**Supplementary information**

# Identification of differently expressed genes, fusion genes and mutated genes associated with the malignant progression of spinal cord gliomas by transcriptome analysis

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**Supplementary Table S1 Characteristics of libraries mapped to reference gene database**

| Sample ID | Raw reads | Clean reads | Total mapped | Multiple mapped | Uniquely mapped |
|---|---|---|---|---|---|
| S01 (grade Ⅱ) | 26374768 | 18281210 | 16581447 (90.7%) | 671553 (3.67%) | 15909894 (87.03%) |
| S02 (grade Ⅱ) | 29287160 | 18308306 | 16430308 (89.74%) | 627639 (3.43%) | 15802669 (86.31%) |
| S03 (grade Ⅱ) | 34812436 | 23540518 | 21447731 (91.11%) | 851822 (3.62%) | 20595909 (87.49%) |
| S04 (grade Ⅱ) | 26773424 | 14352260 | 12497000 (87.07%) | 559883 (3.9%) | 11937117 (83.17%) |
| S05 (grade Ⅳ) | 33204894 | 18916628 | 16046711 (84.83%) | 646156 (3.42%) | 15400555 (81.41%) |
| S06 (grade Ⅳ) | 31100538 | 20312198 | 18626061 (91.7%) | 779340 (3.84%) | 17846721 (87.86%) |
| S07 (grade Ⅳ) | 26275874 | 14021924 | 11365194 (81.05%) | 474856 (3.39%) | 10890338 (77.67%) |
| S08 (grade Ⅳ) | 32218992 | 20453534 | 18004262 (88.03%) | 940983 (4.6%) | 17063279 (83.42%) |
| S09 (grade Ⅳ) | 24513220 | 14860896 | 12943461 (87.1%) | 505235 (3.4%) | 12438226 (83.7%) |

Note: Sample ID: Sample name;
Raw reads: The number of reads in the raw data;
Clean reads: The number of reads filtered from the raw data;
Total mapped: The number of reads mapped to the genome;
Multiple mapped: Reads number compared to multiple locations of the genome;
Uniquely mapped: Number of reads mapped to a single location of the genome;

**Supplementary Table S2 Sum of differentially expressed genes in Ⅳ vs Ⅱ.**

| Gene | $Log_2$ FoldChange Ⅳ vs Ⅱ | *P* value | FDR-adjusted *P*-Value |
|---|---|---|---|
| DSC3 | -7.644464873 | 9.2747E-21 | 2.55E-16 |
| INSM1 | -4.757408157 | 5.60485E-16 | 7.72E-12 |
| HCG11 | 4.048435957 | 2.85798E-15 | 2.62E-11 |
| COL21A1 | 5.848582591 | 2.61561E-14 | 1.80E-10 |
| ANGPTL1 | -3.396304942 | 8.39226E-14 | 4.62E-10 |
| TTC12 | 3.339669539 | 1.55741E-12 | 7.15E-09 |
| MIR663AHG | -8.680383152 | 2.42055E-12 | 9.44E-09 |
| TP53TG3D | -5.185378151 | 2.74279E-12 | 9.44E-09 |
| VPS37B | 2.81244086 | 5.21042E-12 | 1.49E-08 |
| AC003973.3 | -6.749704046 | 5.39692E-12 | 1.49E-08 |
| PDIA2 | -2.789790546 | 6.46502E-12 | 1.62E-08 |
| TEX14 | -3.49220684 | 1.02705E-11 | 2.36E-08 |
| NTS | -7.364034876 | 5.96609E-11 | 1.26E-07 |
| LINC01098 | -7.384175145 | 7.5591E-11 | 1.48E-07 |
| PLAG1 | -3.33033095 | 8.06609E-11 | 1.48E-07 |
| AC107952.2 | -3.020672634 | 1.42343E-10 | 2.45E-07 |
| PDLIM4 | 4.04282121 | 4.28315E-10 | 6.94E-07 |
| ZNF560 | -4.6081876 | 4.65791E-10 | 7.13E-07 |
| AL121904.1 | -8.503642103 | 2.58352E-09 | 3.74E-06 |
| MTHFD2 | -2.184382432 | 3.13129E-09 | 4.31E-06 |
| CERS3-AS1 | -7.124660409 | 3.92797E-09 | 5.05E-06 |
| SALL2 | 2.042423998 | 4.03736E-09 | 5.05E-06 |
| NPPA | -5.117147686 | 5.13175E-09 | 6.14E-06 |
| CD163L1 | -3.916580658 | 5.58061E-09 | 6.40E-06 |
| PAX3 | -3.091501649 | 8.24707E-09 | 9.08E-06 |
| PLEKHG4 | -2.993476157 | 8.78503E-09 | 9.31E-06 |
| ELOVL2 | 2.807287313 | 9.6495E-09 | 9.82E-06 |
| AC012593.1 | 6.116733733 | 9.9855E-09 | 9.82E-06 |
| TCEA3 | 2.50141056 | 1.58874E-08 | 1.51E-05 |
| AC002351.1 | -5.367016888 | 1.71192E-08 | 1.57E-05 |
| AC022893.2 | -4.572351569 | 2.69809E-08 | 2.40E-05 |
| PRAME | -9.147589372 | 2.96841E-08 | 2.55E-05 |
| HERC2P4 | -4.813024781 | 3.50193E-08 | 2.92E-05 |
| OR5AK4P | 3.979787313 | 3.76244E-08 | 3.05E-05 |
| TMEM229A | 3.331206486 | 4.89054E-08 | 3.85E-05 |
| IQGAP2 | -2.867257858 | 7.00629E-08 | 5.36E-05 |
| AL359233.1 | 3.906260429 | 8.56009E-08 | 6.37E-05 |
| ZFHX4 | 4.231190322 | 1.10891E-07 | 8.04E-05 |

