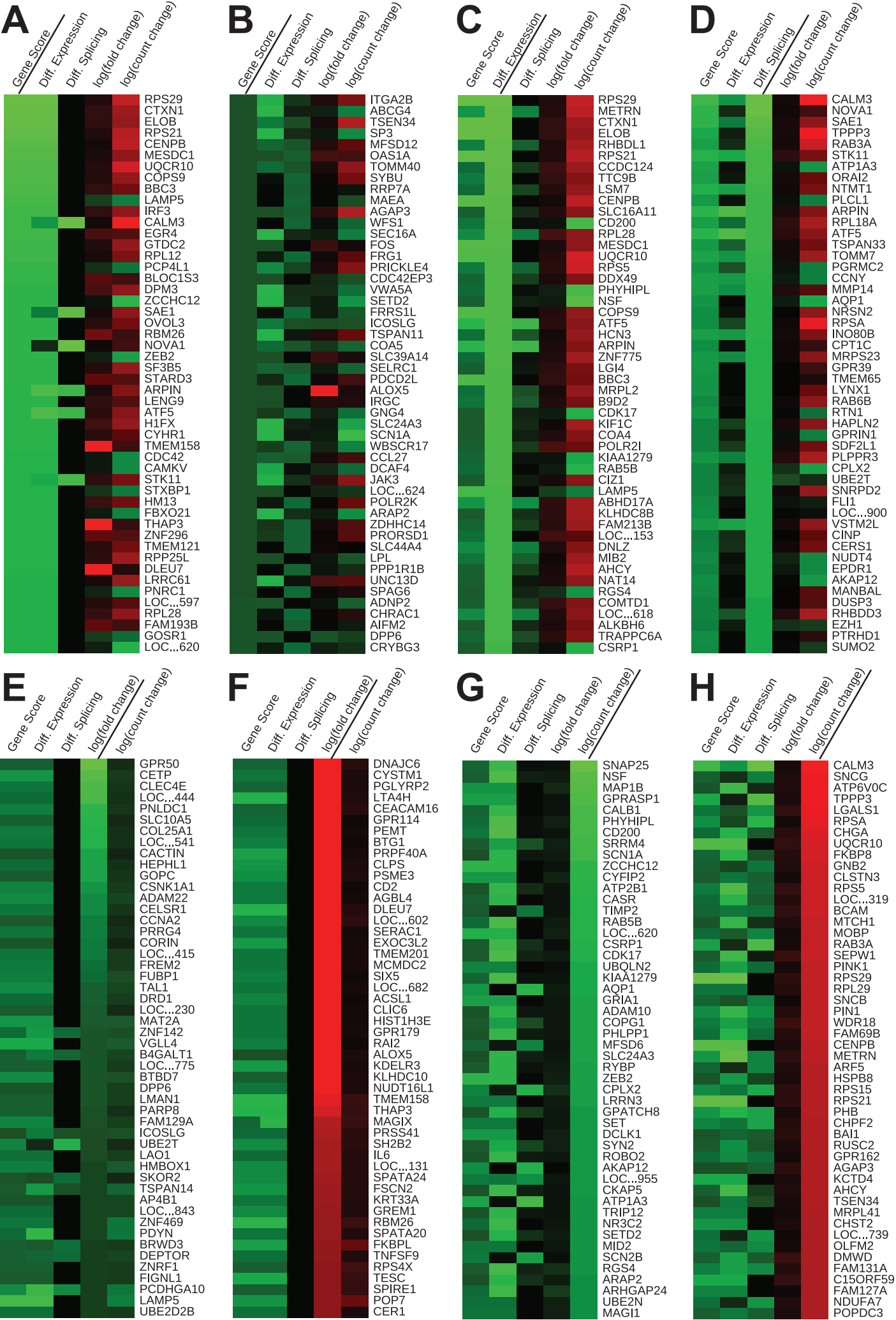
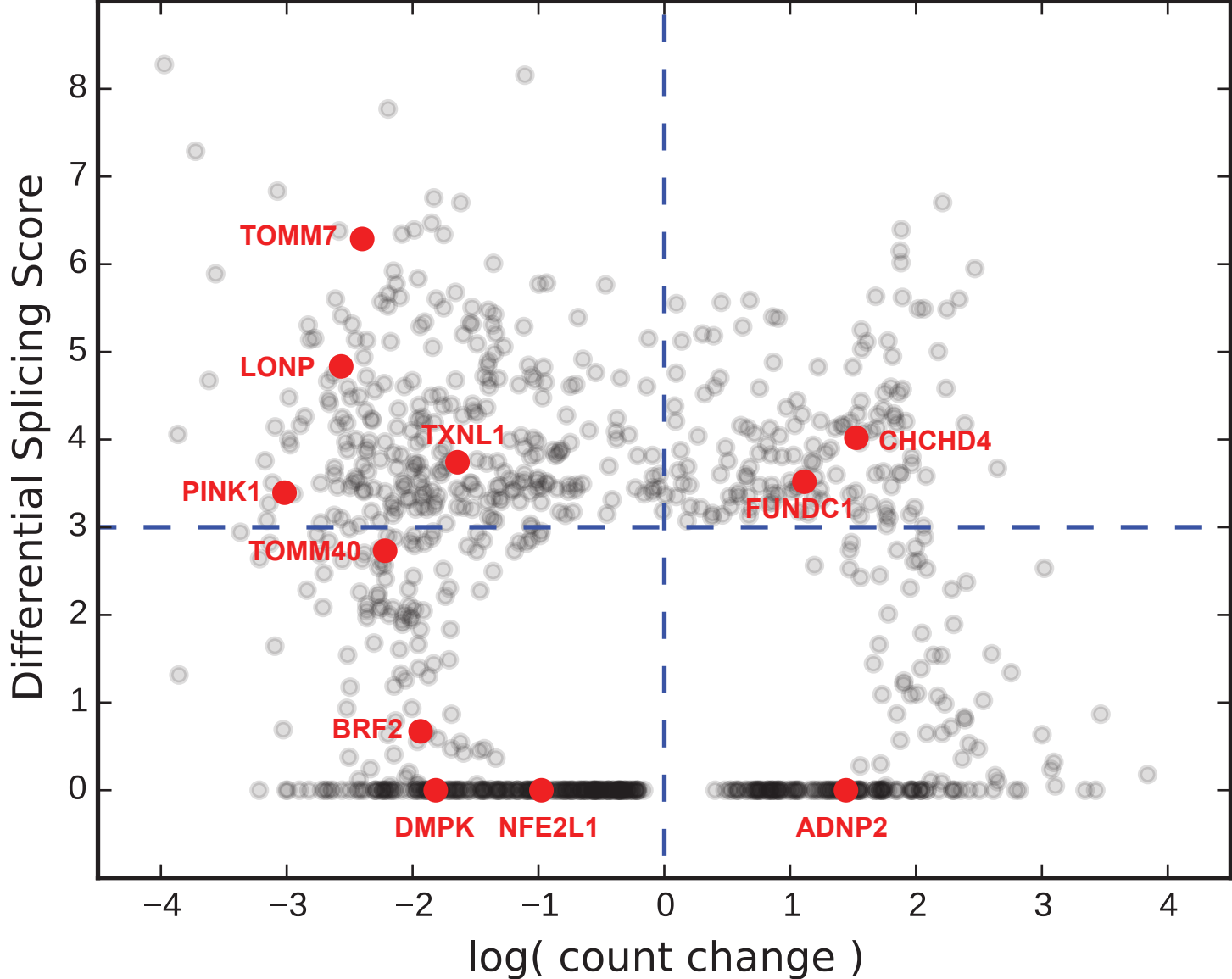


Supplementary Figure 1



Supplementary Figure 2



# Supplementary Table 1

| GO Term        | p-value | Ontology Name                                   | Genes                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|----------------|---------|-------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Level 2</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0009866     | 0.014   | cell surface                                    | ADAM10 AMBP ARSB B4GALT1 BCAM CASR CD2 CLSTN1 CLSTN3 CORIN CX3CL1 DPP6 FLT3L GP5 GREM1 GRIA1 GRM7 HBEGF ITGA2B KCNH2 LGALS1 LPL LRFN3 LRRC8A NTRK2 P2RY12 PHB ROBO1 ROBO2 SCARB1 SLITRK6 TIMP2 TMEM8B TNFRSF1A TSPAN14 TSPAN33 TSPAN8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0003735     | 0.000   | structural constituent of ribosome              | MRPL19 MRPL2 MRPL36 MRPL41 MRPS12 MRPS23 MRPS7 NDUF7 RPL12 RPL15 RPL18A RPL28 RPL29 RPL30 RPL34 RPL35 RPL37 RPL38 RPS15 RPS21 RPS29 RPS4X RPS5 RPSA ATP6V0E2 FUBP1 IL6 LAMTOR1 LAMTOR2 NDNF PRMT6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| GO:0016049     | 0.018   | cell growth                                     | AB13 ARF5 ARF6 ARL10 BACH2 CALB1 CAMKV CDC42 CPG1 CSTB DAB1 DCLK1 DEPTOR EVI5L FAM53A HSPB8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GO:0005622     | 0.037   | intracellular                                   | JAK3 KIF1C LGALS1 MAP1LC3B MID2 MRPL19 MRPL2 MRPL36 MRPS12 NMRK2 NOS2 NR3C1 PARP8 PITPNB RAB5B RAB6B RDH12 RHOU RILPL2 RNF114 RPL15 RPL28 RPL30 RPL38 RPS21 RPS29 RPS4X RPSA TRIM41 TRIM50 TWF2 UNC119B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| GO:0030246     | 0.023   | carbohydrate binding                            | BCAN CLEC2L CLEC4E CRYBG3 DGCR2 GALNT16 LGALS1 LMAN1 NPTX2 PFKM SIGLEC1 WBSCTR17                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <b>Level 3</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0001965     | 0.033   | G-protein alpha-subunit binding                 | DRD1 GRIA1 PPP5C RGS4 RGS8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| GO:0042802     | 0.019   | identical protein