 3.23 | 3.58 | 　 |
| DDIT3 | DNA Repair  | 2.13 | 2.17 | 2.62 | 　 |
| PPP1R15A | DNA Repair  | 2.53 | 3.29 | 11 | 　 |
| GADD45G | DNA Repair  | 11.08 | 14.72 | 38.05 | 　 |
| SNAI1 | Epithelial-to-Mesenchymal Transition | 2.58 | 　 | 　 | 　 |
| SNAI2 | Epithelial-to-Mesenchymal Transition | 2.91 | 3.16 | 　 | 　 |
| CA9 | Response to hypoxia | 3.39 | 11.96 | 3.97 | 　 |
| ARNT | Response to hypoxia | 2.27 | 　 | 2.03 | 　 |
| HMOX1 | Response to hypoxia | 2.41 | 　 | 3.58 | 　 |
| WEE1 | Cell cycle | 2.2 | 　 | 　 | 　 |
| DKC1 | tumor suppressor | 2.33 | 2.22 | 　 | 　 |
| **Genes** | **functions** | **≥ 2 fold-downegulation relative to PBS** | **J47 vs Δ*hly*****(≥2 folds)** |
| **MG1655** | **J47Δ*hly*** | **J47** |
| ANGPT2 | Angiogenesis |  | -2.22 | -2.11 |  |
| CFLAR | Anti-apoptosis |  | -2.73 |  |  |
| TBX2 | Cell Senescence |  |  | -2.41 |  |
| TERF2IP | Telomeres & Telomerase |  |  | -2.08 | -3.18 |
| IGFBP5 | Cell Senescence | -45.89 | 　 | -45.25 | -390.72 |
| IGFBP7 | Cell Senescence | -6.73 | -6.15 | -6.63 | 　 |
| KRT14 | Epithelial-to-Mesenchymal Transition | -4.79 | -4.82 | 　 | 　 |
| ANGPT1 | Angiogenesis | -2.6 | 　 | 　 | 　 |

Grey, gene regulation by MG1655 that is irrelevant to adenoma/CRC development

Yellow, *hly*-dependent gene regulation