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|---|---|---|---|
| AP002840.2 | 5.046766807 | 1.27343E-07 | 8.99E-05 |
| AC016717.2 | -4.694015645 | 1.60249E-07 | 0.000110327 |
| ZNF208 | -5.133979464 | 1.64882E-07 | 0.000110748 |
| BEAN1 | -2.862682419 | 1.69141E-07 | 0.000110904 |
| CPXM2 | 3.831338999 | 2.32447E-07 | 0.000148869 |
| GPR17 | 5.148566557 | 2.46582E-07 | 0.000154332 |
| CCDC8 | 3.441994921 | 2.67014E-07 | 0.000163407 |
| DMKN | 4.802693541 | 2.73979E-07 | 0.000164024 |
| PAPPA2 | -3.223563981 | 2.83056E-07 | 0.000164735 |
| MAB21L1 | -3.838732851 | 2.87131E-07 | 0.000164735 |
| AC008556.1 | 2.416191027 | 3.74578E-07 | 0.000210521 |
| PNPLA4 | 2.853256819 | 4.08164E-07 | 0.000224808 |
| NPY5R | -3.656681678 | 4.31307E-07 | 0.000228688 |
| LINC01993 | -5.14714583 | 4.31817E-07 | 0.000228688 |
| ARAP3 | -2.749019938 | 4.70472E-07 | 0.000244459 |
| ALX3 | -7.154724083 | 5.2235E-07 | 0.000266389 |
| LIMS2 | 4.163685291 | 5.37501E-07 | 0.000267441 |
| ZFHX4-AS1 | 5.083927683 | 5.43835E-07 | 0.000267441 |
| GRM5 | 4.10187018 | 6.13001E-07 | 0.000296166 |
| TKTL1 | -4.500305761 | 6.84177E-07 | 0.000324854 |
| FABP5 | 2.736760314 | 7.02857E-07 | 0.000328068 |
| AL512380.1 | -4.944123346 | 7.15801E-07 | 0.000328541 |
| LINC01436 | -5.053067136 | 7.50135E-07 | 0.000338655 |
| CNN2P8 | 5.322943855 | 8.16575E-07 | 0.000362704 |
| FILIP1L | -2.352645647 | 9.88889E-07 | 0.000429082 |
| LINC00944 | -6.012477291 | 9.97178E-07 | 0.000429082 |
| AC104041.1 | -6.105182941 | 1.10744E-06 | 0.000468092 |
| TP63 | -4.569705164 | 1.12183E-06 | 0.000468092 |
| MRO | 2.69626528 | 1.16117E-06 | 0.000477276 |
| FRMD6 | 1.937745695 | 1.26201E-06 | 0.000511096 |
| ANKRD34C | 5.702175037 | 1.3833E-06 | 0.000552096 |
| CACNB3 | -2.450926087 | 1.45727E-06 | 0.000573311 |
| SPX | 3.766180047 | 1.61298E-06 | 0.000625632 |
| CNMD | 3.730431934 | 1.64038E-06 | 0.000627424 |
| AL355974.3 | -3.751578875 | 1.75819E-06 | 0.000663271 |
| RAB34 | 2.785875496 | 1.87693E-06 | 0.000698497 |
| GLIS1 | -2.647677692 | 1.95661E-06 | 0.00071844 |
| WSCD2 | 3.721535607 | 1.99745E-06 | 0.000723785 |
| FAM162B | -2.636745292 | 2.35023E-06 | 0.00084056 |
| OSR1 | -4.768696952 | 2.44743E-06 | 0.000857315 |
| ACSM4 | -4.735939035 | 2.45934E-06 | 0.000857315 |
| NPY2R | -6.927528924 | 2.50691E-06 | 0.000862973 |
| HSPA2 | 3.115854541 | 2.57299E-06 | 0.000869136 |
| MUC12 | -3.775541276 | 2.59765E-06 | 0.000869136 |

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|---|---|---|---|
| LIF | -3.056087175 | 2.6195E-06 | 0.000869136 |
| AC109466.1 | -6.734968879 | 2.90094E-06 | 0.000951059 |
| NMU | -4.878662637 | 3.05069E-06 | 0.000987559 |
| PCDHGA9 | 4.072507508 | 3.08399E-06 | 0.000987559 |
| TBX5 | 5.891410841 | 3.12977E-06 | 0.000990697 |
| GPD1 | 2.749639667 | 3.33804E-06 | 0.001044618 |
| MGAT5B | -1.98115571 | 3.47755E-06 | 0.001076048 |
| AC138761.4 | -7.145596302 | 3.73913E-06 | 0.001144132 |
| A2MP1 | 1.493783104 | 4.31055E-06 | 0.001304487 |
| AC100863.1 | -5.630074048 | 4.409E-06 | 0.001319777 |
| CCT7P2 | 3.622224281 | 4.58626E-06 | 0.001341594 |
| RP11-435B5.5 | -4.731831825 | 4.62139E-06 | 0.001341594 |
| GALR1 | -2.986850688 | 4.62803E-06 | 0.001341594 |
| COL5A1 | -3.236190007 | 4.88889E-06 | 0.001402449 |
| COPZ2 | 2.45764328 | 4.95963E-06 | 0.001408075 |
| PRICKLE3 | 2.281443846 | 5.08847E-06 | 0.001429912 |
| MFAP2 | -3.081022594 | 5.40668E-06 | 0.001503987 |
| RPS28P7 | -2.377599865 | 5.49237E-06 | 0.001512545 |
| APC | 1.286704968 | 5.61789E-06 | 0.001531794 |
| CHSY1 | -1.543770817 | 6.14144E-06 | 0.001658129 |
| AC010636.1 | -6.53741555 | 6.29978E-06 | 0.001669941 |
| LINC00870 | 4.640031031 | 6.30647E-06 | 0.001669941 |
| AL845331.1 | 4.645493422 | 6.45725E-06 | 0.001693583 |
| AC021218.1 | -5.402962907 | 6.54571E-06 | 0.001700588 |
| AC073365.1 | -9.088799312 | 6.75998E-06 | 0.001739842 |
| CHDH | 1.477829771 | 7.0082E-06 | 0.001787026 |
| BSPRY | 3.314865659 | 7.29544E-06 | 0.001829074 |
| DLG5-AS1 | -1.919400462 | 7.33662E-06 | 0.001829074 |
| HPSE2 | 4.969459944 | 7.37235E-06 | 0.001829074 |
| CLEC2B | -2.176180598 | 7.7678E-06 | 0.001909978 |
| RHOD | 3.211622741 | 8.0926E-06 | 0.001972232 |
| NRN1 | 3.622332004 | 8.8322E-06 | 0.002133596 |
| FABP5P7 | 2.77419541 | 8.94595E-06 | 0.002142282 |
| SLC39A12 | 3.351338244 | 9.06446E-06 | 0.00215195 |
| NPAS1 | 4.122628687 | 9.20431E-06 | 0.002166474 |
| SPOCD1 | -3.956560042 | 9.82323E-06 | 0.00229256 |
| NPY1R | -2.117313312 | 1.00139E-05 | 0.002317425 |
| SLC43A2 | 1.814651239 | 1.04447E-05 | 0.00239697 |
| DNAJC15 | 1.269704813 | 1.12576E-05 | 0.002562168 |
| AGTR1 | -5.170728093 | 1.18406E-05 | 0.00267278 |
| SPTSSB | -3.195173809 | 1.23227E-05 | 0.002758979 |
| FKBP5 | -3.909012656 | 1.25845E-05 | 0.002794867 |
| SIGLEC1 | -2.882725491 | 1.28938E-05 | 0.002825899 |
| ACOT1 | 2.431159478 | 1.29294E-05 | 0.002825899 |

