Supplementary material

Hub gene identification and prognostic model establishment for patients with HBV-related hepatocellular carcinoma

Lianmei Wang1, Jing Liu1, Zhong Xian1, Jingzhuo Tian1, Chunying Li1, Yushi Zhang1, Suyan Liu1, Jiayin Han1, Chen Pan1, Yan Yi1, Yong Zhao1, Hongbing Zhang2, Aihua Liang1\*

1Key Laboratory of Beijing for Identification and Safety Evaluation of Chinese Medicine, Institute of Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing, China

2State Key Laboratory of Medical Molecular Biology, Department of Physiology, Institute of Basic Medical Sciences and School of Basic Medicine, Graduate School of Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing, China.

**\****Correspondence to*: Professor Aihua Liang. 16. Dongzhimen Nanxioejie, Dongcheng District, Beijing, China. Email: [ahliang@icmm.ac.cn](mailto:ahliang@icmm.ac.cn).

**Supplementary Table S1. DEGs integrated with RRA**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene | GSE121248  limma FC | GSE55092  limma FC | GSE62232  limma FC | P. value | Adj P. value | Log FC |
| GPC3 | 3.86 | 3.42 | 5.99 | 2.26E-10 | 4.82E-06 | 4.42 |
| SPINK1 | 3.67 | 3.90 | 4.73 | 2.48E-12 | 5.29E-08 | 4.10 |
| AKR1B10 | 3.04 | 3.50 | 4.66 | 1.07E-10 | 2.27E-06 | 3.73 |
| TOP2A | 3.26 | 3.79 | 4.14 | 1.07E-10 | 2.27E-06 | 3.73 |
| ASPM | 2.85 | 3.04 | 4.30 | 2.48E-09 | 5.29E-05 | 3.40 |
| RRM2 | 2.75 | 2.48 | 4.26 | 7.05E-08 | 1.50E-03 | 3.16 |
| HMMR | 2.21 | 3.25 | 3.70 | 6.82E-10 | 1.45E-05 | 3.05 |
| COL15A1 | 2.99 | 2.03 | 3.88 | 3.39E-07 | 7.23E-03 | 2.97 |
| CDK1 | 2.03 | 2.75 | 3.88 | 1.70E-08 | 3.63E-04 | 2.89 |
| DTL | 2.20 | 2.46 | 3.96 | 7.40E-08 | 1.58E-03 | 2.87 |
| ROBO1 | 2.00 | 3.32 | 3.24 | 4.29E-09 | 9.14E-05 | 2.85 |
| CCNB1 | 2.05 | 2.59 | 3.46 | 4.37E-08 | 9.30E-04 | 2.70 |
| CAP2 | 2.33 | 2.87 | 2.70 | 4.12E-08 | 8.77E-04 | 2.63 |
| PRC1 | 2.09 | 2.53 | 3.24 | 5.17E-08 | 1.10E-03 | 2.62 |
| PBK | 2.23 | 2.61 | 3.00 | 3.65E-08 | 7.78E-04 | 2.61 |
| ECT2 | 2.05 | 2.41 | 3.32 | 8.14E-08 | 1.73E-03 | 2.59 |
| NDC80 | 1.81 | 2.88 | 3.00 | 1.45E-08 | 3.09E-04 | 2.56 |
| GINS1 | 1.93 | 2.30 | 3.42 | 1.26E-07 | 2.68E-03 | 2.55 |
| NEK2 | 2.32 | 2.09 | 3.21 | 2.26E-07 | 4.82E-03 | 2.54 |
| SULT1C2 | 1.78 | 3.49 | 2.19 | 2.58E-07 | 5.49E-03 | 2.49 |
| BUB1B | 2.06 | 2.71 | 2.53 | 6.06E-08 | 1.29E-03 | 2.43 |
| KIF20A | 1.89 | 2.49 | 2.91 | 6.71E-08 | 1.43E-03 | 2.43 |
| DKK1 | 1.69 | 3.80 | 1.71 | 2.27E-06 | 4.83E-02 | 2.40 |
| ZWINT | 1.69 | 1.91 | 3.46 | 4.72E-07 | 1.01E-02 | 2.36 |
| LCN2 | 1.83 | 3.13 | 2.09 | 4.02E-07 | 8.57E-03 | 2.35 |
| NUSAP1 | 1.87 | 2.05 | 3.12 | 3.11E-07 | 6.61E-03 | 2.35 |
| FGF13 | 1.35 | 2.89 | 2.70 | 1.21E-07 | 2.57E-03 | 2.31 |
| CENPU | 1.81 | 2.11 | 2.99 | 2.05E-07 | 4.36E-03 | 2.30 |
| KIAA0101 | 1.65 | 2.05 | 3.19 | 2.92E-07 | 6.23E-03 | 2.30 |
| MELK | 1.47 | 2.89 | 2.47 | 8.14E-08 | 1.73E-03 | 2.27 |
| NCAPG | 1.83 | 2.39 | 2.56 | 8.53E-08 | 1.82E-03 | 2.26 |
| TTK | 1.68 | 2.32 | 2.74 | 1.21E-07 | 2.57E-03 | 2.25 |
| DLGAP5 | 1.55 | 2.19 | 2.90 | 1.84E-07 | 3.92E-03 | 2.21 |
| CDKN2C | 1.34 | 2.09 | 3.00 | 2.42E-07 | 5.15E-03 | 2.14 |
| CDC20 | 1.60 | 2.33 | 2.45 | 1.07E-07 | 2.27E-03 | 2.13 |
| TRIM16 | 1.38 | 2.98 | 1.99 | 5.92E-07 | 1.26E-02 | 2.11 |
| CCNB2 | 1.77 | 2.06 | 2.36 | 2.66E-07 | 5.67E-03 | 2.06 |
| LINC01419 | 2.06 | 2.19 | 1.80 | 1.18E-06 | 2.51E-02 | 2.02 |
| EZH2 | 1.64 | 1.62 | 2.72 | 1.75E-06 | 3.73E-02 | 1.99 |
| BUB1 | 1.63 | 1.75 | 2.50 | 8.89E-07 | 1.89E-02 | 1.96 |
| KIF4A | 1.72 | 1.97 | 2.17 | 3.81E-07 | 8.10E-03 | 1.95 |
| RAD51AP1 | 1.64 | 2.03 | 2.16 | 3.30E-07 | 7.02E-03 | 1.94 |
| DNAJC6 | 1.86 | 2.26 | 1.71 | 2.23E-06 | 4.76E-02 | 1.94 |
| LYZ | 1.85 | 1.83 | 2.08 | 6.51E-07 | 1.39E-02 | 1.92 |
| KIF11 | 1.38 | 2.09 | 2.28 | 2.34E-07 | 4.98E-03 | 1.92 |
| APOBEC3B | 1.63 | 1.67 | 2.43 | 1.53E-06 | 3.25E-02 | 1.91 |
| CCNE2 | 1.42 | 1.70 | 2.58 | 1.18E-06 | 2.51E-02 | 1.90 |
| PTTG1 | 1.49 | 1.73 | 2.32 | 9.67E-07 | 2.06E-02 | 1.85 |
| E2F8 | 1.57 | 1.91 | 1.99 | 5.64E-07 | 1.20E-02 | 1.82 |
| AURKA | 1.15 | 1.76 | 2.52 | 8.52E-07 | 1.82E-02 | 1.81 |
| ITGA6 | 1.32 | 2.05 | 2.03 | 5.10E-07 | 1.09E-02 | 1.80 |
| NQO1 | 1.29 | 1.67 | 2.41 | 1.45E-06 | 3.08E-02 | 1.79 |
| FOXM1 | 1.13 | 1.80 | 2.16 | 6.98E-07 | 1.49E-02 | 1.70 |
| CDC7 | 1.20 | 1.79 | 1.99 | 7.47E-07 | 1.59E-02 | 1.66 |
| TP53I3 | 1.26 | 1.92 | 1.78 | 1.35E-06 | 2.86E-02 | 1.65 |
| TTC39A | 1.09 | 1.86 | 1.95 | 6.98E-07 | 1.49E-02 | 1.63 |
| TRIP13 | 1.19 | 1.70 | 1.91 | 1.23E-06 | 2.61E-02 | 1.60 |
| LINC01093 | -4.20 | -4.64 | -5.25 | 6.71E-11 | 1.43E-06 | -4.70 |
| MT1M | -2.86 | -3.78 | -6.01 | 2.88E-09 | 6.13E-05 | -4.22 |
| KCNN2 | -4.03 | -3.22 | -5.08 | 3.88E-08 | 8.27E-04 | -4.11 |
| SLCO1B3 | -2.94 | -3.80 | -5.46 | 2.48E-09 | 5.29E-05 | -4.07 |
| SLC22A1 | -2.57 | -4.70 | -4.36 | 4.85E-09 | 1.03E-04 | -3.88 |
| FCN3 | -3.35 | -4.07 | -4.16 | 5.46E-09 | 1.16E-04 | -3.86 |
| CXCL14 | -3.84 | -3.57 | -4.12 | 1.12E-08 | 2.38E-04 | -3.85 |
| C9 | -2.80 | -5.22 | -3.49 | 6.06E-08 | 1.29E-03 | -3.84 |
| CLEC4G | -3.21 | -3.67 | -4.44 | 7.58E-09 | 1.61E-04 | -3.77 |
| CYP1A2 | -3.37 | -3.32 | -4.38 | 2.47E-08 | 5.26E-04 | -3.69 |
| AKR1D1 | -2.57 | -4.78 | -3.43 | 7.40E-08 | 1.58E-03 | -3.60 |
| CRHBP | -3.05 | -3.63 | -3.97 | 1.45E-08 | 3.09E-04 | -3.55 |
| CLEC4M | -2.97 | -3.27 | -4.24 | 3.65E-08 | 7.78E-04 | -3.49 |
| MT1F | -2.44 | -3.22 | -4.66 | 4.12E-08 | 8.77E-04 | -3.44 |
| CYP26A1 | -2.76 | -3.33 | -4.16 | 2.30E-08 | 4.90E-04 | -3.42 |
| ESR1 | -2.33 | -3.27 | -4.41 | 3.44E-08 | 7.32E-04 | -3.34 |
| C7 | -2.91 | -4.55 | -2.43 | 1.47E-06 | 3.14E-02 | -3.29 |
| CYP2B6 | -2.22 | -3.30 | -4.30 | 3.22E-08 | 6.87E-04 | -3.27 |
| APOF | -2.73 | -3.14 | -3.86 | 7.05E-08 | 1.50E-03 | -3.24 |
| CYP2A6 | -2.35 | -3.13 | -4.11 | 8.14E-08 | 1.73E-03 | -3.20 |
| GYS2 | -2.34 | -2.99 | -4.24 | 1.31E-07 | 2.79E-03 | -3.19 |
| HGF | -2.78 | -3.69 | -3.10 | 1.91E-07 | 4.06E-03 | -3.19 |
| GPR128 | -2.27 | -3.88 | -3.38 | 8.53E-08 | 1.82E-03 | -3.18 |
| IDO2 | -3.35 | -3.01 | -2.97 | 2.83E-07 | 6.04E-03 | -3.11 |
| GHR | -2.31 | -3.27 | -3.74 | 3.44E-08 | 7.32E-04 | -3.11 |
| BBOX1 | -3.34 | -2.60 | -3.36 | 3.60E-07 | 7.66E-03 | -3.10 |
| NAT2 | -2.52 | -2.72 | -4.01 | 2.50E-07 | 5.32E-03 | -3.08 |
| DCN | -2.49 | -3.88 | -2.72 | 5.23E-07 | 1.11E-02 | -3.03 |
| CYP2B7P | -1.82 | -3.69 | -3.58 | 2.34E-07 | 4.98E-03 | -3.03 |
| ALDOB | -2.22 | -4.00 | -2.83 | 4.02E-07 | 8.57E-03 | -3.02 |
| SRPX | -2.86 | -3.18 | -2.74 | 4.85E-07 | 1.03E-02 | -2.93 |
| GBA3 | -2.36 | -2.45 | -3.97 | 6.21E-07 | 1.32E-02 | -2.93 |
| GNMT | -1.60 | -3.45 | -3.69 | 7.31E-07 | 1.56E-02 | -2.91 |
| GPM6A | -2.70 | -3.13 | -2.89 | 3.39E-07 | 7.23E-03 | -2.91 |
| SPP2 | -1.72 | -4.15 | -2.81 | 4.36E-07 | 9.29E-03 | -2.89 |
| IGF1 | -2.37 | -2.98 | -3.31 | 1.36E-07 | 2.90E-03 | -2.89 |
| LCAT | -2.54 | -2.60 | -3.50 | 3.81E-07 | 8.10E-03 | -2.88 |
| CYP2C8 | -1.71 | -3.09 | -3.84 | 3.91E-07 | 8.33E-03 | -2.88 |
| FOS | -2.21 | -3.94 | -2.47 | 1.25E-06 | 2.66E-02 | -2.87 |
| MT1G | -1.92 | -2.64 | -3.96 | 3.11E-07 | 6.61E-03 | -2.84 |
| ASPA | -1.98 | -2.74 | -3.67 | 2.19E-07 | 4.66E-03 | -2.80 |
| FBP1 | -1.82 | -3.76 | -2.69 | 5.92E-07 | 1.26E-02 | -2.76 |
| CXCL12 | -2.23 | -3.36 | -2.54 | 9.28E-07 | 1.98E-02 | -2.71 |
| MT1E | -1.57 | -2.68 | -3.75 | 8.89E-07 | 1.89E-02 | -2.67 |
| CYP2E1 | -1.64 | -2.34 | -3.98 | 7.64E-07 | 1.63E-02 | -2.65 |
| ANXA10 | -1.83 | -2.72 | -3.41 | 2.42E-07 | 5.15E-03 | -2.65 |
| CYP39A1 | -1.65 | -3.06 | -3.24 | 5.92E-07 | 1.26E-02 | -2.65 |
| SLC10A1 | -1.50 | -2.60 | -3.77 | 1.42E-06 | 3.03E-02 | -2.62 |
| KMO | -2.15 | -3.14 | -2.57 | 7.81E-07 | 1.66E-02 | -2.62 |
| MT1X | -1.50 | -2.58 | -3.77 | 1.47E-06 | 3.14E-02 | -2.62 |
| MT1H | -1.65 | -2.64 | -3.55 | 5.78E-07 | 1.23E-02 | -2.62 |
| PLAC8 | -2.12 | -3.11 | -2.60 | 7.14E-07 | 1.52E-02 | -2.61 |
| FCN2 | -2.05 | -3.04 | -2.70 | 5.78E-07 | 1.23E-02 | -2.60 |
| HGFAC | -2.87 | -2.20 | -2.69 | 1.05E-06 | 2.23E-02 | -2.59 |
| MARCO | -1.74 | -3.50 | -2.48 | 1.11E-06 | 2.37E-02 | -2.57 |
| VNN1 | -1.84 | -2.98 | -2.90 | 3.30E-07 | 7.02E-03 | -2.57 |
| RDH16 | -1.96 | -2.38 | -3.33 | 7.14E-07 | 1.52E-02 | -2.56 |
| PCK1 | -1.49 | -3.75 | -2.33 | 2.06E-06 | 4.40E-02 | -2.52 |
| LOC101928916 | -1.93 | -3.16 | -2.48 | 1.20E-06 | 2.56E-02 | -2.52 |
| ZG16 | -2.18 | -2.78 | -2.49 | 1.07E-06 | 2.28E-02 | -2.49 |
| C6 | -1.60 | -2.83 | -2.99 | 7.14E-07 | 1.52E-02 | -2.47 |
| IL13RA2 | -1.89 | -2.91 | -2.52 | 9.87E-07 | 2.10E-02 | -2.44 |
| OLFML3 | -2.04 | -2.51 | -2.74 | 5.10E-07 | 1.09E-02 | -2.43 |
| CD5L | -2.11 | -2.68 | -2.44 | 1.35E-06 | 2.86E-02 | -2.41 |
| GRAMD1C | -1.51 | -3.11 | -2.58 | 1.40E-06 | 2.97E-02 | -2.40 |
| FETUB | -1.52 | -2.49 | -3.09 | 1.32E-06 | 2.81E-02 | -2.37 |
| CETP | -1.96 | -2.63 | -2.40 | 1.66E-06 | 3.55E-02 | -2.33 |
| AFM | -1.87 | -2.54 | -2.55 | 8.71E-07 | 1.85E-02 | -2.32 |
| CFHR3 | -1.84 | -2.07 | -3.01 | 1.75E-06 | 3.73E-02 | -2.30 |
| NPY1R | -1.73 | -2.58 | -2.43 | 1.50E-06 | 3.19E-02 | -2.25 |
| HPGD | -1.70 | -2.51 | -2.51 | 1.03E-06 | 2.19E-02 | -2.24 |
| ANK3 | -2.10 | -2.30 | -2.29 | 2.23E-06 | 4.76E-02 | -2.23 |
| KDM8 | -1.93 | -2.07 | -2.67 | 1.78E-06 | 3.79E-02 | -2.22 |
| ACADL | -1.58 | -2.39 | -2.68 | 7.99E-07 | 1.70E-02 | -2.22 |
| RCAN1 | -1.65 | -2.46 | -2.40 | 1.64E-06 | 3.48E-02 | -2.17 |
| SOCS2 | -1.54 | -2.09 | -2.85 | 1.58E-06 | 3.37E-02 | -2.16 |
| CYP3A43 | -1.41 | -2.09 | -2.90 | 2.34E-06 | 4.98E-02 | -2.14 |
| BHMT | -1.47 | -2.08 | -2.77 | 1.72E-06 | 3.67E-02 | -2.11 |

FC, fold change.