binding                       | AB13 AHCY APIP APLP2 BAG2 BAIAP2 C10L4 CASP8 CDCD155 CEACAM16 CLDN3 ERBB3 FKBP8 FR33 GALE GP1BB GPR50 GRIA1 HMOX1 HSPB8 IIGP1 IRF3 ITGA2B ITPA JUN KCNH2 LMAN1 MAP1S MAT2A MID2 MSANTD3 NDEL1 PFKM PPARG PPP5C PSME3 PYCRL RABAC1 RASSF1 RBMX RILPL2 ROBO1 ROBO2 SDSL SH2B2 SNX1 SNX33 STXBP1 SYT3 TRIM41 TRIM50 UBE2G2 VWA1 WAS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0048306     | 0.027   | calcium-dependent protein binding               | CALM3 CPLX2 DDX5 GRM7 NSMF SNAP25 SYN2 WFS1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GO:0043679     | 0.008   | axon terminus                                   | AQP1 CASR CHRMS1 DRD1 GRM7 KCNC3 NTRK2 PDYN SNCB SNCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0032809     | 0.013   | neuronal cell body membrane                     | AQP1 ATP2B1 KCNB1 KCNC3 RGS8 UNC5A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| GO:0003707     | 0.007   | steroid hormone receptor activity               | NR0B1 NR1H3 NR3C1 NR3C2 PAQR7 PAQR9 PPARG RARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0030742     | 0.007   | GTP-dependent protein binding                   | CDC42 GCH1 RAB3A RAB5B RAPGEF6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0005496     | 0.014   | steroid binding                                 | NR3C1 NR3C2 PAQR7 PAQR9 PGRMC2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0042493     | 0.046   | response to drug                                | AQP1 ATP1A3 BLOC1S3 DGCR2 DRD1 FOS JUN KCNJ11 MAT2A PEMT SRP14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0043195     | 0.043   | terminal bouton                                 | CALB1 CALB2 CPLX2 GRM7 NTRK2 PVALB RAB3A SNAP25 SNCB STXBP1 SYN2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0043025     | 0.029   | neuronal cell body                              | ATP1A3 BAIAP2 CALB1 CASK CASR CIB1 CPLX2 DAB1 DPP6 DRD1 EFHC1 GRIA1 GRIN3B GRM7 GRM8 HCN3 INHA KCNB1 KCNJ11 KCNN4 MAP1B MAP1LC3B MAP1S NRNS2 NTRK2 PDYN PLXDC1 PPP1R1B PPP5C PTK2B PVALB RARA ROBO1 RPSA SCN1A SNAP25 SNCB SNCG TIMP2 VGF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| GO:0016021     | 0.013   | integral component of