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|---|---|---|---|
| AC073578.2 | -4.879862715 | 1.34528E-05 | 0.00291713 |
| MTND1P23 | -6.437867426 | 1.41355E-05 | 0.003041232 |
| LINC02094 | -3.408775539 | 1.57807E-05 | 0.003345308 |
| LINC01257 | -5.33304191 | 1.58814E-05 | 0.003345308 |
| CBX2 | -2.68419043 | 1.59133E-05 | 0.003345308 |
| CXCL10 | -3.387200186 | 1.65208E-05 | 0.003446718 |
| BEX2 | 1.801355602 | 1.67899E-05 | 0.00347652 |
| BCL11A | -3.294846315 | 1.70709E-05 | 0.003508334 |
| LINC00900 | 1.966832175 | 1.73059E-05 | 0.003530283 |
| HSF4 | -2.158418587 | 1.76127E-05 | 0.003566445 |
| SAMD14 | -1.64610371 | 1.79426E-05 | 0.003606729 |
| STXBP6 | 1.879392512 | 1.82002E-05 | 0.003622027 |
| LGSN | -4.513488141 | 1.82818E-05 | 0.003622027 |
| SERPINE1 | -2.844319491 | 1.96211E-05 | 0.003859601 |
| GSX1 | -3.653817453 | 2.02564E-05 | 0.00395632 |
| AC108156.1 | 5.650797199 | 2.24583E-05 | 0.004331141 |
| OCIAD2 | -2.464085196 | 2.26165E-05 | 0.004331141 |
| SVEP1 | -3.235852787 | 2.27874E-05 | 0.004331141 |
| MUM1L1 | -2.241059001 | 2.28046E-05 | 0.004331141 |
| TMEM184A | -4.493275624 | 2.45048E-05 | 0.004622177 |
| TMSB10 | -1.433457103 | 2.54658E-05 | 0.004770774 |
| DNM1 | -1.557955363 | 2.58555E-05 | 0.00481104 |
| AC112255.1 | -6.432565448 | 2.67073E-05 | 0.004919971 |
| AC027290.2 | 2.36600108 | 2.69298E-05 | 0.004919971 |
| LINC02388 | -5.556839856 | 2.69769E-05 | 0.004919971 |
| DRAXIN | -2.938571849 | 2.74469E-05 | 0.004972762 |
| C6orf141 | -4.477223764 | 2.80134E-05 | 0.005022783 |
| AF279873.3 | -4.658063865 | 2.80878E-05 | 0.005022783 |
| MROH3P | 3.256099892 | 3.05796E-05 | 0.00543311 |
| FABP6 | -3.68180446 | 3.08902E-05 | 0.005453114 |
| PDLIM1 | -2.945507139 | 3.17195E-05 | 0.005504303 |
| BMP7 | 1.906375184 | 3.17755E-05 | 0.005504303 |
| GYPE | -2.34190573 | 3.17798E-05 | 0.005504303 |
| LINC00639 | 2.395847562 | 3.28555E-05 | 0.005655056 |
| C2CD4C | -2.383600399 | 3.30988E-05 | 0.005661536 |
| CLVS2 | 4.118044393 | 3.48813E-05 | 0.0059296 |
| MMP23B | -3.695747026 | 3.54976E-05 | 0.005997354 |
| ERVW-1 | 1.731842783 | 3.6021E-05 | 0.006037212 |
| HOXB5 | 1.878242281 | 3.6172E-05 | 0.006037212 |
| EMX2OS | 2.98752369 | 3.69428E-05 | 0.006128722 |
| EMX2 | 3.146923035 | 3.74421E-05 | 0.006173335 |
| DLK1 | -7.924022069 | 3.76601E-05 | 0.006173335 |
| B4GALNT1 | -2.30361355 | 4.38385E-05 | 0.007143594 |
| GPD1L | 2.450590631 | 4.47442E-05 | 0.00721667 |

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|---|---|---|---|
| DNAH3 | -3.665192461 | 4.48163E-05 | 0.00721667 |
| NR3C2 | 2.595548419 | 4.50731E-05 | 0.00721667 |
| AP000525.10 | -3.412986557 | 4.68682E-05 | 0.00746071 |
| GPR37L1 | 2.868855656 | 4.73541E-05 | 0.007494734 |
| AC022215.1 | -3.042312805 | 4.77844E-05 | 0.007519628 |
| RASD1 | -3.351039617 | 4.90338E-05 | 0.007672398 |
| AC006946.3 | -2.732593984 | 5.14534E-05 | 0.008005504 |
| CRYGD | -3.756098054 | 5.47911E-05 | 0.008440118 |
| SYT7 | -2.735527023 | 5.48597E-05 | 0.008440118 |
| WNT6 | -4.2294029 | 5.57359E-05 | 0.008527289 |
| AC006548.3 | -3.444037561 | 5.61748E-05 | 0.008546943 |
| AC099654.7 | -5.942090208 | 5.8194E-05 | 0.00880552 |
| KCNS1 | 3.539331534 | 5.92269E-05 | 0.00891284 |
| LINC00346 | -2.865412172 | 6.05361E-05 | 0.009060339 |
| SCN5A | -3.389938577 | 6.33631E-05 | 0.009432203 |
| TNFRSF12A | -1.816032417 | 6.40089E-05 | 0.009435857 |
| PCDHGC4 | 4.081426323 | 6.44991E-05 | 0.009435857 |
| NPSR1-AS1 | -5.347191345 | 6.47053E-05 | 0.009435857 |
| SLC6A15 | -3.634437722 | 6.47971E-05 | 0.009435857 |
| GSX2 | -3.57899244 | 6.51009E-05 | 0.009435857 |
| KHDRBS2 | -3.552391119 | 6.71771E-05 | 0.009685815 |
| PCDHGC3 | 3.450061259 | 6.95072E-05 | 0.009947335 |
| TLR10 | 2.740048268 | 6.97133E-05 | 0.009947335 |
| ACOT2 | 1.348741288 | 7.09435E-05 | 0.010057304 |
| AC005220.1 | 4.08690331 | 7.12144E-05 | 0.010057304 |
| SLITRK5 | 1.326492477 | 7.22384E-05 | 0.010149861 |
| HOXB7 | 1.983641441 | 7.45504E-05 | 0.010421535 |
| TNFRSF18 | -2.486586367 | 7.60124E-05 | 0.010572251 |
| STK26 | -2.368553784 | 7.87033E-05 | 0.010845459 |
| JADE1 | -1.334598177 | 7.87644E-05 | 0.010845459 |
| PCA3 | -2.983461013 | 7.97887E-05 | 0.010931844 |
| MYO7A | -2.312450221 | 8.28123E-05 | 0.011289936 |
| LINC01170 | 3.447144926 | 8.39522E-05 | 0.011388958 |
| AC022905.1 | -4.795460462 | 8.50185E-05 | 0.011477075 |
| HLA-F | -4.880337682 | 8.68899E-05 | 0.011639023 |
| BCAS1 | 3.113002467 | 8.75285E-05 | 0.011639023 |
| HOXB-AS2 | 2.967564223 | 8.75816E-05 | 0.011639023 |
| MOV10L1 | 2.136691132 | 8.79355E-05 | 0.011639023 |
| AC040160.1 | -2.269562401 | 8.83313E-05 | 0.011639023 |
| AP001372.1 | -2.858658204 | 9.12E-05 | 0.011959799 |
| KRT18P14 | -3.160451216 | 9.16663E-05 | 0.011963968 |
| SNORD3B-2 | -3.74735665 | 9.90954E-05 | 0.012872588 |
| KCNB2 | -4.785326382 | 9.98768E-05 | 0.012913179 |
| RNU2-57P | -6.045551001 | 0.000102031 | 0.013130109 |

