

Table S5: Gene ontology analysis for 5hmC-specific peaks at promoters

| Cluster | GO ID | GO Term | Count | P Value | Genes |
|------------|--|--|-------|----------|---|
| Cluster 1 | GO:0003012 | muscle system process | 17 | 2.45E-02 | ADORA2B, BDKRB2, CRYAB, DYSF, EDNRA, GAL, GDNF, KCNE1, KCNIP2, MYLK2, NMUR1, P2RX3, P2RX4, TACR2, TMOD4, TNNT1, TNNT2 |
| | GO:0006939 | smooth muscle contraction | | | |
| | GO:0006936 | muscle contraction | | | |
| Cluster 2 | GO:0010524 | positive regulation of calcium ion transport into cytosol | 27 | 2.57E-02 | ADORA2B, BCL2, BGLAP, CADM1, CREB1, CREB3, EDNRA, GDNF, GIMAP1, GIMAP5, HRH1, HTR2C, INPP5D, LCK, LHCGR, NEDD4L, NLRP12, P2RX3, P2RX4, PRKCZ, SLN, SMAD3, TAC4, THY1, TRIP6, UNC13D, XDH |
| | GO:0010522 | regulation of calcium ion transport into cytosol | | | |
| | GO:0051928 | positive regulation of calcium ion transport | | | |
| | GO:0043270 | positive regulation of ion transport | | | |
| | GO:0010959 | regulation of metal ion transport | | | |
| | GO:0051924 | regulation of calcium ion transport | | | |
| | GO:0032846 | positive regulation of homeostatic process | | | |
| | GO:0051050 | positive regulation of transport | | | |
| | GO:0043269 | regulation of ion transport | | | |
| | GO:0051281 | positive regulation of release of sequestered calcium ion into cytosol | | | |
| | GO:0032844 | regulation of homeostatic process | | | |
| | GO:0045428 | regulation of nitric oxide biosynthetic process | | | |
| | GO:0051279 | regulation of release of sequestered calcium ion into cytosol | | | |
| | GO:0050850 | positive regulation of calcium-mediated signaling | | | |
| GO:0050848 | regulation of calcium-mediated signaling | | | | |
| GO:0048871 | multicellular organismal homeostasis | | | | |
| Cluster 3 | GO:0048812 | neuron projection morphogenesis | 46 | 3.09E-02 | ALDH1A2, ANTXR1, B3GNT2, BAIAP2L2, BCL2, BIN3, BTG2, CCKAR, CDH23, CHST3, CREB1, CRYGB, DMD, DSCAML1, EFNB3, EMX2, EPHA2, FEZ1, GAS7, GDNF, GLI2, GSX2, HOXC8, ITGB4, KCNIP2, MACF1, MAP2, MC1R, NCAM2, NFATC1, NGFR, NTM, NUMBL, OBSL1, PARD6B, PMP22, ROBO3, SLIT1, SOX1, TBR1, THY1, TNNT2, TSGA10, TULP3, UCHL1, ULK2 |
| | GO:0030182 | neuron differentiation | | | |
| | GO:0000904 | cell morphogenesis involved in differentiation | | | |
| | GO:0007409 | axonogenesis | | | |
| | GO:0048667 | cell morphogenesis involved in neuron differentiation | | | |
| | GO:0031175 | neuron projection development | | | |
| | GO:0048666 | neuron development | | | |
| | GO:0048858 | cell projection morphogenesis | | | |
| | GO:0032990 | cell part morphogenesis | | | |
| | GO:0032989 | cellular component morphogenesis | | | |
| | GO:0030030 | cell projection organization | | | |
| | GO:0000902 | cell morphogenesis | | | |
| GO:0007411 | axon guidance | | | | |
| Cluster 4 | GO:0007389 | pattern specification process | 24 | 3.16E-02 | ALDH1A2, AXIN1, BTG2, C6ORF59, DSCAML1, EDNRA, EMX2, GDF11, GLI2, GNA13, GRHL3, GSX2, HES7, HIPK2, HNF1B, HOXC8, LFNG, MDFI, MID1, MYF5, RTTN, SFRP1, SFRP2, TULP3 |
| | GO:0003002 | regionalization | | | |

