**Supplementary Table 4.** Functional enrichment analysis of genes negatively related to TK2 in cervical cancer

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Category** | **Description** | **GeneRatio** | **p.adjust** | **q-value** | **Count** |
| GO:0010948 | BP | negative regulation of cell cycle process | 31/358 | 6.72E-09 | 5.48E-09 | 31 |
| GO:0008544 | BP | epidermis development | 35/358 | 6.72E-09 | 5.48E-09 | 35 |
| GO:1901988 | BP | negative regulation of cell cycle phase transition | 26/358 | 1.27E-08 | 1.03E-08 | 26 |
| GO:0043588 | BP | skin development | 32/358 | 1.77E-08 | 1.44E-08 | 32 |
| GO:1901991 | BP | negative regulation of mitotic cell cycle phase transition | 24/358 | 5.06E-08 | 4.13E-08 | 24 |
| GO:0098687 | CC | chromosomal region | 26/365 | 8.72E-07 | 7.12E-07 | 26 |
| GO:0030057 | CC | desmosome | 8/365 | 2.55E-06 | 2.08E-06 | 8 |
| GO:0005911 | CC | cell-cell junction | 28/365 | 2.21E-05 | 1.80E-05 | 28 |
| GO:0071162 | CC | CMG complex | 5/365 | 5.83E-05 | 4.75E-05 | 5 |
| GO:0000775 | CC | chromosome, centromeric region | 16/365 | 8.26E-05 | 6.74E-05 | 16 |
| GO:0045296 | MF | cadherin binding | 22/362 | 0.00049 | 0.000429 | 22 |
| GO:0044183 | MF | protein folding chaperone | 6/362 | 0.020215 | 0.01768 | 6 |
| GO:0003697 | MF | single-stranded DNA binding | 10/362 | 0.020375 | 0.01782 | 10 |
| GO:0005149 | MF | interleukin-1 receptor binding | 4/362 | 0.039694 | 0.034716 | 4 |
| GO:0017116 | MF | single-stranded DNA helicase activity | 4/362 | 0.039694 | 0.034716 | 4 |
| hsa04110 | KEGG | Cell cycle | 18/222 | 2.10E-05 | 1.76E-05 | 18 |
| hsa03050 | KEGG | Proteasome | 9/222 | 0.000229 | 0.000192 | 9 |
| hsa03440 | KEGG | Homologous recombination | 8/222 | 0.0006 | 0.000503 | 8 |
| hsa04657 | KEGG | IL-17 signaling pathway | 11/222 | 0.00142 | 0.001191 | 11 |
| hsa03030 | KEGG | DNA replication | 7/222 | 0.00142 | 0.001191 | 7 |