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|---|---|---|---|
| AL139393.2 | -2.737111897 | 0.000104213 | 0.013243384 |
| SOWAHA | 2.399463172 | 0.000104258 | 0.013243384 |
| PSMC1P7 | -4.742793634 | 0.000104354 | 0.013243384 |
| GADD45A | -2.377299928 | 0.000105753 | 0.013359327 |
| ITPR2 | 1.57304713 | 0.000107934 | 0.013552805 |
| ACBD7 | 2.99762363 | 0.00010853 | 0.013552805 |
| AL109924.4 | -4.473908192 | 0.000108761 | 0.013552805 |
| MGAM | -2.328648574 | 0.00011112 | 0.013784375 |
| HSD17B6 | 2.730204159 | 0.000112973 | 0.013951423 |
| GAP43 | -2.26486927 | 0.000115538 | 0.014204439 |
| HS3ST3A1 | -4.460078887 | 0.000116277 | 0.014231768 |
| AC007681.1 | -1.997136562 | 0.000118242 | 0.014368883 |
| AL109924.2 | -4.47356612 | 0.000118539 | 0.014368883 |
| PRODH | 2.168578578 | 0.000118962 | 0.014368883 |
| RGS20 | 2.745971632 | 0.000119506 | 0.014371495 |
| UBL4B | -5.010769611 | 0.000120379 | 0.014413532 |
| XK | 1.54164891 | 0.000123675 | 0.014744059 |
| IL36G | -5.172160671 | 0.00012622 | 0.014982664 |
| NOS2 | -1.663714216 | 0.000130438 | 0.01536706 |
| AQP7P2 | -4.359000364 | 0.000130724 | 0.01536706 |
| AP003900.1 | -9.724557949 | 0.000131133 | 0.01536706 |
| FZD10-AS1 | -2.825637462 | 0.000135628 | 0.015758105 |
| EBF1 | -2.267007974 | 0.000135914 | 0.015758105 |
| ENTPD2 | 3.515811129 | 0.000136186 | 0.015758105 |
| GNRH1 | -1.887017916 | 0.000138916 | 0.016006712 |
| Z73979.1 | -3.042659485 | 0.000141743 | 0.016264452 |
| ATP2B3 | 3.412077788 | 0.000142409 | 0.016273075 |
| EXTL1 | 1.929599317 | 0.000146868 | 0.016713257 |
| TENM2 | -2.934680186 | 0.000148112 | 0.016713661 |
| CIPC | 1.512977644 | 0.000148452 | 0.016713661 |
| PGR | 2.745098119 | 0.000148693 | 0.016713661 |
| AC015712.6 | -2.30657579 | 0.000153082 | 0.017137133 |
| LL22NC03-N64E9.1 | -4.332723457 | 0.000156145 | 0.017409214 |
| AC092652.1 | 5.729327765 | 0.000157139 | 0.017449435 |
| PCDHGC5 | 2.496088166 | 0.000158609 | 0.017500532 |
| ERI2 | 1.176714944 | 0.00015887 | 0.017500532 |
| FAM160A1 | -5.136766007 | 0.000160546 | 0.017614682 |
| FREM3 | -3.65706256 | 0.000166361 | 0.018180251 |
| BIRC7 | -2.867909262 | 0.000167728 | 0.018257109 |
| CNGB1 | -6.149890342 | 0.000169499 | 0.01837725 |
| TSPAN2 | -2.752825626 | 0.000175839 | 0.018982422 |
| AL031728.1 | -2.433397618 | 0.000176459 | 0.018982422 |
| BANCR | -4.094502173 | 0.000179876 | 0.019274743 |
| AC107375.1 | -1.197009306 | 0.000181675 | 0.019392006 |

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|---|---|---|---|
| PCDHA11 | 2.848181708 | 0.000183629 | 0.019524975 |
| MAGEC2 | -7.968210488 | 0.000186563 | 0.019760557 |
| AC145098.2 | -2.208041003 | 0.000187298 | 0.019762484 |
| NYAP2 | -4.082996618 | 0.000192352 | 0.020218259 |
| GABRE | -2.487780459 | 0.000194767 | 0.020394237 |
| CLIC5 | 1.995243061 | 0.000198968 | 0.020755187 |
| CASZ1 | -2.441336768 | 0.000204451 | 0.021246701 |
| NPC1L1 | -2.961674862 | 0.000206315 | 0.021359849 |
| AC008554.1 | -3.983514984 | 0.000208035 | 0.021457215 |
| LINC00871 | -5.358204506 | 0.000209965 | 0.021575503 |
| BEAN1-AS1 | -3.228103654 | 0.000214311 | 0.021896648 |
| HIRAP1 | -3.605382397 | 0.000214681 | 0.021896648 |
| MEGF10 | 2.151133403 | 0.000217707 | 0.022123383 |
| AC008708.1 | -5.453672264 | 0.000223953 | 0.02267441 |
| LDHB | 1.527915183 | 0.000234176 | 0.023548782 |
| CAB39L | 1.55738958 | 0.000234588 | 0.023548782 |
| FGF13 | -1.594590977 | 0.00023576 | 0.023548782 |
| PIN4P1 | -2.886581191 | 0.000236009 | 0.023548782 |
| EPOR | 1.359105489 | 0.000239111 | 0.023772106 |
| BX255923.3 | -3.463643935 | 0.000245417 | 0.024276411 |
| AC060766.1 | 2.806481709 | 0.000245946 | 0.024276411 |
| AC004877.1 | 2.92905524 | 0.000247951 | 0.024386874 |
| PPP1R16B | 2.428561335 | 0.000251281 | 0.024531604 |
| STX8P1 | -2.500614108 | 0.000251516 | 0.024531604 |
| RINL | 1.865257067 | 0.00025215 | 0.024531604 |
| ATP1A2 | 2.589111897 | 0.000252986 | 0.024531604 |
| RDH10 | -1.53154111 | 0.000257265 | 0.024772075 |
| OR7E115P | 5.201241917 | 0.000258952 | 0.024822834 |
| AC017006.2 | -3.085818938 | 0.000260349 | 0.024822834 |
| LINC01060 | -5.764420013 | 0.000260496 | 0.024822834 |
| AC136424.2 | -3.380664538 | 0.000267817 | 0.025345406 |
| GAL | -4.192149813 | 0.000268375 | 0.025345406 |
| FOXF2 | 1.794376037 | 0.000268741 | 0.025345406 |
| AC011195.2 | -5.059456383 | 0.000270307 | 0.025406088 |
| LL22NC03-N14H11.1 | -3.454807382 | 0.000277948 | 0.026035365 |
| HAGLROS | 2.748682983 | 0.000278932 | 0.02603902 |
| AP003119.3 | -2.269643835 | 0.00028193 | 0.026201945 |
| IGHV3-9 | 6.237014823 | 0.000283135 | 0.026201945 |
| FGF13-AS1 | -2.67206446 | 0.000284347 | 0.026201945 |
| TDRD9 | 3.298061077 | 0.000285267 | 0.026201945 |
| DUSP5P1 | -3.065241725 | 0.000285656 | 0.026201945 |
| CITED1 | -3.014429331 | 0.000286386 | 0.026201945 |
| ERMP1 | 1.278817831 | 0.000289406 | 0.026390593 |
| MICA | 2.682244157 | 0.00029153 | 0.026496495 |

