The most enriched pathway terms

Statistic method: hypergeometric test
FDR correction method: Benjamini and Hochberg

| Term | Description | Sample number | Background number | P-value | Corrected P-value | Gene_id | Gene_name |
|------|-------------|---------------|-------------------|---------|-------------------|---------|-----------|
| hsa04668 | TNF signaling pathway | 37/1188 | 94/5573 | 4.67047556586705e-05 | 0.0143383599872118 | ENSG00000136244 | IL6 | TNFAIP |
| | | | | | | ENSG000000182158 | MAP2K6 |
| | | | | | | ENSG00000108984 | BIRC3 |
| | | | | | | ENSG000001177606 | ATF |
| | | | | | | ENSG00000073756 | CCL20 |
| | | | | | | ENSG00000110330 | BCL |
| | | | | | | ENSG00000166840 | RPS6KA4 |
| | | | | | | ENSG00000090339 | CEBPB |
| | | | | | | ENSG00000131323 | NFKB |
| | | | | | | ENSG00000163739 | CREB3L2 |
| | | | | | | ENSG00000168040 | JU |
| | | | | | | ENSG00000157625 | PTGS2 |
| | | | | | | ENSG00000128272 | BIRC |
| | | | | | | ENSG00000115009 | MLKL |
| | | | | | | ENSG00000069399 | ICAM |
| | | | | | | ENSG00000100906 | NFKBIA |
| | | | | | | ENSG00000073756 | TRAF3 |
| | | | | | | ENSG00000136244 | CXCL |
| | | | | | | ENSG00000169429 | DAP |
| | | | | | | ENSG00000082701 | CASP |
| | | | | | | ENSG00000162772 | THBS1 |
| | | | | | | ENSG00000128272 | CXCL |
| | | | | | | ENSG00000114251 | DAP |
| hsa05219 | Bladder cancer | 18/1188 | 38/5573 | 0.00030111143160324 | 0.0365222017434792 | ENSG00000136244 | IL6 | CRTC3 |
| | | | | | | ENSG00000196730 | NFKB2 |
| | | | | | | ENSG00000068028 | ATF |
| | | | | | | ENSG00000110099 | GSK3B |
| | | | | | | ENSG00000132155 | NFKB2 |
| | | | | | | ENSG00000135446 | RAF |
| | | | | | | ENSG00000174775 | WNT5A |
| | | | | | | ENSG00000068078 | RELA |
| | | | | | | ENSG00000100784 | CCN1 |
| | | | | | | ENSG00000147889 | RAF |
| | | | | | | ENSG00000197122 | HRA |
| | | | | | | ENSG00000102882 | FGFR3 |
| | | | | | | ENSG0000025708 | RPS6KA5 |
| | | | | | | ENSG00000112242 | CDFN2A |
| | | | | | | ENSG00000117399 | MAPK3 |
| | | | | | | ENSG00000131323 | TLY |
| | | | | | | ENSG00000104856 | WNT7B |
| | | | | | | ENSG00000117399 | CCND1 |
| hsa05166 | Human T-cell leukemia virus 1 infection | 64/1188 | 205/5573 | 0.000475214435277415 | 0.0365222017434792 | ENSG00000136244 | IL6 | CRTC3 |
| | | | | | | ENSG00000140577 | NFkB2 |
| | | | | | | ENSG00000077150 | GSK3B |
| | | | | | | ENSG00000162772 | ATF |
| | | | | | | ENSG00000082701 | WNT5A |
| | | | | | | ENSG00000128272 | RELA |
| | | | | | | ENSG00000114251 | CCN1 |
| | | | | | | ENSG00000104856 | CCND1 |
| | | | | | | ENSG00000117399 | WNT7B |
| Gene ID   | Gene Symbol | Pathway Name     |
|----------|-------------|------------------|
| ENSG0000166949 | CCND3  | JUN      |
| ENSG0000108773  | POLE4   | FOSI     |
| ENSG0000107404  | SMAD2   | FZC      |
| ENSG0000109320  | ICAM1   | CAL      |
| ENSG0000162434  | NRF2B   | JIA      |
| ENSG0000110092  | POLE3   | CREBBP   |
| ENSG0000188064  | CDC26   | ETS      |
| ENSG0000112576  | TERT    | XIAF     |
| ENSG0000177606  | CDK4    | HRA      |
| ENSG0000155387  | ADCY6   | CCNE     |
| ENSG00001555760 | CDKN2A  | FZI      |
| ENSG00000900339 | TCF3    | MSX      |
| ENSG0000179218  | DGL1    | CCNE     |
| ENSG00001000906 | ADCY9   |         |
| ENSG0000148229  | WNT10B  | FC       |
| ENSG0000005339  | CREM    | IL2R     |
| ENSG00000132341 | WNT6    | FZD      |
| ENSG000000132341 | ATM     | POLD     |
| ENSG00000176386 | SLC2A1  |         |
| ENSG00000175592 | ANAPC11 |         |
| ENSG00000175387 | IL15    | PIK3C    |
| ENSG00000174775 | FZD1    |         |
| ENSG00000174233 | TP53    |         |
| ENSG00000180340 | STAT5A  |         |
| ENSG00000071564 | POLD1   | IL2R     |
| ENSG00000163132 | TP53    |         |
| ENSG00000075711 |         |         |
| ENSG00000157456 |         |         |
| ENSG00000162104 |         |         |
| ENSG0000199884 |         |         |
| ENSG00001700345 |         |         |
| ENSG0000095794 |         |         |
| ENSG00000100385 |         |         |
| ENSG00000115596 |         |         |
| ENSG00000163251 |         |         |
| ENSG00000149311 |         |         |
| ENSG00000106628 |         |         |
| ENSG00000117394 |         |         |
| ENSG00000141452 |         |         |
| ENSG00000164136 |         |         |
| ENSG00000121879 |         |         |
| ENSG00000157240 |         |         |
| ENSG00000121281 |         |         |
| ENSG00000123268 |         |         |
| ENSG0000065539 |         |         |
| ENSG00000164109 |         |         |
| ENSG00000112242 |         |         |
| ENSG00000126561 |         |         |
| ENSG0000062822 |         |         |
| ENSG00000147168 |         |         |
| ENSG00000141510 |         |         |
| ENSG00000080206 |         |         |
| ENSG00000143574 |         |         |
| ENSG0000015414 |         |         |
| ENSG00000130702 |         |         |
| ENSG00000100960 |         |         |
| ENSG00000131323 |         |         |
| ENSG00000101966 |         |         |
| ENSG00000188513 |         |         |
| ENSG00000135446 |         |         |
| ENSG00000030110 |         |         |
| ENSG00000076604 |         |         |
| ENSG00000123975 |         |         |
| ENSG00000164171 |         |         |
| ENSG00000197565 |         |         |
| ENSG00000101680 |         |         |
| ENSG00000171862 |         |         |
| ENSG00000121879 |         |         |

**hsa05222**  Small cell lung cancer  32/1188  86/5573  0.000497862951348489  0.0365222017434392

| Gene ID   | Gene Symbol | Pathway Name     |
|----------|-------------|------------------|
| ENSG00000023445 | BIRC3  | LAMI     |
| ENSG00000196878 | LAM4    |         |
| ENSG00000161717 | LAM1    |         |
| ENSG00000109320 | NFKB1   |         |
| ENSG00000172037 | CDK6    |         |
| ENSG00000105810 | CCNE    |         |
| ENSG00000110092 | CKS1B   |         |
| ENSG00000173207 | GADD45A |         |
| ENSG00000099860 | PTPG52  |         |
| ENSG00000073756 | BIRC2   |         |
| ENSG00000110330 | DDR2    |         |
| ENSG00000134574 | FN1     |         |
| ENSG0000015414 | TRAF3   |         |
| ENSG00000130702 | COL4A5  |         |
| ENSG00000106006 | TRAF    |         |
| ENSG00000131323 | COL4A6  |         |
| ENSG00000101966 | BAK1    |         |
| ENSG00000188513 | TRAF3   |         |
| ENSG00000135446 | CKS2    |         |
| ENSG00000030110 | ITGA4   |         |
| ENSG00000076604 | ITGA3   |         |
| ENSG00000123975 | LAM1    |         |
| ENSG00000164171 | PTE     |         |
| ENSG00000197565 | LAM1C   |         |
| ENSG00000101680 | EZF     |         |
| ENSG00000171862 | ITGA3   |         |
| ENSG00000121879 | LAM1    |         |

file:///Users/dawen/Desktop/诺禾致源测序/2保1/0710结果交付.差原始数据/X101SC21061603-Z01-F001-B1-16.result/5.Enrichment/2.KEGG/K223Rvsgenes.txt
### Pathway Enrichment

**hsa05169**  
**Epstein-Barr virus infection**  
49/1188  
149/5573  
0.0005948241326954  
0.0365222017434792

| Gene ID | Gene Name 1 | Gene Name 2 | Gene Name 3 | Gene Name 4 | Gene Name 5 | Gene Name 6 | Gene Name 7 | Gene Name 8 | Gene Name 9 | Gene Name 10 | Gene Name 11 | Gene Name 12 | Gene Name 13 | Gene Name 14 | Gene Name 15 | Gene Name 16 | Gene Name 17 | Gene Name 18 | Gene Name 19 | Gene Name 20 | Gene Name 21 |
|---------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| ENSG00000135862 | IL6 | TNFAIP | NFKB2 | MAP2K6 | GADD45A | RELB | NFKB | CDK6 | RUNX | JAK1 | CCNC | CCND3 | JUN | NFKBIE | GADD45B | DBB2 | SIN3 | IFNAR1 | ICA1 | CAL | NFKBIA | PDL1 | IRAK1 | TRAF | CDK4 | FADI | BAK1 | PSMC | MAPK11 | MAPK12 | ISG15 | STAT | OAS2 | PSMC | PLCG2 | PSMI | PIK3CA | PSMC4 | MAP2K4 | NFKBIB | IKBK | E2F3 | SAP3 | TAB1 | ENTP1 | VIM | CIR1 | CASP8 | TP5 |

**hsa04550**  
**Signaling pathways regulating pluripotency of stem cells**  
38/1188  
113/5573  
0.00149734778478924  
0.0736741054270069

| Gene ID | Gene Name 1 | Gene Name 2 | Gene Name 3 | Gene Name 4 | Gene Name 5 | Gene Name 6 | Gene Name 7 | Gene Name 8 | Gene Name 9 | Gene Name 10 | Gene Name 11 | Gene Name 12 | Gene Name 13 | Gene Name 14 | Gene Name 15 | Gene Name 16 | Gene Name 17 | Gene Name 18 | Gene Name 19 | Gene Name 20 | Gene Name 21 |
|---------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| ENSG00000135111 | TBX3 | GSK3 | WNT5A | SMAD3 | INH1 | DVL1 | JAK | WNT7B | ZFHX3 | SMAI | FZD7 | JARID | FGFR4 | RAF | HRAS | ID3 | FGF3 | OTX | EZF3 | SAP3 | TAB1 | ENTP1 | VIM | CIR1 | CASP8 | TP5 | BMPR1A | PIK3CA | FZD | ID1 | ACVR1 | PCGF6 | 
| ID     | Pathway                          | Gene Count | Enrichment Count | Pathway Score | Pathway FDR |
|--------|----------------------------------|------------|------------------|---------------|-------------|
| hsa04657 | IL-17 signaling pathway         | 26/1188    | 70/5573          | 0.0016798655960553 | 0.0736741054270069 |
| hsa05200 | Pathways in cancer               | 119/1188   | 442/5573         | 0.0020323189706997 | 0.077992045006112 |

**Pathway Enrichment**

| ID     | Pathway                          | Gene Count | Enrichment Count | Pathway Score | Pathway FDR |
|--------|----------------------------------|------------|------------------|---------------|-------------|
|        |                                  |            |                  |               |             |

**hsa04657**

- IL6
- TNFAIP
- CXCL8
- GSK3
- IL6
- TNFAIP
- CXCL8
- GSK3
- HSP90AA1
- CEBPB
- NFkB1
- HSP90B1
- FOSL1
- PTGS
- NFKBIA
- TRAF3
- CXCL12
- FADD
- TRAF1
- HSP90AB1
- MAPK11
- MAPK3
- MAPK12
- FC
- IKBKE
- CASP

**hsa05200**

- IL6
- NFKB2
- BIRC3
- LAM1
- CXCL8
- GSK3
- DAPK1
- WNT5A
- GADD45A
- JI
- HSP90AA1
- JAG2
- SMAD
- DVL1
- NFKB
- LAMB2
- ROCK2
- AE
- CDK6
- JAK
- RASSF1
- CCND1
- PLC1
- WNT7B
- CCND3
- HSP90B1
- JL
- CK51B
- GADD45B
- PIM1
- PTGS
- BIRC2
- DDB
- SMA2
- FZC
- IFNAR1
- EPAS1
- IIL12
- FN1
- IFNGR
- LAM5
- NFKBIA
- DLI
- NOTCH1
- MGST3
- CREBBP
- FGF4
- RUNG
- RAF1
- TRAF
- TERT
- XIAF
- COL4A5
- RAI
- COL4A5
- IRI
- CDK4
- BMP
- HRAS
- FADI
- BAK1
- TRAF
- SOS2
- FGFR
- ADCY6
- HSP90B1
- RPS6KA5
- CNK2A
- STI
- TCF7L2
- CK1
- MGST2
- FZC
- MTIF2
- EGNL
- PAX8
- LRP
| ENSG00000160867 | GNB2 | MAP2K1 | ARHGEF11 | COL4A6 | LAMA1 | NCOA3 | PTE1E1 |
|-----------------|------|-------|----------|--------|--------|--------|--------|
| ENSG00000132155 | VEGFB | ADC    | PMAIP1   | AXL    | MAGI3  | ITPR   | BIRC3  |
| ENSG00000131323 | NFE2L2 |        | AXIN     |        |        |        |        |
| ENSG00000164362 |        |        | VEGFA    |        |        |        |        |
| ENSG000001888153 |        |        | WNT10B   |        |        |        |        |
| ENSG00000144118 |        |        | VEGFA    |        |        |        |        |
| ENSG00000135446 |        |        | HIF1A    |        |        |        |        |
| ENSG00000125845 |        |        | IL2RB    |        |        |        |        |
| ENSG000000174775 |        |        | IL7RB    |        |        |        |        |
| ENSG00000168040 |        |        | IL18RB   |        |        |        |        |
| ENSG00000030110 |        |        | IL27RB   |        |        |        |        |
| ENSG00000076604 |        |        | IL32RB   |        |        |        |        |
| ENSG00000100485 |        |        | IL15RB   |        |        |        |        |
| ENSG00000068078 |        |        | IL10RB   |        |        |        |        |
| ENSG00000039484 |        |        | IL6RB    |        |        |        |        |
| ENSG00000009484 |        |        | IL1RB    |        |        |        |        |
| ENSG00000086884 |        |        | IL2RB    |        |        |        |        |
| ENSG00000112715 |        |        | IL5RB    |        |        |        |        |
| ENSG00000170345 |        |        | IL28RB   |        |        |        |        |
| ENSG00000100644 |        |        | IL27RA   |        |        |        |        |
| ENSG0000015415 |        |        | IL18RA   |        |        |        |        |
| ENSG00000100385 |        |        | IL15RA   |        |        |        |        |
| ENSG00000111596 |        |        | IL10RA   |        |        |        |        |
| ENSG00000197943 |        |        | IL6RA    |        |        |        |        |
| ENSG00000163251 |        |        | IL1RA    |        |        |        |        |
| ENSG00000134184 |        |        | IL2RA    |        |        |        |        |
| ENSG00000164171 |        |        | IL5RA    |        |        |        |        |
| ENSG00000117394 |        |        | IL28RA   |        |        |        |        |
| ENSG00000089685 |        |        | IL27RO   |        |        |        |        |
| ENSG00000163235 |        |        | IL18RO   |        |        |        |        |
| ENSG00000196914 |        |        | IL10RO   |        |        |        |        |
| ENSG00000197565 |        |        | IL6RO    |        |        |        |        |
| ENSG00000101680 |        |        | IL1RA    |        |        |        |        |
| ENSG00000124151 |        |        | IL2RA    |        |        |        |        |
| ENSG000001171862 |        |        | IL5RA    |        |        |        |        |
| ENSG00000164136 |        |        | IL2RA    |        |        |        |        |
| ENSG00000121879 |        |        | IL5RA    |        |        |        |        |
| ENSG00000157240 |        |        | IL2RA    |        |        |        |        |
| ENSG00000121281 |        |        | IL5RA    |        |        |        |        |
| ENSG00000100387 |        |        | IL6RA    |        |        |        |        |
| ENSG00000135862 |        |        | IL1RA    |        |        |        |        |
| ENSG00000111242 |        |        | IL2RA    |        |        |        |        |
| ENSG00000126561 |        |        | IL5RA    |        |        |        |        |
| ENSG00000157764 |        |        | IL2RA    |        |        |        |        |
| ENSG00000058884 |        |        | IL6RA    |        |        |        |        |
| ENSG00000164683 |        |        | IL1RA    |        |        |        |        |
| ENSG00000198431 |        |        | IL2RA    |        |        |        |        |
| ENSG00000147168 |        |        | IL5RA    |        |        |        |        |
| ENSG00000050555 |        |        | IL2RA    |        |        |        |        |
| ENSG00000120296 |        |        | IL5RA    |        |        |        |        |
| ENSG00000064012 |        |        | IL2RA    |        |        |        |        |
| ENSG00000141510 |        |        | IL5RA    |        |        |        |        |