membrane                  | ABCG4 ACSL1 ADAM10 ADAM22 ADCCK2 AGPAT1 AGPAT2 AGPAT4 AIFM2 AKAP1 ALG10B APLP2 AQP1 ARV1 ASPHD2 ATP1A3 ATP2B1 ATP6V0C ATP6V0E2 B3GALT4 B3GAT1 B4GALT1 BCAM BEAN1 CABP7 CASR CDCD155 CD2 CD200 CDH9 CELSR1 CHRMS1 CHST1 CHST2 CIDSD1 CLDN19 CLDN3 CLEC2L CLEC4E CLIC6 CLPTM1L CLSTN1 CLSTN3 COL25A1 COMTD1 CORIN CPT1C CTXN1 CX3CL1 CYSTM1 DGCR2 DIO1 DMPK DNAJC22 DPM3 DPP6 DRD1 ECEL1 EMC10 ERBB3 FAM134B FAM155A FAM171A2 FAM210B FAM69B FIBCD1 FKBP8 FLT3L FREM2 FRRS1L FUNDC1 FYCO1 GALNT16 GJB1 GOSR1 GP1BB GPRBAR1 GPR108 GPR162 GPR39 GPR50 GPR88 GRIA1 GRIN3B GRM7 GRM8 GXYLT1 HBEGF HCN3 HEPLH1 HS3ST3A1 IER3IP1 ITGA2B KCNB1 KCNC3 KCNH2 KCNJ11 KCNJ9 KCNN4 KDELR3 LAMP5 LHFP13 LMAN1 LRFN3 LRRC4 LRRN3 MANBAL MCOLN3 MERTTL23 MFSO12 MFSO6 MMP14 MOSPD3 MTCH1 MXRA7 NAT14 NAT8L NCAM2 NFE2L1 NIPAL3 NRSN2 NTRK2 ORAI2 P2RY12 P2RY6 PAQR4 PAQR7 PAQR9 PEMT PEX2 PGRMC2 PINK1 PLPP5 PLPPR3 PLXDC1 PLXNA3 PNLOC1 POPDC3 PRRG4 PTAFR PTCHD1 QRFRP RABAC1 RHBDD3 RHBDL1 RNF182 ROBO1 ROBO2 RTN1 S1PR1 SCARB1 SCN1A SCN1B SCN2B SCNN1A SERAC1 SERP1 SERP2 SIGLEC1 SIRPA SLC10A5 SLC10A7 SLC16A8 SLC1A5 SLC24A3 SLC39A1 SLC39A14 SLC44A4 SLITRK3 SLITRK6 STARD3 STEAP4 STXBP5L SURF4 SUSD2 SYBU SYT3 TM7SF3 TMCC1 TMEM114 TMEM121 TMEM141 TMEM158 TMEM168 TMEM184B TMEM201 TMEM65 TMEM88B TMEM8B TMEM9 TMNRSF1A TMNRSF9 TOMM40 TOMM7 TOR1AIP1 TSPAN11 TSPAN14 TSPAN33 TSPAN8 TTYH2 UBIAD1 UCP1 UCP2 UNC5A VSTM4 WBSCTR17 WFS1 ZDHHC14 ZDHHC9                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0000149     | 0.043   | SNARE binding                                   | CPLX2 EXOC3L2 GOSR1 KCNB1 SNAP25 STXBP1 SYT3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| <b>Level 4</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0016363     | 0.046   | nuclear matrix                                  | ALOX5 ANP32A ATN1 CASK MAEA NSMF PRKCZ PRPF40A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0006914     | 0.040   | autophagy                                       | ARSB ATGA4 FAM134B FUNDC1 GOPC LRSAAM1 MAP1LC3B NRBF2 PINK1 RAB12 RAB33B STK11 UBQLN2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0005840     | 0.001   | ribosome                                        | MRPL19 MRPL2 