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|---|---|---|---|
| AC092112.1 | -3.142721798 | 0.000292814 | 0.026525629 |
| MT1G | 3.665337323 | 0.000294722 | 0.026610998 |
| GJB6 | 6.194612287 | 0.000297907 | 0.026810665 |
| C17orf67 | -1.713445595 | 0.000320513 | 0.028751184 |
| MTSS1L | 1.625864702 | 0.000321753 | 0.028768714 |
| LIN7A | -1.622614285 | 0.000326415 | 0.029091113 |
| EFNA5 | -3.747240945 | 0.000333239 | 0.029603462 |
| PWRN1 | -3.463571147 | 0.00033572 | 0.029643301 |
| AC022113.1 | -2.151622225 | 0.000336035 | 0.029643301 |
| CHCHD2P11 | -4.446998958 | 0.00033753 | 0.029643301 |
| GLT1D1 | -1.824932363 | 0.000337993 | 0.029643301 |
| DSG2 | -3.386520571 | 0.000342497 | 0.029942938 |
| AC016044.1 | 5.988822729 | 0.000343856 | 0.029966637 |
| PNCK | 2.182920915 | 0.000345293 | 0.029996885 |
| AC068987.3 | -3.750669577 | 0.000347105 | 0.030059501 |
| CCNYL2 | -3.066793003 | 0.000350915 | 0.030248219 |
| AC018695.7 | 4.848871869 | 0.000351481 | 0.030248219 |
| HMGA1P7 | 6.242618376 | 0.000354118 | 0.030380277 |
| LINC01405 | -3.925305003 | 0.000356004 | 0.030447154 |
| SCARF2 | -1.661394647 | 0.000359741 | 0.030671548 |
| ELAVL4 | -2.325372411 | 0.000367775 | 0.031259716 |
| AC093642.2 | 2.923813657 | 0.000388673 | 0.032934319 |
| KRT16P2 | -7.571760694 | 0.000390064 | 0.03295084 |
| RSPO3 | -3.597557925 | 0.000392118 | 0.033023011 |
| SNORD124 | -5.084888543 | 0.000400462 | 0.033538941 |
| LINC02058 | 3.452324622 | 0.000401699 | 0.033538941 |
| AC078917.1 | -5.115471492 | 0.000402616 | 0.033538941 |
| GPR161 | -1.090718872 | 0.000403587 | 0.033538941 |
| LINC02100 | -2.667363744 | 0.000404333 | 0.033538941 |
| ACAA2 | 1.298204011 | 0.000411733 | 0.034050199 |
| ANKRD28 | 1.156119363 | 0.000422876 | 0.034867047 |
| CCNA1 | -3.058787455 | 0.000425885 | 0.035010305 |
| FOXQ1 | 2.327984883 | 0.000427774 | 0.035041206 |
| ALDH6A1 | 1.464744058 | 0.000428806 | 0.035041206 |
| COL24A1 | -3.338398779 | 0.000431795 | 0.035171743 |
| AC093895.1 | -4.176665931 | 0.000432958 | 0.035171743 |
| UPK3A | 3.028871934 | 0.000436218 | 0.035309435 |
| AACSP1 | -4.471332115 | 0.000437677 | 0.035309435 |
| IGFBP3 | -3.155122921 | 0.000438499 | 0.035309435 |
| SEPT7P3 | 2.902712767 | 0.000440168 | 0.03534048 |
| NNMT | -3.561347309 | 0.000443672 | 0.035401024 |
| CHADL | 2.167714384 | 0.000444408 | 0.035401024 |
| KLF6 | -1.094197598 | 0.000444778 | 0.035401024 |
| PCDHA4 | 3.134398727 | 0.000448959 | 0.035630808 |

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|---|---|---|---|
| PLPP4 | 1.163189491 | 0.000451911 | 0.035706526 |
| IGF2BP2-AS1 | -2.403379259 | 0.000452507 | 0.035706526 |
| FBN2 | -2.517646438 | 0.000459283 | 0.036137735 |
| PDE10A | -2.043510665 | 0.000471367 | 0.036877771 |
| FAM84B | -1.39580359 | 0.000473434 | 0.036934554 |
| AC080100.1 | 1.49847605 | 0.000475087 | 0.036958799 |
| LINC01829 | -4.651596088 | 0.000482068 | 0.037396291 |
| FBXL22 | 1.534961982 | 0.000490516 | 0.037944702 |
| MIR5690 | -4.792159491 | 0.000493016 | 0.038031305 |
| LINC01140 | 2.530813954 | 0.000500009 | 0.038462999 |
| HHIP-AS1 | -1.729221196 | 0.000515983 | 0.039581205 |
| GJB2 | 3.026247291 | 0.000521139 | 0.039831892 |
| TEX22 | 1.620395508 | 0.00052268 | 0.039831892 |
| LINC01561 | 1.387266819 | 0.00052426 | 0.039831892 |
| IP6K3 | -2.741733677 | 0.000525036 | 0.039831892 |
| EDARADD | -2.571972833 | 0.000526853 | 0.039859918 |
| AP001521.1 | 4.933134532 | 0.000538828 | 0.040654197 |
| HLA-A | -5.581744431 | 0.000541247 | 0.040725151 |
| CEL | -1.790452862 | 0.000549527 | 0.041235471 |
| ISYNA1 | -1.237400937 | 0.000555983 | 0.041520946 |
| C8orf4 | -2.303681602 | 0.000556347 | 0.041520946 |
| RNF141 | 1.074970691 | 0.000558294 | 0.041553704 |
| AC024451.4 | -2.050352898 | 0.000564002 | 0.041816883 |
| SLC47A1P1 | -5.025964089 | 0.000565908 | 0.041816883 |
| FGR | -1.448398265 | 0.000566386 | 0.041816883 |
| PAH | 2.778270873 | 0.000575488 | 0.042341617 |
| LINC01679 | -3.686348503 | 0.000576568 | 0.042341617 |
| HIST1H2BH | -2.609847102 | 0.000584614 | 0.0427867 |
| FAM50B | 2.327432222 | 0.000586965 | 0.0427867 |
| SORCS2 | 1.74592075 | 0.00058729 | 0.0427867 |
| LINC01535 | 1.33461199 | 0.000597126 | 0.043388513 |
| SLC25A5 | 1.517676479 | 0.000604647 | 0.043819385 |
| FGF5 | -4.734752983 | 0.000607309 | 0.043830486 |
| AC004448.4 | -2.138803399 | 0.000608119 | 0.043830486 |
| METTL24 | 3.260404154 | 0.000609575 | 0.043830486 |
| HOXB6 | 2.811615802 | 0.000616736 | 0.044158994 |
| HACD3 | 1.476853425 | 0.00061735 | 0.044158994 |
| AC104461.1 | 3.309378208 | 0.000627284 | 0.044753305 |
| GPRC5A | -3.415520467 | 0.000633136 | 0.044962436 |
| RP11-782C8.2 | -3.337924452 | 0.000633481 | 0.044962436 |
| CDH18 | -2.305964548 | 0.000643266 | 0.045539587 |
| LINC01750 | -2.107347203 | 0.000651334 | 0.045992559 |
| AL162731.1 | -4.376203643 | 0.000654183 | 0.04607554 |
| MDGA2 | 1.806972757 | 0.000657477 | 0.046114886 |