**hsa04210**  | Apoptosis |
|-------------|-----------|
| 40/1188     | 123/5573  | 0.00231653754838153 | 0.0790196697059033 |

Pathway Enrichment
| Pathway ID | Pathway Name                  | Enriched Genes                                                                 | Pathway ID | Pathway Name                  | Enriched Genes                                                                 |
|------------|-------------------------------|--------------------------------------------------------------------------------|------------|-------------------------------|--------------------------------------------------------------------------------|
| hsa05140   | Leishmaniasis                 | C3 NFKB1 JAK1 JUN PTGS2 IL12 IFNGR1 NFKB1 IAI MAPK11 MAPK3 MAPK12 FC STAT1 NCF NFKB1 IAI TAM | hsa05165   | Human papillomavirus infection | ITGB8 LAM1 THBS1 GSK WNT3A VT OASL DVL COL1A1 NFKB1 LAM1 ATP6V0B CREB3L2 CDK6 JAK CCND1 NWC7 LAM1 NOTCH1 CREBBP LF3 RAF1 TRAF TERT COL4. PSE11 CDK HRAS FADI BAK1 HES5 S052 COL9A TCF7L2 CHI FZD2 DLG MAPK3 AX12 ITGA2 |
| Pathway Enrichment | hsa04621 NOD-like receptor signaling pathway | 41/1188 | 133/5573 | 0.00601627891467234 | 0.153916468900367 |
|----------------------|---------------------------------------------|---------|----------|----------------------|----------------------|
| ENSG00000135446 | | | | | |
| ENSG00000174775 | | | | | |
| ENSG00000168040 | | | | | |
| ENSG00000030110 | | | | | |
| ENSG00000182820 | | | | | |
| ENSG00000100485 | | | | | |
| ENSG00000092758 | | | | | |
| ENSG00000148737 | | | | | |
| ENSG00000111642 | | | | | |
| ENSG00000180340 | | | | | |
| ENSG00000075711 | | | | | |
| ENSG00000102882 | | | | | |
| ENSG00000103126 | | | | | |
| ENSG00000169884 | | | | | |
| ENSG00000151276 | | | | | |
| ENSG00000005884 | | | | | |
| ENSG00000115415 | | | | | |
| ENSG00000111642 | | | | | |
| ENSG00000186039 | | | | | |
| ENSG00000197565 | | | | | |
| ENSG00000101680 | | | | | |
| ENSG00000171862 | | | | | |
| ENSG00000121879 | | | | | |
| ENSG00000147099 | | | | | |
| ENSG00000157240 | | | | | |
| ENSG00000114573 | | | | | |
| ENSG00000135862 | | | | | |
| ENSG00000142156 | | | | | |
| ENSG00000263528 | | | | | |
| ENSG00000185825 | | | | | |
| ENSG00000103479 | | | | | |
| ENSG00000184384 | | | | | |
| ENSG00000067606 | | | | | |
| ENSG0000005884 | | | | | |
| ENSG00000164683 | | | | | |
| ENSG00000187840 | | | | | |
| ENSG00000050555 | | | | | |
| ENSG0000064012 | | | | | |
| ENSG00000141510 | | | | | |
| ENSG00000169733 | | | | | |
| ATP6V1B1 | | | | | |
| COL4A6 | | | | | |
| LAMA1 | | | | | |
| PTE | | | | | |
| PIK3CA | | | | | |
| HDAC8 | | | | | |
| FZD | | | | | |
| ATP6V1A | | | | | |
| LAMC1 | | | | | |
| COL6A1 | | | | | |
| IKBKE | | | | | |
| BCAP31 | | | | | |
| RBL | | | | | |
| PRKCZ | | | | | |
| ITGA | | | | | |
| HEY1 | | | | | |
| EIF4EBP1 | | | | | |
| LAMC3 | | | | | |
| CASI | | | | | |
| TP53 | | | | | |
| RNFK1 | | | | | |
| hsa04621 NOD-like receptor signaling pathway | 41/1188 | 133/5573 | 0.00601627891467234 | 0.153916468900367 |
| ENSG00000136244 | | | | | |
| ENSG0000018503 | | | | | |
| ENSG00000150995 | | | | | |
| ENSG00000023445 | | | | | |
| ENSG00000169429 | | | | | |
| ENSG00000162645 | | | | | |
| ENSG00000080824 | | | | | |
| ENSG00000109320 | | | | | |
| ENSG00000162434 | | | | | |
| ENSG00000149782 | | | | | |
| ENSG00000177606 | | | | | |
| ENSG00000110330 | | | | | |
| ENSG00000142166 | | | | | |
| ENSG00000164733 | | | | | |
| ENSG00000112851 | | | | | |
| ENSG00000100906 | | | | | |
| ENSG00000139112 | | | | | |
| ENSG00000131323 | | | | | |
| ENSG00000163739 | | | | | |
| ENSG00000087077 | | | | | |
| ENSG00000101966 | | | | | |
| ENSG00000110218 | | | | | |
| ENSG00000168040 | | | | | |
| ENSG00000096384 | | | | | |
| ENSG00000157625 | | | | | |
| ENSG00000142185 | | | | | |
| ENSG00000185386 | | | | | |
| ENSG00000169604 | | | | | |
| ENSG0000006433 | | | | | |
| ENSG000001202882 | | | | | |
| ENSG00000188130 | | | | | |
| ENSG00000136560 | | | | | |
| ENSG0000015145 | | | | | |
| ENSG00000111335 | | | | | |
| ENSG00000166888 | | | | | |
| ILS | | | | | |
| Tnfap | | | | | |
| Itpr1 | | | | | |
| Birc | | | | | |
| Cxcl8 | | | | | |
| Gbp | | | | | |
| Hsp90aa1 | | | | | |
| Nfkbi | | | | | |
| Jak | | | | | |
| Plcb1 | | | | | |
| Junc | | | | | |
| Ctsb | | | | | |
| Erbii | | | | | |
| Nfkb | | | | | |
| Gabarapl | | | | | |
| Traf3 | | | | | |
| Cxci | | | | | |
| Trp6 | | | | | |
| Xai | | | | | |
| Panx1 | | | | | |
| Fad | | | | | |
| Hsp90ab1 | | | | | |
| Tab3 | | | | | |
| Trpw | | | | | |
| Mapk11 | | | | | |
| Antxr1 | | | | | |
| Itpr3 | | | | | |
| Mapk12 | | | | | |
| Tank | | | | | |
| Stat | | | | | |
| Oas2 | | | | | |
| Mfn | | | | | |
| Nod1 | | | | | |
| Nfkb | | | | | |
| Ikbke | | | | | |
| Tab | | | | | |
| Tmem173 | | | | | |
| Casp8 | | | | | |
| Pathway Description                  | ID    | Count | Enrichment | p-value | FDR        |
|-------------------------------------|-------|-------|------------|---------|------------|
| Hepatocellular carcinoma            | has05225 | 44/1188 | 147/5573  | 0.0081224509374697 | 0.186267049645831 |
| AGE-RAGE signaling pathway in diabetic complications | has04933 | 29/1188 | 89/5573   | 0.0084942628502985  | 0.186267049645831  |
| Protein processing in endoplasmic reticulum | has04141 | 44/1188 | 149/5573  | 0.01048953296920317 | 0.20626522579005  |
| Pathway Enrichment | DNAJB2 | SEC24D | HSP90B1 | MBTPS1 | FBXO2 | HSPBP1 | BAG | DNAJB1 | CAL | UGGT2 | PDIA | PREB | HSPH | RAD23A | NFE2L2 | MOI | P4HB | RPN1 | CRYAB | PPN1R | UBQLN4 | TRAM1 | SSR | SELENOS | RBX1 | BCAP |
|-------------------|--------|--------|--------|--------|-------|--------|-----|--------|-----|-------|------|-------|-----|--------|------|-------|------|-------|-------|-------|-------|-----|-------|-----|-------|
| **hsa03010**      | Ribosome | 38/1188 | 126/5573 | 0.0116999295191911 | 0.20626522579005 |
| **hsa04620**      | Toll-like receptor signaling pathway | 24/1188 | 72/5573 | 0.0117631092866874 | 0.20626522579005 | 0.20626522579005 |
|                   |        | MRPL9  | RPS27L | MRPS12 | MRPL2 | RPL: | RPS27 | MRPS18C | RPS2 RPS; | RPLP1 | MRPI | MRPL3 | RPL18 RPS; | RSL24D1 | MRPL34 | RPL13 | RPL; | UBA52 | RPL; | MRPS7 | MRPL10 | RPS20 | MRPL14 | RPL18A | ARPS15 | RPL23A | RPL10A | MRPL32 | RPL22 RPS; | RPL10 RPL; | RPL8 RPL3; | RPL14 | MRPL12 |
| Pathway Enrichment | Non-small cell lung cancer | Cushing syndrome |
|-------------------|---------------------------|------------------|
| hsa05223          | 21/1188  61/5573  0.0120937265935534  0.206265225790050 | 38/1188  128/5573  0.0152212732694476  0.226735260095891 |
| ENSG00000169429   | JUN  IL12A  NFKB  IRAK1  TRAF  FADD  MAPK  MXK3  MAPK12  FC  TLR  PIK3CA  MAP2K4  IKKBE  TAB  CTSDK  CXCL  CASP8 |
| ENSG00000109320   | GADD45A  CDK6  RASSI  CCND1  GADD45B  DDB2  RAF  CDK4  HRA  BAK1  SOS1  CDKN2A  STI  MAPK3  PLCG  TGFA  PIK3C  EZF3  STAT1  BRAF  TP5  |
| ENSG00000177606   | LDLR  ITPR  GSK3B  ATF  WNT5A  DVI  MEN1  CREB3L2  CDK6  CCNE  PLCB3  WNT7B  PBD  KCN13  FZD  ORAI1  CDK  ADCY6  CDKN2A  TCF7L2  PDEB1  FZD  NCEH1  ITPPI  MAPK3  AXII  ADCY9  WDFI  WNT10B  WNT6  FZD  CYP11A1  FZD1  ADCY  EZF3  BRAF  WDR5B  NR4A1  |
| Pathway ID | Pathway Name                                      | Fold Change | Raw Count | Enrichment Score | Adjusted p-value |
|-----------|--------------------------------------------------|-------------|-----------|------------------|------------------|
| hsa05134  | Legionellosis                                    | 16/1188     | 44/5573   | 0.0155429428558278 | 0.226735260095891 |
| hsa00533  | Glycosaminoglycan biosynthesis - keratan sulfate | 6/1188      | 11/5573   | 0.0158848063957023 | 0.226735260095891 |
| hsa05224  | Breast cancer                                    | 37/1188     | 125/5573  | 0.0172702821335468 | 0.226735260095891 |
| hsa05145  | Toxoplasmosis                                    | 25/1188     | 78/5573   | 0.0172760507155868 | 0.226735260095891 |

**Enriched Pathways**
- Legionellosis
- Glycosaminoglycan biosynthesis - keratan sulfate
- Breast cancer
- Toxoplasmosis

**Related Genes**
- C3 IL6 BNIIF NFKB2 CXCL1 NFKB1 HSP1 IL12A NFKB CXCL1 HSP1 TLR5 CLK1 ARF1 HSF1 CASP8
- BGALT1 ST3GAL1 CHST2 BGALT2 ST3GAL3 ST3GAL2
- NFKB2 GSK3 WNT5A GADD45A JAG2 DVL CDK6 CCNE WNT7B JU GADD45B DDB2 FZD DLL4 NOTC1 RAF1 CDK HRAS BAK SOS2 TCF7F FZD2 LRP1 MAPK3 AKII WNT10B FC WNT6 FZD NCOA3 PTE PIK3CA FZIE2F3 BRAF HEY1 TPS1
- LDLR MAP2I BIRC3 LAMI NFKB1 LAMI JAK1 BIRC IL12A IFNGI LAMAS NFKBIA IRAI XIAP HSPA MAPK11 MAPK9 MAPK12 STAT1 LAMI NFKB1S LAMC1 TAE LAMC3 CASI

file:///Users/dawen/Desktop/诺禾致源测序2保1?/0710结果交付，差异数据/X101SC21061603-Z01-F001-B1-16.result/5.Enrichment/2.KEGG/K223Rv...
| Pathway | Description | Start/Stop | Genes | Enrichment Score |
|---------|-------------|------------|-------|-----------------|
| hsa04512 | ECM-receptor interaction | 22/1188 67/5573 | 0.0185371482241989 | 0.226735260095989 |
| hsa00790 | Folate biosynthesis | 10/1188 24/5573 | 0.0193497377977696 | 0.226735260095989 |
| hsa04510 | Focal adhesion | 49/1188 175/5573 | 0.0201639515927901 | 0.226735260095989 |
| Pathway ID | Description                                      | Count in Pathway | Count in Dataset | p-value | Enrichment Score | Log Odds Ratio |
|------------|--------------------------------------------------|------------------|------------------|---------|------------------|---------------|
| `hsa04658` | Th1 and Th2 cell differentiation                  | 21/1188          | 64/5573          | 0.0212883381225639 | 0.226735260095891 |
| `hsa00515` | Mannose type O-glycan biosynthesis                | 9/1188           | 21/5573          | 0.021412073626457  | 0.226735260095891 |
| `hsa05162` | Measles                                          | 28/1188          | 91/5573          | 0.0214179887386998  | 0.226735260095891 |
| `hsa04927` | Cortisol synthesis and secretion                 | 16/1188          | 46/5573          | 0.0241248470705576  | 0.233312331422579 |
| `hsa05120` | Epithelial cell signaling in Helicobacter pylori infection | 20/1188          | 61/5573          | 0.0244652650609664  | 0.233312331422579 |
hsa04380  Osteoclast differentiation  28/1188  92/5573  0.0247247846946687  0.233312331422579

hsa04115  p53 signaling pathway  22/1188  69/5573  0.0260611519738397  0.233312331422579

hsa05202  Transcriptional misregulation in cancer  43/1188  153/5573  0.0265859989695248  0.233312331422579
| Pathway Enrichment | Gene Symbols | P-values | q-values |
|---------------------|--------------|----------|----------|
| hsa05230 Central carbon metabolism in cancer | ENSG00000171988, ENSG00000099860, ENSG00000185630, ENSG00000134574, ENSG00000169375, ENSG00000159216, ENSG00000175832, ENSG00000158715, ENSG00000164438, ENSG0000019083, ENSG00000175197, ENSG00000168283, ENSG00000113916, ENSG000001253293, ENSG00000100385, ENSG00000149311, ENSG00000171843, ENSG00000115738, ENSG00000123268, ENSG00000104885, ENSG00000138756, ENSG00000136807, ENSG00000198728, ENSG00000141510 | 0.0269978591944065 | 0.233312331422579 |
| hsa04137 Mitophagy - animal | ENSG00000152256, ENSG00000105976, ENSG00000105281, ENSG00000138413, ENSG00000132155, ENSG00000174775, ENSG00000168209, ENSG00000137801, ENSG00000139112, ENSG0000012149, ENSG00000174775, ENSG000001586828, ENSG00000187098, ENSG00000197124, ENSG00000190644, ENSG00000116688, ENSG00000136436, ENSG00000141526, ENSG00000156510, ENSG00000077463, ENSG0000017394, ENSG00000177169, ENSG0000012749, ENSG00000177606, ENSG00000177169, ENSG00000139112 | 0.0291081190161847 | 0.233312331422579 |
| hsa05206 MicroRNAs in cancer | ENSG00000168209, ENSG00000137801, ENSG0000012149, ENSG00000174775, ENSG000001586828, ENSG00000187098, ENSG00000197124, ENSG00000190644, ENSG00000116688, ENSG00000136436, ENSG00000141526, ENSG00000156510, ENSG00000077463, ENSG0000017394, ENSG00000177169, ENSG0000012749, ENSG00000177606, ENSG00000177169, ENSG00000139112 | 0.0295319246616885 | 0.233312331422579 |
| ID     | Pathway Description               | Genes                                                                 | P-value 1  | P-value 2 |
|--------|-----------------------------------|----------------------------------------------------------------------|-----------|-----------|
| hsa00514 | Other types of O-glycan biosynthesis | ENSG00000158715, ENSG00000174775, ENSG00000137807, etc.             | 0.0295523 | 0.2333123 |
| hsa04350 | TGF-beta signaling pathway         | B4GALT1, B4GALT2, B4GALT3, LFGN, PLOD, POMT1, POGSLT1, RFNG          | 0.0311589 | 0.2333123 |
| hsa04659 | Th17 cell differentiation          | I6L, HSP90A, SMAD3, NFKB, JAK1, JUN, NFKBIE, SMAD2, IFNGR1, RUNX1, etc. | 0.0311589 | 0.2333123 |