MRPL36 MRPL41 MRPS12 MRPS23 MRPS7 RPL12 RPL15 RPL18A RPL28 RPL29 RPL30 RPL38 RPS15 RPS21 RPS29 RPS4X RPS5 RPSA TMA16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| GO:0046928     | 0.001   | regulation of neurotransmitter secretion        | CELSR1 GRM8 KCNC3 NGF NTRK2 SNCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0007030     | 0.042   | Golgi organization                              | CDC42 CSNK1A1 GORASP1 KIFC3 LMAN1 PLEKHM2 RAB30 SURF4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0034599     | 0.037   | cellular response to oxidative stress           | ADNP2 BRF2 CHCHD4 LONP1 NFE2L1 PINK1 TXNL1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| GO:0070412     | 0.003   | R-SMAD binding                                  | DDX5 FOS FOXH1 JUN RANBP3 ZEB2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0043401     | 0.022   | steroid hormone mediated signaling pathway      | BMP7 NR0B1 NR1H3 NR3C1 NR3C2 PPARG RARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| GO:0032590     | 0.024   | dendrite membrane                               | ATP2B1 GRIA1 KCNB1 KCNC3 LAMP5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0042127     | 0.01    | regulation of cell proliferation                | ATF5 B4GALT1 BCL6B CDK6 CIB1 ERBB3 IL6 INHA MAFG MATK NOS2 NR3C1 NR3C2 PIN1 PTK2B RNF126 TAL1 TNFRSF1A TMNRSF9 TOPORS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0030424     | 0.026   | axon                                            | ADAM22 AQP1 ATP1A3 CALB1 CASR CIB1 CPT1C DRD1 GRM7 HCN3 KCNB1 MAP1B MAP1LC3B MAP3K12 NCAM2 NDEL1 NRN1L NTRK2 PINK1 PTK2B PVALB RAB3A ROBO1 SCN1A SNAP25 SNCG TNFRSF1A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0005634     | 0.047   | nucleus                                         | ADAM10 ADNP2 AGAP3 AHCY ALKBH6 ALOX5 ANKRD23 ANKRD54 ANP32A APLP2 AQP1 ARL6IP4 ATF5 ATN1 ATP1A3 ATP2B1 AUTS2 B9D2 BACH2 BCL6B BRF2 BRWD3 BTBD7 BTG1 CACTIN CALB1 CALB2 CALM3 CASK CASP3 CASP8 CASR CBR1 CBX4 CBX5 CDCD106 CDCD155 CCNA2 CCNK CCNY CDC34 CDK17 CDK6 CDKL1 CENPB CHRA2C CIB1 C1NP CIZ1 CLDN19 CLIC6 CLSTN1 COMMD10 COP9S CSNK1A1 CSRP1 CSTB CSTF2 CYFIP2 DCLRE1B DDX5 DEDD2 DGKZ DGUOQ DMPK DNAJB1 DRD1 DUSP3 DYRK3 