**Supplementary Table S2. The GO annotation of up-regulated genes**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Oncology | ID | Description | Gene Ratio | Bg Ratio | P.value | P.adjust | Q value | Gene ID | Count |
| BP | GO:0098813 | nuclear chromosome segregation | 18/55 | 262/18670 | 2.24E-20 | 3.13E-17 | 2.20E-17 | TOP2A/CCNB1/PRC1/ECT2/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/CCNE2/PTTG1/TRIP13 | 18 |
| BP | GO:0000280 | nuclear division | 20/55 | 407/18670 | 9.27E-20 | 6.25E-17 | 4.40E-17 | TOP2A/ASPM/CCNB1/PRC1/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/KIF11/CCNE2/PTTG1/AURKA/TRIP13 | 20 |
| BP | GO:0000819 | sister chromatid segregation | 16/55 | 189/18670 | 1.35E-19 | 6.25E-17 | 4.40E-17 | TOP2A/CCNB1/PRC1/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/PTTG1/TRIP13 | 16 |
| BP | GO:0000070 | mitotic sister chromatid segregation | 15/55 | 151/18670 | 1.84E-19 | 6.40E-17 | 4.51E-17 | CCNB1/PRC1/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/PTTG1/TRIP13 | 15 |
| BP | GO:0048285 | organelle fission | 20/55 | 449/18670 | 6.41E-19 | 1.78E-16 | 1.26E-16 | TOP2A/ASPM/CCNB1/PRC1/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/KIF11/CCNE2/PTTG1/AURKA/TRIP13 | 20 |
| BP | GO:0007059 | chromosome segregation | 18/55 | 321/18670 | 8.68E-19 | 1.81E-16 | 1.27E-16 | TOP2A/CCNB1/PRC1/ECT2/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/CCNE2/PTTG1/TRIP13 | 18 |
| BP | GO:0140014 | mitotic nuclear division | 17/55 | 264/18670 | 9.09E-19 | 1.81E-16 | 1.27E-16 | CCNB1/PRC1/NDC80/NEK2/BUB1B/ZWINT/NUSAP1/NCAPG/TTK/DLGAP5/CDC20/BUB1/KIF4A/KIF11/PTTG1/AURKA/TRIP13 | 17 |
| BP | GO:0010948 | negative regulation of cell cycle process | 17/55 | 361/18670 | 1.78E-16 | 3.09E-14 | 2.18E-14 | RRM2/CDK1/DTL/CCNB1/NDC80/NEK2/BUB1B/TTK/CDKN2C/CDC20/EZH2/BUB1/PTTG1/E2F8/AURKA/CDC7/TRIP13 | 17 |
| BP | GO:0007088 | regulation of mitotic nuclear division | 13/55 | 164/18670 | 1.21E-15 | 1.87E-13 | 1.32E-13 | CCNB1/NDC80/NEK2/BUB1B/NUSAP1/TTK/DLGAP5/CDC20/BUB1/KIF11/PTTG1/AURKA/TRIP13 | 13 |
| BP | GO:1901990 | regulation of mitotic cell cycle phase transition | 17/55 | 444/18670 | 5.47E-15 | 7.62E-13 | 5.37E-13 | HMMR/CDK1/DTL/CCNB1/NDC80/NEK2/BUB1B/TTK/DLGAP5/CDKN2C/CDC20/EZH2/BUB1/E2F8/AURKA/CDC7/TRIP13 | 17 |
| BP | GO:0051783 | regulation of nuclear division | 13/55 | 188/18670 | 7.22E-15 | 9.15E-13 | 6.44E-13 | CCNB1/NDC80/NEK2/BUB1B/NUSAP1/TTK/DLGAP5/CDC20/BUB1/KIF11/PTTG1/AURKA/TRIP13 | 13 |
| BP | GO:0051983 | regulation of chromosome segregation | 11/55 | 103/18670 | 8.15E-15 | 9.46E-13 | 6.66E-13 | CCNB1/ECT2/NDC80/NEK2/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 11 |
| BP | GO:1901987 | regulation of cell cycle phase transition | 17/55 | 480/18670 | 1.96E-14 | 2.10E-12 | 1.48E-12 | HMMR/CDK1/DTL/CCNB1/NDC80/NEK2/BUB1B/TTK/DLGAP5/CDKN2C/CDC20/EZH2/BUB1/E2F8/AURKA/CDC7/TRIP13 | 17 |
| BP | GO:0045930 | negative regulation of mitotic cell cycle | 15/55 | 338/18670 | 3.34E-14 | 3.32E-12 | 2.34E-12 | TOP2A/CDK1/CCNB1/NDC80/BUB1B/ZWINT/TTK/CDKN2C/CDC20/EZH2/BUB1/PTTG1/E2F8/AURKA/TRIP13 | 15 |
| BP | GO:0000075 | cell cycle checkpoint | 13/55 | 216/18670 | 4.38E-14 | 4.07E-12 | 2.86E-12 | TOP2A/CDK1/DTL/CCNB1/NDC80/BUB1B/ZWINT/TTK/CDC20/BUB1/E2F8/AURKA/TRIP13 | 13 |
| BP | GO:0007093 | mitotic cell cycle checkpoint | 12/55 | 165/18670 | 4.79E-14 | 4.17E-12 | 2.93E-12 | TOP2A/CDK1/CCNB1/NDC80/BUB1B/ZWINT/TTK/CDC20/BUB1/E2F8/AURKA/TRIP13 | 12 |
| BP | GO:0010965 | regulation of mitotic sister chromatid separation | 9/55 | 57/18670 | 6.78E-14 | 5.56E-12 | 3.91E-12 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:0051304 | chromosome separation | 10/55 | 90/18670 | 9.92E-14 | 7.68E-12 | 5.41E-12 | TOP2A/CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 10 |
| BP | GO:0051306 | mitotic sister chromatid separation | 9/55 | 60/18670 | 1.11E-13 | 8.12E-12 | 5.72E-12 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:1905818 | regulation of chromosome separation | 9/55 | 62/18670 | 1.51E-13 | 1.05E-11 | 7.42E-12 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:2000816 | negative regulation of mitotic sister chromatid separation | 8/55 | 39/18670 | 1.91E-13 | 1.27E-11 | 8.93E-12 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:1905819 | negative regulation of chromosome separation | 8/55 | 40/18670 | 2.38E-13 | 1.51E-11 | 1.06E-11 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:0033047 | regulation of mitotic sister chromatid segregation | 9/55 | 68/18670 | 3.63E-13 | 2.11E-11 | 1.49E-11 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:0033048 | negative regulation of mitotic sister chromatid segregation | 8/55 | 42/18670 | 3.64E-13 | 2.11E-11 | 1.49E-11 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:0033046 | negative regulation of sister chromatid segregation | 8/55 | 44/18670 | 5.45E-13 | 3.03E-11 | 2.14E-11 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:0051985 | negative regulation of chromosome segregation | 8/55 | 45/18670 | 6.61E-13 | 3.43E-11 | 2.41E-11 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:1901988 | negative regulation of cell cycle phase transition | 13/55 | 267/18670 | 6.64E-13 | 3.43E-11 | 2.41E-11 | CDK1/DTL/CCNB1/NDC80/BUB1B/TTK/CDKN2C/CDC20/EZH2/BUB1/E2F8/AURKA/TRIP13 | 13 |
| BP | GO:0033045 | regulation of sister chromatid segregation | 9/55 | 80/18670 | 1.66E-12 | 8.26E-11 | 5.82E-11 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:0030071 | regulation of mitotic metaphase/anaphase transition | 8/55 | 51/18670 | 1.93E-12 | 9.25E-11 | 6.51E-11 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/TRIP13 | 8 |
| BP | GO:0045839 | negative regulation of mitotic nuclear division | 8/55 | 52/18670 | 2.27E-12 | 1.05E-10 | 7.43E-11 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:1902099 | regulation of metaphase/anaphase transition of cell cycle | 8/55 | 53/18670 | 2.67E-12 | 1.20E-10 | 8.45E-11 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/TRIP13 | 8 |
| BP | GO:0007091 | metaphase/anaphase transition of mitotic cell cycle | 8/55 | 54/18670 | 3.13E-12 | 1.36E-10 | 9.58E-11 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/TRIP13 | 8 |
| BP | GO:0044784 | metaphase/anaphase transition of cell cycle | 8/55 | 56/18670 | 4.25E-12 | 1.79E-10 | 1.26E-10 | CCNB1/NDC80/BUB1B/TTK/DLGAP5/CDC20/BUB1/TRIP13 | 8 |
| BP | GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 10/55 | 131/18670 | 4.57E-12 | 1.87E-10 | 1.32E-10 | CCNB1/PRC1/NDC80/NEK2/NUSAP1/TTK/CDC20/KIF4A/KIF11/AURKA | 10 |
| BP | GO:1901991 | negative regulation of mitotic cell cycle phase transition | 12/55 | 248/18670 | 6.12E-12 | 2.34E-10 | 1.65E-10 | CDK1/CCNB1/NDC80/BUB1B/TTK/CDKN2C/CDC20/EZH2/BUB1/E2F8/AURKA/TRIP13 | 12 |
| BP | GO:0007094 | mitotic spindle assembly checkpoint | 7/55 | 34/18670 | 6.56E-12 | 2.34E-10 | 1.65E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:0031577 | spindle checkpoint | 7/55 | 34/18670 | 6.56E-12 | 2.34E-10 | 1.65E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:0071173 | spindle assembly checkpoint | 7/55 | 34/18670 | 6.56E-12 | 2.34E-10 | 1.65E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:0071174 | mitotic spindle checkpoint | 7/55 | 34/18670 | 6.56E-12 | 2.34E-10 | 1.65E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:0051784 | negative regulation of nuclear division | 8/55 | 60/18670 | 7.58E-12 | 2.64E-10 | 1.86E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 8 |
| BP | GO:0045841 | negative regulation of mitotic metaphase/anaphase transition | 7/55 | 36/18670 | 1.01E-11 | 3.44E-10 | 2.42E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:1902100 | negative regulation of metaphase/anaphase transition of cell cycle | 7/55 | 37/18670 | 1.25E-11 | 4.13E-10 | 2.91E-10 | CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/TRIP13 | 7 |
| BP | GO:0007052 | mitotic spindle organization | 9/55 | 106/18670 | 2.22E-11 | 7.19E-10 | 5.06E-10 | CCNB1/PRC1/NDC80/NEK2/TTK/CDC20/KIF4A/KIF11/AURKA | 9 |
| BP | GO:0007051 | spindle organization | 10/55 | 170/18670 | 6.17E-11 | 1.95E-09 | 1.38E-09 | ASPM/CCNB1/PRC1/NDC80/NEK2/TTK/CDC20/KIF4A/KIF11/AURKA | 10 |
| BP | GO:0140013 | meiotic nuclear division | 10/55 | 172/18670 | 6.93E-11 | 2.14E-09 | 1.51E-09 | TOP2A/ASPM/BUB1B/TTK/CDC20/BUB1/CCNE2/PTTG1/AURKA/TRIP13 | 10 |
| BP | GO:0051321 | meiotic cell cycle | 11/55 | 249/18670 | 1.36E-10 | 4.11E-09 | 2.90E-09 | TOP2A/ASPM/NEK2/BUB1B/TTK/CDC20/BUB1/CCNE2/PTTG1/AURKA/TRIP13 | 11 |
| BP | GO:1903046 | meiotic cell cycle process | 10/55 | 188/18670 | 1.67E-10 | 4.93E-09 | 3.48E-09 | TOP2A/ASPM/BUB1B/TTK/CDC20/BUB1/CCNE2/PTTG1/AURKA/TRIP13 | 10 |
| BP | GO:2001251 | negative regulation of chromosome organization | 9/55 | 146/18670 | 3.99E-10 | 1.16E-08 | 8.16E-09 | TOP2A/CCNB1/NDC80/BUB1B/TTK/CDC20/BUB1/PTTG1/TRIP13 | 9 |
| BP | GO:0090068 | positive regulation of cell cycle process | 11/55 | 298/18670 | 9.14E-10 | 2.60E-08 | 1.83E-08 | CDK1/DTL/CCNB1/ECT2/NDC80/NUSAP1/DLGAP5/EZH2/E2F8/AURKA/CDC7 | 11 |
| BP | GO:0000086 | G2/M transition of mitotic cell cycle | 10/55 | 247/18670 | 2.38E-09 | 6.62E-08 | 4.66E-08 | HMMR/CDK1/DTL/CCNB1/NEK2/MELK/CCNB2/AURKA/FOXM1/CDC7 | 10 |