*Note: The table includes genes associated with specific pathways and their corresponding P-values.*
hsa05146  Amoebiasis  23/1188  74/5573  0.0311589758577386  0.233312331422579

hsa05167  Kaposi sarcoma-associated herpesvirus infection  42/1188  151/5573  0.0331523208755073  0.242327678780494

hsa04218  Cellular senescence  39/1188  140/5573  0.0381797388624261  0.265035046583717
| Pathway Enrichment | hsa05217 | Basal cell carcinoma | 18/1188 | 56/5573 | 0.0385442469217226 | 0.26503504653717 | ENSG0000032155 | ENSG00000152518 | ENSG00000135446 | ENSG00000174775 | ENSG00000147889 | ENSG00000110422 | ENSG00000112242 | ENSG00000188130 | ENSG00000096433 | ENSG00000157456 | ENSG00000102882 | ENSG00000094190 | HIPK3 | MAPK11 | ITPR3 | CCN1 | MAPK3 | MAPK12 | E2I | ATM | PPD | HIPK2 | PTE | PIK3CA | CDC25A | E2I | RBL2 | FOXM | E2F5 | E4BP1 | LIN9 | TP5 |
| hsa04120 | Ubiquitin mediated proteolysis | 36/1188 | 128/5573 | 0.0395525440141355 | 0.26503504653717 | ENSG00000023445 | ENSG00000117399 | ENSG0000014979 | ENSG00000072422 | ENSG00000116661 | ENSG00000110330 | ENSG00000134574 | ENSG00000176386 | ENSG00000099860 | ENSG00000134574 | ENSG00000155760 | ENSG00000125845 | ENSG00000030110 | ENSG00000148737 | ENSG00000180340 | ENSG00000103126 | ENSG00000169884 | ENSG00000155996 | ENSG00000163251 | ENSG00000157240 | ENSG00000141510 | BIRC3 | CDC2 | NEDD4L | RHOBTB1 | FBXO2 | BIRC | DDB2 | CDC2 | CDC34 | XIA | STUB1 | UBE2J2 | RNI | KHL13 | SOCS3 | UBE | WWP2 | TRIM37 | PIA | UBE25 | RCH | WWP1 | RHOBTB2 | UBE2H | ANAPC11 | ICH | REX1 | CUL4A | MGRN1 | PPII | CUL7 | PIA5 | AIRE | HERC | SMURF1 | UBE2E1 |
| hsa00190 | Oxidative phosphorylation | 35/1188 | 124/5573 | 0.0399737752032815 | 0.26503504653717 | ENSG00000198804 | ENSG00000117140 | MT-CO1 | ATP6V0B | ENSG00000000132155 | ENSG000001527518 | ENSG00000135446 | ENSG00000174775 | ENSG00000147889 | ENSG00000110422 | ENSG00000185386 | ENSG00000096433 | ENSG00000125476 | ENSG00000102882 | ENSG000001187840 | ENSG00000183814 | ENSG00000141510 | ENSG00000030101 | ENSG00000148737 | ENSG00000180340 | ENSG00000103126 | ENSG00000169884 | ENSG00000155996 | ENSG00000163251 | ENSG00000157240 | ENSG00000141510 | BIRC3 | CDC2 | NEDD4L | RHOBTB1 | FBXO2 | BIRC | DDB2 | CDC2 | CDC34 | XIA | STUB1 | UBE2J2 | RNI | KHL13 | SOCS3 | UBE | WWP2 | TRIM37 | PIA | UBE25 | RCH | WWP1 | RHOBTB2 | UBE2H | ANAPC11 | ICH | REX1 | CUL4A | MGRN1 | PPII | CUL7 | PIA5 | AIRE | HERC | SMURF1 | UBE2E1 |

file:///Users/dawen/Desktop/诺禾致源测序2保17/0710结果交付，差原始数据/X101SC21061603-Z01-F001-B1-16.result/Enrichment/2.KEGG/K23Rv...
| Gene Symbol | Description | hsa05205 Proteoglycans in cancer | hsa05212 Pancreatic cancer |
|-------------|-------------|---------------------------------|---------------------------|
| TNFSF11    | TNF-α      | 47/1188 174/5573 0.0410983227549801 0.265035046583717 | 22/1188 72/5573 0.0414387043518515 0.265035046583717 |
| NDUFC2     | NADH-ubiquinone oxidoreductase complex flavoprotein subunit C2 | | |
| Pathway Enrichment | Reactome ID | Canonical Pathway | Gene Count | Gene ID | Enrichment P-Value | Gene URI | Enrichment Depth |
|---------------------|-------------|--------------------|------------|---------|--------------------|----------|-----------------|
| C-type lectin receptor signaling pathway | hsa04625 | C-type lectin receptor signaling pathway | 24/1188 | ENSG00000109320, ENSG00000105810, ENSG00000162434, ENSG00000110092, ENSG00000099860, ENSG00000134574, ENSG00000175387, ENSG00000132155, ENSG00000144118, ENSG00000135446, ENSG0000012715, ENSG0000012788, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENSG00000136244, ENSG00000130880, ENSG00000102882, ENSG00000112715, ENSG00000115415, ENSG00000163235, ENSG00000121879, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENCG00000136244 | 0.0480740580904671 | 0.301198690485171 | 24/1188 | 81/5573 |
| N-Glycan biosynthesis | hsa00510 | N-Glycan biosynthesis | 15/1188 | ENSG00000109320, ENSG00000105810, ENSG00000162434, ENSG00000110092, ENSG00000099860, ENSG00000134574, ENSG00000175387, ENSG00000132155, ENSG00000144118, ENSG00000135446, ENSG0000012715, ENSG0000012788, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENSG00000136244, ENSG00000130880, ENSG00000102882, ENSG00000112715, ENSG00000115415, ENSG00000163235, ENSG00000121879, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENCG00000136244 | 0.0497360368337934 | 0.305340122368427 | 15/1188 | 46/5573 |
| Purine metabolism | hsa00230 | Purine metabolism | 40/1188 | ENSG00000109320, ENSG00000105810, ENSG00000162434, ENSG00000110092, ENSG00000099860, ENSG00000134574, ENSG00000175387, ENSG00000132155, ENSG00000144118, ENSG00000135446, ENSG0000012715, ENSG0000012788, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENSG00000136244, ENSG00000130880, ENSG00000102882, ENSG00000112715, ENSG00000115415, ENSG00000163235, ENSG00000121879, ENSG00000112242, ENSG00000157764, ENSG00000141510, ENCG00000136244 | 0.0507242548559928 | 0.305340122368427 | 40/1188 | 147/5573 |
| Pathway ID | Pathway Name        | Gene IDs | P-value 1  | P-value 2 |
|-----------|---------------------|----------|-----------|-----------|
| hsa05010  | Alzheimer disease   | ENSG00000103024, ENSG00000198931, ENSG00000162104, ENSG00000147853, ENSG0000058600, ENSG00000160191, ENSG00000076685, ENSG00000106628, ENSG0000099817, ENSG0000133805, ENSG0000121281, ENSG0000185100, ENSG0000115252, ENSG0000140057, ENSG0000062822, ENSG0000138185, ENSG0000159899, ENSG0000198805 | 0.0538128451774168 | 0.305572903683738 |
| hsa01522  | Endocrine resistance| ENSG000000103024, ENSG00000198931, ENSG00000162104, ENSG00000147853, ENSG0000058600, ENSG00000160191, ENSG00000076685, ENSG00000106628, ENSG0000099817, ENSG0000133805, ENSG0000121281, ENSG0000185100, ENSG0000115252, ENSG0000140057, ENSG0000062822, ENSG0000138185, ENSG0000159899, ENSG0000198805 | 0.0545426335476288 | 0.305572903683738 |

**Alzheimer disease**

- ENSG00000103024
- ENSG00000198931
- ENSG00000162104
- ENSG00000147853
- ENSG0000058600
- ENSG00000160191
- ENSG00000076685
- ENSG00000106628
- ENSG0000099817
- ENSG0000133805
- ENSG0000121281
- ENSG0000185100
- ENSG0000115252
- ENSG0000140057
- ENSG0000062822
- ENSG0000138185
- ENSG0000159899
- ENSG0000198805

**Endocrine resistance**

- ENSG000000103024
- ENSG00000198931
- ENSG00000162104
- ENSG00000147853
- ENSG0000058600
- ENSG00000160191
- ENSG00000076685
- ENSG00000106628
- ENSG0000099817
- ENSG0000133805
- ENSG0000121281
- ENSG0000185100
- ENSG0000115252
- ENSG0000140057
- ENSG0000062822
- ENSG0000138185
- ENSG0000159899
- ENSG0000198805

| Pathway ID | Pathway Name        | Gene IDs | P-value 1  | P-value 2 |
|-----------|---------------------|----------|-----------|-----------|
| hsa05010  | Alzheimer disease   | ENSG00000103024, ENSG00000198931, ENSG00000162104, ENSG00000147853, ENSG0000058600, ENSG00000160191, ENSG00000076685, ENSG00000106628, ENSG0000099817, ENSG0000133805, ENSG0000121281, ENSG0000185100, ENSG0000115252, ENSG0000140057, ENSG0000062822, ENSG0000138185, ENSG0000159899, ENSG0000198805 | 0.0538128451774168 | 0.305572903683738 |
| hsa01522  | Endocrine resistance| ENSG000000103024, ENSG00000198931, ENSG00000162104, ENSG00000147853, ENSG0000058600, ENSG00000160191, ENSG00000076685, ENSG00000106628, ENSG0000099817, ENSG0000133805, ENSG0000121281, ENSG0000185100, ENSG0000115252, ENSG0000140057, ENSG0000062822, ENSG0000138185, ENSG0000159899, ENSG0000198805 | 0.0545426335476288 | 0.305572903683738 |
| Pathway Enrichment | **hsa04064** | NF-kappa B signaling pathway | 21/1188 | 70/5573 | 0.0547155228096473 | 0.305572903683738 | ENSG00000112242, ENSG00000157764, ENSG00000141510, TNFAIP3, NFKB2, BIRC, CXCL8, CARD14, REI, NFKB1, GADD45B, PTPG2, BIRC, ICAM1, NFKBIA, IRAK, TRAF3, XI, TAB3, CFLA, PLEC2, AT7, ERC1, TAB |
|-------------------|-------------|-----------------------------|--------|----------|---------------------|-----------------|---------------------|
| **hsa05210**      | Colorectal cancer | 24/1188 | 82/5573 | 0.0547443312788456 | 0.305572903683738 | ENSG00000118503, ENSG00000077150, ENSG00000110092, GSK3B, GADD45A, SMAD3, CCND1, JUI, GADD45B, DDB2, SMAC, RAF, RALI, HRAS, BAK, SOS2, TCF7I, EREG, MAPP, PMAIP1, AXIN, FOS, BIRC, TGFA, PIK3C, BRAF, TP5 |
| **hsa05323**      | Rheumatoid arthritis | 17/1188 | 55/5573 | 0.0613820874001706 | 0.336505371997364 | ENSG00000136244, ENSG00000169429, ENSG00000115009, G6C3, CCLL20, ATPI60, JU, ICAM1, IL1, CXCL1, VEGI, FOS, TClRG, CTSI, ATPI6V1, B1, CTSF, IL15, ATPI6V, A1, CTSK |
| **hsa05161**      | Hepatitis B | 33/1188 | 121/5573 | 0.37192395219477 | 0.3809539952036162 | ENSG00000136244, ENSG00000169429, ENSG00000115009, G6C3, CCLL20, ATPI60, JU, ICAM1, IL1, CXCL1, VEGI, FOS, TClRG, CTSI, ATPI6V1, B1, CTSF, IL15, ATPI6V, A1, CTSK |
| Pathway Enrichment | Gene IDs | P-values | q-values |
|---------------------|----------|----------|----------|
| hsa05142            | 22/1188  | 0.0710743615961856 | 0.376203948448775 |
| Chagas disease (American trypanosomiasis) | 22/1188  | 0.0710743615961856 | 0.376203948448775 |
| hsa04926            | 30/1188  | 0.0724547443934073 | 0.377010280148747 |
| Relaxin signaling pathway | 30/1188  | 0.0724547443934073 | 0.377010280148747 |
| hsa05216            | 11/1188  | 0.0746822912827918 | 0.382124390396952 |
| Thyroid cancer      | 11/1188  | 0.0746822912827918 | 0.382124390396952 |
| hsa00480            | 13/1188  | 0.0793419238534166 | 0.39111776996337 |
| Glutathione metabolism | 13/1188  | 0.0793419238534166 | 0.39111776996337 |
| Dataset ID  | Disease               | Pathway                          | # GOs | # ALLMols | p value 1  | q value 1  | # GOs | # ALLMols | p value 2  | q value 2  |
|------------|-----------------------|----------------------------------|-------|-----------|-----------|------------|-------|-----------|-----------|------------|
| hsa05220   | Chronic myeloid leukemia | hsa05220 Chronic myeloid leukemia | 21/1188 | 73/5573 | 0.0809959129923018 | 0.391117769965337 |       |           |           |            |
| hsa05214   | Glioma                | hsa05214 Glioma                  | 19/1188 | 65/5573 | 0.0820021366079631 | 0.391117769965337 |       |           |           |            |
| hsa05218   | Melanoma              | hsa05218 Melanoma                | 18/1188 | 61/5573 | 0.0822631261758009 | 0.391117769965337 |       |           |           |            |
| hsa00410   | beta-Alanine metabolism | hsa00410 beta-Alanine metabolism | 9/1188 | 26/5573 | 0.082809951295924 | 0.391117769965337 |       |           |           |            |
| hsa05012   | Parkinson disease     | hsa05012 Parkinson disease       | 34/1188 | 128/5573 | 0.0897193078021153 | 0.417330719624991 |       |           |           |            |
| Pathway ID | Pathway Name                  | ID | ID | FDR   | pval   |
|-----------|-------------------------------|----|----|-------|--------|
| hsa04330  | Notch signaling pathway       | 14/1188 | 46/5573 | 0.0942597485947848 | 0.420977362895348 |
| hsa04917  | Prolactin signaling pathway   | 17/1188 | 58/5573 | 0.0943387635819127 | 0.420977362895348 |
| hsa05213  | Endometrial cancer            | 16/1188 | 54/5573 | 0.0946170620188691 | 0.420977362895348 |
| hsa03013  | RNA transport                 | 40/1188 | 155/5573 | 0.101226294005626 | 0.443949603710387 |

ID: Entrez Gene ID
FDR: False Discovery Rate
pval: p-value
| Pathway ID | Pathway Name                        | Count 1 | Count 2 | P-value 1   | P-value 2   |
|-----------|------------------------------------|---------|---------|-------------|-------------|
| hsa051302 | Salmonella infection               | 20/1188 | 71/5573 | 0.10392587345369 | 0.449368384718709 |
| hsa01524  | Platinum drug resistance           | 10/1188 | 63/5573 | 0.106391717032112 | 0.45159461459689 |
| hsa05163  | Human cytomegalovirus infection    | 44/1188 | 173/5573| 0.107382432786883 | 0.45159461459689 |

| Pathway ID | Pathway Name                        | Count 1 | Count 2 | P-value 1   | P-value 2   |
|-----------|------------------------------------|---------|---------|-------------|-------------|
| hsa051302 | Salmonella infection               | 20/1188 | 71/5573 | 0.10392587345369 | 0.449368384718709 |
| hsa01524  | Platinum drug resistance           | 10/1188 | 63/5573 | 0.106391717032112 | 0.45159461459689 |
| hsa05163  | Human cytomegalovirus infection    | 44/1188 | 173/5573| 0.107382432786883 | 0.45159461459689 |

| Pathway ID | Pathway Name                        | Count 1 | Count 2 | P-value 1   | P-value 2   |
|-----------|------------------------------------|---------|---------|-------------|-------------|
| hsa051302 | Salmonella infection               | 20/1188 | 71/5573 | 0.10392587345369 | 0.449368384718709 |
| hsa01524  | Platinum drug resistance           | 10/1188 | 63/5573 | 0.106391717032112 | 0.45159461459689 |
| hsa05163  | Human cytomegalovirus infection    | 44/1188 | 173/5573| 0.107382432786883 | 0.45159461459689 |

| Pathway ID | Pathway Name                        | Count 1 | Count 2 | P-value 1   | P-value 2   |
|-----------|------------------------------------|---------|---------|-------------|-------------|
| hsa051302 | Salmonella infection               | 20/1188 | 71/5573 | 0.10392587345369 | 0.449368384718709 |
| hsa01524  | Platinum drug resistance           | 10/1188 | 63/5573 | 0.106391717032112 | 0.45159461459689 |
| hsa05163  | Human cytomegalovirus infection    | 44/1188 | 173/5573| 0.107382432786883 | 0.45159461459689 |
Pathway Enrichment