| | | | | | |
|-----------|------------|--|----|----------|--|
| | GO:0009952 | anterior/posterior pattern formation | | | |
| Cluster 5 | GO:0006812 | cation transport | 56 | 3.29E-02 | ACCN1, AQP6, ATP1B1, ATP1B2, ATP2A2, ATP2B4, ATP2C2, ATP6V0A2, BSPRY, C1QTNF3, CATSPER4, FKBP4, FTL, GABRE, GLRA4, GRIA4, GRID1, HCN1, HTR3E, HVCN1, KCNA6, KCNE1, KCNIP1, KCNIP2, KCNJ11, KCNJ2, KCNJ4, KCTD12, KCTD6, LCK, MCOLN2, MFI2, MPST, NEDD4L, NFATC1, NMUR1, P2RX3, P2RX4, PKD2L2, SFXN4, SLC12A8, SLC20A1, SLC22A17, SLC22A2, SLC22A3, SLC26A9, SLC34A1, SLC38A3, SLC5A10, SLC5A7, SLC9A8, SLN, STEAP4, TCIRG1, TRPV6, TTYH2 |
| | GO:0006811 | ion transport | | | |
| | GO:0030001 | metal ion transport | | | |
| | GO:0015672 | monovalent inorganic cation transport | | | |
| | GO:0015674 | di-, tri-valent inorganic cation transport | | | |
| | GO:0006813 | potassium ion transport | | | |
| Cluster 6 | GO:0010810 | regulation of cell-substrate adhesion | 16 | 3.56E-02 | BCL2, CADM1, CCDC80, CDKN2A, COL1A1, DDR1, DMP1, EMILIN1, GSN, LAMA3, LGALS3, MYF5, NID1, PRKCZ, SMAD3, TGFB1 |
| | GO:0010811 | positive regulation of cell-substrate adhesion | | | |
| | GO:0030155 | regulation of cell adhesion | | | |
| | GO:0045785 | positive regulation of cell adhesion | | | |
| | GO:0030198 | extracellular matrix organization | | | |
| | GO:0043062 | extracellular structure organization | | | |

Table S6: Gene ontology analysis for 5mC-specific peaks at promoters

| Cluster | GO ID | GO Term | Count | P Value | Genes |
|------------|--------------------|--|-------|----------|--|
| Cluster 1 | GO:0007126 | meiosis | 34 | 5.65E-03 | ADAD1, ASZ1, BCL6, BOLL, CATSPER2, CETN1, DAZ1, DAZ2, DAZ3, DAZ4, DAZL, HORMAD1, ITGB1, MAD1L1, MAEL, MEI1, MORC1, OOEP, OVOL1, PIWIL1, PIWIL2, PRKACG, RAD51C, RBMY1F, SOHLH2, SPDYA, SYCE1, SYCE1L, TDRD1, TDRD6, TP73, TTN, USP22, VCPIP1 |
| | GO:0051327 | M phase of meiotic cell cycle | | | |
| | GO:0051321 | meiotic cell cycle | | | |
| | GO:0048232 | male gamete generation | | | |
| | GO:0007283 | spermatogenesis | | | |
| | GO:0007128 | meiotic prophase I | | | |
| | GO:0051324 | prophase | | | |
| | GO:0007276 | gamete generation | | | |
| | GO:0019953 | sexual reproduction | | | |
| | GO:0048609 | reproductive process in a multicellular organism | | | |
| | GO:0032504 | multicellular organism reproduction | | | |
| | GO:0007127 | meiosis I | | | |
| | GO:0000279 | M phase | | | |
| | GO:0022403 | cell cycle phase | | | |
| | GO:0048610 | reproductive cellular process | | | |
| GO:0022402 | cell cycle process | | | | |
| GO:0007049 | cell cycle | | | | |
| Cluster 2 | GO:0006334 | nucleosome assembly | 33 | 6.76E-03 | ASZ1, C1QTNF7, CAT, H2AFB1, H2AFB2, H2AFB3, H2BFWT, H3F3C, HIST1H2AA, HIST1H2BA, HIST1H2BI, HIST1H3E, HIST1H3G, HIST3H3, IRF7, LCAT, MAEL, MTERF, NAP1L5, NAT14, OOEP, RAD51C, SFRS6, SKAP2, SOAT2, TADA3, TRRAP, TTN, TUBA3D, TUBA3E, USP22, WDR77, WHSC1L1 |
| | GO:0031497 | chromatin assembly | | | |
| | GO:0065004 | protein-DNA complex assembly | | | |
| | GO:0034728 | nucleosome organization | | | |
| | GO:0006323 | DNA packaging | | | |
| | GO:0034622 | cellular macromolecular complex assembly | | | |
| | GO:0006333 | chromatin assembly or disassembly | | | |
| | GO:0034621 | cellular macromolecular complex subunit organization | | | |
| | GO:0043933 | macromolecular complex subunit organization | | | |
| | GO:0065003 | macromolecular complex assembly | | | |
| | GO:0051276 | chromosome organization | | | |
| | GO:0006325 | chromatin organization | | | |
| | GO:0043623 | cellular protein complex assembly | | | |
| | GO:0006461 | protein complex assembly | | | |
| | GO:0070271 | protein complex biogenesis | | | |
| | GO:0045727 | positive regulation of translation | | | BIRC7, BOLL, DAZ1, DAZ2, DAZ3, DAZ4, DAZL, EIF5AL1, FEM1A, KIAA0427, NDUFA13, PIWIL1, PIWIL2, RPS4X, TLR4, TNRC6A, TP73 |
| | GO:0006417 | regulation of translation | | | |
| | GO:0045948 | positive regulation of translational initiation | | | |