| BP | GO:0033044 | regulation of chromosome organization | 11/55 | 342/18670 | 3.87E-09 | 1.06E-07 | 7.44E-08 | TOP2A/CCNB1/NDC80/NEK2/BUB1B/TTK/DLGAP5/CDC20/BUB1/PTTG1/TRIP13 | 11 |
| BP | GO:0044839 | cell cycle G2/M phase transition | 10/55 | 266/18670 | 4.84E-09 | 1.30E-07 | 9.14E-08 | HMMR/CDK1/DTL/CCNB1/NEK2/MELK/CCNB2/AURKA/FOXM1/CDC7 | 10 |
| BP | GO:0045132 | meiotic chromosome segregation | 7/55 | 90/18670 | 8.02E-09 | 2.11E-07 | 1.49E-07 | TOP2A/BUB1B/TTK/BUB1/CCNE2/PTTG1/TRIP13 | 7 |
| BP | GO:0045787 | positive regulation of cell cycle | 11/55 | 389/18670 | 1.47E-08 | 3.79E-07 | 2.67E-07 | CDK1/DTL/CCNB1/ECT2/NDC80/NUSAP1/DLGAP5/EZH2/E2F8/AURKA/CDC7 | 11 |
| BP | GO:0010639 | negative regulation of organelle organization | 11/55 | 393/18670 | 1.63E-08 | 4.13E-07 | 2.91E-07 | TOP2A/CCNB1/NDC80/NEK2/BUB1B/FGF13/TTK/CDC20/BUB1/PTTG1/TRIP13 | 11 |
| BP | GO:0045931 | positive regulation of mitotic cell cycle | 8/55 | 163/18670 | 2.44E-08 | 6.07E-07 | 4.28E-07 | CDK1/DTL/CCNB1/NDC80/NUSAP1/DLGAP5/AURKA/CDC7 | 8 |
| BP | GO:0000082 | G1/S transition of mitotic cell cycle | 9/55 | 279/18670 | 1.14E-07 | 2.78E-06 | 1.96E-06 | RRM2/CDK1/CCNB1/CDKN2C/EZH2/CCNE2/E2F8/AURKA/CDC7 | 9 |
| BP | GO:0031145 | anaphase-promoting complex-dependent catabolic process | 6/55 | 81/18670 | 1.35E-07 | 3.25E-06 | 2.29E-06 | CDK1/CCNB1/BUB1B/CDC20/PTTG1/AURKA | 6 |
| BP | GO:0044843 | cell cycle G1/S phase transition | 9/55 | 298/18670 | 1.99E-07 | 4.70E-06 | 3.31E-06 | RRM2/CDK1/CCNB1/CDKN2C/EZH2/CCNE2/E2F8/AURKA/CDC7 | 9 |
| BP | GO:0030261 | chromosome condensation | 5/55 | 47/18670 | 2.57E-07 | 5.97E-06 | 4.20E-06 | TOP2A/CDK1/CCNB1/NUSAP1/NCAPG | 5 |
| BP | GO:0000910 | cytokinesis | 7/55 | 171/18670 | 6.70E-07 | 1.51E-05 | 1.06E-05 | PRC1/ECT2/KIF20A/NUSAP1/KIF4A/E2F8/AURKA | 7 |
| BP | GO:1901989 | positive regulation of cell cycle phase transition | 6/55 | 106/18670 | 6.72E-07 | 1.51E-05 | 1.06E-05 | CDK1/DTL/CCNB1/DLGAP5/EZH2/CDC7 | 6 |
| BP | GO:0051225 | spindle assembly | 6/55 | 108/18670 | 7.50E-07 | 1.66E-05 | 1.17E-05 | ASPM/NEK2/CDC20/KIF4A/KIF11/AURKA | 6 |
| BP | GO:0010971 | positive regulation of G2/M transition of mitotic cell cycle | 4/55 | 27/18670 | 1.12E-06 | 2.45E-05 | 1.72E-05 | CDK1/DTL/CCNB1/CDC7 | 4 |
| BP | GO:0010389 | regulation of G2/M transition of mitotic cell cycle | 7/55 | 196/18670 | 1.67E-06 | 3.58E-05 | 2.52E-05 | HMMR/CDK1/DTL/CCNB1/NEK2/AURKA/CDC7 | 7 |
| BP | GO:1902751 | positive regulation of cell cycle G2/M phase transition | 4/55 | 30/18670 | 1.74E-06 | 3.68E-05 | 2.59E-05 | CDK1/DTL/CCNB1/CDC7 | 4 |
| BP | GO:2000134 | negative regulation of G1/S transition of mitotic cell cycle | 6/55 | 125/18670 | 1.77E-06 | 3.68E-05 | 2.59E-05 | CDK1/CCNB1/CDKN2C/EZH2/E2F8/AURKA | 6 |
| BP | GO:0007143 | female meiotic nuclear division | 4/55 | 31/18670 | 2.00E-06 | 4.09E-05 | 2.88E-05 | TOP2A/TTK/AURKA/TRIP13 | 4 |
| BP | GO:0008608 | attachment of spindle microtubules to kinetochore | 4/55 | 32/18670 | 2.28E-06 | 4.60E-05 | 3.24E-05 | CCNB1/ECT2/NDC80/NEK2 | 4 |
| BP | GO:1902807 | negative regulation of cell cycle G1/S phase transition | 6/55 | 131/18670 | 2.33E-06 | 4.60E-05 | 3.24E-05 | CDK1/CCNB1/CDKN2C/EZH2/E2F8/AURKA | 6 |
| BP | GO:0072401 | signal transduction involved in DNA integrity checkpoint | 5/55 | 73/18670 | 2.38E-06 | 4.60E-05 | 3.24E-05 | CDK1/DTL/CCNB1/E2F8/AURKA | 5 |
| BP | GO:0072422 | signal transduction involved in DNA damage checkpoint | 5/55 | 73/18670 | 2.38E-06 | 4.60E-05 | 3.24E-05 | CDK1/DTL/CCNB1/E2F8/AURKA | 5 |
| BP | GO:0042770 | signal transduction in response to DNA damage | 6/55 | 133/18670 | 2.54E-06 | 4.79E-05 | 3.37E-05 | CDK1/DTL/CCNB1/E2F8/AURKA/FOXM1 | 6 |
| BP | GO:0072395 | signal transduction involved in cell cycle checkpoint | 5/55 | 74/18670 | 2.54E-06 | 4.79E-05 | 3.37E-05 | CDK1/DTL/CCNB1/E2F8/AURKA | 5 |
| BP | GO:0007292 | female gamete generation | 6/55 | 136/18670 | 2.89E-06 | 5.33E-05 | 3.75E-05 | TOP2A/ASPM/CCNB1/TTK/AURKA/TRIP13 | 6 |
| BP | GO:1902749 | regulation of cell cycle G2/M phase transition | 7/55 | 213/18670 | 2.91E-06 | 5.33E-05 | 3.75E-05 | HMMR/CDK1/DTL/CCNB1/NEK2/AURKA/CDC7 | 7 |
| BP | GO:0007077 | mitotic nuclear envelope disassembly | 3/55 | 12/18670 | 5.22E-06 | 9.33E-05 | 6.57E-05 | CDK1/CCNB1/CCNB2 | 3 |
| BP | GO:0051988 | regulation of attachment of spindle microtubules to kinetochore | 3/55 | 12/18670 | 5.22E-06 | 9.33E-05 | 6.57E-05 | CCNB1/ECT2/NEK2 | 3 |
| BP | GO:0032465 | regulation of cytokinesis | 5/55 | 89/18670 | 6.34E-06 | 1.12E-04 | 7.87E-05 | PRC1/ECT2/KIF20A/E2F8/AURKA | 5 |
| BP | GO:0031570 | DNA integrity checkpoint | 6/55 | 157/18670 | 6.63E-06 | 1.15E-04 | 8.13E-05 | TOP2A/CDK1/DTL/CCNB1/E2F8/AURKA | 6 |
| BP | GO:1901992 | positive regulation of mitotic cell cycle phase transition | 5/55 | 91/18670 | 7.07E-06 | 1.22E-04 | 8.56E-05 | CDK1/DTL/CCNB1/DLGAP5/CDC7 | 5 |
| BP | GO:2000241 | regulation of reproductive process | 6/55 | 160/18670 | 7.39E-06 | 1.26E-04 | 8.84E-05 | SPINK1/ASPM/TTK/CDC20/AURKA/TRIP13 | 6 |
| BP | GO:0007100 | mitotic centrosome separation | 3/55 | 14/18670 | 8.61E-06 | 1.44E-04 | 1.02E-04 | NEK2/KIF11/AURKA | 3 |
| BP | GO:0051302 | regulation of cell division | 6/55 | 168/18670 | 9.77E-06 | 1.62E-04 | 1.14E-04 | ASPM/PRC1/ECT2/KIF20A/E2F8/AURKA | 6 |
| BP | GO:0070301 | cellular response to hydrogen peroxide | 5/55 | 99/18670 | 1.07E-05 | 1.74E-04 | 1.22E-04 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0051299 | centrosome separation | 3/55 | 15/18670 | 1.07E-05 | 1.74E-04 | 1.22E-04 | NEK2/KIF11/AURKA | 3 |
| BP | GO:0051445 | regulation of meiotic cell cycle | 4/55 | 49/18670 | 1.29E-05 | 2.06E-04 | 1.45E-04 | ASPM/TTK/CDC20/TRIP13 | 4 |
| BP | GO:0030397 | membrane disassembly | 3/55 | 16/18670 | 1.32E-05 | 2.06E-04 | 1.45E-04 | CDK1/CCNB1/CCNB2 | 3 |
| BP | GO:0051081 | nuclear envelope disassembly | 3/55 | 16/18670 | 1.32E-05 | 2.06E-04 | 1.45E-04 | CDK1/CCNB1/CCNB2 | 3 |
| BP | GO:0006260 | DNA replication | 7/55 | 273/18670 | 1.47E-05 | 2.28E-04 | 1.61E-04 | RRM2/CDK1/DTL/GINS1/CCNE2/E2F8/CDC7 | 7 |
| BP | GO:0044774 | mitotic DNA integrity checkpoint | 5/55 | 106/18670 | 1.49E-05 | 2.28E-04 | 1.61E-04 | TOP2A/CDK1/CCNB1/E2F8/AURKA | 5 |
| BP | GO:0030330 | DNA damage response, signal transduction by p53 class mediator | 5/55 | 107/18670 | 1.56E-05 | 2.36E-04 | 1.66E-04 | CDK1/CCNB1/E2F8/AURKA/FOXM1 | 5 |
| BP | GO:0034501 | protein localization to kinetochore | 3/55 | 17/18670 | 1.60E-05 | 2.39E-04 | 1.69E-04 | CDK1/NDC80/TTK | 3 |
| BP | GO:0071156 | regulation of cell cycle arrest | 5/55 | 108/18670 | 1.63E-05 | 2.40E-04 | 1.69E-04 | CDK1/CCNB1/E2F8/AURKA/FOXM1 | 5 |
| BP | GO:2000045 | regulation of G1/S transition of mitotic cell cycle | 6/55 | 184/18670 | 1.64E-05 | 2.40E-04 | 1.69E-04 | CDK1/CCNB1/CDKN2C/EZH2/E2F8/AURKA | 6 |
| BP | GO:0007127 | meiosis I | 5/55 | 114/18670 | 2.12E-05 | 3.08E-04 | 2.17E-04 | TOP2A/CCNE2/PTTG1/AURKA/TRIP13 | 5 |
| BP | GO:0006977 | DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 4/55 | 56/18670 | 2.21E-05 | 3.14E-04 | 2.21E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0090307 | mitotic spindle assembly | 4/55 | 56/18670 | 2.21E-05 | 3.14E-04 | 2.21E-04 | NEK2/CDC20/KIF4A/KIF11 | 4 |
| BP | GO:0072431 | signal transduction involved in mitotic G1 DNA damage checkpoint | 4/55 | 57/18670 | 2.37E-05 | 3.30E-04 | 2.33E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:1902400 | intracellular signal transduction involved in G1 DNA damage checkpoint | 4/55 | 57/18670 | 2.37E-05 | 3.30E-04 | 2.33E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0061982 | meiosis I cell cycle process | 5/55 | 119/18670 | 2.61E-05 | 3.60E-04 | 2.53E-04 | TOP2A/CCNE2/PTTG1/AURKA/TRIP13 | 5 |
| BP | GO:0072413 | signal transduction involved in mitotic cell cycle checkpoint | 4/55 | 59/18670 | 2.72E-05 | 3.64E-04 | 2.57E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:1902402 | signal transduction involved in mitotic DNA damage checkpoint | 4/55 | 59/18670 | 2.72E-05 | 3.64E-04 | 2.57E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:1902403 | signal transduction involved in mitotic DNA integrity checkpoint | 4/55 | 59/18670 | 2.72E-05 | 3.64E-04 | 2.57E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:1902806 | regulation of cell cycle G1/S phase transition | 6/55 | 202/18670 | 2.78E-05 | 3.68E-04 | 2.59E-04 | CDK1/CCNB1/CDKN2C/EZH2/E2F8/AURKA | 6 |
| BP | GO:0071459 | protein localization to chromosome, centromeric region | 3/55 | 21/18670 | 3.10E-05 | 4.07E-04 | 2.87E-04 | CDK1/NDC80/TTK | 3 |
| BP | GO:0031571 | mitotic G1 DNA damage checkpoint | 4/55 | 63/18670 | 3.53E-05 | 4.55E-04 | 3.21E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0044819 | mitotic G1/S transition checkpoint | 4/55 | 63/18670 | 3.53E-05 | 4.55E-04 | 3.21E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0044783 | G1 DNA damage checkpoint | 4/55 | 64/18670 | 3.76E-05 | 4.80E-04 | 3.38E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0070192 | chromosome organization involved in meiotic cell cycle | 4/55 | 65/18670 | 3.99E-05 | 5.06E-04 | 3.56E-04 | BUB1B/BUB1/CCNE2/TRIP13 | 4 |
| BP | GO:0000281 | mitotic cytokinesis | 4/55 | 72/18670 | 5.98E-05 | 7.46E-04 | 5.25E-04 | ECT2/KIF20A/NUSAP1/KIF4A | 4 |