EAF1 EGR4 ELL3 ELOB EPS15L1 ERBB3 EXOSC4 EZH1 FAM193B FAM53A FAM83G FIGNL1 FIGNL2 FLJ1 FOS FOXH1 FOXJ1 FRA10AC1 FRG1 FUBP1 GCH1 GLIS1 GNA13 GNL1 GPR88 GPRASP1 H1FX H2AFX HINT3 HIST1H3E HMOX1 HMG20B HOXD1 HR HSF4 HSF5 HSPB2 HSPB8 IIGP1 INO80B IQSEC1 IRF2BPL IRF3 JUNK KLHDC10 LDCC1 LGAL51 LONP1 LSM4 LTA4H MAEA MAFG MAGI1 MAGI3 MAP1S MBD5 MED1 MED25 MED27 MED29 MED31 MEF2A METTL22 MEK3B MGRN1 MIER2 MMP14 MPG MRPL19 MVB12A MYCL MZF1 NACC1 NFE2L1 NHLH2 NIP7 NME2 NOS2 NOVA1 NR0B1 NR1H3 NR3C1 NR3C2 NRBF2 NSMF NTMT1 NUDT16L1 NUDT4 OAS1A OLFM2 OVOL3 PAF1 PATZ1 PCIF1 PDCCD7 POLIM7 PHB PHLPP1 PIN1 PINK1 PLXNA3 PNMA1 PNRC1 POLR2E POLR2I POLR2K POP7 PPARG PPIL2 PPP1R1B PPP5C PQBP1 PRKCZ PRMT6 PRPF40A PRPF6 PSM27 PSMO9 PSME3 PTK2B PVALB RAD17 RAD51D RANBP3 RARA RASSF1 RBM42 RBMX RDM1 RFWD2 RFXANK RGS4 RGS8 RNF114 RNF126 RNPS1 RPL12 RPL15 RPL30 RPP25L RPPD18 RPS4X RPS5 RUSC1 RYBP SAE1 SAFB SCAF11 SCAND1 SDR39U1 SERTAD1 SET SETD2 SF3A1 SF3B4 SF3B5 SIN3B SIVA1 SIX5 SKOR2 SMU1 SNRNP35 SNRPD2 SOX12 SP1 SP3 SPATA24 SRP14 SRRM4 SS18L1 ST18 STK11 SUMO2 SURF6 SWSAP1 SYMPK TAL1 TCF15 TCF20 TESC TIGD5 TMA16 TMEM201 TMEM8B TNFRSF1A TOPORS TOR1AIP1 TOX2 TRIB1 TRIM41 TRIP12 TSEN34 TSHZ2 TSSK6 TUBB2A TXNDC9 TXNL1 U2AF1L4 U2AF2 UBE2N UBE2T UBIAD1 UBOX5 UBQLN2 UBXN6 USF2 VGLL4 WBSCTR22 WDR18 XPC YPEL4 ZBTB22 ZBTB43 ZCCHC12 ZEB2 ZMAT5 ZNHIT1 ZSCAN21 |
| <b>Level 5</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0022627     | 0.014   | cytosolic small ribosomal subunit               | RPS15 RPS21 RPS29 RPS4X RPS5 RPSA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| GO:0017075     | 0.012   | syntaxin-1 binding                              | CPLX2 NSF SNAP25 STXBP1 SYBU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| GO:0022625     | 0.000   | cytosolic large ribosomal subunit               | RPL12 RPL15 RPL18A RPL28 RPL29 RPL30 RPL34 RPL35 RPL37 RPL38 SURF6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| GO:0048487     | 0.024   | beta-tubulin binding                            | AKAP1 B4GALT1 MAP1S NDEL1 SNCB SNCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| GO:0019228     | 0.042   | neuronal action potential                       | DPP6 DRD1 GPR88 GRIA1 