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|---|---|---|---|
| ALX1 | -7.801851928 | 0.00065809 | 0.046114886 |
| AC090692.1 | -2.48181863 | 0.00065982 | 0.046118772 |
| FCRLA | 3.240039808 | 0.000663481 | 0.046257226 |
| SGCD | 1.502176983 | 0.000674355 | 0.046820027 |
| AC007240.1 | -3.50070573 | 0.000674954 | 0.046820027 |
| AL354919.2 | -5.278010553 | 0.000677284 | 0.046863645 |
| CDK18 | 2.646107571 | 0.000686913 | 0.047410777 |
| AC118942.1 | -5.485185233 | 0.000695344 | 0.047872706 |
| ASIC2 | 2.703498696 | 0.000704608 | 0.048271825 |
| AC021683.3 | -3.714653592 | 0.000704647 | 0.048271825 |
| AC023794.3 | 2.442013728 | 0.000706434 | 0.04827417 |
| AC006058.4 | 3.0081952 | 0.000711838 | 0.048523067 |
| RPS3AP14 | -2.65973728 | 0.000716734 | 0.048533634 |
| AL160286.2 | -3.179367667 | 0.000719349 | 0.048533634 |
| AC009902.2 | 3.366317782 | 0.000720448 | 0.048533634 |
| GPR135 | 1.152219671 | 0.000720805 | 0.048533634 |
| APOL4 | -2.23186537 | 0.000728605 | 0.048939173 |
| AC020913.3 | -2.354072807 | 0.000736052 | 0.049319041 |
| TYRP1 | -4.042966946 | 0.0007395 | 0.049377417 |
| AC068491.4 | -2.718734003 | 0.000742103 | 0.049377417 |
| NAPEPLD | 1.410854247 | 0.000743852 | 0.049377417 |
| FA2H | 3.018440872 | 0.000746911 | 0.049377417 |
| KY | 2.096585794 | 0.000747149 | 0.049377417 |
| CADPS | -1.680534177 | 0.000747681 | 0.049377417 |
| SEC11C | 1.471961517 | 0.00075615 | 0.049762054 |
| PITX1 | -6.557106128 | 0.000757119 | 0.049762054 |

Note:

Log$_2$ FoldChange (Ⅳ vs Ⅱ): The multiple value of difference between two samples or comparison combinations, expressed as log$_2$ (group1/group2), calculated according to the difference analysis software

*P* value: *P* value of significance test

FDR-adjusted *P*-Value: *P* value of multiple hypothesis test correction

**Supplementary Table S3 Pathway analysis of differentially expressed genes in Ⅳ vs Ⅱ.**

| Pathway ID | Description | *P* value | FDR-adjusted *P*-Value | Gene ID | Count |
|---|---|---|---|---|---|
| hsa04080 | Neuroactive ligand-receptor interaction | 0.007960251 | 0.39403243 | NTS/NPY5R/GRM5/NPY2R/NMU/GALR1/NPY1R/AGTR1/GNRH1/GABRE/GAL | 11 |
| hsa04218 | Cellular senescence | 0.00269618 | 0.177947873 | SERPINE1/HLA-F/GADD45A/ITPR2/CCNA1/IGFBP3/HLA-A/SLC25A5 | 8 |
| hsa04022 | cGMP-PKG signaling pathway | 0.011902866 | 0.44819415 | NPPA/AGTR1/ITPR2/ATP2B3/CNGB1/ATP1A2/SLC25A5 | 7 |
| hsa04024 | cAMP signaling pathway | 0.038984128 | 0.689750173 | NPPA/ARAP3/NPY1R/ATP2B3/CNGB1/ATP1A2/PDE10A | 7 |
| hsa04060 | Cytokine-cytokine receptor interaction | 0.09985891 | 0.689750173 | LIF/CXCL10/BMP7/TNFRSF12A/TNFRSF18/IL36G/EPOR | 7 |
| hsa04020 | Calcium signaling pathway | 0.064603668 | 0.689750173 | GRM5/AGTR1/ITPR2/NOS2/ATP2B3/SLC25A5 | 6 |
| hsa04144 | Endocytosis | 0.176337224 | 0.799081256 | VPS37B/ARAP3/HSPA2/DNM1/HLA-F/HLA-A | 6 |
| hsa00062 | Fatty acid elongation | 5.19E-05 | 0.010268165 | ELOVL2/ACOT1/ACOT2/ACAA2/HACD3 | 5 |
| hsa04925 | Aldosterone synthesis and secretion | 0.013581641 | 0.44819415 | NPPA/AGTR1/ITPR2/ATP2B3/ATP1A2 | 5 |
| hsa04261 | Adrenergic signaling in cardiomyocytes | 0.067382076 | 0.689750173 | CACNB3/AGTR1/SCN5A/ATP2B3/ATP1A2 | 5 |
| hsa05224 | Breast cancer | 0.072390199 | 0.689750173 | APC/WNT6/GADD45A/PGR/FGF5 | 5 |
| hsa04934 | Cushing syndrome | 0.083004586 | 0.689750173 | APC/AGTR1/RASD1/WNT6/ITPR2 | 5 |
| hsa04390 | Hippo signaling pathway | 0.090517673 | 0.689750173 | FRMD6/APC/SERPINE1/BMP7/WNT6 | 5 |
| hsa05167 | Kaposi sarcoma-associated herpesvirus infection | 0.128454983 | 0.748061373 | CLEC2B/HLA-F/ITPR2/MICA/HLA-A | 5 |
| hsa05169 | Epstein-Barr virus infection | 0.157205345 | 0.799081256 | CXCL10/HLA-F/GADD45A/CCNA1/HLA-A | 5 |
| hsa04010 | MAPK signaling pathway | 0.457200665 | 0.812762779 | CACNB3/HSPA2/GADD45A/EFNA5/FGF5 | 5 |
| hsa05165 | Human | 0.5466930 | 0.846330358 | APC/WNT6/HLA-F/CCNA1/HLA-A | 5 |

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|---|---|---|---|---|---|
| | papillomavirus infection | 4 | | | |
| hsa01040 | Biosynthesis of unsaturated fatty acids | 0.000747028 | 0.073955787 | ELOVL2/ACOT1/ACOT2/HACD3 | 4 |
| hsa04974 | Protein digestion and absorption | 0.040300319 | 0.689750173 | COL21A1/COL5A1/ATP1A2/COL24A1 | 4 |
| hsa04972 | Pancreatic secretion | 0.049929865 | 0.689750173 | ITPR2/ATP2B3/ATP1A2/CEL | 4 |
| hsa04915 | Estrogen signaling pathway | 0.107208477 | 0.689750173 | HSPA2/FKBP5/ITPR2/PGR | 4 |
| hsa04371 | Apelin signaling pathway | 0.15368691 | 0.799081256 | AGTR1/SERPINE1/ITPR2/NOS2 | 4 |
| hsa04723 | Retrograde endocannabinoid signaling | 0.168621549 | 0.799081256 | GRM5/ITPR2/GABRE/NAPEPLD | 4 |
| hsa05226 | Gastric cancer | 0.187192803 | 0.799276255 | APC/WNT6/GADD45A/FGF5 | 4 |
| hsa04310 | Wnt signaling pathway | 0.222825788 | 0.812762779 | PRICKLE3/APC/WNT6/RSPO3 | 4 |
| hsa05202 | Transcriptional misregulation in cancer | 0.312632896 | 0.812762779 | PAX3/GADD45A/CCNA1/IGFBP3 | 4 |
| hsa05203 | Viral carcinogenesis | 0.351823623 | 0.812762779 | HLA-F/CCNA1/HLA-A/HIST1H2BH | 4 |
| hsa05205 | Proteoglycans in cancer | 0.369686872 | 0.812762779 | COL21A1/HPSE2/WNT6/ITPR2 | 4 |
| hsa05166 | Human T-cell leukemia virus 1 infection | 0.412403555 | 0.812762779 | HLA-F/CCNA1/HLA-A/SLC25A5 | 4 |
| hsa05168 | Herpes simplex virus 1 infection | 0.9397386 | 0.944508847 | ZNF560/ZNF208/HLA-F/HLA-A | 4 |
| hsa00830 | Retinol metabolism | 0.04056605 | 0.689750173 | PNPLA4/HSD17B6/RDH10 | 3 |
| hsa01212 | Fatty acid metabolism | 0.04934615 | 0.689750173 | ELOVL2/ACAA2/HACD3 | 3 |
| hsa05416 | Viral myocarditis | 0.04934615 | 0.689750173 | HLA-F/HLA-A/SGCD | 3 |
| hsa04612 | Antigen processing and presentation | 0.064097253 | 0.689750173 | HSPA2/HLA-F/HLA-A | 3 |
| hsa04924 | Renin secretion | 0.074934009 | 0.689750173 | NPPA/AGTR1/ITPR2 | 3 |
| hsa05217 | Basal cell carcinoma | 0.074934009 | 0.689750173 | APC/WNT6/GADD45A | 3 |