| BP | GO:0001556 | oocyte maturation | 3/55 | 26/18670 | 5.99E-05 | 7.46E-04 | 5.25E-04 | CCNB1/AURKA/TRIP13 | 3 |
| BP | GO:0000077 | DNA damage checkpoint | 5/55 | 145/18670 | 6.71E-05 | 8.27E-04 | 5.83E-04 | CDK1/DTL/CCNB1/E2F8/AURKA | 5 |
| BP | GO:0007050 | cell cycle arrest | 6/55 | 237/18670 | 6.77E-05 | 8.27E-04 | 5.83E-04 | CDK1/CCNB1/CDKN2C/E2F8/AURKA/FOXM1 | 6 |
| BP | GO:0042542 | response to hydrogen peroxide | 5/55 | 146/18670 | 6.93E-05 | 8.40E-04 | 5.92E-04 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0071236 | cellular response to antibiotic | 5/55 | 147/18670 | 7.16E-05 | 8.60E-04 | 6.06E-04 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0006323 | DNA packaging | 6/55 | 247/18670 | 8.50E-05 | 1.00E-03 | 7.07E-04 | TOP2A/CDK1/CCNB1/NUSAP1/CENPU/NCAPG | 6 |
| BP | GO:0097237 | cellular response to toxic substance | 6/55 | 247/18670 | 8.50E-05 | 1.00E-03 | 7.07E-04 | AKR1B10/CDK1/ECT2/LCN2/EZH2/NQO1 | 6 |
| BP | GO:0022412 | cellular process involved in reproduction in multicellular organism | 7/55 | 361/18670 | 8.71E-05 | 1.02E-03 | 7.18E-04 | SPINK1/TOP2A/ASPM/CCNB1/TTK/AURKA/TRIP13 | 7 |
| BP | GO:0071103 | DNA conformation change | 7/55 | 364/18670 | 9.17E-05 | 1.06E-03 | 7.50E-04 | TOP2A/CDK1/CCNB1/GINS1/NUSAP1/CENPU/NCAPG | 7 |
| BP | GO:0071158 | positive regulation of cell cycle arrest | 4/55 | 82/18670 | 9.94E-05 | 1.14E-03 | 8.06E-04 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0040020 | regulation of meiotic nuclear division | 3/55 | 31/18670 | 1.03E-04 | 1.17E-03 | 8.25E-04 | TTK/CDC20/TRIP13 | 3 |
| BP | GO:0034502 | protein localization to chromosome | 4/55 | 83/18670 | 1.04E-04 | 1.18E-03 | 8.31E-04 | CDK1/NDC80/TTK/EZH2 | 4 |
| BP | GO:0048477 | oogenesis | 4/55 | 87/18670 | 1.25E-04 | 1.41E-03 | 9.90E-04 | ASPM/CCNB1/AURKA/TRIP13 | 4 |
| BP | GO:0034614 | cellular response to reactive oxygen species | 5/55 | 168/18670 | 1.34E-04 | 1.50E-03 | 1.05E-03 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0045740 | positive regulation of DNA replication | 3/55 | 36/18670 | 1.61E-04 | 1.78E-03 | 1.26E-03 | CDK1/E2F8/CDC7 | 3 |
| BP | GO:0016572 | histone phosphorylation | 3/55 | 38/18670 | 1.90E-04 | 2.07E-03 | 1.46E-03 | CDK1/CCNB1/AURKA | 3 |
| BP | GO:0044773 | mitotic DNA damage checkpoint | 4/55 | 97/18670 | 1.91E-04 | 2.07E-03 | 1.46E-03 | CDK1/CCNB1/E2F8/AURKA | 4 |
| BP | GO:0061640 | cytoskeleton-dependent cytokinesis | 4/55 | 100/18670 | 2.14E-04 | 2.31E-03 | 1.63E-03 | ECT2/KIF20A/NUSAP1/KIF4A | 4 |
| BP | GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process | 7/55 | 419/18670 | 2.19E-04 | 2.34E-03 | 1.65E-03 | CDK1/CCNB1/PBK/BUB1B/CDC20/PTTG1/AURKA | 7 |
| BP | GO:0000079 | regulation of cyclin-dependent protein serine/threonine kinase activity | 4/55 | 102/18670 | 2.31E-04 | 2.46E-03 | 1.73E-03 | CCNB1/CDKN2C/CCNB2/CCNE2 | 4 |
| BP | GO:0070317 | negative regulation of G0 to G1 transition | 3/55 | 41/18670 | 2.38E-04 | 2.51E-03 | 1.77E-03 | RRM2/EZH2/CDC7 | 3 |
| BP | GO:0018105 | peptidyl-serine phosphorylation | 6/55 | 299/18670 | 2.41E-04 | 2.52E-03 | 1.77E-03 | CDK1/CCNB1/DKK1/TTK/AURKA/CDC7 | 6 |
| BP | GO:0034599 | cellular response to oxidative stress | 6/55 | 302/18670 | 2.54E-04 | 2.64E-03 | 1.86E-03 | CDK1/ECT2/LCN2/MELK/EZH2/NQO1 | 6 |
| BP | GO:1904029 | regulation of cyclin-dependent protein kinase activity | 4/55 | 106/18670 | 2.68E-04 | 2.76E-03 | 1.95E-03 | CCNB1/CDKN2C/CCNB2/CCNE2 | 4 |
| BP | GO:0070316 | regulation of G0 to G1 transition | 3/55 | 45/18670 | 3.14E-04 | 3.22E-03 | 2.27E-03 | RRM2/EZH2/CDC7 | 3 |
| BP | GO:0048599 | oocyte development | 3/55 | 46/18670 | 3.36E-04 | 3.41E-03 | 2.40E-03 | CCNB1/AURKA/TRIP13 | 3 |
| BP | GO:0018209 | peptidyl-serine modification | 6/55 | 322/18670 | 3.58E-04 | 3.59E-03 | 2.53E-03 | CDK1/CCNB1/DKK1/TTK/AURKA/CDC7 | 6 |
| BP | GO:0045023 | G0 to G1 transition | 3/55 | 47/18670 | 3.58E-04 | 3.59E-03 | 2.53E-03 | RRM2/EZH2/CDC7 | 3 |
| BP | GO:0007135 | meiosis II | 2/55 | 10/18670 | 3.78E-04 | 3.68E-03 | 2.59E-03 | BUB1B/BUB1 | 2 |
| BP | GO:0051231 | spindle elongation | 2/55 | 10/18670 | 3.78E-04 | 3.68E-03 | 2.59E-03 | PRC1/KIF4A | 2 |
| BP | GO:0061983 | meiosis II cell cycle process | 2/55 | 10/18670 | 3.78E-04 | 3.68E-03 | 2.59E-03 | BUB1B/BUB1 | 2 |
| BP | GO:1903862 | positive regulation of oxidative phosphorylation | 2/55 | 10/18670 | 3.78E-04 | 3.68E-03 | 2.59E-03 | CDK1/CCNB1 | 2 |
| BP | GO:0051653 | spindle localization | 3/55 | 48/18670 | 3.81E-04 | 3.68E-03 | 2.60E-03 | ASPM/NDC80/NUSAP1 | 3 |
| BP | GO:0009994 | oocyte differentiation | 3/55 | 51/18670 | 4.56E-04 | 4.34E-03 | 3.05E-03 | CCNB1/AURKA/TRIP13 | 3 |
| BP | GO:0035404 | histone-serine phosphorylation | 2/55 | 11/18670 | 4.61E-04 | 4.34E-03 | 3.05E-03 | CCNB1/AURKA | 2 |
| BP | GO:0045835 | negative regulation of meiotic nuclear division | 2/55 | 11/18670 | 4.61E-04 | 4.34E-03 | 3.05E-03 | TTK/TRIP13 | 2 |
| BP | GO:0055015 | ventricular cardiac muscle cell development | 2/55 | 11/18670 | 4.61E-04 | 4.34E-03 | 3.05E-03 | CDK1/CCNB1 | 2 |
| BP | GO:0010498 | proteasomal protein catabolic process | 7/55 | 477/18670 | 4.78E-04 | 4.47E-03 | 3.15E-03 | CDK1/CCNB1/PBK/BUB1B/CDC20/PTTG1/AURKA | 7 |
| BP | GO:0006998 | nuclear envelope organization | 3/55 | 52/18670 | 4.83E-04 | 4.48E-03 | 3.16E-03 | CDK1/CCNB1/CCNB2 | 3 |
| BP | GO:0007098 | centrosome cycle | 4/55 | 124/18670 | 4.87E-04 | 4.49E-03 | 3.16E-03 | CDK1/NEK2/KIF11/AURKA | 4 |
| BP | GO:0045840 | positive regulation of mitotic nuclear division | 3/55 | 53/18670 | 5.11E-04 | 4.68E-03 | 3.30E-03 | NUSAP1/DLGAP5/AURKA | 3 |
| BP | GO:0070601 | centromeric sister chromatid cohesion | 2/55 | 12/18670 | 5.52E-04 | 4.99E-03 | 3.52E-03 | BUB1B/BUB1 | 2 |
| BP | GO:2000105 | positive regulation of DNA-dependent DNA replication | 2/55 | 12/18670 | 5.52E-04 | 4.99E-03 | 3.52E-03 | E2F8/CDC7 | 2 |
| BP | GO:0062197 | cellular response to chemical stress | 6/55 | 350/18670 | 5.56E-04 | 5.00E-03 | 3.52E-03 | CDK1/ECT2/LCN2/MELK/EZH2/NQO1 | 6 |
| BP | GO:0000302 | response to reactive oxygen species | 5/55 | 232/18670 | 5.95E-04 | 5.32E-03 | 3.74E-03 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0045143 | homologous chromosome segregation | 3/55 | 57/18670 | 6.32E-04 | 5.59E-03 | 3.93E-03 | CCNE2/PTTG1/TRIP13 | 3 |
| BP | GO:0031023 | microtubule organizing center organization | 4/55 | 133/18670 | 6.34E-04 | 5.59E-03 | 3.93E-03 | CDK1/NEK2/KIF11/AURKA | 4 |
| BP | GO:0000212 | meiotic spindle organization | 2/55 | 13/18670 | 6.51E-04 | 5.67E-03 | 3.99E-03 | ASPM/AURKA | 2 |
| BP | GO:2000052 | positive regulation of non-canonical Wnt signaling pathway | 2/55 | 13/18670 | 6.51E-04 | 5.67E-03 | 3.99E-03 | GPC3/DKK1 | 2 |
| BP | GO:0046605 | regulation of centrosome cycle | 3/55 | 58/18670 | 6.66E-04 | 5.76E-03 | 4.06E-03 | NEK2/KIF11/AURKA | 3 |
| BP | GO:0090231 | regulation of spindle checkpoint | 2/55 | 14/18670 | 7.58E-04 | 6.44E-03 | 4.53E-03 | CCNB1/NDC80 | 2 |
| BP | GO:0090266 | regulation of mitotic cell cycle spindle assembly checkpoint | 2/55 | 14/18670 | 7.58E-04 | 6.44E-03 | 4.53E-03 | CCNB1/NDC80 | 2 |
| BP | GO:1903504 | regulation of mitotic spindle checkpoint | 2/55 | 14/18670 | 7.58E-04 | 6.44E-03 | 4.53E-03 | CCNB1/NDC80 | 2 |
| BP | GO:0007062 | sister chromatid cohesion | 3/55 | 63/18670 | 8.48E-04 | 7.16E-03 | 5.04E-03 | BUB1B/CDC20/BUB1 | 3 |
| BP | GO:0003128 | heart field specification | 2/55 | 15/18670 | 8.73E-04 | 7.24E-03 | 5.10E-03 | ROBO1/DKK1 | 2 |
| BP | GO:0055057 | neuroblast division | 2/55 | 15/18670 | 8.73E-04 | 7.24E-03 | 5.10E-03 | ASPM/FGF13 | 2 |
| BP | GO:2000095 | regulation of Wnt signaling pathway, planar cell polarity pathway | 2/55 | 15/18670 | 8.73E-04 | 7.24E-03 | 5.10E-03 | GPC3/DKK1 | 2 |
| BP | GO:0051785 | positive regulation of nuclear division | 3/55 | 66/18670 | 9.71E-04 | 8.00E-03 | 5.64E-03 | NUSAP1/DLGAP5/AURKA | 3 |
| BP | GO:0048385 | regulation of retinoic acid receptor signaling pathway | 2/55 | 16/18670 | 9.96E-04 | 8.06E-03 | 5.68E-03 | TRIM16/EZH2 | 2 |
| BP | GO:0051447 | negative regulation of meiotic cell cycle | 2/55 | 16/18670 | 9.96E-04 | 8.06E-03 | 5.68E-03 | TTK/TRIP13 | 2 |
| BP | GO:0055012 | ventricular cardiac muscle cell differentiation | 2/55 | 16/18670 | 9.96E-04 | 8.06E-03 | 5.68E-03 | CDK1/CCNB1 | 2 |
| BP | GO:0006261 | DNA-dependent DNA replication | 4/55 | 151/18670 | 1.02E-03 | 8.20E-03 | 5.77E-03 | GINS1/CCNE2/E2F8/CDC7 | 4 |
| BP | GO:0007281 | germ cell development | 5/55 | 262/18670 | 1.03E-03 | 8.23E-03 | 5.80E-03 | SPINK1/ASPM/CCNB1/AURKA/TRIP13 | 5 |
| BP | GO:0072331 | signal transduction by p53 class mediator | 5/55 | 267/18670 | 1.12E-03 | 8.90E-03 | 6.27E-03 | CDK1/CCNB1/E2F8/AURKA/FOXM1 | 5 |
| BP | GO:0007076 | mitotic chromosome condensation | 2/55 | 17/18670 | 1.13E-03 | 8.92E-03 | 6.28E-03 | NUSAP1/NCAPG | 2 |
| BP | GO:0044786 | cell cycle DNA replication | 3/55 | 71/18670 | 1.20E-03 | 9.44E-03 | 6.65E-03 | GINS1/E2F8/CDC7 | 3 |
| BP | GO:0051782 | negative regulation of cell division | 2/55 | 18/18670 | 1.26E-03 | 9.90E-03 | 6.97E-03 | ASPM/E2F8 | 2 |
| BP | GO:0031100 | animal organ regeneration | 3/55 | 73/18670 | 1.30E-03 | 1.01E-02 | 7.13E-03 | CDK1/EZH2/AURKA | 3 |
| BP | GO:0051303 | establishment of chromosome localization | 3/55 | 75/18670 | 1.41E-03 | 1.09E-02 | 7.66E-03 | CCNB1/NDC80/DLGAP5 | 3 |