SCN1A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GO:0007616     | 0.049   | long-term memory                                | CALB1 GRIA1 NTRK2 PRKCZ SNAP25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0005689     | 0.000   | U12-type spliceosomal complex                   | LSM7 PDCCD7 RBM41 SF3B4 SF3B5 SNRNP35 SNRPD2 ZMAT5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| GO:0030307     | 0.026   | positive regulation of cell growth              | ADAM10 ADNP2 CIB1 EXOSC4 HBEGF MMP14 NGF PTK2B SLC44A4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| GO:0071300     | 0.021   | cellular response to retinoic acid              | ADNP2 AQP1 PTK2B RARA TESC TWF2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0006412     | 0.001   | translation                                     | EIF4E3 FARS2 MRPL19 MRPL2 MRPL36 MRPL41 MRPS12 MRPS23 MRPS7 RPL12 RPL15 RPL18A RPL28 RPL29 RPL30 RPL34 RPL35 RPL37 RPL38 RPS15 RPS21 RPS29 RPS4X RPS5 RPSA SARS2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0013107     | 0.011   | integral component of mitochondrial outer mem.  | DMPK FUNDC1 PINK1 TOMM40 TOMM7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0061630     | 0.013   | ubiquitin protein ligase activity               | CDC34 FBXO30 KCMF1 LRSAAM1 MED1 MED27 MED31 MGRN1 MIB2 PEX2 PPIL2 RFWD2 RNF114 RNF126 TOPORS TRIP12 UBE2G2 UBE2N UBE2T UBOX5 ZNRF1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| <b>Level 6</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0042593     | 0.032   | glucose homeostasis                             | GPR39 IL6 KCNB1 MBD5 PFKM PPARG SH2B2 STK11 STXBP5L VGF WFS1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| GO:0071347     | 0.034   | cellular response to interleukin-1              | CACTIN CX3CL1 HYAL3 IL6 RBMX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| GO:0000028     | 0.002   | ribosomal small subunit assembly                | MRPS7 RPS15 RPS5 RPSA RRP7A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GO:0030218     | 0.015   | erythrocyte differentiation                     | CASP3 DYRK3 JAK3 NFE2L1 SP3 TAL1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0007601     | 