**hsa04310**  Wnt signaling pathway  31/1188  118/5573  0.113839148505683  0.468022278604662

**hsa04919**  Thyroid hormone signaling pathway  26/1188  97/5573  0.115533956088888  0.468022278604662

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| ID     | Pathway Enrichment                     | Pathway Name                        | FPKM   | Homo sapiens IDs                                      | Function          |
|--------|----------------------------------------|-------------------------------------|--------|------------------------------------------------------|-------------------|
| hsa01230 | Biosynthesis of amino acids            | 19/1188                            | 0.118218260718879 | ENSG000000174775, ENSG000000173599, ENSG000000135069, ENSG000000109107, ENSG000000102144, ENSG000000111640, ENSG000000138413, ENSG000000166411, ENSG00000070669, ENSG00000081181, ENSG000000166123, ENSG000000108515, ENSG000000143811, ENSG00000030707, ENSG00000016984, ENSG000000183010 | PC, PSAT1, ALDOC, PGK, IDH2, P53, CS5, GPD, IDH1, IDH3, ASNS, ARG, GPT2, ENO, PYCR2, RPL, AS51, MTR, PYCR1 |
| hsa04390 | Hippo signaling pathway                | 36/1188                            | 0.119823478489088 | ENSG000000187079, ENSG000000150457, ENSG000000082701, ENSG000000114251, ENSG000000118852, ENSG000000166949, ENSG000000107404, ENSG000000068028, ENSG000000110092, ENSG000000188064, ENSG000000125756, ENSG000000184009, ENSG000000129474, ENSG000000110330, ENSG000000175387, ENSG0000001555760, ENSG000000125845, ENSG000000116985, ENSG000000148737, ENSG000000180340, ENSG000000075711, ENSG000000128245, ENSG000000184008, ENSG000000103126, ENSG000000169884, ENSG000000132849, ENSG000000115596, ENSG0000001613251, ENSG000000089685, ENSG000000134376, ENSG000000013738, ENSG00000015738, ENSG000000107779, ENSG000000135924, ENSG00000015920, ENSG000000067606, ENSG000000125968, ENSG000000139926 | TEAD1, LATS1, GSK3B, WNT5A, CTG, SMAD3, DVL, RASSF1, CCND1, WNT7B, CCND3, ACTG1, AJSUB, BIRC, SMAD2, FXZ, BMP2, BMP4, TCF7L2, FZL, DLG1, YWH/A, WNTTR1, AXIN1, WNT10B, PATJ, WNT, FZD5, BIRC, CRB1, ID2, BMP1, AFA, FZ, PCR3, ID1, FRMD6 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 35/1188                            | 0.122625355988637 | ENSG000000136244, ENSG000000169429, ENSG000000082701, ENSG000000128272, ENSG000000198804, ENSG000000109320, ENSG000000177606, ENSG000000151366, ENSG000000105573, ENSG000000185633, ENSG000000198712, ENSG000000179091 | IL6, CXCL8, GSK3B, ATF, MT-C01, NFkB1, JUN, NDUF2, GSK3A, NDUF4, MT-C02, CY1, NDUF1, C0X7B, SOC, SREBF1, MT, CO3 |
| Gene ID | Gene Name | Pathway | Path ID | Log2 Freq | p-value |
|--------|-----------|---------|---------|-----------|---------|
| ENSG00000109390 | NDUFB10 | hsa04068 | FoxO signaling pathway | 31/1188 | 119/5573 | 0.123946938528155 | 0.468022278604662 |
| ENSG00000131174 | UQCR10 |
| ENSG00000184557 | NDUF57 IN |
| ENSG00000072310 | NDUFB7 |
| ENSG00000198938 | UQCR11 |
| ENSG00000171118 | DDT3 SDH |
| ENSG00000184076 | NDUFS4 |
| ENSG00000152586 | COX7C |
| ENSG00000171105 | NDUFA8 |
| ENSG00000097955 | NDUFB1 |
| ENSG00000127540 | PIK3CA ITC |
| ENSG00000175197 | NDUF58 |
| ENSG00000117118 | UQCRHL |
| ENSG00000164258 | CASP8 |
| ENSG00000121879 | UQRC2 |

| Gene ID | Gene Name | Pathway | Path ID | Log2 Freq | p-value |
|--------|-----------|---------|---------|-----------|---------|
| ENSG00000183648 | NDUFB1 |
| ENSG00000121879 | PIK3CA ITC |
| ENSG00000140990 | NDUFS4 |
| ENSG00000198938 | COX7C |
| ENSG00000171118 | DDT3 SDH |
| ENSG00000184076 | NDUF57 IN |
| ENSG00000152586 | NDUFB7 |
| ENSG00000198938 | UQCR11 |
| ENSG00000127540 | PIK3CA ITC |
| ENSG00000175197 | NDUF58 |
| ENSG00000117118 | UQCRHL |
| ENSG00000164258 | CASP8 |
| ENSG00000121879 | UQRC2 |

| Gene ID | Gene Name | Pathway | Path ID | Log2 Freq | p-value |
|--------|-----------|---------|---------|-----------|---------|
| ENSG00000082701 | IL6 BNIP3 |
| ENSG00000116717 | GADD45A |
| ENSG000001166949 | SMAD3 |
| ENSG00000112096 | SOC |
| ENSG00000087095 | NLK CCND |
| ENSG00000110092 | GADD45B |
| ENSG00000083860 | SGK1 |
| ENSG00000175387 | SMAD |
| ENSG00000053339 | CREBBP |
| ENSG00000139112 | GADD45B |
| ENSG00000132155 | CEBP |
| ENSG00000126457 | GABARAPL |
| ENSG00000174775 | RAP1 | PRMT |
| ENSG00000100485 | HRAS |
| ENSG00000101109 | SOS |
| ENSG00000166851 | STK4 |
| ENSG00000184481 | PKL |
| ENSG00000185386 | FOXO4 |
| ENSG00000171105 | MAPK11 IN |
| ENSG00000157456 | CCNB2 |
| ENSG00000102882 | MIF |
| ENSG00000188130 | MAPK3 |
| ENSG000001313916 | MAPK12 |
| ENSG00000149311 | BC |
| ENSG00000171862 | ATM |
| ENSG00000121879 | PTE1 |
| ENSG00000103479 | PIK3CA RBL |
| ENSG00000121691 | BAI |
| ENSG00000103479 | RB1 |
| ENSG00000157764 | BRAF |

| Gene ID | Gene Name | Pathway | Path ID | Log2 Freq | p-value |
|--------|-----------|---------|---------|-----------|---------|
| ENSG00000082701 | GSK3B |
| ENSG00000116717 | GADD45A |
| ENSG000001166949 | CDC20 |
| ENSG00000105810 | SMAD |
| ENSG00000110092 | CCND |
| ENSG00000112576 | GADD45B |
| ENSG00000099860 | RAD21 |
| ENSG00000164754 | SMAD |
| ENSG00000175387 | CREBBP |
| ENSG00000053339 | PKMYT1 |
| ENSG00000127564 | CDC26 |
| ENSG00000176386 | CDK2 |
| ENSG00000135446 | CDK6 |
| ENSG00000147889 | CCNC |
| ENSG00000166851 | CCNB2 |
| ENSG00000157456 | CDC2 |
| ENSG00000128245 | CCNH |
| ENSG00000114126 | MAD2L2 |
| ENSG00000205250 | CCNB2 |
| ENSG00000149311 | YWHAA |
| ENSG00000141552 | TFDP2 |
| ENSG00000116670 | E2F |
| ENSG00000134480 | ATM |
| ENSG00000164109 | ANAPC11 |
| ENSG00000103087 | MAD2L1 |
| ENSG00000164045 | CDC25A E2I |
| ENSG000000112242 | RBL2 E2F |
| ENSG00000116670 | TP53 |

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| Pathway Enrichment | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
|---------------------|---------|---------|-------------------|-------------------|
| hsa04215 Apoptosis - multiple species | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
| hsa05321 Inflammatory bowel disease (IBD) | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
| hsa00240 Pyrimidine metabolism | 25/1188 | 94/5573 | 0.129616754222647 | 0.479425825859671 |
| hsa04810 Regulation of actin cytoskeleton | 44/1188 | 177/5573 | 0.141416612472752 | 0.516169871709596 |

| Pathway Enrichment | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
|---------------------|---------|---------|-------------------|-------------------|
| hsa04215 Apoptosis - multiple species | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
| hsa05321 Inflammatory bowel disease (IBD) | 10/1188 | 32/5573 | 0.125009207966066 | 0.468022278604662 |
| hsa00240 Pyrimidine metabolism | 25/1188 | 94/5573 | 0.129616754222647 | 0.479425825859671 |
| hsa04810 Regulation of actin cytoskeleton | 44/1188 | 177/5573 | 0.141416612472752 | 0.516169871709596 |

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| ID      | Pathway Description                  | P-value 1 | P-value 2 | Fold Change |
|---------|--------------------------------------|-----------|-----------|-------------|
| hsa04925| Aldosterone synthesis and secretion | 0.14401   | 0.51619   | 1709596     |
| hsa05226| Gastric cancer                      | 0.14578   | 0.51619   | 1709596     |
| hsa05416| Viral myocarditis                   | 0.14627   | 0.51619   | 1709596     |
| hsa04151| PI3K-Akt signaling pathway          | 0.14963   | 0.52203   | 19511929    |

**Pathway Enrichment**

- **hsa04925**: Aldosterone synthesis and secretion
- **hsa05226**: Gastric cancer
- **hsa05416**: Viral myocarditis
- **hsa04151**: PI3K-Akt signaling pathway

**Gene List**

- **hsa04925**
  - ENSG00000196914
  - ENSG0000016683
  - ENSG00000143398
  - ENSG00000147065
  - ENSG00000121879
  - ENSG00000101608
  - ENSG00000157764
  - ENSG00000070087
  - ENSG00000083457
  - ENSG00000058884
  - ENSG00000137710

- **hsa05226**
  - LDLR
  - ITPR
  - ATP4
  - ATP5
  - CREB3L2
  - PLCB3
  - KCNK
  - PRKD2
  - PRKC

- **hsa05416**
  - GSK3B
  - WNT5A
  - GADD45A
  - JI
  - SMAD3
  - DVL
  - MET
  - CCND

- **hsa04151**
  - IL6
  - ITGB8
  - DDIT4
  - LAMB
  - THBS1
  - GSK3
  - EFNA1
  - ATF

**Additional Pathways**

- **hsa00019**: Aldosterone synthesis and secretion
  - ENSG00000116717
  - ENSG00000173801
  - ENSG00000166949
  - ENSG00000107404

- **hsa00018**: Gastric cancer
  - ENSG00000030110
  - ENSG00000082701
  - ENSG00000114251

- **hsa00017**: Viral myocarditis
  - ENSG00000090339
  - ENSG00000143322

- **hsa00016**: PI3K-Akt signaling pathway
  - ENSG00000136244
  - ENSG00000110092
  - ENSG00000184009

**Note**: P-values and fold changes indicate the statistical significance of pathway enrichment.
| Pathway ID | Pathway Name | Genes | Enrichment Score | FDR Score |
|-----------|--------------|-------|------------------|-----------|
| hsa05131  | Shigellosis  | 17/1188 62/5573 | 0.152933247161476 | 0.527047903000609 |
| hsa04611  | Platelet activation | 25/1188 96/5573 | 0.155127582325496 | 0.527047903000609 |
| Pathway Enrichment | Pathway Description | DEGs | Pathway Enrichment | Pathway Description | DEGs |
|-------------------|---------------------|------|-------------------|---------------------|------|
| *hsa04622*        | RIG-I-like receptor signaling pathway | 15/1188 | 54/5573 | 0.158769491658617 | 0.527047903000609 |
| *hsa04666*        | Fc gamma R-mediated phagocytosis | 20/1188 | 75/5573 | 0.15907180414047 | 0.527047903000609 |
| *hsa04370*        | VEGF signaling pathway | 14/1188 | 50/5573 | 0.16572086807244 | 0.527047903000609 |
| *hsa05414*        | Dilated cardiomyopathy (DCM) | 18/1188 | 67/5573 | 0.166398945223157 | 0.527047903000609 |
| Pathway ID | Pathway Name                                      | Count1 | Count2 | p-value1     | p-value2     |
|------------|--------------------------------------------------|--------|--------|--------------|--------------|
| hsa03420   | Nucleotide excision repair                       | 12/1188| 42/5573| 0.166696539693234 | 0.527047903000609 |
|            |                                                  |        |        |              |              |
| hsa04150   | mTOR signaling pathway                           | 34/1188| 136/5573| 0.169065756385785 | 0.527047903000609 |
|            |                                                  |        |        |              |              |
| hsa04630   | JAK-STAT signaling pathway                       | 28/1188| 110/5573| 0.169754006627054 | 0.527047903000609 |
|            |                                                  |        |        |              |              |
| hsa00980   | Metabolism of xenobiotics by cytochrome P450      | 10/1188| 34/5573| 0.170579713613723 | 0.527047903000609 |

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| Pathway | Description | ID | Count | Pathway | Description | ID | Count |
|---------|-------------|-----|-------|---------|-------------|-----|-------|
| hsa00640 | Propanoate metabolism | 9/1188 | 30/5573 | 0.17165315196086 | 0.527047903000609 |
| hsa05144 | Malaria | 8/1188 | 26/5573 | 0.171804027639036 | 0.527047903000609 |
| hsa05168 | Herpes simplex infection | 33/1188 | 132/5573 | 0.173393609781959 | 0.527047903000609 |
| hsa04915 | Estrogen signaling pathway | 25/1188 | 98/5573 | 0.183263278271239 | 0.547664130436135 |
| hsa04520 | Adherens junction | 18/1188 | 68/5573 | 0.183743991644697 | 0.547664130436135 |
| Pathway                          | ID     | Genes                                      | Upregulated | Downregulated | P-value   | FDR       |
|---------------------------------|--------|--------------------------------------------|-------------|---------------|-----------|-----------|
| B cell receptor signaling       | hsa0462| ENSG00000124216, ENSG00000140576, ENSG00000187095, ENSG00000142949, ENSG00000175387, ENSG00000198561, ENSG00000053339, ENSG00000148737, ENSG00000171105, ENSG00000197122, ENSG00000102882, ENSG0000035403, ENSG00000151422, ENSG00000136153 | 16/1188     | 60/5573        | 0.192950191769141 | 0.567286448353374 |
| Thermogenesis                   | hsa04714| ENSG00000198804, ENSG00000182158, ENSG00000184009, ENSG00000151336, ENSG00000099624, ENSG00000185633, ENSG00000198712, ENSG00000196786, ENSG00000179091, ENSG0000024030, ENSG00000110909, ENSG00000174775, ENSG0000010930, ENSG00000212907, ENSG00000131174, ENSG00000100485, ENSG00000174233, ENSG00000198938, ENSG00000140990, ENSG00000198886, ENSG00000181924, ENSG00000116985, ENSG00000184076, ENSG00000115286, ENSG00000168275, ENSG00000185386, ENSG00000099795, ENSG00000127540, ENSG00000117118, ENSG00000146258, ENSG00000188130, ENSG00000127184, ENSG00000162104, ENSG00000077463, ENSG00000162377, ENSG00000154723, ENSG00000119421, ENSG00000198840, ENSG00000197179, ENSG00000183648, ENSG00000121281, ENSG00000108604, ENSG00000124172, ENSG00000198695, ENSG00000134962, ENSG00000203667, ENSG00000110717 | 50/1188     | 209/5573        | 0.1960008172424  | 0.567286448353374 |