| BP | GO:0050000 | chromosome localization | 3/55 | 76/18670 | 1.46E-03 | 1.12E-02 | 7.92E-03 | CCNB1/NDC80/DLGAP5 | 3 |
| BP | GO:0021700 | developmental maturation | 5/55 | 284/18670 | 1.47E-03 | 1.12E-02 | 7.92E-03 | SPINK1/CCNB1/CDC20/AURKA/TRIP13 | 5 |
| BP | GO:0021543 | pallium development | 4/55 | 169/18670 | 1.54E-03 | 1.17E-02 | 8.27E-03 | ASPM/ROBO1/FGF13/EZH2 | 4 |
| BP | GO:0008356 | asymmetric cell division | 2/55 | 20/18670 | 1.56E-03 | 1.18E-02 | 8.34E-03 | ASPM/FGF13 | 2 |
| BP | GO:0001933 | negative regulation of protein phosphorylation | 6/55 | 429/18670 | 1.59E-03 | 1.20E-02 | 8.44E-03 | SPINK1/CCNB1/PBK/DKK1/CDKN2C/FOXM1 | 6 |
| BP | GO:0048469 | cell maturation | 4/55 | 177/18670 | 1.83E-03 | 1.37E-02 | 9.64E-03 | SPINK1/CCNB1/AURKA/TRIP13 | 4 |
| BP | GO:0001759 | organ induction | 2/55 | 22/18670 | 1.90E-03 | 1.41E-02 | 9.94E-03 | ROBO1/DKK1 | 2 |
| BP | GO:0006979 | response to oxidative stress | 6/55 | 451/18670 | 2.05E-03 | 1.52E-02 | 1.07E-02 | CDK1/ECT2/LCN2/MELK/EZH2/NQO1 | 6 |
| BP | GO:2000050 | regulation of non-canonical Wnt signaling pathway | 2/55 | 23/18670 | 2.07E-03 | 1.53E-02 | 1.08E-02 | GPC3/DKK1 | 2 |
| BP | GO:0070507 | regulation of microtubule cytoskeleton organization | 4/55 | 186/18670 | 2.19E-03 | 1.60E-02 | 1.13E-02 | NEK2/FGF13/KIF11/AURKA | 4 |
| BP | GO:0051307 | meiotic chromosome separation | 2/55 | 25/18670 | 2.45E-03 | 1.79E-02 | 1.26E-02 | TOP2A/TTK | 2 |
| BP | GO:0042326 | negative regulation of phosphorylation | 6/55 | 468/18670 | 2.46E-03 | 1.79E-02 | 1.26E-02 | SPINK1/CCNB1/PBK/DKK1/CDKN2C/FOXM1 | 6 |
| BP | GO:0050769 | positive regulation of neurogenesis | 6/55 | 474/18670 | 2.63E-03 | 1.89E-02 | 1.33E-02 | ASPM/ROBO1/ECT2/DKK1/EZH2/ITGA6 | 6 |
| BP | GO:0046677 | response to antibiotic | 5/55 | 327/18670 | 2.72E-03 | 1.95E-02 | 1.37E-02 | CDK1/ECT2/LCN2/EZH2/NQO1 | 5 |
| BP | GO:0031099 | regeneration | 4/55 | 198/18670 | 2.74E-03 | 1.96E-02 | 1.38E-02 | CDK1/CCNB1/EZH2/AURKA | 4 |
| BP | GO:0071902 | positive regulation of protein serine/threonine kinase activity | 5/55 | 334/18670 | 2.97E-03 | 2.11E-02 | 1.49E-02 | CDK1/ROBO1/CCNB1/DKK1/EZH2 | 5 |
| BP | GO:0051984 | positive regulation of chromosome segregation | 2/55 | 28/18670 | 3.07E-03 | 2.17E-02 | 1.53E-02 | CCNB1/DLGAP5 | 2 |
| BP | GO:0055024 | regulation of cardiac muscle tissue development | 3/55 | 100/18670 | 3.20E-03 | 2.25E-02 | 1.58E-02 | CDK1/CCNB1/DKK1 | 3 |
| BP | GO:0051642 | centrosome localization | 2/55 | 29/18670 | 3.29E-03 | 2.29E-02 | 1.61E-02 | ASPM/AURKA | 2 |
| BP | GO:0060914 | heart formation | 2/55 | 29/18670 | 3.29E-03 | 2.29E-02 | 1.61E-02 | ROBO1/DKK1 | 2 |
| BP | GO:0010975 | regulation of neuron projection development | 6/55 | 499/18670 | 3.38E-03 | 2.35E-02 | 1.65E-02 | ROBO1/DKK1/FGF13/CDC20/EZH2/ITGA6 | 6 |
| BP | GO:0048384 | retinoic acid receptor signaling pathway | 2/55 | 30/18670 | 3.52E-03 | 2.40E-02 | 1.69E-02 | TRIM16/EZH2 | 2 |
| BP | GO:0061842 | microtubule organizing center localization | 2/55 | 30/18670 | 3.52E-03 | 2.40E-02 | 1.69E-02 | ASPM/AURKA | 2 |
| BP | GO:0097421 | liver regeneration | 2/55 | 30/18670 | 3.52E-03 | 2.40E-02 | 1.69E-02 | EZH2/AURKA | 2 |
| BP | GO:1902750 | negative regulation of cell cycle G2/M phase transition | 3/55 | 105/18670 | 3.67E-03 | 2.49E-02 | 1.76E-02 | CDK1/DTL/AURKA | 3 |
| BP | GO:0002082 | regulation of oxidative phosphorylation | 2/55 | 31/18670 | 3.75E-03 | 2.51E-02 | 1.77E-02 | CDK1/CCNB1 | 2 |
| BP | GO:0031572 | G2 DNA damage checkpoint | 2/55 | 31/18670 | 3.75E-03 | 2.51E-02 | 1.77E-02 | CDK1/DTL | 2 |
| BP | GO:0043457 | regulation of cellular respiration | 2/55 | 31/18670 | 3.75E-03 | 2.51E-02 | 1.77E-02 | CDK1/CCNB1 | 2 |
| BP | GO:0032886 | regulation of microtubule-based process | 4/55 | 218/18670 | 3.87E-03 | 2.58E-02 | 1.82E-02 | NEK2/FGF13/KIF11/AURKA | 4 |
| BP | GO:0006275 | regulation of DNA replication | 3/55 | 108/18670 | 3.97E-03 | 2.63E-02 | 1.85E-02 | CDK1/E2F8/CDC7 | 3 |
| BP | GO:1901976 | regulation of cell cycle checkpoint | 2/55 | 32/18670 | 3.99E-03 | 2.64E-02 | 1.86E-02 | CCNB1/NDC80 | 2 |
| BP | GO:0040001 | establishment of mitotic spindle localization | 2/55 | 33/18670 | 4.24E-03 | 2.79E-02 | 1.96E-02 | NDC80/NUSAP1 | 2 |
| BP | GO:0010092 | specification of animal organ identity | 2/55 | 34/18670 | 4.50E-03 | 2.92E-02 | 2.06E-02 | ROBO1/DKK1 | 2 |
| BP | GO:0031128 | developmental induction | 2/55 | 34/18670 | 4.50E-03 | 2.92E-02 | 2.06E-02 | ROBO1/DKK1 | 2 |
| BP | GO:0021987 | cerebral cortex development | 3/55 | 113/18670 | 4.51E-03 | 2.92E-02 | 2.06E-02 | ASPM/ROBO1/FGF13 | 3 |
| BP | GO:0042752 | regulation of circadian rhythm | 3/55 | 114/18670 | 4.62E-03 | 2.98E-02 | 2.10E-02 | TOP2A/CDK1/EZH2 | 3 |
| BP | GO:0045666 | positive regulation of neuron differentiation | 5/55 | 371/18670 | 4.65E-03 | 2.98E-02 | 2.10E-02 | ROBO1/ECT2/DKK1/EZH2/ITGA6 | 5 |
| BP | GO:0001701 | in utero embryonic development | 5/55 | 373/18670 | 4.75E-03 | 3.04E-02 | 2.14E-02 | CCNB1/GINS1/NEK2/CCNB2/E2F8 | 5 |
| BP | GO:0071695 | anatomical structure maturation | 4/55 | 232/18670 | 4.83E-03 | 3.07E-02 | 2.16E-02 | SPINK1/CCNB1/AURKA/TRIP13 | 4 |
| BP | GO:0046777 | protein autophosphorylation | 4/55 | 235/18670 | 5.05E-03 | 3.20E-02 | 2.25E-02 | NEK2/MELK/TTK/AURKA | 4 |
| BP | GO:0030900 | forebrain development | 5/55 | 381/18670 | 5.20E-03 | 3.28E-02 | 2.31E-02 | ASPM/ROBO1/DKK1/FGF13/EZH2 | 5 |
| BP | GO:0003156 | regulation of animal organ formation | 2/55 | 37/18670 | 5.31E-03 | 3.33E-02 | 2.35E-02 | ROBO1/DKK1 | 2 |
| BP | GO:0060045 | positive regulation of cardiac muscle cell proliferation | 2/55 | 38/18670 | 5.60E-03 | 3.50E-02 | 2.46E-02 | CDK1/CCNB1 | 2 |
| BP | GO:0032506 | cytokinetic process | 2/55 | 39/18670 | 5.89E-03 | 3.65E-02 | 2.57E-02 | ECT2/KIF20A | 2 |
| BP | GO:2000826 | regulation of heart morphogenesis | 2/55 | 39/18670 | 5.89E-03 | 3.65E-02 | 2.57E-02 | ROBO1/DKK1 | 2 |
| BP | GO:0018107 | peptidyl-threonine phosphorylation | 3/55 | 126/18670 | 6.10E-03 | 3.74E-02 | 2.64E-02 | CDK1/TTK/CDC7 | 3 |
| BP | GO:0006302 | double-strand break repair | 4/55 | 248/18670 | 6.10E-03 | 3.74E-02 | 2.64E-02 | RAD51AP1/FOXM1/CDC7/TRIP13 | 4 |
| BP | GO:0021537 | telencephalon development | 4/55 | 249/18670 | 6.18E-03 | 3.76E-02 | 2.65E-02 | ASPM/ROBO1/FGF13/EZH2 | 4 |
| BP | GO:0021795 | cerebral cortex cell migration | 2/55 | 40/18670 | 6.19E-03 | 3.76E-02 | 2.65E-02 | ROBO1/FGF13 | 2 |
| BP | GO:0006997 | nucleus organization | 3/55 | 130/18670 | 6.65E-03 | 4.03E-02 | 2.84E-02 | CDK1/CCNB1/CCNB2 | 3 |
| BP | GO:0017145 | stem cell division | 2/55 | 42/18670 | 6.80E-03 | 4.08E-02 | 2.88E-02 | ASPM/FGF13 | 2 |
| BP | GO:0051154 | negative regulation of striated muscle cell differentiation | 2/55 | 42/18670 | 6.80E-03 | 4.08E-02 | 2.88E-02 | DKK1/EZH2 | 2 |
| BP | GO:0055007 | cardiac muscle cell differentiation | 3/55 | 132/18670 | 6.93E-03 | 4.14E-02 | 2.92E-02 | CDK1/CCNB1/DKK1 | 3 |
| BP | GO:0043406 | positive regulation of MAP kinase activity | 4/55 | 258/18670 | 7.00E-03 | 4.17E-02 | 2.93E-02 | CDK1/ROBO1/DKK1/EZH2 | 4 |
| BP | GO:0051293 | establishment of spindle localization | 2/55 | 43/18670 | 7.12E-03 | 4.22E-02 | 2.97E-02 | NDC80/NUSAP1 | 2 |
| BP | GO:0018210 | peptidyl-threonine modification | 3/55 | 134/18670 | 7.23E-03 | 4.26E-02 | 3.00E-02 | CDK1/TTK/CDC7 | 3 |
| BP | GO:0001889 | liver development | 3/55 | 135/18670 | 7.37E-03 | 4.33E-02 | 3.05E-02 | EZH2/E2F8/AURKA | 3 |
| BP | GO:0007080 | mitotic metaphase plate congression | 2/55 | 44/18670 | 7.45E-03 | 4.36E-02 | 3.07E-02 | CCNB1/NDC80 | 2 |
| BP | GO:0061008 | hepaticobiliary system development | 3/55 | 138/18670 | 7.83E-03 | 4.56E-02 | 3.21E-02 | EZH2/E2F8/AURKA | 3 |
| BP | GO:0007129 | synapsis | 2/55 | 46/18670 | 8.12E-03 | 4.71E-02 | 3.32E-02 | CCNE2/TRIP13 | 2 |
| BP | GO:1903580 | positive regulation of ATP metabolic process | 2/55 | 47/18670 | 8.46E-03 | 4.89E-02 | 3.44E-02 | CDK1/CCNB1 | 2 |
| CC | GO:0005819 | spindle | 16/55 | 347/19717 | 9.58E-16 | 1.19E-13 | 8.07E-14 | ASPM/CDK1/CCNB1/PRC1/ECT2/NEK2/BUB1B/KIF20A/NUSAP1/TTK/DLGAP5/CDC20/KIF4A/KIF11/AURKA/CDC7 | 16 |
| CC | GO:0000779 | condensed chromosome, centromeric region | 9/55 | 118/19717 | 3.65E-11 | 2.26E-09 | 1.54E-09 | CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/NCAPG/BUB1/AURKA | 9 |
| CC | GO:0000775 | chromosome, centromeric region | 10/55 | 193/19717 | 1.28E-10 | 5.04E-09 | 3.42E-09 | CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/NCAPG/TTK/BUB1/AURKA | 10 |
| CC | GO:0098687 | chromosomal region | 12/55 | 347/19717 | 1.63E-10 | 5.04E-09 | 3.42E-09 | CDK1/CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/NCAPG/TTK/EZH2/BUB1/AURKA | 12 |
| CC | GO:0000793 | condensed chromosome | 10/55 | 223/19717 | 5.25E-10 | 1.30E-08 | 8.84E-09 | TOP2A/CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/NCAPG/BUB1/AURKA | 10 |
| CC | GO:0000776 | kinetochore | 8/55 | 135/19717 | 3.64E-09 | 7.52E-08 | 5.11E-08 | CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/TTK/BUB1 | 8 |
| CC | GO:0000780 | condensed nuclear chromosome, centromeric region | 5/55 | 26/19717 | 8.82E-09 | 1.56E-07 | 1.06E-07 | CCNB1/NDC80/BUB1B/BUB1/AURKA | 5 |
| CC | GO:0005876 | spindle microtubule | 6/55 | 59/19717 | 1.43E-08 | 2.09E-07 | 1.42E-07 | CDK1/PRC1/NUSAP1/KIF4A/KIF11/AURKA | 6 |
| CC | GO:0000777 | condensed chromosome kinetochore | 7/55 | 105/19717 | 1.63E-08 | 2.09E-07 | 1.42E-07 | CCNB1/NDC80/NEK2/BUB1B/ZWINT/CENPU/BUB1 | 7 |
| CC | GO:0000922 | spindle pole | 8/55 | 164/19717 | 1.69E-08 | 2.09E-07 | 1.42E-07 | ASPM/CCNB1/PRC1/NEK2/DLGAP5/CDC20/KIF11/AURKA | 8 |
| CC | GO:0072686 | mitotic spindle | 7/55 | 109/19717 | 2.12E-08 | 2.39E-07 | 1.62E-07 | ASPM/CDK1/ECT2/NUSAP1/KIF11/AURKA/CDC7 | 7 |
| CC | GO:0030496 | midbody | 8/55 | 173/19717 | 2.56E-08 | 2.64E-07 | 1.80E-07 | ASPM/CDK1/PRC1/ECT2/NEK2/KIF20A/KIF4A/AURKA | 8 |
| CC | GO:0000940 | condensed chromosome outer kinetochore | 4/55 | 14/19717 | 5.31E-08 | 5.07E-07 | 3.44E-07 | CCNB1/NDC80/BUB1B/BUB1 | 4 |
| CC | GO:0000778 | condensed nuclear chromosome kinetochore | 4/55 | 15/19717 | 7.23E-08 | 6.40E-07 | 4.35E-07 | CCNB1/NDC80/BUB1B/BUB1 | 4 |
| CC | GO:0005874 | microtubule | 10/55 | 416/19717 | 1.97E-07 | 1.63E-06 | 1.10E-06 | ASPM/CDK1/PRC1/NEK2/KIF20A/NUSAP1/FGF13/KIF4A/KIF11/AURKA | 10 |
| CC | GO:0000794 | condensed nuclear chromosome | 6/55 | 99/19717 | 3.27E-07 | 2.53E-06 | 1.72E-06 | CCNB1/NDC80/NEK2/BUB1B/BUB1/AURKA | 6 |
| CC | GO:0000307 | cyclin-dependent protein kinase holoenzyme complex | 4/55 | 42/19717 | 5.61E-06 | 4.09E-05 | 2.78E-05 | CDK1/CCNB1/CCNB2/CCNE2 | 4 |
| CC | GO:1902554 | serine/threonine protein kinase complex | 4/55 | 88/19717 | 1.06E-04 | 7.32E-04 | 4.97E-04 | CDK1/CCNB1/CCNB2/CCNE2 | 4 |
| CC | GO:1902911 | protein kinase complex | 4/55 | 109/19717 | 2.43E-04 | 1.58E-03 | 1.08E-03 | CDK1/CCNB1/CCNB2/CCNE2 | 4 |
| CC | GO:0072687 | meiotic spindle | 2/55 | 11/19717 | 4.13E-04 | 2.56E-03 | 1.74E-03 | ASPM/AURKA | 2 |
| CC | GO:0005871 | kinesin complex | 3/55 | 55/19717 | 4.86E-04 | 2.87E-03 | 1.95E-03 | KIF20A/KIF4A/KIF11 | 3 |
| CC | GO:0045171 | intercellular bridge | 3/55 | 59/19717 | 5.98E-04 | 3.37E-03 | 2.29E-03 | KIF20A/KIF4A/CDC7 | 3 |
| CC | GO:0031616 | spindle pole centrosome | 2/55 | 15/19717 | 7.84E-04 | 4.05E-03 | 2.75E-03 | DLGAP5/AURKA | 2 |
| CC | GO:0045120 | pronucleus | 2/55 | 15/19717 | 7.84E-04 | 4.05E-03 | 2.75E-03 | EZH2/AURKA | 2 |
| CC | GO:0005875 | microtubule associated complex | 4/55 | 152/19717 | 8.53E-04 | 4.23E-03 | 2.87E-03 | KIF20A/KIF4A/KIF11/AURKA | 4 |
| CC | GO:0043073 | germ cell nucleus | 2/55 | 19/19717 | 1.27E-03 | 6.04E-03 | 4.10E-03 | AURKA/TRIP13 | 2 |
| CC | GO:0005680 | anaphase-promoting complex | 2/55 | 21/19717 | 1.55E-03 | 7.12E-03 | 4.84E-03 | BUB1B/CDC20 | 2 |
| CC | GO:0097431 | mitotic spindle pole | 2/55 | 27/19717 | 2.56E-03 | 1.14E-02 | 7.71E-03 | ASPM/AURKA | 2 |
| CC | GO:0061695 | transferase complex, transferring phosphorus-containing groups | 4/55 | 259/19717 | 5.87E-03 | 2.51E-02 | 1.70E-02 | CDK1/CCNB1/CCNB2/CCNE2 | 4 |
| CC | GO:0000152 | nuclear ubiquitin ligase complex | 2/55 | 43/19717 | 6.41E-03 | 2.65E-02 | 1.80E-02 | BUB1B/CDC20 | 2 |
| CC | GO:0031461 | cullin-RING ubiquitin ligase complex | 3/55 | 158/19717 | 9.77E-03 | 3.91E-02 | 2.65E-02 | DTL/BUB1B/CDC20 | 3 |
| CC | GO:0032154 | cleavage furrow | 2/55 | 55/19717 | 1.03E-02 | 4.00E-02 | 2.72E-02 | ECT2/KIF20A | 2 |
| CC | GO:0035580 | specific granule lumen | 2/55 | 62/19717 | 1.30E-02 | 4.88E-02 | 3.31E-02 | LCN2/LYZ | 2 |
| MF | GO:0004674 | protein serine/threonine kinase activity | 9/55 | 439/17696 | 7.58E-06 | 9.49E-04 | 7.89E-04 | CDK1/PBK/NEK2/BUB1B/MELK/TTK/BUB1/AURKA/CDC7 | 9 |
| MF | GO:0016538 | cyclin-dependent protein serine/threonine kinase regulator activity | 4/55 | 49/17696 | 1.59E-05 | 9.49E-04 | 7.89E-04 | CCNB1/CDKN2C/CCNB2/CCNE2 | 4 |
| MF | GO:0035173 | histone kinase activity | 3/55 | 17/17696 | 1.87E-05 | 9.49E-04 | 7.89E-04 | CDK1/CCNB1/AURKA | 3 |
| MF | GO:0008017 | microtubule binding | 6/55 | 246/17696 | 1.11E-04 | 4.23E-03 | 3.52E-03 | PRC1/KIF20A/NUSAP1/FGF13/KIF4A/KIF11 | 6 |
| MF | GO:0019887 | protein kinase regulator activity | 5/55 | 180/17696 | 2.37E-04 | 7.22E-03 | 6.00E-03 | CCNB1/FGF13/CDKN2C/CCNB2/CCNE2 | 5 |
| MF | GO:0019207 | kinase regulator activity | 5/55 | 207/17696 | 4.51E-04 | 1.14E-02 | 9.50E-03 | CCNB1/FGF13/CDKN2C/CCNB2/CCNE2 | 5 |
| MF | GO:0015631 | tubulin binding | 6/55 | 336/17696 | 5.94E-04 | 1.29E-02 | 1.07E-02 | PRC1/KIF20A/NUSAP1/FGF13/KIF4A/KIF11 | 6 |
| MF | GO:0003777 | microtubule motor activity | 3/55 | 84/17696 | 2.27E-03 | 4.30E-02 | 3.58E-02 | KIF20A/KIF4A/KIF11 | 3 |

**Supplementary Table S3. The GO annotation of down-regulated genes**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Oncology | ID | Description | Gene Ratio | Bg Ratio | P. value | P. adjust | Q value | Gene ID | Count |
| BP | GO:0071276 | cellular response to cadmium ion | 8/72 | 37/18670 | 1.16E-12 | 1.51E-09 | 1.24E-09 | MT1M/CYP1A2/MT1F/FOS/MT1G/MT1E/MT1X/MT1H | 8 |
| BP | GO:0008202 | steroid metabolic process | 15/72 | 331/18670 | 1.82E-12 | 1.51E-09 | 1.24E-09 | CYP1A2/AKR1D1/CYP26A1/ESR1/CYP2B6/APOF/CYP2A6/LCAT/CYP2C8/CYP2E1/CYP39A1/RDH16/CETP/ACADL/CYP3A43 | 15 |
| BP | GO:0071280 | cellular response to copper ion | 7/72 | 27/18670 | 7.85E-12 | 4.30E-09 | 3.52E-09 | MT1M/CYP1A2/MT1F/MT1G/MT1E/MT1X/MT1H | 7 |
| BP | GO:0010273 | detoxification of copper ion | 6/72 | 15/18670 | 1.29E-11 | 4.30E-09 | 3.52E-09 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:1990169 | stress response to copper ion | 6/72 | 15/18670 | 1.29E-11 | 4.30E-09 | 3.52E-09 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0061687 | detoxification of inorganic compound | 6/72 | 17/18670 | 3.18E-11 | 7.55E-09 | 6.18E-09 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0097501 | stress response to metal ion | 6/72 | 17/18670 | 3.18E-11 | 7.55E-09 | 6.18E-09 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0046686 | response to cadmium ion | 8/72 | 63/18670 | 1.07E-10 | 2.23E-08 | 1.82E-08 | MT1M/CYP1A2/MT1F/FOS/MT1G/MT1E/MT1X/MT1H | 8 |
| BP | GO:0071248 | cellular response to metal ion | 11/72 | 188/18670 | 1.43E-10 | 2.63E-08 | 2.15E-08 | MT1M/CYP1A2/CRHBP/MT1F/FOS/MT1G/FBP1/MT1E/MT1X/MT1H/ANK3 | 11 |
| BP | GO:0046688 | response to copper ion | 7/72 | 42/18670 | 2.28E-10 | 3.79E-08 | 3.10E-08 | MT1M/CYP1A2/MT1F/MT1G/MT1E/MT1X/MT1H | 7 |
| BP | GO:0071294 | cellular response to zinc ion | 6/72 | 23/18670 | 2.55E-10 | 3.85E-08 | 3.15E-08 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0071241 | cellular response to inorganic substance | 11/72 | 215/18670 | 5.97E-10 | 8.27E-08 | 6.77E-08 | MT1M/CYP1A2/CRHBP/MT1F/FOS/MT1G/FBP1/MT1E/MT1X/MT1H/ANK3 | 11 |
| BP | GO:0071466 | cellular response to xenobiotic stimulus | 10/72 | 180/18670 | 1.73E-09 | 2.21E-07 | 1.81E-07 | CYP1A2/CRHBP/CYP26A1/CYP2B6/CYP2A6/GHR/NAT2/CYP2C8/CYP2E1/PCK1 | 10 |
| BP | GO:0006882 | cellular zinc ion homeostasis | 6/72 | 36/18670 | 4.73E-09 | 5.61E-07 | 4.59E-07 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0055069 | zinc ion homeostasis | 6/72 | 38/18670 | 6.66E-09 | 7.37E-07 | 6.04E-07 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0019373 | epoxygenase P450 pathway | 5/72 | 20/18670 | 1.10E-08 | 1.14E-06 | 9.33E-07 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1 | 5 |
| BP | GO:0006805 | xenobiotic metabolic process | 8/72 | 125/18670 | 2.69E-08 | 2.63E-06 | 2.15E-06 | CYP1A2/CYP26A1/CYP2B6/CYP2A6/GHR/NAT2/CYP2C8/CYP2E1 | 8 |
| BP | GO:0042738 | exogenous drug catabolic process | 5/72 | 24/18670 | 2.97E-08 | 2.74E-06 | 2.25E-06 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1 | 5 |
| BP | GO:0010043 | response to zinc ion | 6/72 | 53/18670 | 5.29E-08 | 4.63E-06 | 3.79E-06 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0046394 | carboxylic acid biosynthetic process | 11/72 | 355/18670 | 1.08E-07 | 8.78E-06 | 7.19E-06 | CYP1A2/AKR1D1/DCN/CYP2C8/ASPA/CYP2E1/CYP39A1/KMO/HPGD/ACADL/BHMT | 11 |
| BP | GO:0016053 | organic acid biosynthetic process | 11/72 | 356/18670 | 1.11E-07 | 8.78E-06 | 7.19E-06 | CYP1A2/AKR1D1/DCN/CYP2C8/ASPA/CYP2E1/CYP39A1/KMO/HPGD/ACADL/BHMT | 11 |
| BP | GO:0010038 | response to metal ion | 11/72 | 362/18670 | 1.31E-07 | 9.92E-06 | 8.12E-06 | MT1M/CYP1A2/CRHBP/MT1F/FOS/MT1G/FBP1/MT1E/MT1X/MT1H/ANK3 | 11 |
| BP | GO:0009410 | response to xenobiotic stimulus | 10/72 | 292/18670 | 1.71E-07 | 1.24E-05 | 1.01E-05 | CYP1A2/CRHBP/CYP26A1/CYP2B6/CYP2A6/GHR/NAT2/CYP2C8/CYP2E1/PCK1 | 10 |
| BP | GO:0001676 | long-chain fatty acid metabolic process | 7/72 | 109/18670 | 2.05E-07 | 1.42E-05 | 1.16E-05 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/HPGD/ACADL | 7 |
| BP | GO:0072330 | monocarboxylic acid biosynthetic process | 9/72 | 237/18670 | 3.12E-07 | 2.08E-05 | 1.70E-05 | CYP1A2/AKR1D1/DCN/CYP2C8/CYP2E1/CYP39A1/KMO/HPGD/ACADL | 9 |
| BP | GO:0045926 | negative regulation of growth | 9/72 | 249/18670 | 4.73E-07 | 3.02E-05 | 2.47E-05 | MT1M/MT1F/MT1G/FBP1/MT1E/MT1X/MT1H/PLAC8/SOCS2 | 9 |
| BP | GO:0006066 | alcohol metabolic process | 10/72 | 370/18670 | 1.49E-06 | 8.99E-05 | 7.36E-05 | CYP1A2/AKR1D1/APOF/IGF1/LCAT/CYP39A1/RDH16/PCK1/CETP/ACADL | 10 |
| BP | GO:0019369 | arachidonic acid metabolic process | 5/72 | 51/18670 | 1.52E-06 | 8.99E-05 | 7.36E-05 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1 | 5 |