0.039   | visual perception                               | CRYBA4 GPR179 HSF4 NGB OLFM2 PDE6D RDH12 SLITRK6 WFS1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| GO:0008380     | 0.020   | RNA splicing                                    | ARL6IP4 CACTIN DCAF4 DDX5 FRG1 LSM4 PQBP1 PRPF40A PRPF6 RBMX RNPS1 SCF11 SF3A1 SF3B4 SF3B5 SNRNP35 SNRPD2 SRRM4 U2AF1L4 U2AF2 ZMAT5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <b>Level 7</b> |         |                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| GO:0051291     | 0.024   | protein heterooligomerization                   | CLDN3 GCH1 HR KCNH2 MAT2A PPP5C PRKCZ SEPT9 STK11 TNFRSF1A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| GO:0048814     | 0.008   | regulation of dendrite morphogenesis            | NSMF PQBP1 ROBO1 SKOR2 STK11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| GO:0005272     | 0.024   | sodium channel activity                         | HCN3 SCN1A SCN1B SCN2B SCNN1A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| GO:0043524     | 0.042   | negative regulation of neuron apoptotic process | ERBB3 FAM134B JUN NDNF NGF NTRK2 PIN1 PINK1 PTK2B SET SNCB STXBP1 VSTM2L WFS1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| GO:0043525     | 0.043   | positive regulation of neuron apoptotic process | BBC3 CASP3 CDC34 CDC42 JUN NR3C1 PIN1 TNFRSF1A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| GO:0050772     | 0.009   | positive regulation of axonogenesis             | METRN NTRK2 ROBO1 ROBO2 STK11 ZEB2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| GO:0003924     | 0.034   | GTPase activity                                 | AGAP3 ARF6 CDC42 GCH1 GNA11 GNA13 GNB2 GNG4 GNL1 GPN3 IIGP1 MMAA RAB12 RAB30 RAB33B RAB3A RAB5B RAB6B RHOU TUBB2A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| GO:0000398     | 0.033   | mRNA splicing, via spliceosome                  | LSM4 NOVA1 PRPF40A PRPF6 RBM41 SF3A1 SF3B5 SNRNP35 U2AF1L4 U2AF2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| GO:0032024     | 0.038   | positive regulation of insulin secretion        | CASK CASR GPR39 PFKM PSMO9 SERP1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |