

Table S1 Full information of 104 HCC enriched sub-pathway (FRD < 0.1)

| Sub-pathway ID | Pathway Name | p-value | fdr |
|----------------|--|----------|----------|
| path:04512_11 | ECM-receptor interaction | 3.54E-11 | 8.16E-08 |
| path:04512_13 | ECM-receptor interaction | 1.04E-10 | 8.16E-08 |
| path:04512_14 | ECM-receptor interaction | 1.04E-10 | 8.16E-08 |
| path:05146_9 | Amoebiasis | 2.73E-10 | 1.61E-07 |
| path:03320_2 | PPAR signaling pathway | 9.05E-09 | 4.26E-06 |
| path:04062_2 | Chemokine signaling pathway | 2.24E-08 | 8.79E-06 |
| path:04512_12 | ECM-receptor interaction | 3.46E-08 | 1.17E-05 |
| path:00280_1 | Valine, leucine and isoleucine degradation | 7.70E-08 | 2.02E-05 |
| path:00280_2 | Valine, leucine and isoleucine degradation | 7.70E-08 | 2.02E-05 |
| path:04062_1 | Chemokine signaling pathway | 1.09E-07 | 2.57E-05 |
| path:00071_11 | Fatty acid metabolism | 2.00E-07 | 3.93E-05 |
| path:00910_3 | Nitrogen metabolism | 2.00E-07 | 3.93E-05 |
| path:00650_8 | Butanoate metabolism | 2.38E-07 | 4.32E-05 |
| path:00071_2 | Fatty acid metabolism | 2.79E-07 | 4.61E-05 |
| path:04512_3 | ECM-receptor interaction | 3.13E-07 | 4.61E-05 |
| path:04512_27 | ECM-receptor interaction | 3.13E-07 | 4.61E-05 |
| path:00071_7 | Fatty acid metabolism | 4.64E-07 | 6.05E-05 |
| path:00071_8 | Fatty acid metabolism | 4.64E-07 | 6.05E-05 |
| path:04512_10 | ECM-receptor interaction | 4.88E-07 | 6.05E-05 |
| path:00982_4 | Drug metabolism - cytochrome P450 | 6.97E-07 | 7.32E-05 |
| path:00982_5 | Drug metabolism - cytochrome P450 | 6.97E-07 | 7.32E-05 |
| path:00982_9 | Drug metabolism - cytochrome P450 | 6.97E-07 | 7.32E-05 |
| path:04512_9 | ECM-receptor interaction | 7.35E-07 | 7.32E-05 |
| path:04512_5 | ECM-receptor interaction | 7.45E-07 | 7.32E-05 |
| path:04512_6 | ECM-receptor interaction | 2.39E-06 | 0.000225 |
| path:00830_2 | Retinol metabolism | 3.38E-06 | 0.000303 |
| path:00071_4 | Fatty acid metabolism | 3.48E-06 | 0.000303 |
| path:00650_7 | Butanoate metabolism | 5.52E-06 | 0.000435 |
| path:00982_12 | Drug metabolism - cytochrome P450 | 5.52E-06 | 0.000435 |
| path:05146_2 | Amoebiasis | 5.54E-06 | 0.000435 |
| path:00071_9 | Fatty acid metabolism | 6.92E-06 | 0.000526 |
| path:05146_1 | Amoebiasis | 1.21E-05 | 0.000819 |
| path:00071_10 | Fatty acid metabolism | 1.23E-05 | 0.000819 |
| path:00982_10 | Drug metabolism - cytochrome P450 | 1.23E-05 | 0.000819 |
| path:04970_1 | Salivary secretion | 1.29E-05 | 0.000819 |
| path:00350_2 | Tyrosine metabolism | 1.29E-05 | 0.000819 |
| path:00350_3 | Tyrosine metabolism | 1.29E-05 | 0.000819 |
| path:05414_1 | Dilated cardiomyopathy | 1.51E-05 | 0.000934 |
| path:00590_1 | Arachidonic acid metabolism | 1.66E-05 | 0.001005 |
| path:00330_12 | Arginine and proline metabolism | 1.93E-05 | 0.001136 |
| path:00280_8 | Valine, leucine and isoleucine degradation | 2.26E-05 | 0.001297 |
| path:00071_3 | Fatty acid metabolism | 2.48E-05 | 0.0013 |
| path:00071_5 | Fatty acid metabolism | 2.48E-05 | 0.0013 |
| path:00071_6 | Fatty acid metabolism | 2.48E-05 | 0.0013 |
| path:00280_3 | Valine, leucine and isoleucine degradation | 2.48E-05 | 0.0013 |