| BP | GO:0016125 | sterol metabolic process | 7/72 | 166/18670 | 3.51E-06 | 0.000201 | 0.000165 | AKR1D1/CYP26A1/APOF/LCAT/CYP39A1/CETP/ACADL | 7 |
| BP | GO:0033559 | unsaturated fatty acid metabolic process | 6/72 | 110/18670 | 4.15E-06 | 0.000223 | 0.000182 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/HPGD | 6 |
| BP | GO:0046916 | cellular transition metal ion homeostasis | 6/72 | 110/18670 | 4.15E-06 | 0.000223 | 0.000182 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0006690 | icosanoid metabolic process | 6/72 | 114/18670 | 5.11E-06 | 0.00026 | 0.000213 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/HPGD | 6 |
| BP | GO:0042759 | long-chain fatty acid biosynthetic process | 4/72 | 30/18670 | 5.16E-06 | 0.00026 | 0.000213 | CYP1A2/CYP2C8/CYP2E1/HPGD | 4 |
| BP | GO:0040014 | regulation of multicellular organism growth | 5/72 | 66/18670 | 5.51E-06 | 0.000269 | 0.000221 | GHR/IGF1/PLAC8/NPY1R/SOCS2 | 5 |
| BP | GO:0034754 | cellular hormone metabolic process | 6/72 | 129/18670 | 1.04E-05 | 0.000476 | 0.00039 | CYP1A2/AKR1D1/CYP26A1/ESR1/CYP2C8/RDH16 | 6 |
| BP | GO:0016054 | organic acid catabolic process | 8/72 | 275/18670 | 1.06E-05 | 0.000476 | 0.00039 | AKR1D1/CYP26A1/IDO2/ASPA/CYP39A1/KMO/PCK1/ACADL | 8 |
| BP | GO:0046395 | carboxylic acid catabolic process | 8/72 | 275/18670 | 1.06E-05 | 0.000476 | 0.00039 | AKR1D1/CYP26A1/IDO2/ASPA/CYP39A1/KMO/PCK1/ACADL | 8 |
| BP | GO:0055076 | transition metal ion homeostasis | 6/72 | 133/18670 | 1.24E-05 | 0.000542 | 0.000444 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0098754 | detoxification | 6/72 | 137/18670 | 1.47E-05 | 0.000625 | 0.000512 | MT1M/MT1F/MT1G/MT1E/MT1X/MT1H | 6 |
| BP | GO:0042737 | drug catabolic process | 6/72 | 140/18670 | 1.66E-05 | 0.00069 | 0.000565 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/PCK1 | 6 |
| BP | GO:0008203 | cholesterol metabolic process | 6/72 | 150/18670 | 2.46E-05 | 0.000995 | 0.000815 | AKR1D1/APOF/LCAT/CYP39A1/CETP/ACADL | 6 |
| BP | GO:0042445 | hormone metabolic process | 7/72 | 233/18670 | 3.19E-05 | 0.00126 | 0.001032 | CYP1A2/AKR1D1/CYP26A1/ESR1/GHR/CYP2C8/RDH16 | 7 |
| BP | GO:0006577 | amino-acid betaine metabolic process | 3/72 | 17/18670 | 3.60E-05 | 0.001381 | 0.001131 | BBOX1/ACADL/BHMT | 3 |
| BP | GO:1902652 | secondary alcohol metabolic process | 6/72 | 161/18670 | 3.66E-05 | 0.001381 | 0.001131 | AKR1D1/APOF/LCAT/CYP39A1/CETP/ACADL | 6 |
| BP | GO:1901568 | fatty acid derivative metabolic process | 6/72 | 167/18670 | 4.49E-05 | 0.001657 | 0.001357 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/HPGD | 6 |
| BP | GO:0070989 | oxidative demethylation | 3/72 | 19/18670 | 5.10E-05 | 0.001822 | 0.001492 | CYP1A2/CYP2C8/CYP3A43 | 3 |
| BP | GO:0044282 | small molecule catabolic process | 9/72 | 445/18670 | 5.16E-05 | 0.001822 | 0.001492 | AKR1D1/CYP26A1/IDO2/ALDOB/ASPA/CYP39A1/KMO/PCK1/ACADL | 9 |
| BP | GO:0006956 | complement activation | 6/72 | 175/18670 | 5.83E-05 | 0.002016 | 0.001651 | FCN3/C9/C7/FCN2/C6/CD5L | 6 |
| BP | GO:0015850 | organic hydroxy compound transport | 7/72 | 262/18670 | 6.70E-05 | 0.00227 | 0.001859 | SLCO1B3/SLC22A1/LCAT/CXCL12/SLC10A1/GRAMD1C/CETP | 7 |
| BP | GO:0042402 | cellular biogenic amine catabolic process | 3/72 | 21/18670 | 6.96E-05 | 0.002312 | 0.001893 | IDO2/KMO/BHMT | 3 |
| BP | GO:0009310 | amine catabolic process | 3/72 | 23/18670 | 9.21E-05 | 0.003001 | 0.002457 | IDO2/KMO/BHMT | 3 |
| BP | GO:0006721 | terpenoid metabolic process | 5/72 | 120/18670 | 0.0001 | 0.003197 | 0.002618 | CYP1A2/CYP26A1/CYP2C8/CYP2E1/RDH16 | 5 |
| BP | GO:0006631 | fatty acid metabolic process | 8/72 | 383/18670 | 0.000111 | 0.003479 | 0.002848 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/PCK1/HPGD/ACADL | 8 |
| BP | GO:0042537 | benzene-containing compound metabolic process | 3/72 | 25/18670 | 0.000119 | 0.003661 | 0.002997 | IDO2/CYP2E1/KMO | 3 |
| BP | GO:0006006 | glucose metabolic process | 6/72 | 204/18670 | 0.000136 | 0.004095 | 0.003353 | ALDOB/GNMT/IGF1/FBP1/PCK1/NPY1R | 6 |
| BP | GO:0006706 | steroid catabolic process | 3/72 | 27/18670 | 0.000151 | 0.004393 | 0.003597 | CYP1A2/AKR1D1/CYP39A1 | 3 |
| BP | GO:0016051 | carbohydrate biosynthetic process | 6/72 | 208/18670 | 0.000151 | 0.004393 | 0.003597 | GYS2/ALDOB/GNMT/IGF1/FBP1/PCK1 | 6 |
| BP | GO:0070988 | demethylation | 4/72 | 70/18670 | 0.000154 | 0.004405 | 0.003607 | CYP1A2/CYP2C8/KDM8/CYP3A43 | 4 |
| BP | GO:0072329 | monocarboxylic acid catabolic process | 5/72 | 132/18670 | 0.000157 | 0.004413 | 0.003613 | AKR1D1/CYP26A1/CYP39A1/PCK1/ACADL | 5 |
| BP | GO:0032355 | response to estradiol | 5/72 | 134/18670 | 0.000168 | 0.004655 | 0.003812 | CYP1A2/CRHBP/ESR1/HPGD/SOCS2 | 5 |
| BP | GO:0006720 | isoprenoid metabolic process | 5/72 | 139/18670 | 0.0002 | 0.005433 | 0.004449 | CYP1A2/CYP26A1/CYP2C8/CYP2E1/RDH16 | 5 |
| BP | GO:0035264 | multicellular organism growth | 5/72 | 146/18670 | 0.000251 | 0.006717 | 0.0055 | GHR/IGF1/PLAC8/NPY1R/SOCS2 | 5 |
| BP | GO:0006094 | gluconeogenesis | 4/72 | 82/18670 | 0.000283 | 0.007471 | 0.006117 | ALDOB/GNMT/FBP1/PCK1 | 4 |
| BP | GO:0016042 | lipid catabolic process | 7/72 | 333/18670 | 0.000294 | 0.007632 | 0.006249 | CYP1A2/AKR1D1/CYP26A1/GBA3/CYP39A1/PCK1/ACADL | 7 |
| BP | GO:0019319 | hexose biosynthetic process | 4/72 | 85/18670 | 0.000325 | 0.00831 | 0.006804 | ALDOB/GNMT/FBP1/PCK1 | 4 |
| BP | GO:0034637 | cellular carbohydrate biosynthetic process | 4/72 | 86/18670 | 0.00034 | 0.008558 | 0.007007 | GYS2/IGF1/FBP1/PCK1 | 4 |
| BP | GO:0019318 | hexose metabolic process | 6/72 | 244/18670 | 0.000356 | 0.008831 | 0.00723 | ALDOB/GNMT/IGF1/FBP1/PCK1/NPY1R | 6 |
| BP | GO:0046364 | monosaccharide biosynthetic process | 4/72 | 91/18670 | 0.000422 | 0.010304 | 0.008437 | ALDOB/GNMT/FBP1/PCK1 | 4 |
| BP | GO:0006633 | fatty acid biosynthetic process | 5/72 | 164/18670 | 0.000428 | 0.010309 | 0.008441 | CYP1A2/CYP2C8/CYP2E1/HPGD/ACADL | 5 |
| BP | GO:0019835 | cytolysis | 3/72 | 40/18670 | 0.00049 | 0.011638 | 0.009529 | C9/C7/C6 | 3 |
| BP | GO:0072503 | cellular divalent inorganic cation homeostasis | 8/72 | 493/18670 | 0.000608 | 0.014213 | 0.011638 | MT1M/MT1F/ESR1/MT1G/CXCL12/MT1E/MT1X/MT1H | 8 |
| BP | GO:0006569 | tryptophan catabolic process | 2/72 | 10/18670 | 0.000647 | 0.014327 | 0.011731 | IDO2/KMO | 2 |
| BP | GO:0030388 | fructose 1,6-bisphosphate metabolic process | 2/72 | 10/18670 | 0.000647 | 0.014327 | 0.011731 | ALDOB/FBP1 | 2 |
| BP | GO:0042436 | indole-containing compound catabolic process | 2/72 | 10/18670 | 0.000647 | 0.014327 | 0.011731 | IDO2/KMO | 2 |
| BP | GO:0046218 | indolalkylamine catabolic process | 2/72 | 10/18670 | 0.000647 | 0.014327 | 0.011731 | IDO2/KMO | 2 |
| BP | GO:0001523 | retinoid metabolic process | 4/72 | 104/18670 | 0.000699 | 0.015275 | 0.012507 | CYP1A2/CYP26A1/CYP2C8/RDH16 | 4 |
| BP | GO:0043277 | apoptotic cell clearance | 3/72 | 46/18670 | 0.000741 | 0.015988 | 0.013091 | FCN3/FCN2/MARCO | 3 |
| BP | GO:0044262 | cellular carbohydrate metabolic process | 6/72 | 282/18670 | 0.000763 | 0.016255 | 0.013309 | GYS2/GBA3/GNMT/IGF1/FBP1/PCK1 | 6 |
| BP | GO:0040015 | negative regulation of multicellular organism growth | 2/72 | 11/18670 | 0.000789 | 0.016316 | 0.01336 | PLAC8/SOCS2 | 2 |
| BP | GO:0070189 | kynurenine metabolic process | 2/72 | 11/18670 | 0.000789 | 0.016316 | 0.01336 | IDO2/KMO | 2 |
| BP | GO:0006575 | cellular modified amino acid metabolic process | 5/72 | 188/18670 | 0.000796 | 0.016316 | 0.01336 | BBOX1/GNMT/VNN1/ACADL/BHMT | 5 |
| BP | GO:0005996 | monosaccharide metabolic process | 6/72 | 287/18670 | 0.000836 | 0.01694 | 0.01387 | ALDOB/GNMT/IGF1/FBP1/PCK1/NPY1R | 6 |
| BP | GO:0016101 | diterpenoid metabolic process | 4/72 | 110/18670 | 0.000862 | 0.017259 | 0.014131 | CYP1A2/CYP26A1/CYP2C8/RDH16 | 4 |
| BP | GO:0006568 | tryptophan metabolic process | 2/72 | 12/18670 | 0.000944 | 0.018234 | 0.01493 | IDO2/KMO | 2 |
| BP | GO:0034372 | very-low-density lipoprotein particle remodeling | 2/72 | 12/18670 | 0.000944 | 0.018234 | 0.01493 | LCAT/CETP | 2 |
| BP | GO:1904181 | positive regulation of membrane depolarization | 2/72 | 12/18670 | 0.000944 | 0.018234 | 0.01493 | DCN/ANK3 | 2 |
| BP | GO:0009066 | aspartate family amino acid metabolic process | 3/72 | 51/18670 | 0.001003 | 0.019146 | 0.015677 | GNMT/ASPA/BHMT | 3 |
| BP | GO:0030449 | regulation of complement activation | 4/72 | 115/18670 | 0.001018 | 0.019213 | 0.015732 | C9/C7/C6/CD5L | 4 |
| BP | GO:0001867 | complement activation, lectin pathway | 2/72 | 13/18670 | 0.001113 | 0.020094 | 0.016452 | FCN3/FCN2 | 2 |
| BP | GO:0006707 | cholesterol catabolic process | 2/72 | 13/18670 | 0.001113 | 0.020094 | 0.016452 | AKR1D1/CYP39A1 | 2 |
| BP | GO:0009437 | carnitine metabolic process | 2/72 | 13/18670 | 0.001113 | 0.020094 | 0.016452 | BBOX1/ACADL | 2 |
| BP | GO:0016127 | sterol catabolic process | 2/72 | 13/18670 | 0.001113 | 0.020094 | 0.016452 | AKR1D1/CYP39A1 | 2 |
| BP | GO:1901605 | alpha-amino acid metabolic process | 5/72 | 204/18670 | 0.001146 | 0.020474 | 0.016763 | IDO2/GNMT/ASPA/KMO/BHMT | 5 |
| BP | GO:0046718 | viral entry into host cell | 4/72 | 121/18670 | 0.001229 | 0.021723 | 0.017787 | FCN3/CLEC4G/CLEC4M/SLC10A1 | 4 |