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|---|---|---|---|---|---|
| hsa04115 | p53 signaling pathway | 0.098827783 | 0.689750173 | SERPINE1/GADD45A/IGFBP3 | 3 |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 0.102008832 | 0.689750173 | CACNB3/DSG2/SGCD | 3 |
| hsa04970 | Salivary secretion | 0.118509363 | 0.71105618 | ITPR2/ATP2B3/ATP1A2 | 3 |
| hsa05222 | Small cell lung cancer | 0.17314178 | 0.799081256 | GADD45A/NOS2/BIRC7 | 3 |
| hsa00564 | Glycerophospholipid metabolism | 0.184828406 | 0.799276255 | GPD1/GPD1L/PLPP4 | 3 |
| hsa04066 | HIF-1 signaling pathway | 0.196719207 | 0.799276255 | NPPA/SERPINE1/NOS2 | 3 |
| hsa05145 | Toxoplasmosis | 0.225143758 | 0.812762779 | HSPA2/NOS2/BIRC7 | 3 |
| hsa04270 | Vascular smooth muscle contraction | 0.305396096 | 0.812762779 | NPPA/AGTR1/ITPR2 | 3 |
| hsa04514 | Cell adhesion molecules (CAMs) | 0.352627588 | 0.812762779 | SIGLEC1/HLA-F/HLA-A | 3 |
| hsa04550 | Signaling pathways regulating pluripotency of stem cells | 0.361197546 | 0.812762779 | LIF/APC/WNT6 | 3 |
| hsa04072 | Phospholipase D signaling pathway | 0.38680085 | 0.812762779 | GRM5/AGTR1/DNM1 | 3 |
| hsa04921 | Oxytocin signaling pathway | 0.403745609 | 0.812762779 | NPPA/CACNB3/ITPR2 | 3 |
| hsa05225 | Hepatocellular carcinoma | 0.478060836 | 0.823096049 | APC/WNT6/GADD45A | 3 |
| hsa05016 | Huntington disease | 0.505836664 | 0.831854934 | GRM5/DNAH3/SLC25A5 | 3 |
| hsa04360 | Axon guidance | 0.536641695 | 0.846330358 | RHOD/BMP7/EFNA5 | 3 |
| hsa05170 | Human immunodeficiency virus 1 infection | 0.591392246 | 0.869717016 | HLA-F/ITPR2/HLA-A | 3 |
| hsa04015 | Rap1 signaling pathway | 0.601839913 | 0.869717016 | ARAP3/EFNA5/FGF5 | 3 |
| hsa04810 | Regulation of actin cytoskeleton | 0.628846048 | 0.881084419 | IQGAP2/APC/FGF5 | 3 |
| hsa05163 | Human cytomegalovirus infection | 0.635400709 | 0.881084419 | HLA-F/ITPR2/HLA-A | 3 |

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|---|---|---|---|---|---|
| hsa04151 | PI3K-Akt signaling pathway | 0.894976831 | 0.939502295 | EPOR/EFNA5/FGF5 | 3 |
| hsa00534 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 0.05329203 | 0.689750173 | HS3ST3A1/EXTL1 | 2 |
| hsa05330 | Allograft rejection | 0.08374233 | 0.689750173 | HLA-F/HLA-A | 2 |
| hsa05332 | Graft-versus-host disease | 0.08374233 | 0.689750173 | HLA-F/HLA-A | 2 |
| hsa00640 | Propanoate metabolism | 0.088445033 | 0.689750173 | LDHB/ALDH6A1 | 2 |
| hsa04940 | Type I diabetes mellitus | 0.103001161 | 0.689750173 | HLA-F/HLA-A | 2 |
| hsa04960 | Aldosterone-regulated sodium reabsorption | 0.107991189 | 0.689750173 | NR3C2/ATP1A2 | 2 |
| hsa04975 | Fat digestion and absorption | 0.107991189 | 0.689750173 | NPC1L1/CEL | 2 |
| hsa05320 | Autoimmune thyroid disease | 0.118158683 | 0.71105618 | HLA-F/HLA-A | 2 |
| hsa04973 | Carbohydrate digestion and absorption | 0.144529334 | 0.799081256 | MGAM/ATP1A2 | 2 |
| hsa04961 | Endocrine and other factor-regulated calcium reabsorption | 0.160891655 | 0.799081256 | DNM1/ATP1A2 | 2 |
| hsa00280 | Valine, leucine and isoleucine degradation | 0.171981467 | 0.799081256 | ACAA2/ALDH6A1 | 2 |
| hsa00330 | Arginine and proline metabolism | 0.177573613 | 0.799081256 | PRODH/NOS2 | 2 |
| hsa04978 | Mineral absorption | 0.177573613 | 0.799081256 | ATP1A2/MT1G | 2 |
| hsa04923 | Regulation of lipolysis in adipocytes | 0.194511787 | 0.799276255 | NPPA/NPY1R | 2 |
| hsa00561 | Glycerolipid metabolism | 0.22892813 | 0.812762779 | PLPP4/CEL | 2 |
| hsa05213 | Endometrial cancer | 0.22892813 | 0.812762779 | APC/GADD45A | 2 |
| hsa04927 | Cortisol synthesis and secretion | 0.240504025 | 0.812762779 | AGTR1/ITPR2 | 2 |