**Pathway Enrichment**

**hsa0462** B cell receptor signaling pathway

**hsa04714** Thermogenesis
| Pathway Enrichment |  |  | ENSG00000233954 | ENSG00000140740 |
|--------------------|--------------------------|----------------|--------------------------------|----------------|
| hsa05221 Acute myeloid leukemia | 15/1188 | 56/5573 | 0.19772403314944 | 0.56726448353374 |
| hsa00250 Alanine, aspartate and glutamate metabolism | 9/1188 | 31/5573 | 0.198922865022369 | 0.567286448353374 |
| hsa00360 Phenylalanine metabolism | 5/1188 | 15/5573 | 0.199566568150373 | 0.567286448353374 |
| hsa05143 African trypanosomiasis | 7/1188 | 23/5573 | 0.2027220843443 | 0.57096382838256 |
| hsa05164 Influenza A | 29/1188 | 117/5573 | 0.206335105225315 | 0.575862520947016 |
| hsa04062 Chemokine signaling pathway | 31/1188 | 126/5573 | 0.209463503495726 | 0.579326987145838 |

| Pathway Enrichment |  |  | ENSG00000173801 | ENSG00000109320 |
|--------------------|--------------------------|----------------|--------------------------------|----------------|
| hsa05221 Acute myeloid leukemia | 15/1188 | 56/5573 | 0.19772403314944 | 0.56726448353374 |
| hsa00250 Alanine, aspartate and glutamate metabolism | 9/1188 | 31/5573 | 0.198922865022369 | 0.567286448353374 |
| hsa00360 Phenylalanine metabolism | 5/1188 | 15/5573 | 0.199566568150373 | 0.567286448353374 |
| hsa05143 African trypanosomiasis | 7/1188 | 23/5573 | 0.2027220843443 | 0.57096382838256 |
| hsa05164 Influenza A | 29/1188 | 117/5573 | 0.206335105225315 | 0.575862520947016 |
| hsa04062 Chemokine signaling pathway | 31/1188 | 126/5573 | 0.209463503495726 | 0.579326987145838 |

| Pathway Enrichment |  |  | ENSG00000166532 | ENSG00000109320 |
|--------------------|--------------------------|----------------|--------------------------------|----------------|
| hsa05221 Acute myeloid leukemia | 15/1188 | 56/5573 | 0.19772403314944 | 0.56726448353374 |
| hsa00250 Alanine, aspartate and glutamate metabolism | 9/1188 | 31/5573 | 0.198922865022369 | 0.567286448353374 |
| hsa00360 Phenylalanine metabolism | 5/1188 | 15/5573 | 0.199566568150373 | 0.567286448353374 |
| hsa05143 African trypanosomiasis | 7/1188 | 23/5573 | 0.2027220843443 | 0.57096382838256 |
| hsa05164 Influenza A | 29/1188 | 117/5573 | 0.206335105225315 | 0.575862520947016 |
| hsa04062 Chemokine signaling pathway | 31/1188 | 126/5573 | 0.209463503495726 | 0.579326987145838 |

| Pathway Enrichment |  |  | ENSG00000166532 | ENSG00000109320 |
|--------------------|--------------------------|----------------|--------------------------------|----------------|
| hsa05221 Acute myeloid leukemia | 15/1188 | 56/5573 | 0.19772403314944 | 0.56726448353374 |
| hsa00250 Alanine, aspartate and glutamate metabolism | 9/1188 | 31/5573 | 0.198922865022369 | 0.567286448353374 |
| hsa00360 Phenylalanine metabolism | 5/1188 | 15/5573 | 0.199566568150373 | 0.567286448353374 |
| hsa05143 African trypanosomiasis | 7/1188 | 23/5573 | 0.2027220843443 | 0.57096382838256 |
| hsa05164 Influenza A | 29/1188 | 117/5573 | 0.206335105225315 | 0.575862520947016 |
| hsa04062 Chemokine signaling pathway | 31/1188 | 126/5573 | 0.209463503495726 | 0.579326987145838 |

| Pathway Enrichment |  |  | ENSG00000166532 | ENSG00000109320 |
|--------------------|--------------------------|----------------|--------------------------------|----------------|
| hsa05221 Acute myeloid leukemia | 15/1188 | 56/5573 | 0.19772403314944 | 0.56726448353374 |
| hsa00250 Alanine, aspartate and glutamate metabolism | 9/1188 | 31/5573 | 0.198922865022369 | 0.567286448353374 |
| hsa00360 Phenylalanine metabolism | 5/1188 | 15/5573 | 0.199566568150373 | 0.567286448353374 |
| hsa05143 African trypanosomiasis | 7/1188 | 23/5573 | 0.2027220843443 | 0.57096382838256 |
| hsa05164 Influenza A | 29/1188 | 117/5573 | 0.206335105225315 | 0.575862520947016 |
| hsa04062 Chemokine signaling pathway | 31/1188 | 126/5573 | 0.209463503495726 | 0.579326987145838 |
| Pathway Enrichment | 19/1188 | 74/5573 | 0.214959398549061 | 0.589219065665731 |
|---------------------|---------|---------|-------------------|-------------------|
| hsa03008 Ribosome biogenesis in eukaryotes | 15/1188 | 57/5573 | 0.218732275031037 | 0.594254941898481 |
| hsa05133 Pertussis | 18/1188 | 70/5573 | 0.22098389986165 | 0.595105765752215 |
| hsa01521 EGFR tyrosine kinase inhibitor resistance | 14/1188 | 53/5573 | 0.224737326982852 | 0.597851276242852 |
| Pathway Enrichment          | Description                                           | Gene ID | Enrichment Score | Pathway ID |
|-----------------------------|-------------------------------------------------------|---------|------------------|------------|
| hsa04612                    | Antigen processing and presentation                   | 9/1188  | 32/5573          | 0.227845600392227 | 0.597851276242852 |
| hsa04913                    | Ovarian steroidogenesis                               | 9/1188  | 32/5573          | 0.227845600392227 | 0.597851276242852 |
| hsa04960                    | Aldosterone-regulated sodium reabsorption             | 8/1188  | 28/5573          | 0.232655692887    | 0.60529913318906   |
| hsa04916                    | Melanogenesis                                          | 21/1188 | 84/5573          | 0.239170829190022 | 0.605561022616364  |
| hsa05215                    | Prostate cancer                                       | 21/1188 | 84/5573          | 0.239170829190022 | 0.605561022616364  |
| hsa05412                    | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 15/1188 | 58/5573          | 0.240658212099482  | 0.605561022616364  |

Gene IDs and Enrichment Scores are provided for each pathway.
| Pathway Enrichment | Gene IDs | Results |
|---------------------|----------|---------|
| **hsa00670** | One carbon pool by folate | 5/1188 16/5573 0.242589887419026 0.605561022616364 |
| **hsa04723** | Retrograde endocannabinoid signaling | 28/1188 115/5573 0.24261891134141 0.605561022616364 |
| **hsa05418** | Fluid shear stress and atherosclerosis | 28/1188 116/5573 0.258658038217017 0.640387239779228 |
| **hsa04540** | Gap junction | 18/1188 72/5573 0.261257904614699 0.641649413733702 |

**hsa00670** | One carbon pool by folate | 5/1188 16/5573 0.242589887419026 0.605561022616364 |

**hsa04723** | Retrograde endocannabinoid signaling | 28/1188 115/5573 0.24261891134141 0.605561022616364 |

**hsa05418** | Fluid shear stress and atherosclerosis | 28/1188 116/5573 0.258658038217017 0.640387239779228 |

**hsa04540** | Gap junction | 18/1188 72/5573 0.261257904614699 0.641649413733702 |
| Pathway ID | Pathway Name                      | Enrichment Scores | Gene IDs |
|-----------|-----------------------------------|-------------------|----------|
| hsa04145  | Phagosome                         | 25/1188           | 103/5573 |
|           |                                   | 0.263924861313736 | 0.643055019232674 |
| hsa00330  | Arginine and proline metabolism   | 11/1188           | 42/5573  |
|           |                                   | 0.271586962384536 | 0.656513365764194 |
| hsa04918  | Thyroid hormone synthesis         | 13/1188           | 51/5573  |
|           |                                   | 0.280601120990367 | 0.672000409871236 |
| hsa04211  | Longevity regulating pathway      | 18/1188           | 73/5573  |
|           |                                   | 0.28237150773091  | 0.672000409871236 |
| hsa04912  | GnRH signaling pathway            | 20/1188           | 82/5573  |
|           |                                   | 0.285675940681025 | 0.674634721454421 |
| Pathway Name                                      | Annotation | Count | Adjusted | P.value | Count | Adjusted | P.value |
|--------------------------------------------------|------------|-------|----------|---------|-------|----------|---------|
| RNA polymerase                                   | hsa03020   | 8/1188 | 30/5573  | 0.299706500524127 | 0.699874620969842 |
| Renal cell carcinoma                             | hsa05211   | 16/1188 | 65/5573  | 0.300923289798108 | 0.699874620969842 |
| Protein digestion and absorption                 | hsa04974   | 15/1188 | 61/5573  | 0.311018627625035 | 0.716508664483417 |
| Huntington disease                               | hsa05016   | 41/1188 | 178/5573 | 0.312743195572566 | 0.716508664483417 |
| Pathway | Description | Gene Symbols | Score 1 | Score 2 |
|---------|-------------|--------------|---------|---------|
| hsa01040 | Biosynthesis of unsaturated fatty acids | ENSG00000183648, ENSG00000099817, ENSG00000124172, ENSG00000108064, ENSG00000110717, ENSG00000233954, ENSG00000064012, ENSG00000141510, ENSG00000140740 | 6/1188 | 22/5573 | 0.321822169407309 |
| hsa04722 | Neurotrophin signaling pathway | UQCRH1, CASP8, TP53, UQCRCL | 25/1188 | 107/5573 | 0.336841878189829 |
| hsa04961 | Endocrine and other factor-regulated calcium reabsorption | SCD, ELOVL, PEER, HAD, ACOT7, ACOT1 | 9/1188 | 36/5573 | 0.355349005492774 |
| hsa05160 | Hepatitis C | LDLR, CXCL, GSK3B, CDL1, NFKB1, JAK, IFNAR1, NFKBIA, RAI, TRAF3, HR, SOS2, SOC5, MAPK11, MAPK12, PLCG2, PIK3CA, NFKBIB, SH2B2, BRAF, TP53 | 25/1188 | 108/5573 | 0.35584481981354 |
| hsa04914 | Progesterone-mediated oocyte maturation | HSP90AA1, PKMYT1, RA, CDC26, ADC | 20/1188 | 86/5573 | 0.370037802062063 |
| Pathway Enrichment | Inflammatory mediator regulation of TRP channels | MAPK signaling pathway |
|---------------------|-----------------------------------------------|------------------------|
| hsa04750            | 18/1188                                      | 56/1188                |
|                     | 77/5573                                      | 251/5573               |
|                     | 0.371584527976532                           | 0.371921642568696      |
|                     | 0.807182039659756                           | 0.807182039659756      |
| ENSG00000185386     | MAPK12                                        | NFKB2                  |
| ENSG00000157456     | ADCY9 CPEI                                    | MAP2K6                 |
| ENSG00000102882     | ANAPC11                                       | AS1CL PLCE             |
| ENSG00000188130     | MAD2L2                                        | P2RY2 PKRI             |
| ENSG00000162104     | PIK3CA                                        | TRPV3 ADC              |
| ENSG00000107864     | ADCY7 MAD2L1                                  | MAPK11 SR              |
| ENSG00000141552     | K223Rv                                       | ITPR1                  |
| ENSG00000116670     |                                                               |
| ENSG00000121879     |                                                               |
| ENSG00000121281     |                                                               |
| ENSG00000164045     |                                                               |
| ENSG00000157764     |                                                               |
| Enrichment ID | Pathway Name                                      | Size | Number of Genes | Number of Loci | Pathway Enrichment Score | Pathway Correction Score |
|---------------|--------------------------------------------------|------|----------------|----------------|--------------------------|--------------------------|
| hsa05032      | Morphine addiction                              | 14/1188 | 59/5573       | 0.373729379188082 | 0.807182039659756        |                          |
| hsa04931      | Insulin resistance                               | 21/1188 | 91/5573       | 0.379799238072944 | 0.807182039659756        |                          |
| hsa00340      | Histidine metabolism                             | 5/1188  | 19/5573       | 0.381242331435389 | 0.807182039659756        |                          |
| hsa00532      | Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate | 5/1188  | 19/5573       | 0.381242331435389 | 0.807182039659756        |                          |
| hsa00983      | Drug metabolism - other enzymes                  | 11/1188 | 46/5573       | 0.388747668040592 | 0.80861151516974         |                          |
| hsa05152      | Tuberculosis                                     | 28/1188 | 124/5573      | 0.39913917514802  | 0.80861151516974         |                          |
| **hsa0040** | Pentose and glucuronate interconversions | 4/1188 | 15/5573 | 0.40152907325353 | 0.80861151516974 |
|-----------------|--------------------------------------|--------|---------|------------------|------------------|
|                  |                                      |        |         |                  |                  |
| **hsa00730**     | Thiamine metabolism                 | 4/1188 | 15/5573 | 0.40152907325353 | 0.80861151516974 |
|                  |                                      |        |         |                  |                  |
| **hsa04072**     | Phospholipase D signaling pathway    | 26/1188| 115/5573| 0.402609986520786| 0.80861151516974 |
|                  |                                      |        |         |                  |                  |
| **hsa05130**     | Pathogenic Escherichia coli infection| 12/1188| 51/5573 | 0.402680616222708| 0.80861151516974 |
|                  |                                      |        |         |                  |                  |
| **hsa04623**     | Cytosolic DNA-sensing pathway        | 10/1188| 42/5573 | 0.404853672496411| 0.80861151516974 |
|                  |                                      |        |         |                  |                  |
| **hsa03410**     | Base excision repair                | 8/1188 | 33/5573 | 0.40630328222387 | 0.80861151516974 |
|                  |                                      |        |         |                  |                  |
| **hsa04660**     | T cell receptor signaling pathway    | 17/1188| 74/5573 | 0.408034084441562| 0.80861151516974 |

**Pathway Enrichment**

| Pathway Name                                      | KEGG ID | KEGG Name                        | q-value | p-value |
|--------------------------------------------------|---------|----------------------------------|---------|---------|
| Pentose and glucuronate interconversions         | hsa00040| Pentose and glucuronate interconversions | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Thiamine metabolism                              | hsa00730| Thiamine metabolism              | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Phospholipase D signaling pathway                | hsa04072| Phospholipase D signaling pathway | 26/1188 | 115/5573| 0.402609986520786| 0.80861151516974 |
| Pathogenic Escherichia coli infection            | hsa05130| Pathogenic Escherichia coli infection | 12/1188 | 51/5573 | 0.402680616222708| 0.80861151516974 |
| Cytosolic DNA-sensing pathway                    | hsa04623| Cytosolic DNA-sensing pathway     | 10/1188 | 42/5573 | 0.404853672496411| 0.80861151516974 |
| Base excision repair                             | hsa03410| Base excision repair             | 8/1188  | 33/5573 | 0.40630328222387 | 0.80861151516974 |
| T cell receptor signaling pathway                | hsa04660| T cell receptor signaling pathway | 17/1188 | 74/5573 | 0.408034084441562| 0.80861151516974 |

**KEGG Enrichment**

| Pathway Name                                      | KEGG ID | KEGG Name                        | q-value | p-value |
|--------------------------------------------------|---------|----------------------------------|---------|---------|
| Pentose and glucuronate interconversions         | hsa00040| Pentose and glucuronate interconversions | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Thiamine metabolism                              | hsa00730| Thiamine metabolism              | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Phospholipase D signaling pathway                | hsa04072| Phospholipase D signaling pathway | 26/1188 | 115/5573| 0.402609986520786| 0.80861151516974 |
| Pathogenic Escherichia coli infection            | hsa05130| Pathogenic Escherichia coli infection | 12/1188 | 51/5573 | 0.402680616222708| 0.80861151516974 |
| Cytosolic DNA-sensing pathway                    | hsa04623| Cytosolic DNA-sensing pathway     | 10/1188 | 42/5573 | 0.404853672496411| 0.80861151516974 |
| Base excision repair                             | hsa03410| Base excision repair             | 8/1188  | 33/5573 | 0.40630328222387 | 0.80861151516974 |
| T cell receptor signaling pathway                | hsa04660| T cell receptor signaling pathway | 17/1188 | 74/5573 | 0.408034084441562| 0.80861151516974 |