| | | | |
|---------------|--|----------|----------|
| path:04010_2 | MAPK signaling pathway | 2.83E-05 | 0.00145 |
| path:00591_1 | Linoleic acid metabolism | 3.95E-05 | 0.001979 |
| path:00280_7 | Valine, leucine and isoleucine degradation | 4.17E-05 | 0.002048 |
| path:04110_23 | Cell cycle | 5.59E-05 | 0.002688 |
| path:00350_4 | Tyrosine metabolism | 6.05E-05 | 0.002837 |
| path:04610_11 | Complement and coagulation cascades | 6.29E-05 | 0.002837 |
| path:00330_11 | Arginine and proline metabolism | 6.29E-05 | 0.002837 |
| path:00590_2 | Arachidonic acid metabolism | 6.50E-05 | 0.002837 |
| path:00590_3 | Arachidonic acid metabolism | 6.50E-05 | 0.002837 |
| path:04350_13 | TGF-beta signaling pathway | 8.05E-05 | 0.003451 |
| path:00980_3 | Metabolism of xenobiotics by cytochrome P450 | 8.98E-05 | 0.003781 |
| path:00010_3 | Glycolysis / Gluconeogenesis | 0.000107 | 0.004405 |
| path:00590_4 | Arachidonic acid metabolism | 0.000108 | 0.004407 |
| path:04970_2 | Salivary secretion | 0.000167 | 0.006574 |
| path:00071_1 | Fatty acid metabolism | 0.000167 | 0.006574 |
| path:00980_1 | Metabolism of xenobiotics by cytochrome P450 | 0.000191 | 0.007397 |
| path:00790_4 | Folate biosynthesis | 0.0002 | 0.007587 |
| path:04270_9 | Vascular smooth muscle contraction | 0.00029 | 0.010663 |
| path:05200_52 | Pathways in cancer | 0.00029 | 0.010663 |
| path:04110_17 | Cell cycle | 0.000327 | 0.011858 |
| path:04110_3 | Cell cycle | 0.000435 | 0.015519 |
| path:04270_8 | Vascular smooth muscle contraction | 0.000472 | 0.016362 |
| path:00330_10 | Arginine and proline metabolism | 0.000472 | 0.016362 |
| path:04914_4 | Progesterone-mediated oocyte maturation | 0.00056 | 0.019136 |
| path:00280_10 | Valine, leucine and isoleucine degradation | 0.000614 | 0.020668 |
| path:04114_16 | Oocyte meiosis | 0.000676 | 0.022447 |
| path:04610_6 | Complement and coagulation cascades | 0.000944 | 0.0309 |
| path:04920_5 | Adipocytokine signaling pathway | 0.00105 | 0.033458 |
| path:00640_5 | Propanoate metabolism | 0.00105 | 0.033458 |
| path:00280_9 | Valine, leucine and isoleucine degradation | 0.001093 | 0.034349 |
| path:04010_11 | MAPK signaling pathway | 0.001186 | 0.036315 |
| path:04530_10 | Tight junction | 0.001186 | 0.036315 |
| path:04145_1 | Phagosome | 0.001223 | 0.036495 |
| path:00790_6 | Folate biosynthesis | 0.001223 | 0.036495 |
| path:00270_2 | Cysteine and methionine metabolism | 0.001574 | 0.04581 |
| path:00270_8 | Cysteine and methionine metabolism | 0.001574 | 0.04581 |
| path:00410_5 | beta-Alanine metabolism | 0.001681 | 0.047742 |
| path:00650_4 | Butanoate metabolism | 0.001681 | 0.047742 |
| path:05200_14 | Pathways in cancer | 0.001838 | 0.051583 |
| path:05146_7 | Amoebiasis | 0.001986 | 0.054417 |
| path:00650_13 | Butanoate metabolism | 0.001986 | 0.054417 |
| path:04610_4 | Complement and coagulation cascades | 0.002201 | 0.058292 |
| path:00250_1 | Alanine, aspartate and glutamate metabolism | 0.002201 | 0.058292 |
| path:00270_1 | Cysteine and methionine metabolism | 0.002201 | 0.058292 |
| path:04360_19 | Axon guidance | 0.002266 | 0.059308 |

| | | | |
|---------------|--------------------------------|----------|----------|
| path:05215_7 | Prostate cancer | 0.00229 | 0.059308 |
| path:04020_3 | Calcium signaling pathway | 0.002368 | 0.060662 |
| path:05222_1 | Small cell lung cancer | 0.002551 | 0.063965 |
| path:00410_4 | beta-Alanine metabolism | 0.002551 | 0.063965 |
| path:04114_11 | Oocyte meiosis | 0.002631 | 0.065281 |
| path:04930_5 | Type II diabetes mellitus | 0.002999 | 0.073632 |
| path:04510_1 | Focal adhesion | 0.003427 | 0.083271 |
| path:00650_3 | Butanoate metabolism | 0.003706 | 0.08889 |
| path:04110_12 | Cell cycle | 0.003734 | 0.08889 |
| path:04114_21 | Oocyte meiosis | 0.003995 | 0.091408 |
| path:04514_81 | Cell adhesion molecules (CAMs) | 0.003995 | 0.091408 |
| path:04514_84 | Cell adhesion molecules (CAMs) | 0.003995 | 0.091408 |
| path:00140_11 | Steroid hormone biosynthesis | 0.003995 | 0.091408 |
| path:04062_13 | Chemokine signaling pathway | 0.004061 | 0.092027 |