| BP | GO:0006576 | cellular biogenic amine metabolic process | 3/72 | 55/18670 | 0.00125 | 0.021847 | 0.017888 | IDO2/KMO/BHMT | 3 |
| BP | GO:0034370 | triglyceride-rich lipoprotein particle remodeling | 2/72 | 14/18670 | 0.001295 | 0.022179 | 0.01816 | LCAT/CETP | 2 |
| BP | GO:0071391 | cellular response to estrogen stimulus | 2/72 | 14/18670 | 0.001295 | 0.022179 | 0.01816 | CRHBP/ESR1 | 2 |
| BP | GO:0006000 | fructose metabolic process | 2/72 | 15/18670 | 0.001491 | 0.025267 | 0.020688 | ALDOB/FBP1 | 2 |
| BP | GO:0006555 | methionine metabolic process | 2/72 | 16/18670 | 0.001699 | 0.028113 | 0.023019 | GNMT/BHMT | 2 |
| BP | GO:0006957 | complement activation, alternative pathway | 2/72 | 16/18670 | 0.001699 | 0.028113 | 0.023019 | C9/C7 | 2 |
| BP | GO:0032496 | response to lipopolysaccharide | 6/72 | 330/18670 | 0.001709 | 0.028113 | 0.023019 | CYP1A2/DCN/FOS/KMO/PCK1/HPGD | 6 |
| BP | GO:0002920 | regulation of humoral immune response | 4/72 | 134/18670 | 0.00179 | 0.028861 | 0.023631 | C9/C7/C6/CD5L | 4 |
| BP | GO:0044409 | entry into host | 4/72 | 134/18670 | 0.00179 | 0.028861 | 0.023631 | FCN3/CLEC4G/CLEC4M/SLC10A1 | 4 |
| BP | GO:0006586 | indolalkylamine metabolic process | 2/72 | 17/18670 | 0.001921 | 0.030685 | 0.025124 | IDO2/KMO | 2 |
| BP | GO:0097305 | response to alcohol | 5/72 | 233/18670 | 0.002057 | 0.032536 | 0.02664 | CRHBP/FOS/CYP2E1/GRAMD1C/HPGD | 5 |
| BP | GO:0002237 | response to molecule of bacterial origin | 6/72 | 343/18670 | 0.002076 | 0.032536 | 0.02664 | CYP1A2/DCN/FOS/KMO/PCK1/HPGD | 6 |
| BP | GO:0034375 | high-density lipoprotein particle remodeling | 2/72 | 18/18670 | 0.002156 | 0.032855 | 0.026901 | LCAT/CETP | 2 |
| BP | GO:0060749 | mammary gland alveolus development | 2/72 | 18/18670 | 0.002156 | 0.032855 | 0.026901 | ESR1/SOCS2 | 2 |
| BP | GO:0061377 | mammary gland lobule development | 2/72 | 18/18670 | 0.002156 | 0.032855 | 0.026901 | ESR1/SOCS2 | 2 |
| BP | GO:0048638 | regulation of developmental growth | 6/72 | 347/18670 | 0.0022 | 0.033227 | 0.027206 | GHR/IGF1/CXCL12/PLAC8/NPY1R/SOCS2 | 6 |
| BP | GO:0030258 | lipid modification | 5/72 | 238/18670 | 0.002256 | 0.033759 | 0.027641 | LCAT/CYP2C8/CYP2E1/ACADL/SOCS2 | 5 |
| BP | GO:0032026 | response to magnesium ion | 2/72 | 19/18670 | 0.002404 | 0.035332 | 0.02893 | FBP1/ANK3 | 2 |
| BP | GO:0090201 | negative regulation of release of cytochrome c from mitochondria | 2/72 | 19/18670 | 0.002404 | 0.035332 | 0.02893 | HGF/IGF1 | 2 |
| BP | GO:0006959 | humoral immune response | 6/72 | 356/18670 | 0.0025 | 0.036426 | 0.029825 | FCN3/C9/C7/FCN2/C6/CD5L | 6 |
| BP | GO:0042180 | cellular ketone metabolic process | 5/72 | 246/18670 | 0.002603 | 0.037594 | 0.030781 | CYP2B6/IDO2/KMO/ACADL/BHMT | 5 |
| BP | GO:0043691 | reverse cholesterol transport | 2/72 | 20/18670 | 0.002664 | 0.038148 | 0.031235 | LCAT/CETP | 2 |
| BP | GO:0006090 | pyruvate metabolic process | 4/72 | 150/18670 | 0.002696 | 0.03828 | 0.031343 | ALDOB/IGF1/FBP1/PCK1 | 4 |
| BP | GO:0005977 | glycogen metabolic process | 3/72 | 74/18670 | 0.00293 | 0.041246 | 0.033772 | GYS2/GNMT/IGF1 | 3 |
| BP | GO:0006073 | cellular glucan metabolic process | 3/72 | 75/18670 | 0.003044 | 0.042133 | 0.034498 | GYS2/GNMT/IGF1 | 3 |
| BP | GO:0044042 | glucan metabolic process | 3/72 | 75/18670 | 0.003044 | 0.042133 | 0.034498 | GYS2/GNMT/IGF1 | 3 |
| BP | GO:0052126 | movement in host environment | 4/72 | 158/18670 | 0.00325 | 0.044619 | 0.036533 | FCN3/CLEC4G/CLEC4M/SLC10A1 | 4 |
| BP | GO:0006869 | lipid transport | 6/72 | 380/18670 | 0.00345 | 0.046966 | 0.038455 | SLCO1B3/APOF/LCAT/SLC10A1/GRAMD1C/CETP | 6 |
| CC | GO:0072562 | blood microparticle | 6/73 | 147/19717 | 1.75E-05 | 0.002029 | 0.001842 | FCN3/C9/FCN2/CD5L/AFM/CFHR3 | 6 |
| CC | GO:0046930 | pore complex | 3/73 | 23/19717 | 8.18E-05 | 0.004604 | 0.004178 | C9/C7/C6 | 3 |
| CC | GO:0034364 | high-density lipoprotein particle | 3/73 | 26/19717 | 0.000119 | 0.004604 | 0.004178 | APOF/LCAT/CETP | 3 |
| CC | GO:0005581 | collagen trimer | 4/73 | 87/19717 | 0.000305 | 0.006682 | 0.006063 | FCN3/DCN/FCN2/MARCO | 4 |
| CC | GO:0034358 | plasma lipoprotein particle | 3/73 | 37/19717 | 0.000346 | 0.006682 | 0.006063 | APOF/LCAT/CETP | 3 |
| CC | GO:1990777 | lipoprotein particle | 3/73 | 37/19717 | 0.000346 | 0.006682 | 0.006063 | APOF/LCAT/CETP | 3 |
| CC | GO:0032994 | protein-lipid complex | 3/73 | 39/19717 | 0.000404 | 0.006701 | 0.006081 | APOF/LCAT/CETP | 3 |
| CC | GO:0016323 | basolateral plasma membrane | 5/73 | 217/19717 | 0.001262 | 0.018296 | 0.016603 | SLCO1B3/SLC22A1/SLC10A1/HPGD/ANK3 | 5 |
| MF | GO:0016705 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 12/70 | 159/17696 | 1.24E-12 | 3.26E-10 | 2.48E-10 | CYP1A2/AKR1D1/CYP26A1/CYP2B6/CYP2A6/BBOX1/CYP2C8/CYP2E1/CYP39A1/KMO/KDM8/CYP3A43 | 12 |
| MF | GO:0004497 | monooxygenase activity | 10/70 | 99/17696 | 5.67E-12 | 7.48E-10 | 5.70E-10 | CYP1A2/AKR1D1/CYP26A1/CYP2B6/CYP2A6/CYP2C8/CYP2E1/CYP39A1/KMO/CYP3A43 | 10 |
| MF | GO:0008395 | steroid hydroxylase activity | 7/70 | 38/17696 | 1.28E-10 | 1.12E-08 | 8.55E-09 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/CYP39A1/CYP3A43 | 7 |
| MF | GO:0016712 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | 6/70 | 32/17696 | 2.57E-09 | 1.55E-07 | 1.18E-07 | CYP1A2/CYP2B6/CYP2A6/CYP2C8/CYP2E1/CYP3A43 | 6 |
| MF | GO:0020037 | heme binding | 9/70 | 135/17696 | 2.93E-09 | 1.55E-07 | 1.18E-07 | CYP1A2/CYP26A1/CYP2B6/CYP2A6/IDO2/CYP2C8/CYP2E1/CYP39A1/CYP3A43 | 9 |
| MF | GO:0046906 | tetrapyrrole binding | 9/70 | 145/17696 | 5.52E-09 | 2.43E-07 | 1.85E-07 | CYP1A2/CYP26A1/CYP2B6/CYP2A6/IDO2/CYP2C8/CYP2E1/CYP39A1/CYP3A43 | 9 |
| MF | GO:0005506 | iron ion binding | 9/70 | 152/17696 | 8.35E-09 | 3.15E-07 | 2.40E-07 | CYP1A2/CYP26A1/CYP2B6/CYP2A6/BBOX1/CYP2C8/CYP2E1/CYP39A1/CYP3A43 | 9 |
| MF | GO:0008392 | arachidonic acid epoxygenase activity | 4/70 | 16/17696 | 3.94E-07 | 1.30E-05 | 9.91E-06 | CYP2B6/CYP2A6/CYP2C8/CYP2E1 | 4 |
| MF | GO:0008391 | arachidonic acid monooxygenase activity | 4/70 | 17/17696 | 5.14E-07 | 1.51E-05 | 1.15E-05 | CYP2B6/CYP2A6/CYP2C8/CYP2E1 | 4 |
| MF | GO:0016725 | oxidoreductase activity, acting on CH or CH2 groups | 3/70 | 13/17696 | 1.65E-05 | 0.000399 | 0.000304 | CYP1A2/CYP2C8/CYP3A43 | 3 |
| MF | GO:0016709 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen | 4/70 | 39/17696 | 1.66E-05 | 0.000399 | 0.000304 | AKR1D1/CYP26A1/CYP2E1/KMO | 4 |
| MF | GO:0005496 | steroid binding | 5/70 | 95/17696 | 3.68E-05 | 0.00081 | 0.000617 | AKR1D1/ESR1/APOF/GRAMD1C/CETP | 5 |
| MF | GO:0030246 | carbohydrate binding | 7/70 | 271/17696 | 9.62E-05 | 0.001954 | 0.001488 | FCN3/CLEC4G/CLEC4M/ALDOB/FBP1/FCN2/ZG16 | 7 |
| MF | GO:0005319 | lipid transporter activity | 5/70 | 131/17696 | 0.00017 | 0.003197 | 0.002434 | SLCO1B3/APOF/SLC10A1/GRAMD1C/CETP | 5 |
| MF | GO:1901618 | organic hydroxy compound transmembrane transporter activity | 3/70 | 44/17696 | 0.000699 | 0.012301 | 0.009368 | SLCO1B3/SLC22A1/SLC10A1 | 3 |
| MF | GO:0015485 | cholesterol binding | 3/70 | 49/17696 | 0.000959 | 0.015818 | 0.012046 | APOF/GRAMD1C/CETP | 3 |
| MF | GO:0032934 | sterol binding | 3/70 | 56/17696 | 0.001414 | 0.02196 | 0.016724 | APOF/GRAMD1C/CETP | 3 |
| MF | GO:0005159 | insulin-like growth factor receptor binding | 2/70 | 16/17696 | 0.001786 | 0.026192 | 0.019947 | IGF1/SOCS2 | 2 |
| MF | GO:0015125 | bile acid transmembrane transporter activity | 2/70 | 17/17696 | 0.002019 | 0.02805 | 0.021362 | SLCO1B3/SLC10A1 | 2 |
| MF | GO:0120020 | cholesterol transfer activity | 2/70 | 18/17696 | 0.002265 | 0.029902 | 0.022772 | GRAMD1C/CETP | 2 |
| MF | GO:0120015 | sterol transfer activity | 2/70 | 19/17696 | 0.002525 | 0.031747 | 0.024177 | GRAMD1C/CETP | 2 |
| MF | GO:0033218 | amide binding | 6/70 | 356/17696 | 0.002823 | 0.03388 | 0.025802 | CRHBP/CLEC4M/GHR/GNMT/MARCO/ACADL | 6 |
| MF | GO:0001618 | virus receptor activity | 3/70 | 74/17696 | 0.003143 | 0.03448 | 0.026259 | CLEC4G/CLEC4M/SLC10A1 | 3 |
| MF | GO:0140272 | exogenous protein binding | 3/70 | 74/17696 | 0.003143 | 0.03448 | 0.026259 | CLEC4G/CLEC4M/SLC10A1 | 3 |
| MF | GO:0048029 | monosaccharide binding | 3/70 | 75/17696 | 0.003265 | 0.03448 | 0.026259 | CLEC4M/ALDOB/FBP1 | 3 |
| MF | GO:0030247 | polysaccharide binding | 2/70 | 25/17696 | 0.004363 | 0.044302 | 0.033739 | CLEC4G/FCN2 | 2 |
| MF | GO:0043178 | alcohol binding | 3/70 | 85/17696 | 0.004644 | 0.045404 | 0.034578 | APOF/GRAMD1C/CETP | 3 |
| MF | GO:0016702 | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | 2/70 | 27/17696 | 0.005079 | 0.047887 | 0.036469 | IDO2/BBOX1 | 2 |
| MF | GO:0016701 | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | 2/70 | 28/17696 | 0.005456 | 0.049422 | 0.037638 | IDO2/BBOX1 | 2 |
| MF | GO:0051213 | dioxygenase activity | 3/70 | 91/17696 | 0.005616 | 0.049422 | 0.037638 | IDO2/BBOX1/KDM8 | 3 |

**Supplementary Table S4. Primer list**

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| --- | --- |
| Name | Sequence |
| m-Cdk11-F | 5’-AGGTACTTACGGTGTGGTGTAT-3’ |
| m-Cdk1-R | 5’-CTCGCTTTCAAGTCTGATCTTCT-3’ |
| m-Foxm1-F | 5’-ATCGCTACTTGACATTGGACCA-3’ |
| m-Foxm1-R | 5’-GATTGGGTCGTTTCTGCTGTG-3’ |
| m-Actin-F | 5’-AGAGGGAAATCGTGCGTGAC-3’ |
| m-Actin-R | 5’-CAATAGTGATGACCTGGCCGT-3’ |