**Enrichment**

| Pathway Name                                      | KEGG ID | KEGG Name                        | q-value | p-value |
|--------------------------------------------------|---------|----------------------------------|---------|---------|
| Pentose and glucuronate interconversions         | hsa00040| Pentose and glucuronate interconversions | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Thiamine metabolism                              | hsa00730| Thiamine metabolism              | 4/1188  | 15/5573 | 0.40152907325353 | 0.80861151516974 |
| Phospholipase D signaling pathway                | hsa04072| Phospholipase D signaling pathway | 26/1188 | 115/5573| 0.402609986520786| 0.80861151516974 |
| Pathogenic Escherichia coli infection            | hsa05130| Pathogenic Escherichia coli infection | 12/1188 | 51/5573 | 0.402680616222708| 0.80861151516974 |
| Cytosolic DNA-sensing pathway                    | hsa04623| Cytosolic DNA-sensing pathway     | 10/1188 | 42/5573 | 0.404853672496411| 0.80861151516974 |
| Base excision repair                             | hsa03410| Base excision repair             | 8/1188  | 33/5573 | 0.40630328222387 | 0.80861151516974 |
| T cell receptor signaling pathway                | hsa04660| T cell receptor signaling pathway | 17/1188 | 74/5573 | 0.408034084441562| 0.80861151516974 |
| Pathway ID | Pathway Name                     | Genes                                                                 | p-value (FDR) | Adjusted p-value |
|------------|----------------------------------|----------------------------------------------------------------------|---------------|-----------------|
| hsa05203   | Viral carcinogenesis             | ENSG00000135446, ENSG00000174775, ENSG00000100485, ENSG00000185386, ENSG00000075711, ENSG00000102882, ENSG00000188130, ENSG00000170345, ENSG00000121879, ENSG00000104825 | 0.414885477928796 | 0.80861151516974 |
| hsa00590   | Arachidonic acid metabolism      | ENSG00000135446, ENSG00000174775, ENSG00000100485, ENSG00000185386, ENSG00000075711, ENSG00000102882, ENSG00000188130, ENSG00000170345, ENSG00000121879, ENSG00000104825 | 0.422539904699296 | 0.80861151516974 |
| hsa05204   | Chemical carcinogenesis          | ENSG00000135446, ENSG00000174775, ENSG00000100485, ENSG00000185386, ENSG00000075711, ENSG00000102882, ENSG00000188130, ENSG00000170345, ENSG00000121879, ENSG00000104825 | 0.422539904699296 | 0.80861151516974 |
| hsa00062   | Fatty acid elongation            | ENSG00000135446, ENSG00000174775, ENSG00000100485, ENSG00000185386, ENSG00000075711, ENSG00000102882, ENSG00000188130, ENSG00000170345, ENSG00000121879, ENSG00000104825 | 0.42584676396206 | 0.80861151516974 |
| hsa00982   | Drug metabolism - cytochrome P450 | ENSG00000135446, ENSG00000174775, ENSG00000100485, ENSG00000185386, ENSG00000075711, ENSG00000102882, ENSG00000188130, ENSG00000170345, ENSG00000121879, ENSG00000104825 | 0.42584676396206 | 0.80861151516974 |

References:
- C3 NFkB2
- ATF4 CDC2
- KAT2A NFkB
- CREB3L2
- CDK6 JAK
- HIST2H4B
- CCND1 CCND3 JUN
- GSTN NFkB1
- CREBBP
- TRAF3 CDK
- HRAS BAK
- CDKN2A
- CHK4
- HIST2H2BI
- DIL1 SRC
- MAPK3 PMAIP1
- YWHAH
- HDAC7 SCI PIK3CA
- HDAC8 HIST1H2BI
- RBL2 STAT1 GTF2H2C
- CASP8 TP5
- AKR1C3 PTGS1 PTGES2 PTGES3 GPX PL2G4B
- ALDH3B1 MGT3 CBF MGST2 GST GSTM1 ALDH3A1
- ABHD17B ALDH1A1 ELOVL5 HADHA ACOT7 ACOT1
- ALDH3B1 MGST3 MGST2 GST GSTM1 ALDH3A1

file:///Users/dawen/Desktop/诺禾致源测序/2021-07-10结果交付-差异原始数据/X101SC21061603-Z01-F001-B1-16.result/5.Enrichment/2.KEGG/K223Rv... 4/7/2021/7/11 Pathway Enrichment
| Pathway ID | Pathway Name                                      | P.Value | q.Value | GO IDs                                                                 | Genes                                                                 |
|-----------|--------------------------------------------------|---------|---------|-----------------------------------------------------------------------|-----------------------------------------------------------------------|
| hsa04940  | Type I diabetes mellitus                         | 3/1188  | 11/5573 | 0.426311858525028 0.80861151516974 | ENSG000000144381 ENSG000001668811 ENSG00000109472                |
| hsa04928  | Parathyroid hormone synthesis, secretion and action | 19/1188 | 84/5573 | 0.4271735456466047 0.80861151516974 | ENSG00000113448 ENSG00000170776 ENSG00000109995 ENSG00000128272 ENSG00000182158 ENSG000001494972 ENSG00000240103 ENSG00000132155 ENSG00000174233 ENSG00000125966 ENSG00000162337 ENSG00000069589 ENSG00000069433 ENSG00000102882 ENSG00000162104 EN | PDE4D AKAP13 ITPR1 ATF CREB3L2 PLCB3 RAF1 ADCY MAPK24 LRF PDE4A ITPF MAPK3 ADCY9 FO ADCC7 BRA ARRB1 |
| hsa00601  | Glycosphingolipid biosynthesis - lacto and neolacto series | 5/1188  | 20/5573 | 0.428121691392198 0.80861151516974 | ENSG00000086062 ENSG0000117411 ENSG00000196371 ENSG00000158850 | B4GALT1 B4GALT2 FUT4 B4GALT3 ST3GAL4 |
| hsa04066  | HIF-1 signaling pathway                           | 20/1188 | 89/5573 | 0.435896552553974 0.80861151516974 | ENSG00000136244 ENSG00000152256 ENSG00000109320 ENSG00000102144 | IL6 PDK1 NFKB1 PGK GAPDH IFN1G1 CREB B P2M2 E1C1 HIF1 MKK2 ENC E1G1N INS MAPK3 VEGFA HIF1 HKDC1 PLCG2 SLC2A1 PIK3CA RB1 E1F4EBP1 |
| hsa00600  | Sphingolipid metabolism                           | 10/1188 | 43/5573 | 0.436636515706143 0.80861151516974 | ENSG00000176170 ENSG00000198964 ENSG00000143753 ENSG00000103056 ENSG00000067113 ENSG00000141934 ENSG00000164023 ENSG00000143418 ENSG00000148156 ENSG00000162139 | SPHK1 SGM DEG51 SMPI PLP1 PLP2 SGM25 CER UGCG NEU |
| hsa0562   | Inositol phosphate metabolism                     | 15/1188 | 66/5573 | 0.437229679212302 0.80861151516974 | ENSG00000133056 ENSG00000149472 ENSG00000148384 ENSG00000103502 ENSG00000197943 ENSG00000143938 ENSG00000171862 ENSG00000121879 ENSG00000078269 ENSG00000065644 | PIK3CB2 PLCB3 INPP5E CDII PLCG2 PIP5KA1A PTK2 PIK3C SYNJ2 ITPK IPMK MTMF ALDH6A1 PIK4A MTMR14 |
| hsa05410  | Hypertrophic cardiomyopathy (HCM)                 | 15/1188 | 66/5573 | 0.437229679212302 0.80861151516974 | ENSG00000136244 ENSG00000105855 ENSG00000082781 ENSG00000184009 ENSG00000213949 ENSG00000156557 ENSG00000173402 | IL6 ITGB8 ITGB5 AC7 CT ITG5A1 TTF CACNA2D2 DAG1 DES DMD RYR2 ITG4 FIAM EMD ITGA3 |
| Pathway Enrichment | Human Pathway ID | Count | Adjusted p-value | Enrichment Score |
|---------------------|-----------------|-------|------------------|------------------|
| hsa04015 Rap1 signaling pathway | ENSG00000175084 | 37/1188 | 0.441038786288409 | 0.810771900542166 |
| hsa04500 Selenocompound metabolism | ENSG00000178953 | 4/1188 | 0.454508804627462 | 0.828002275810507 |
| hsa04530 Tight junction | ENSG00000170023 | 31/1188 | 0.455805813068325 | 0.828002275810507 |
| hsa04620 Valine, leucine and isoleucine degradation | ENSG00000175084 | 10/1188 | 0.468269927826643 | 0.845640399075173 |
| Pathway Enrichment                                                                 | Pathway ID | GO Term | GO ID | Gene Count | FDR Count | p-value | q-value |
|----------------------------------------------------------------------------------|------------|---------|-------|------------|-----------|---------|---------|
| Glycosphingolipid biosynthesis - globo and isoglobo series                        | hsa00603   | ENSG00000164904 | 12/5573 | 0.48796463480914 | 0.861463660685045 | NAGA ST3GAL1 ST3GAL2 |
| Glycolysis / Gluconeogenesis                                                      | hsa00010   | ENSG00000109107 | 12/5573 | 0.488846457933062 | 0.861463660685045 | ALDOC PG GAPDH ALDH3B1 PG3M1 LDHAL6B LDHB ENO ALDH7A1 HKDC1 GAL ALDH3A1 |
| Proteasome                                                                       | hsa03050   | ENSG00000117054 | 9/1188 | 0.489323703085082 | 0.861463660685045 | PSME1 PSM5 PSMA5 PSM4 PSM6 PSM3 PSM1 PSM4 PSM5 PSMB4 |
| Galactose metabolism                                                             | hsa00052   | ENSG00000117411 | 6/1188 | 0.489490425191813 | 0.861463660685045 | B4GALT1 AKR1B1 B4GALT2 PG3M1 HKDC GALA |
| Cardiac muscle contraction                                                       | hsa04260   | ENSG00000125165 | 13/1188 | 0.497740615279073 | 0.861463660685045 | ATP1B1 MT CO1 MT-CC CYC1 COX7 MT-CO3 UQCR10 CACN2AD UQCR11 COX7C RYF UQCRHL UQCRHC |
| ErbB signaling pathway                                                            | hsa04012   | ENSG00000157445 | 17/1188 | 0.50371558709381 | 0.861463660685045 | GSK3B JUN RAF1 HRA ABL2 SOS EREG SRC MAPK3 PLC1 TGFA NRG PIK3CA MAP2K4 STAT5A BRF EIF4EBP1 |
| Arginine biosynthesis                                                             | hsa00220   | ENSG00000185339 | 4/1188 | 0.505821572997362 | 0.861463660685045 | CPS1 ARG GPT2 ASS |
| 2-Oxocarboxylic acid metabolism                                                  | hsa01210   | ENSG00000185339 | 4/1188 | 0.505821572997362 | 0.861463660685045 | IDHD2 IDH1 IDH3A GPT |
| Vitamin digestion and absorption                                                 | hsa04977   | ENSG00000185339 | 4/1188 | 0.505821572997362 | 0.861463660685045 | TCN2 SLC19A1 |
| Pathway Enrichment | Description | Genes | Enrichment Score | FDR Corrected P Value |
|---------------------|-------------|-------|------------------|----------------------|
| hsa04664            | Fc epsilon RI signaling pathway | 12/1188 55/5573 | 0.517081008394347 | 0.861463660685045 |
|                     |             | ENSG00000138074 |                  |                      |
|                     |             | ENSG00000117479 |                  |                      |
|                     |             | MAP2K6 VAA   |                  |                      |
|                     |             | RAF1 HRA    |                  |                      |
|                     |             | SOS2 MAPK   |                  |                      |
|                     |             | MAPK3       |                  |                      |
|                     |             | MAPK12      |                  |                      |
|                     |             | PLCG2       |                  |                      |
|                     |             | PIK3CA      |                  |                      |
|                     |             | MAP2K4      |                  |                      |
|                     |             | PLA2G4      |                  |                      |
| hsa04966            | Collecting duct acid secretion | 5/1188 22/5573 | 0.519064936810359 | 0.861463660685045 |
|                     |             | ENSG00000010719 |               |                      |
|                     |             | ENSG00000116039 |               |                      |
|                     |             | ENSG00000105675 |               |                      |
|                     |             | ENSG00000114543 |               |                      |
|                     |             | CLCNKB      |                  |                      |
|                     |             | ATP6V1B1    |                  |                      |
|                     |             | ATP4A       |                  |                      |
| hsa05340            | Primary immunodeficiency | 5/1188 22/5573 | 0.519064936810359 | 0.861463660685045 |
|                     |             | ENSG00000105369 |               |                      |
|                     |             | ENSG00000160224 |               |                      |
|                     |             | ENSG00000147168 |               |                      |
|                     |             | ORAI1       |                  |                      |
|                     |             | RFX         |                  |                      |
|                     |             | CD79A       |                  |                      |
|                     |             | AIR         |                  |                      |
| hsa01200            | Carbon metabolism | 23/1188 107/5573 | 0.520608704066263 | 0.861463660685045 |
|                     |             | ENSG00000109107 |               |                      |
|                     |             | ENSG00000102144 |               |                      |
|                     |             | ENSG00000182051 |               |                      |
|                     |             | PC          |                  |                      |
|                     |             | PSAT1       |                  |                      |
|                     |             | ALDOC       |                  |                      |
|                     |             | PGK         |                  |                      |
|                     |             | IDH2        |                  |                      |
|                     |             | PSPH        |                  |                      |
|                     |             | CTSB        |                  |                      |
|                     |             | ALDOC       |                  |                      |
|                     |             | ENO         |                  |                      |
|                     |             | MUT         |                  |                      |
|                     |             | SDHB        |                  |                      |
|                     |             | PGP         |                  |                      |
|                     |             | RPIA        |                  |                      |
|                     |             | ACAT2       |                  |                      |
|                     |             | HKDC1       |                  |                      |
|                     |             | HADHA       |                  |                      |
|                     |             | CAT         |                  |                      |
|                     |             | ADCAI       |                  |                      |
|                     |             | ALDH6A1     |                  |                      |
| hsa04923            | Regulation of lipolysis in adipocytes | 9/1188 41/5573 | 0.522005009205686 | 0.861463660685045 |
|                     |             | ENSG00000117418 |               |                      |
|                     |             | ENSG00000117118 |               |                      |
|                     |             | ENSG000001166123 |             |                      |
|                     |             | ENSG00000108515 |               |                      |
|                     |             | ENSG00000146605 |               |                      |
|                     |             | ENSG00000117118 |               |                      |
|                     |             | ENSG00000106224 |               |                      |
|                     |             | ENSG00000141768 |               |                      |
|                     |             | PTGS1       |                  |                      |
|                     |             | PTG          |                  |                      |
|                     |             | ADCY6       |                  |                      |
|                     |             | ADR         |                  |                      |
|                     |             | INSR        |                  |                      |
|                     |             | ADCY        |                  |                      |
|                     |             | PIK3CA      |                  |                      |
|                     |             | AUR7        |                  |                      |
|                     |             | PLIN        |                  |                      |
| hsa00350            | Tyrosine metabolism | 6/1188 27/5573 | 0.529764272323754 | 0.861463660685045 |
|                     |             | ENSG00000069535 |               |                      |
|                     |             | ENSG00000108602 |               |                      |
|                     |             | HPD         |                  |                      |
|                     |             | ALDH3       |                  |                      |
|                     |             | AOC3        |                  |                      |
|                     |             | MAO         |                  |                      |
|                     |             | TH          |                  |                      |
|                     |             | ALDH3J      |                  |                      |
| hsa00760            | Nicotinate and nicotinamide metabolism | 6/1188 27/5573 | 0.529764272323754 | 0.861463660685045 |
|                     |             | ENSG00000135318 |               |                      |
|                     |             | ENSG00000112299 |               |                      |
|                     |             | ENSG000001076685 |             |                      |
|                     |             | ENSG00000103485 |               |                      |
|                     |             | ENSG00000198805 |               |                      |
|                     |             | NNAT        |                  |                      |
|                     |             | NT5         |                  |                      |
|                     |             | NT5C        |                  |                      |
|                     |             | QPR7        |                  |                      |
|                     |             | PN6         |                  |                      |
| hsa01523            | Antifolate resistance | 6/1188 27/5573 | 0.529764272323754 | 0.861463660685045 |
|                     |             | ENSG00000136244 |               |                      |
|                     |             | ENSG00000173636 |               |                      |
|                     |             | ENSG00000109320 |               |                      |
|                     |             | ENSG00000228716 |               |                      |
|                     |             | ENSG00000110195 |               |                      |
|                     |             | ENSG00000108846 |               |                      |
|                     |             | ILSL         |                  |                      |
|                     |             | SLC19A      |                  |                      |
|                     |             | NFkB1       |                  |                      |
|                     |             | DHF         |                  |                      |
|                     |             | FOLR1       |                  |                      |
|                     |             | ABCI        |                  |                      |
| hsa04976            | Bile secretion | 10/1188 46/5573 | 0.530347335079718 | 0.861463660685045 |
|                     |             | ENSG00000130164 |               |                      |
|                     |             | ENSG00000143153 |               |                      |
|                     |             | ENSG00000143819 |               |                      |
|                     |             | ENSG00000164889 |               |                      |
|                     |             | ENSG00000174233 |               |                      |
|                     |             | LDLR        |                  |                      |
|                     |             | ATP11       |                  |                      |
|                     |             | EPK1        |                  |                      |
|                     |             | SLC4A2      |                  |                      |
|                     |             | ADCCY6      |                  |                      |
|                     |             | NCE1H       |                  |                      |
| Pathway Enrichment | Gene ID | Description | Count | Total Count | P-value | FDR | 
|---------------------|---------|-------------|-------|-------------|---------|-----| 
| Vibrio cholerae infection | hsa05110 | 10/1188 | 46/5573 | 0.530347335079718 | 0.861463660685045 | 
|  |  |  |  |  |  | 
| Autophagy - animal | hsa04140 | 26/1188 | 122/5573 | 0.536996904150428 | 0.865320142248214 | 
| Vascular smooth muscle contraction | hsa04270 | 19/1188 | 89/5573 | 0.539446971885232 | 0.865320142248214 | 
| Insulin secretion | hsa04911 | 12/1188 | 56/5573 | 0.544852487667386 | 0.865320142248214 | 
| Endocytosis | hsa04144 | 46/1188 | 217/5573 | 0.545135271118504 | 0.865320142248214 |
| Pathway ID     | Type                          | P-value       | q-value         |
|----------------|-------------------------------|---------------|-----------------|
| hsa04930       | Type II diabetes mellitus     | 0.546814682723627 | 0.865320142248214 |
| hsa03060       | Protein export                | 0.562178110013211 | 0.877235573417917 |
| hsa05020       | Prion diseases                | 0.562178110013211 | 0.877235573417917 |
| hsa03018       | RNA degradation               | 0.562916638317035 | 0.877235573417917 |
| hsa04213       | Longevity regulating pathway - multiple species | 0.589766566271235 | 0.912857011232122 |
| Pathway Enrichment | Gene ID | Gene Count | Pathway | Gene Count | Pathway Enrichment |
|---------------------|---------|------------|---------|------------|---------------------|
| **Oxytocin signaling pathway** | hsa04921 | 26/1188 | 0.592492943914967 | 0.912857011232122 | ITPR1, ROCK, PLCB, JUN, PTGS2, RAF, PPI1R12A, HRAS, ADC1, TRPM2, CACNA2D1, SRC, MYLK3, ITPR3, ROCK, JUN, ACTG, PTGS2, RAF, EEF2K, RYR, CAMKK2, PLAZG4B, RYR3, NPR3 |
| **Staphylococcus aureus infection** | hsa05150 | 4/1188 | 0.601147707448998 | 0.912857011232122 | C3, ICAM1, C1R |
| **Fat digestion and absorption** | hsa04975 | 5/1188 | 0.603243356382749 | 0.912857011232122 | SLC27A4, PLPP1, PLPP, ACAT2, AGPAT2 |
| **Leukocyte transendothelial migration** | hsa04670 | 19/1188 | 0.603243356382749 | 0.912857011232122 | VAV3, CLDN1, ROCK2, ACTG1, CTNND1, ICAM1, BCA1, MAPK11, MAPK12, VC1, CLDN7, PTK, NCF2, PLCG1, JAM2, RAPGEF3, PI3KCA, MYL2A |
| **Hippo signaling pathway - multiple species** | hsa04392 | 6/1188 | 0.605911920358480 | 0.912857011232122 | TEAD1, LAT1, RASSF1, AJUBA, WWTR1, FRMD6 |
| **Bacterial invasion of epithelial cells** | hsa05100 | 14/1188 | 0.606589023750335 | 0.912857011232122 | MET, ACTG1, CLTCL1, FN1, DMN3, BCA1, ARPC5L, SEPT9, CLT, SRC, VCL, MAD2L2, PI3KCA, ELMO3 |
| **Phosphatidylinositol signaling system** | hsa04070 | 18/1188 | 0.620975648816695 | 0.929948898471831 | ITPR1, PI3K3C2B, DGKZ, PLCG1, INPP5E, CDK, ITPR3, CDI, PLCG2 |
## Pathway Enrichment