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|---|---|---|---|---|---|
| hsa04720 | Long-term potentiation | 0.263729014 | 0.812762779 | GRM5/ITPR2 | 2 |
| hsa04918 | Thyroid hormone synthesis | 0.281163442 | 0.812762779 | ITPR2/ATP1A2 | 2 |
| hsa05218 | Melanoma | 0.286970322 | 0.812762779 | GADD45A/FGF5 | 2 |
| hsa01230 | Biosynthesis of amino acids | 0.310140338 | 0.812762779 | TKTL1/PAH | 2 |
| hsa04971 | Gastric acid secretion | 0.310140338 | 0.812762779 | ITPR2/ATP1A2 | 2 |
| hsa04260 | Cardiac muscle contraction | 0.315912443 | 0.812762779 | CACNB3/ATP1A2 | 2 |
| hsa04742 | Taste transduction | 0.315912443 | 0.812762779 | ENTPD2/ASIC2 | 2 |
| hsa00562 | Inositol phosphate metabolism | 0.321674114 | 0.812762779 | ALDH6A1/ISYNA1 | 2 |
| hsa03320 | PPAR signaling pathway | 0.321674114 | 0.812762779 | FABP5/FABP6 | 2 |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 0.378497669 | 0.812762779 | CACNB3/SGCD | 2 |
| hsa04540 | Gap junction | 0.384081113 | 0.812762779 | GRM5/ITPR2 | 2 |
| hsa05210 | Colorectal cancer | 0.389643406 | 0.812762779 | APC/GADD45A | 2 |
| hsa04912 | GnRH signaling pathway | 0.400701767 | 0.812762779 | ITPR2/GNRH1 | 2 |
| hsa05414 | Dilated cardiomyopathy (DCM) | 0.400701767 | 0.812762779 | CACNB3/SGCD | 2 |
| hsa05032 | Morphine addiction | 0.406196515 | 0.812762779 | GABRE/PDE10A | 2 |
| hsa04922 | Glucagon signaling pathway | 0.433301796 | 0.812762779 | ITPR2/LDHB | 2 |
| hsa04070 | Phosphatidylinositol signaling system | 0.43864531 | 0.812762779 | ITPR2/IP6K3 | 2 |
| hsa04750 | Inflammatory mediator regulation of TRP channels | 0.43864531 | 0.812762779 | ITPR2/ASIC2 | 2 |
| hsa04914 | Progesterone-mediated oocyte maturation | 0.443961798 | 0.812762779 | PGR/CCNA1 | 2 |
| hsa04916 | Melanogenesis | 0.4492508 | 0.812762779 | WNT6/TYRP1 | 2 |
| hsa04933 | AGE-RAGE | 0.4597446 | 0.812762779 | AGTR1/SERPINE1 | 2 |

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|---|---|---|---|---|---|
| | signaling pathway in diabetic complications | 02 | | | |
| hsa05142 | Chagas disease (American trypanosomiasis) | 0.470123428 | 0.823096049 | SERPINE1/NOS2 | 2 |
| hsa04650 | Natural killer cell mediated cytotoxicity | 0.495548617 | 0.831513781 | MICA/HLA-A | 2 |
| hsa04668 | TNF signaling pathway | 0.495548617 | 0.831513781 | LIF/CXCL10 | 2 |
| hsa01200 | Carbon metabolism | 0.520198432 | 0.838358572 | TKTL1/ALDH6A1 | 2 |
| hsa04724 | Glutamatergic synapse | 0.525032641 | 0.838358572 | GRM5/ITPR2 | 2 |
| hsa04152 | AMPK signaling pathway | 0.553352085 | 0.846330358 | CAB39L/CCNA1 | 2 |
| hsa04114 | Oocyte meiosis | 0.557956363 | 0.846330358 | ITPR2/PGR | 2 |
| hsa00230 | Purine metabolism | 0.576039198 | 0.857562115 | ENTPD2/PDE10A | 2 |
| hsa04110 | Cell cycle | 0.576039198 | 0.857562115 | GADD45A/CCNA1 | 2 |
| hsa04210 | Apoptosis | 0.622987587 | 0.881084419 | GADD45A/ITPR2 | 2 |
| hsa04145 | Phagosome | 0.646877464 | 0.881084419 | HLA-F/HLA-A | 2 |
| hsa04630 | JAK-STAT signaling pathway | 0.654573416 | 0.881084419 | LIF/EPOR | 2 |
| hsa04150 | mTOR signaling pathway | 0.676868549 | 0.881514371 | WNT6/CAB39L | 2 |
| hsa05164 | Influenza A | 0.691079871 | 0.881514371 | HSPA2/CXCL10 | 2 |
| hsa04062 | Chemokine signaling pathway | 0.782020436 | 0.916213292 | CXCL10/FGR | 2 |
| hsa05206 | MicroRNAs in cancer | 0.837129846 | 0.938052536 | TP63/APC | 2 |
| hsa04014 | Ras signaling pathway | 0.859718477 | 0.93944805 | EFNA5/FGF5 | 2 |

Note:

Pathway ID: KEGG pathway number

Description: Function description corresponding to the KEGG pathway number

*P* value: *P* value of significance test

FDR-adjusted *P*-Value: *P* value of multiple hypothesis test correction

Gene ID: Differentially expressed genes in this pathway

Count: Number of differentially expressed genes in this pathway

**Supplementary Table S4: The Primers of 11 fusion genes for Real time-PCR**

| Sample ID | Fusion Gene | Forword Primer | Reverse Primer | Fluorescence probe(5’FAM, 3’BHQ1) |
|---|---|---|---|---|
| S01 (Grade II) | RNF213-SLC26A11 | TGAAGATGGAATCCGTAGCG | CAGAAGCACAGCAGGAAGGT | TCAGCTAAGGCTGGACCTGCTGCC |
| S01/ S02/ S03/ S04 (Grade II) | GATSL2-GTF2I | AACTTGCCTTCCTGTCCTCC | GTAGCTCATTGGCCTTTGGT | TCCTCCAAGACCAGATGATGATTATT |
| S03 (Grade II) | CPD-SEZ6 | ATCACAAACGGCGCACATTG | TCCAGGATCGTGGCAGGAAG | ATGATGTGGAAGTGACTTCCTGCCA |
| S06 (Grade IV) | RC3H1-PKLR | CCCAGCAAACTTGAACCGACTA | TCCAACACGGAGGAAGCCAC | ATGATGTGGAAGTGACTTCCTGCCA |
| S06 (Grade IV) | MEX3B-KIAA1199 | TACCCAGTTCTGAGCATGTCG | GCAGTGGCCCAAAGAGTTAT | TGGGGCGGCAAGATCAAGGACGTTG |
| S08 (Grade IV) | ABL2-NCF2 | TCGCTCAGGTACGAGGGACG | TCCTTGGGTTCATCTGGAAA | CAGATGGCAAGGGTGACCAAGGCTT |
| S09 (Grade IV) | KIAA1549-BRAF | CGTCCACAACTCAGCCTACA | TCCATCACCACGAAATCCTT | ATCGGATGCCCAGACTTGATTAGAG |
| S09 (Grade IV) | CASK-SUGP1 | CATTGTAGAGTTATTGGAGAC | GGGAGCAACCCCAAACCACC | ACATGGTTTTCGAATTGAAAGGCT |
| S09 (Grade IV) | TMEM165-PDGFRA | GTCGAGAAAGGCAAAGGCATC | TCGGGGACCGTCAAAGTGTA | TCGAGAAAGGCAAAGGCATCACA |
| S09 (Grade IV) | SLC35F1-ECHDC1 | CTTGTGGGAAGACATCAGGG | GCTTGGTATTATGCCCATCT | AGGGAGCAGGTTAATGACTCCAGAG |
| S09 (Grade IV) | TCF12-SCFD2 | CAATTCAGTGGATCAGGGAG | GATTCATTAGAGCTTTGAGG | ATTCAGTGGATCAGGGAGAGTCACA |