

Supplementary Table 3: GSEA between low- and high- DYRK1A expression HCC samples using LinkedOmics by enriching on WikiPathway

| geneSet | description | enrichment Score | normalized Enrichmen tScore | pValue | FDR | size | leading Edge Num |
|---------|-----------------------------------------------------------------------|---------------------|-----------------------------------|----------|----------|------|------------------------|
| WP366 | TGF-beta Signaling | 0.6533513 | 1.8188485 | 0 | 0.003997 | 132 | 50 |
| WP2857 | Mesodermal Commitment Pathway | 0.640528 | 1.7838839 | 0 | 0.005996 | 144 | 64 |
| WP4331 | Neovascularisation | 0.7410834 | 1.7614212 | 0.002558 | 0.009327 | 37 | 23 |
| WP3651 | Pathways Affected in Adenoid Cystic Carcinoma | 0.6871385 | 1.7415463 | 0 | 0.009993 | 60 | 20 |
| WP3584 | MECP2 and Associated Rett Syndrome | 0.6639486 | 1.7121361 | 0 | 0.016389 | 68 | 27 |
| WP3657 | Hematopoietic Stem Cell Gene Regulation by GABP alpha/beta Complex | 0.8103555 | 1.7110509 | 0 | 0.014324 | 20 | 9 |
| WP2038 | Regulation of Microtubule Cytoskeleton | 0.6850123 | 1.6896294 | 0.002433 | 0.021986 | 46 | 22 |
| WP4533 | Transcription co-factors SKI and SKIL protein partners | 0.8198331 | 1.6829121 | 0 | 0.022235 | 18 | 7 |
| WP364 | IL-6 signaling pathway | 0.6897165 | 1.682824 | 0 | 0.019765 | 43 | 14 |
| WP437 | EGF/EGFR Signaling | 0.6040596 | 1.6686122 | 0 | 0.021786 | 161 | 68 |
| WP2261 | Signaling Pathways in Glioblastoma | 0.6268575 | 1.6628105 | 0 | 0.021804 | 82 | 36 |
| WP710 | DNA Damage Response (only ATM dependent) | 0.6143269 | 1.6621262 | 0 | 0.019987 | 110 | 39 |
| WP363 | Wnt Signaling Pathway (Netpath) | 0.6668647 | 1.654693 | 0 | 0.021986 | 51 | 23 |
| WP4337 | ncRNAs involved in STAT3 signaling in hepatocellular carcinoma | 0.8274906 | 1.6474063 | 0 | 0.023984 | 14 | 6 |
| WP2853 | Endoderm Differentiation | 0.5953693 | 1.6412635 | 0 | 0.025317 | 139 | 56 |
| WP3298 | Melatonin metabolism and effects | 0.6869549 | 1.6407981 | 0 | 0.023984 | 36 | 11 |
| WP4016 | DNA IR-damage and cellular response via ATR | 0.6241997 | 1.636676 | 0.002299 | 0.024572 | 77 | 25 |
| WP3680 | Association Between Physico-Chemical Features and Toxicity Associated | 0.6409993 | 1.6300439 | 0 | 0.027204 | 65 | 21 |
| WP313 | Signaling of Hepatocyte Growth Factor Receptor | 0.702724 | 1.6290907 | 0.002571 | 0.026299 | 34 | 13 |
| WP1539 | Angiogenesis | 0.7284788 | 1.6284453 | 0 | 0.025383 | 24 | 14 |
| WP2324 | AGE/RAGE pathway | 0.6245354 | 1.6276518 | 0 | 0.02465 | 66 | 27 |
| WP51 | Regulation of Actin Cytoskeleton | 0.5781763 | 1.6259658 | 0 | 0.024348 | 144 | 37 |
| WP4540 | Pathways Regulating Hippo Signaling | 0.6015148 | 1.6249045 | 0 | 0.023463 | 98 | 40 |
| WP1541 | Energy Metabolism | 0.65798 | 1.6236196 | 0 | 0.023318 | 47 | 12 |
| WP2446 | Retinoblastoma Gene in Cancer | 0.6153319 | 1.6193992 | 0 | 0.024784 | 86 | 31 |
| WP4655 | Cytosolic DNA-sensing pathway | -0.489778 | -1.571137 | 0 | 0.095313 | 65 | 17 |
| WP3963 | Mevalonate pathway | -0.837901 | -1.585452 | 0.041916 | 0.087093 | 7 | 5 |
| WP134 | Pentose Phosphate Metabolism | -0.830309 | -1.586067 | 0.023952 | 0.090532 | 7 | 5 |
| WP545 | Complement Activation | -0.631033 | -1.588629 | 0.020408 | 0.092096 | 21 | 13 |
| WP357 | Fatty Acid Biosynthesis | -0.628343 | -1.597326 | 0.021898 | 0.087988 | 22 | 10 |

| | | | | | | | |
|--------|--------------------------------------------------------------------|-----------|-----------|----------|----------|-----|----|
| WP4224 | Purine metabolism and related disorders | -0.619534 | -1.608489 | 0.012987 | 0.083169 | 22 | 5 |
| WP2359 | Parkin-Ubiquitin Proteasomal System | -0.520236 | -1.634646 | 0 | 0.065396 | 67 | 19 |
| WP4290 | Metabolic reprogramming in colon cancer | -0.605586 | -1.690905 | 0 | 0.037298 | 40 | 14 |
| WP4718 | Cholesterol metabolism (includes both Bloch and Kandutsch-Russell) | -0.572965 | -1.703154 | 0 | 0.033598 | 44 | 15 |
| WP4752 | Base Excision Repair | -0.623264 | -1.71359 | 0 | 0.030437 | 31 | 12 |
| WP4792 | Purine metabolism | -0.80468 | -1.72358 | 0 | 0.029527 | 13 | 5 |
| WP197 | Cholesterol Biosynthesis Pathway | -0.7919 | -1.742016 | 0.006211 | 0.026053 | 13 | 6 |
| WP4313 | Ferroptosis | -0.609871 | -1.746297 | 0 | 0.026361 | 40 | 7 |
| WP15 | Selenium Micronutrient Network | -0.552895 | -1.749062 | 0 | 0.027055 | 74 | 29 |
| WP107 | Translation Factors | -0.603975 | -1.805682 | 0 | 0.012753 | 50 | 21 |
| WP4521 | Glycosylation and related congenital defects | -0.687513 | -1.808643 | 0.008065 | 0.013427 | 25 | 7 |
| WP4022 | Pyrimidine metabolism | -0.577003 | -1.827483 | 0 | 0.011356 | 83 | 28 |
| WP1946 | Cori Cycle | -0.812488 | -1.949934 | 0 | 0.001754 | 17 | 7 |
| WP100 | Glutathione metabolism | -0.771747 | -1.96583 | 0 | 0.001431 | 21 | 7 |
| WP4396 | Nonalcoholic fatty liver disease | -0.620388 | -2.164443 | 0 | 0 | 148 | 57 |
| WP183 | Proteasome Degradation | -0.787261 | -2.367398 | 0 | 0 | 62 | 36 |
| WP623 | Oxidative phosphorylation Mitochondrial complex I | -0.885722 | -2.437942 | 0 | 0 | 37 | 29 |
| WP4324 | assembly model OXPHOS system | -0.887087 | -2.649891 | 0 | 0 | 44 | 35 |
| WP111 | Electron Transport Chain (OXPHOS system in mitochondria) | -0.869946 | -2.798443 | 0 | 0 | 73 | 48 |
| WP477 | Cytoplasmic Ribosomal Proteins | -0.884494 | -2.806662 | 0 | 0 | 88 | 73 |