| Pathway ID | Pathway Name                                      | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs |
|------------|--------------------------------------------------|----------|----------|----------|----------|----------|----------|----------|----------|
| hsa03440   | Homologous recombination                         | 8/1188   | 40/5573  | 0.642565793663757 | 0.955710593812568 | ENSG00000096433 | ENSG00000103502 | ENSG00000197943 | ENSG00000143398 | ENSG00000171862 | ENSG00000121879 | ENSG00000171862 | ENSG00000151151 | ENSG00000108389 | ENSG00000241973 | ENSG00000163719 | PIP5K1A   |
|            |                                                  |          |          |          |          |          |          |          |          |          |                  |                  |                      |                      |                      |                     |
| hsa04672   | Intestinal immune network for IgA production     | 4/1188   | 20/5573  | 0.644404211463198 | 0.955710593812568 | ENSG00000136492 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | ENSG00000158019 | IL6 CCL28 |
| hsa04217   | Necroptosis                                      | 27/1188  | 133/5573 | 0.648010166908013 | 0.956438082888269 | ENSG00000162909 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | ENSG00000118503 | CAPN2 |
| hsa03015   | mRNA surveillance pathway                        | 16/1188  | 80/5573  | 0.657465970413876 | 0.960653364629427 | ENSG00000165494 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | ENSG00000176102 | PCF11 CSTI |
| hsa01212   | Fatty acid metabolism                            | 9/1188   | 46/5573  | 0.671515285920597 | 0.960653364629427 | ENSG00000100294 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | ENSG000001100941 | PCBP4 PN |
| hsa00970   | Aminoacyl-tRNA biosynthesis                      | 8/1188   | 41/5573  | 0.671792650502076 | 0.960653364629427 | ENSG00000247626 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | ENSG00000179115 | MAR26 F2R |

file:///Users/dawen/Desktop/诺罗病毒测序2保17/0710结果交付．差异数据/X101SC21061603-Z01-F001-B1-16.result/Enrichment/2.KEGG/K223Rv--55/67
| ID     | Pathway                                | Enrichment | p-value | q-value |
|--------|----------------------------------------|------------|---------|---------|
| hsa05014 | Amyotrophic lateral sclerosis (ALS)     | 8/1188     | 41/5573 | 0.671792650502076 | 0.960653364629427 |
|         |                                        |            |         |          | MAP2K6  |
|         |                                        |            |         |          | NEFH    |
|         |                                        |            |         |          | TOMM40   |
|         |                                        |            |         |          | MAPK11   |
|         |                                        |            |         |          | MAPK12   |
|         |                                        |            |         |          | GP       |
|         |                                        |            |         |          | CAT      |
|         |                                        |            |         |          | TP53     |
| hsa00310 | Lysine degradation                      | 11/1188    | 56/5573 | 0.672316577639226 | 0.960653364629427 |
|         |                                        |            |         |          | PLOD2    |
|         |                                        |            |         |          | COLGALT1 |
|         |                                        |            |         |          | KMT2B    |
|         |                                        |            |         |          | ALDH7A1  |
|         |                                        |            |         |          | MAP2K6   |
|         |                                        |            |         |          | NEFH     |
|         |                                        |            |         |          | TOMM40   |
|         |                                        |            |         |          | MAPK11   |
|         |                                        |            |         |          | MAPK12   |
|         |                                        |            |         |          | GP       |
|         |                                        |            |         |          | CAT      |
|         |                                        |            |         |          | TP53     |
| hsa00260 | Glycine, serine and threonine metabolism | 7/1188     | 36/5573 | 0.672770271646016 | 0.960653364629427 |
|         |                                        |            |         |          | PSAT1    |
|         |                                        |            |         |          | PSP      |
|         |                                        |            |         |          | AOC3     |
|         |                                        |            |         |          | ALDH7A1  |
|         |                                        |            |         |          | MAOB     |
|         |                                        |            |         |          | CHD      |
|         |                                        |            |         |          | SARDH    |
| hsa04978 | Mineral absorption                      | 7/1188     | 36/5573 | 0.672770271646016 | 0.960653364629427 |
|         |                                        |            |         |          | CYBRD1   |
|         |                                        |            |         |          | ATP1B    |
|         |                                        |            |         |          | SLC30A1  |
|         |                                        |            |         |          | SLC11A2  |
|         |                                        |            |         |          | ATP2B    |
|         |                                        |            |         |          | HMOX2    |
|         |                                        |            |         |          | ATP7A    |
| hsa04973 | Carbohydrate digestion and absorption  | 5/1188     | 26/5573 | 0.678331532580551 | 0.964110094917728 |
|         |                                        |            |         |          | ATP1B    |
|         |                                        |            |         |          | HKDC1    |
|         |                                        |            |         |          | TAS1R3   |
|         |                                        |            |         |          | PIK3CA   |
|         |                                        |            |         |          | SLC2A5   |
| hsa04022 | cGMP-PKG signaling pathway              | 24/1188    | 121/5573| 0.691176476962942 | 0.977839531924531 |
|         |                                        |            |         |          | PDE3A    |
|         |                                        |            |         |          | ITPF     |
|         |                                        |            |         |          | ATF4     |
|         |                                        |            |         |          | ATP1I    |
|         |                                        |            |         |          | ROCK2    |
|         |                                        |            |         |          | CREB3L2  |
|         |                                        |            |         |          | PLCB3    |
|         |                                        |            |         |          | PRK     |
|         |                                        |            |         |          | RAF1     |
|         |                                        |            |         |          | PPP1R2    |
|         |                                        |            |         |          | ADCY6    |
|         |                                        |            |         |          | ADR      |
|         |                                        |            |         |          | INSR     |
|         |                                        |            |         |          | ATP2E    |
|         |                                        |            |         |          | ATP2B    |
|         |                                        |            |         |          | MYLK3    |
|         |                                        |            |         |          | ITPF     |
|         |                                        |            |         |          | MAPK3    |
|         |                                        |            |         |          | ADCY9    |
|         |                                        |            |         |          | CNGB1    |
|         |                                        |            |         |          | ADCY7    |
|         |                                        |            |         |          | KCNMB4   |
|         |                                        |            |         |          | NPR2     |
|         |                                        |            |         |          | GTF5     |
| hsa04972 | Pancreatic secretion                    | 11/1188    | 57/5573 | 0.69629438400554  | 0.97919797697505  |
|         |                                        |            |         |          | ITPRP1   |
|         |                                        |            |         |          | ATP1B    |
|         |                                        |            |         |          | PLCB3    |
|         |                                        |            |         |          | SLC4A2   |
|         |                                        |            |         |          | ADCY6    |
|         |                                        |            |         |          | ATP2B    |
|         |                                        |            |         |          | ATP2B    |
|         |                                        |            |         |          | ITPRP3   |
|         |                                        |            |         |          | ADC     |
|         |                                        |            |         |          | RYR2     |
|         |                                        |            |         |          | ADCY    |
| hsa04922 | Glucagon signaling pathway              | 17/1188    | 87/5573 | 0.699088045694299 | 0.97919797697505  |
|         |                                        |            |         |          | ITPRP1   |
|         |                                        |            |         |          | ATF      |
|         |                                        |            |         |          | CREB3L2  |
|         |                                        |            |         |          | PLCB3    |
| ID     | Pathway                                                        | genes                                                                 | Enrichment Score 1 | Enrichment Score 2 |
|--------|---------------------------------------------------------------|----------------------------------------------------------------------|---------------------|---------------------|
| hsa00030 | Pentose phosphate pathway                                       | ENSG00000149782, ENSG00000017999, ENSG00000170145, ENSG00000110090, ENSG00000275993, ENSG00000126457, ENSG00000111716, ENSG0000096433, ENSG0000142178, ENSG0000076555, ENSG0000117394, ENSG00000149923, ENSG000000671177 | 0.712096819002551  | 0.97919779679505   |
| hsa00061 | Fatty acid biosynthesis                                        | ENSG00000109107, ENSG00000079739, ENSG00000153574, ENSG00000160211, ENSG0000076555, ENSG0000117174, ENSG000000671177, ALDOC, PGM, RPIA, G6PD, RB5K | 0.71544901328267   | 0.97919779679505   |
| hsa00130 | Ubiquine and other terpenoid-quione biosynthesis              | ENSG00000067113, ENSG00000141934, ENSG00000011666, ENSG00000100644, ENSG00000143398, ENSG00000121879, ENSG00000243708, HIF1A, PIP5K1A, PIK3CA, PL2G4B, EIF4EBP1 | 0.71779101396077   | 0.97919779679505   |
| hsa05231 | Choline metabolism in cancer                                   | ENSG00000109107, ENSG00000079739, ENSG00000153574, ENSG00000160211, ENSG0000076555, ENSG0000117174, CHKA, DGK, JUN, GPCPE, RAF1, HRX, SOS2, PLPP, PLPP2, MAI, CHPT1, FO, HIF1A, PIP5K1A, PIK3CA, PL2G4B, EIF4EBP1 | 0.725692486377153  | 0.97919779679505   |
| hsa00520 | Amino sugar and nucleotide sugar metabolism                   | ENSG00000100485, ENSG00000158104, ENSG00000067113, ENSG00000149923, ENSG00000076555, ENSG00000167397, GNPDA1, PGM1, GNE, UGDH, UAP1L1, HKDC1, CYB5RL, GFPT1 | 0.72954650955365   | 0.97919779679505   |
| hsa03022 | Basal transcription factors                                   | ENSG00000104884, ENSG00000134480, ENSG00000183474, ENSG00000263001, TAF3, TAF1, ERLC2, TAF1, CCHN, GTF2H2C, GTF2I | 0.729754650955365  | 0.97919779679505   |
| hsa04962 | Vasopressin-regulated water reabsorption                      | ENSG00000088986, ENSG00000182158, ENSG00000165272, ENSG000001014981, ENSG00000197355, ENSG00000156510, ENSG00000198380, DYNLL1, CREB3L2, AQP3, RAB5, ADCY6, ARHGDIA, ADCY9 | 0.729754650955365  | 0.97919779679505   |
| hsa00620 | Pyruvate metabolism                                           | ENSG00000165272, ENSG00000115150, ENSG00000174233, ENSG00000141522, ENSG00000162104, PC, LDHAL6, LDHB, ALDH7A1, ACAT2, ACA1 | 0.735380697237882  | 0.97919779679505   |
| hsa00311 | Glycosaminoglycan degradation                                  | ENSG00000165102, ENSG00000088986, ENSG00000182158, ENSG00000165272, ENSG00000115150, ENSG00000174233, ENSG00000141522, ENSG00000162104, PC, LDHAL6, LDHB, ALDH7A1, ACAT2, ACA1 | 0.735705249689614  | 0.97919779679505   |
| hsa00020 | Citrate cycle (TCA cycle)                                     | ENSG00000173599, ENSG00000171989, ENSG00000111716, ENSG00000164904, ENSG00000120437, ENSG00000076555, PC, IDH2, IDH3A, SDH | 0.74327937521853   | 0.97919779679505   |
| hsa00561 | Glycerolipid metabolism                                       | ENSG00000085662, ENSG00000085662, ENSG00000165102, ENSG00000088986, ENSG00000182158, ENSG00000165272, ENSG00000115150, ENSG00000174233, ENSG00000141522, ENSG00000162104, PC, IDH2, IDH3A, SDH | 0.746289250380816  | 0.97919779679505   |

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| Pathway Enrichment | Gene Set | P Value | q Value | Enrichment Score |
|---------------------|----------|---------|---------|------------------|
| hsa05030 Cocaine addiction | 7/1188 | 39/5573 | 0.75531554951902 | 0.979197979679505 |
| hsa04024 cAMP signaling pathway | 29/1188 | 150/5573 | 0.755823514863949 | 0.979197979679505 |
| hsa04060 Cytokine-cytokine receptor interaction | 32/1188 | 165/5573 | 0.758020795986072 | 0.979197979679505 |
| hsa00910 Nitrogen metabolism | 2/1188 | 12/5573 | 0.760940988897737 | 0.979197979679505 |
| hsa02010 ABC transporters | 6/1188 | 34/5573 | 0.76249392368735 | 0.979197979679505 |
| Pathway Enrichment | Genes | Gene Count | Gene Count | p-value | q-value |
|---------------------|-------|------------|------------|---------|---------|
| **Taste transduction** | hsa04742 | 6/1188 | 34/5573 | 0.762493923698735 | 0.979197979679505 |
| | | | | | |
| **Gastric acid secretion** | hsa04971 | 10/1188 | 55/5573 | 0.764560326960954 | 0.979197979679505 |
| | | | | | |
| **Apelin signaling pathway** | hsa04371 | 22/1188 | 116/5573 | 0.767222038492732 | 0.979197979679505 |
| | | | | | |
| **Synaptic vesicle cycle** | hsa04721 | 9/1188 | 50/5573 | 0.768414802898943 | 0.979197979679505 |
| | | | | | |
| **Renin secretion** | hsa04924 | 9/1188 | 50/5573 | 0.768414802898943 | 0.979197979679505 |
| | | | | | |
| **Serotonergic synapse** | hsa04726 | 15/1188 | 81/5573 | 0.771841011915381 | 0.979197979679505 |
| | | | | | |
| **Glycosaminoglycan biosynthesis - heparan sulfate / heparin** | hsa00534 | 3/1188 | 18/5573 | 0.771875931864626 | 0.979197979679505 |
| | | | | | |
| **Axon guidance** | hsa04360 | 29/1188 | 152/5573 | 0.781247834536464 | 0.979600898257564 |

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| Pathway ID | Pathway Name                        | Significantly Enriched Proteins | p-value       |
|-----------|------------------------------------|---------------------------------|--------------|
| hsa04142  | Lysosome                           |                                 | 0.9796       |
| hsa04720  | Long-term potentiation             |                                 | 0.9796       |
| hsa00140  | Steroid hormone biosynthesis       |                                 | 0.9796       |
| hsa00604  | Glycosphingolipid biosynthesis - ganglio series | | 0.9903       |
| hsa04950  | Maturity onset diabetes of the young |                                 | 0.9903       |
| hsa00564  | Glycerophospholipid metabolism     |                                 | 0.9913       |
### Pathway Enrichment

| Pathway                     | Annotation               | DEGs | Total DEGs | q-value | FDR | accession       |
|-----------------------------|--------------------------|------|------------|---------|-----|-----------------|
| hsa04910 Insulin signaling pathway | 22/1188                  | 119/557 | 0.807921057305251 | 0.992127058370848 |       |                 |
| hsa03040 Spliceosome        | 23/1188                  | 125/557 | 0.819336164021668 | 0.997564998291051 |       |                 |
| hsa00051 Fructose and mannose metabolism | 5/1188                  | 31/557  | 0.821711251047486  | 0.997564998291051 |       |                 |
| hsa04340 Hedgehog signaling pathway | 7/1188                  | 42/557  | 0.82209753930826  | 0.997564998291051 |       |                 |
| hsa00071 Fatty acid degradation | 6/1188                  | 37/557  | 0.831402287340321  | 0.99998654289568 |       |                 |
| hsa00500 Starch and sucrose metabolism | 4/1188                  | 26/557  | 0.836520758748482  | 0.99998654289568 |       |                 |
| hsa00630 Glyoxylate and dicarboxylate metabolism | 4/1188                  | 26/557  | 0.836520758748482  | 0.99998654289568 |       |                 |
| hsa04136 Autophagy - other | 5/1188                  | 32/557  | 0.843114084071755  | 0.99998654289568 |       |                 |
| hsa05170 Human immunodeficiency virus 1 infection | 32/1188                  | 173/557 | 0.845012600377722  | 0.99998654289568 |       |                 |
| Pathway Enrichment | p-value | Enrichment Score | q-value | Enriched Genes |
|--------------------|---------|------------------|---------|----------------|
| **Long-term depression** | $0.849866836914825$ | 8/1188 | 0.999998654289568 | `ENSG00000177606` `ENSG00000179218` `ENSG00000100906` `ENSG00000167004` `ENSG00000132155` `ENSG00000184216` `ENSG00000114125` `ENSG00000174775` `ENSG00000168040` `ENSG00000030110` `ENSG00000096433` `ENSG00000157456` `ENSG00000114125` `ENSG00000184216` | **KEGG** `K223Rv` **PPI** | `CALR` `NFkB` `PDIA3` `RAF` `IRAK1` `RNF` `HRAS` `FADD` `BAK1` `MAPK` `ITPR3` `CCNB` `GNB2` `MAPK12` `FC` `CFL1` `PTK2` `PLCG2` `ATI` `LIMK1` `PIK3i` `RXB1` `CUL4` `TAB1` `TREM173` `CASPB` |
| **Peroxisome** | $0.852530302305315$ | 13/1188 | 0.999998654289568 | `ENSG00000124587` `ENSG00000112096` `ENSG00000182054` `ENSG00000138413` `ENSG00000254858` `ENSG00000095321` `ENSG00000174233` `ENSG00000172354` `ENSG00000102882` `ENSG00000162104` `ENSG00000170345` `ENSG00000139842` `ENSG00000197448` `ENSG00000115425` | **Enrichment** | `ITPR1` `PLCB` `RAF1` `HRAS` `ITPR3` `MAPK` `PLA2G4B` `BRAF` `PEX6` `SOD2` `IDH2` `IDH1` `MPV17L2` `CRAT` `GSKT0` `PECR` `PEX5` `NUDT19` `CA` `GNPAT` `PEX` |
| **Terpenoid backbone biosynthesis** | $0.856629584421715$ | 3/1188 | 0.999998654289568 | `ENSG00000167508` `ENSG00000167508` | **Enrichment** | `ICMT` `ACAT` `MVD` |
| **Circadian entrainment** | $0.865157289199486$ | 13/1188 | 0.999998654289568 | `ENSG00000136244` `ENSG00000085063` | **Enrichment** | `IL6` `CD59` `ITGA1` `IL11` `CD24` `ITGA` `CSF1` `ITGA` |
| **Ferroptosis** | $0.867721158109882$ | 6/1188 | 0.999998654289568 | `ENSG00000168003` `ENSG00000106091` | **Enrichment** | `SLC3A2` `SLC11A2` `PCBP1` `SLC39A14` `GSS` `TP53` |
| **Mismatch repair** | $0.878014095222223$ | 3/1188 | 0.999998654289568 | `ENSG00000174371` `ENSG00000106628` | **Enrichment** | `SLC3A2` `SLC11A2` `PCBP1` `SLC39A14` `GSS` `TP53` |
| **Hematopoietic cell lineage** | $0.879567477720803$ | 8/1188 | 0.999998654289568 | `ENSG00000161471` | **Enrichment** | `ITL6` `CD59` `ITGAI` `CD24` `ITGA` `CSF1` `ITGA` |
| Pathway Enrichment                                      | Gene Accession       | Gene Description | P-value     | Adjusted P-value |
|--------------------------------------------------------|----------------------|------------------|-------------|------------------|
| hsa00380 Tryptophan metabolism                         | ENSG00000184371      | ENSG00000005884  | 0.879569131133309 | 0.999998654289568 |
| hsa00511 Other glycan degradation                       | ENSG0000017280       | ENSG00000162139  | 0.885217433623028 | 0.999998654289568 |
| hsa04261 Adrenergic signaling in cardiomyocytes        | ENSG00000167280      | ENSG00000162104  | 0.891261725280964 | 0.999998654289568 |
| hsa04710 Circadian rhythm                              | ENSG00000133794      | ENSG00000103417  | 0.894171839411614 | 0.999998654289568 |
| hsa0565 Ether lipid metabolism                         | ENSG00000067113      | ENSG00000141934  | 0.894914247688192 | 0.999998654289568 |
| hsa0512 Mucin type O-glycan biosynthesis               | ENSG00000008513      | ENSG00000158470  | 0.896515491650005 | 0.999998654289568 |
| hsa0860 Porphyrin and chlorophyll metabolism           | ENSG00000109320      | ENSG00000132155  | 0.897365823186556 | 0.999998654289568 |
| hsa04920 Adipocytokine signaling pathway               | ENSG00000109320      | ENSG00000132155  | 0.90350450925187 | 0.999998654289568 |
| hsa04725 Cholinergic synapse                            | ENSG00000167170      | ENSG00000162104  | 0.908073473473029 | 0.999998654289568 |
| hsa04071 Sphingolipid signaling pathway                | ENSG00000184371      | ENSG00000005884  | 0.90350450925187 | 0.999998654289568 |
| Pathway ID | Pathway Name                          | P-value | q-value | Enriched Genes                                                                 | Gene Symbols | Other Information                  |
|-----------|---------------------------------------|---------|---------|-------------------------------------------------------------------------------|-------------|-------------------------------------|
| hsa04114  | Oocyte meiosis                        | 0.0000  | 0.0000  | ENSG00000171862, ENSG00000121879, ENSG00000141510, ITPR1, CDC2, PKMYT1, CDC26, ADC, PK1, ITPR, CCNB2, MAPK3, MAPK12, YWHAH, ADCC9, CPEI, ANAPC11, MAD2L2, ADCCY7, MAD2L1, RB |
| hsa04650  | Natural killer cell mediated cytotoxicity | 0.0000  | 0.0000  | ENSG00000150995, ENSG00000117399, ENSG00000112182, ENSG00000127564, ENSG00000175476, ENSG00000102288, ENSG00000157609, ENSG00000161670, ENSG00000121281, ENSG00000164109, ENSG00000100387, VAV3, IFNFA1, ICAM1, IFNNG1, RAF, HRAS, SOS, MAPK3, PTK, PLCG2, PIK3CA, BRI |
| hsa04514  | Cell adhesion molecules (CAMs)         | 0.0000  | 0.0000  | ENSG00000134215, ENSG00000121281, ENSG00000132155, ENSG00000174775, ENSG00000100485, ENSG00000120899, ENSG000001197943, ENSG00000121879, ENSG00000157764, SDC4, ITGB, CLDN1, GLC, PTPR, NLGN4X, ICAM1, CNTNAP1, JAM, L1CAM, PVI, SDC3, MPZL |
| hsa00563  | Glycosylphosphatidylinositol (GPI)-anchor biosynthesis | 0.0000  | 0.0000  | ENSG00000135845, ENSG00000135845, ENSG00000109083, ENSG00000100564, PIGC, GPAA, PIH |
| hsa00270  | Cysteine and methionine metabolism     | 0.0000  | 0.0000  | ENSG00000121281, ENSG00000100485, ENSG000001197943, ENSG00000121879, ENSG00000157764, SDC4, ITGB, CLDN1, GLC, PTPR, NLGN4X, ICAM1, CNTNAP1, JAM, L1CAM, PVI, SDC3, MPZL |
| hsa04610  | Complement and coagulation cascades    | 0.0000  | 0.0000  | ENSG00000100983, ENSG00000116984, ENSG00000117167, ENSG00000101444, SDC4, ITGB, CLDN1, GLC, PTPR, NLGN4X, ICAM1, CNTNAP1, JAM, L1CAM, PVI, SDC3, MPZL |
| hsa00120  | Primary bile acid biosynthesis         | 0.0000  | 0.0000  | ENSG00000102437, ENSG000001084754, HSD3B7, HSD3B7, HSD3B7, HSD3B7, HSD3B7 |
| hsa00650  | Butanoate metabolism                  | 0.0000  | 0.0000  | ENSG00000100983, ENSG00000116984, ENSG00000117167, ENSG00000101444, SDC4, ITGB, CLDN1, GLC, PTPR, NLGN4X, ICAM1, CNTNAP1, JAM, L1CAM, PVI, SDC3, MPZL |
| hsa03320  | PPAR signaling pathway                | 0.0000  | 0.0000  | ENSG00000102437, ENSG000001084754, HSD3B7, HSD3B7, HSD3B7, HSD3B7, HSD3B7 |
| hsa04727  | GABAergic synapse                     | 0.0000  | 0.0000  | ENSG00000102437, ENSG000001084754, HSD3B7, HSD3B7, HSD3B7, HSD3B7, HSD3B7 |
| Gene ID | Pathway Description                        | Significance | FDR       | Enrichment Score | Enrichment FDR | Pathways | Enrichment FDR |
|--------|-------------------------------------------|--------------|-----------|------------------|----------------|----------|----------------|
| hsa00770 | Pantothenate and CoA biosynthesis         | 1/1188       | 13/5573   | 0.955863527048067 | 0.999998654289568 | ENSG00000197122 | 0.999998654289568 |
| hsa03030 | DNA replication                           | 4/1188       | 35/5573   | 0.958639710604445 | 0.999998654289568 | ENSG00000162104 | 0.999998654289568 |
| hsa00591 | Linoleic acid metabolism                  | 1/1188       | 14/5573   | 0.965294125944991 | 0.999998654289568 | ENSG00000121281 | 0.999998654289568 |
| hsa04614 | Renin-angiotensin system                  | 1/1188       | 14/5573   | 0.965294125944991 | 0.999998654289568 | ENSG00000102287 | 0.999998654289568 |
| hsa04014 | Ras signaling pathway                     | 30/1188      | 186/5573  | 0.970895733014369 | 0.999998654289568 | ENSG00000106628 | 0.999998654289568 |
| hsa04979 | Cholesterol metabolism                    | 5/1188       | 44/5573   | 0.97220905994802  | 0.999998654289568 | ENSG00000102882 | 0.999998654289568 |
| hsa04964 | Proximal tubule bicarbonate reclamation   | 1/1188       | 15/5573   | 0.972711031571426 | 0.999998654289568 | ENSG00000165527 | 0.999998654289568 |
| hsa05322 | Systemic lupus erythematosus              | 11/1188      | 81/5573   | 0.97307613685546  | 0.999998654289568 | ENSG00000123384 | 0.999998654289568 |
| hsa00592 | alpha-Linolenic acid metabolism           | 1/1188       | 16/5573   | 0.978543938101319 | 0.999998654289568 | ENSG00000102287 | 0.999998654289568 |
| hsa03460 | Fanconi anemia pathway                    | 6/1188       | 53/5573   | 0.981175411529753 | 0.999998654289568 | ENSG00000197943 | 0.999998654289568 |
| hsa05033 | Nicotine addiction                       | 1/1188       | 17/5573   | 0.9831309097651   | 0.999998654289568 | ENSG00000102287 | 0.999998654289568 |
| hsa04724 | Glutamatergic synapse                     | 12/1188      | 91/5573   | 0.983639821127479 | 0.999998654289568 | ENSG00000068082 | 0.999998654289568 |
| Enrichment Term          | Pathway ID | Count | Average FDR | p-value       | Gene Count | Gene Members                                                                 |
|-------------------------|------------|-------|-------------|---------------|------------|-----------------------------------------------------------------------------|
| hsa05031 Amphetamine addiction | hsa05237 | 6/1188 | 54/5573     | 0.983846716418026 | 0.999998654289568 | ENSG00000102882 ENSG00000162104 ENSG00000121281 ENSG00000243708 ATF4 CREB3L2 JU MAOB FOS |
| hsa04728 Dopaminergic synapse          | hsa04728 | 15/1188 | 109/5573    | 0.984315401181613 | 0.999998654289568 | ENSG00000050995 ENSG00000082701 ENSG00000121281 ENSG00000133794 ENSG00000149782 ENSG00000150723 ENSG00000144285 ENSG00000185386 ENSG00000096433 ENSG00000172354 ENSG000000188130 ENSG00000069535 ENSG00000170345 ENSG00000180176 ITPR1 GSK3A SCN1 MAPK11 ITPR3 GNB MAPK12 MAOB FOS |
| hsa00100 Steroid biosynthesis        | hsa00100 | 1/1188 | 18/5573     | 0.986737907461116 | 0.999998654289568 | ENSG00000172893 DHCR7 |
| hsa04744 Phototransduction          | hsa00830 | 19/1188 | 136/5573    | 0.989789395203686 | 0.999998654289568 | SPHK1 ITPF3 PLCB3 ORA ADRB1 ATP2B4 ATP2B1 MYLK3 ITPLC1 ADCY9 PTK2 PLCG2 RYR ADCY7 PDE1 ITPKC P2R RYR3 PHKA |
| hsa00830 Retinol metabolism          | hsa00830 | 2/1188 | 30/5573     | 0.993237233830193 | 0.999998654289568 | CYP251 DHR53 |
| hsa05034 Alcoholism                 | hsa00830 | 20/1188 | 149/5573    | 0.995421946640445 | 0.999998654289568 | ATF4 H3F3 CREB3L2 HIST2H4B CAMKK1 H2AFZ RAF HRAS SOS; HIST1H2AI HIST2H2BI GNB2 MAPK1 MAOB HDAC1 TH1H2D1 CAMK2I HIST1H2BI HIST2H2BI HIST1H2BI BRAF |
| hsa04152 AMPK signaling pathway      | hsa00830 | 12/1188 | 108/5573    | 0.998286594604212 | 0.999998654289568 | CREB3L2 CCND1 ULK1 CPT1A SREBF1 INS SCD EEFF2I ACACB PHK3CA CAMKK2 EIF4EBP1 |
| Pathway ID | Pathway Name                          | Up/Down | Genes | p-value | FDR | Genes |
|------------|---------------------------------------|---------|-------|---------|-----|-------|
| hsa04740   | Olfactory transduction                | 4/1188  | 61/5573 | 0.999633900634011 | 0.999998654289568 | ENSG00000173020, ENSG000000070729, ENSG00000115252, ENSG00000137486 |
| hsa04080   | Neuroactive ligand-receptor interaction | 12/1188 | 153/5573 | 0.999998654289568 | 0.999998654289568 | ENSG00000065325, ENSG000000013580, ENSG00000175591, ENSG000000151090, ENSG00000139874, ENSG00000043591, ENSG000000213903, ENSG00000091718, ENSG00000109451, ENSG00000213218, ENSG00000169006, ENSG000000102287, ENSG000000164251, ENSG00000083454, GLP2R, NR3, P2RY2, THR, SSTR1, ADRB, LTB4R, CSH, NTSR2, GAB1, FZRL1, P2R |