| | | | | |
|-----------|------------|---|----|----------|
| Cluster 3 | GO:0010608 | posttranscriptional regulation of gene expression | 17 | 2.70E-02 |
| | GO:0006446 | regulation of translational initiation | | |
| | GO:0032268 | regulation of cellular protein metabolic process | | |
| | GO:0032270 | positive regulation of cellular protein metabolic process | | |
| | GO:0051247 | positive regulation of protein metabolic process | | |

| Table S7: Gene ontology analysis for 5hmC-specific peaks at gene bodies | | | | | |
|--|-----------------------|---|--------------|----------------|---|
| Cluster | GO ID | GO Term | Count | P Value | Genes |
| Cluster 1 | GO:0030029 | actin filament-based process | 19 | 9.79E-03 | ABL1, ADD1, CRYAA, DIAPH2, DMD, EPB41L1, FSCN1, GAS7, INPP5K, LASP1, MYH10, MYH9, MYO1E, NEDD9, NPHP4, PCNT, PRKCZ, RAC1, TLN1 |
| | GO:0030036 | actin cytoskeleton organization | | | |
| | GO:0007015 | actin filament organization | | | |
| | GO:0007010 | cytoskeleton organization | | | |
| Cluster 2 | GO:0010551 | regulation of specific transcription from RNA polymerase II promoter | 11 | 1.78E-02 | BCOR, GDNF, HDAC4, HEY2, HHEX, INSR, ITGB1BP3, NOTCH1, NR1H2, SMAD3, USF1 |
| | GO:0032583 | regulation of gene-specific transcription | | | |
| | GO:0010553 | negative regulation of specific transcription from RNA polymerase II promoter | | | |
| | GO:0032582 | negative regulation of gene-specific transcription | | | |
| | GO:0016202 | regulation of striated muscle tissue development | | | |
| | GO:0048634 | regulation of muscle development | | | |
| Cluster 3 | GO:0006816 | calcium ion transport | 30 | 2.18E-02 | ANO8, ATP6V0A4, C16ORF7, CACNA1A, CACNA2D3, CACNG7, CAMK2G, CHRNA4, CHRNE, CLCN6, GRIN3A, GRIN3B, HCN2, KCNIP1, KCNK4, KCTD11, LASP1, LCK, NEDD4L, NFATC1, SLC10A3, SLC24A3, SLC26A9, SLC8A2, SLC8A3, SLC9A5, TRAPPC10, TRPM4, TST, TTYH2 |
| | GO:0015674 | di-, tri-valent inorganic cation transport | | | |
| | GO:0006811 | ion transport | | | |
| | GO:0030001 | metal ion transport | | | |
| | GO:0006812 | cation transport | | | |
| | GO:0006814 | sodium ion transport | | | |
| | GO:0015672 | monovalent inorganic cation transport | | | |
| Cluster 4 | GO:0006917 | induction of apoptosis | 41 | 2.25E-02 | ABL1, ALOX12, AXIN1, BBC3, CACNA1A, CBX4, CDKN1A, CRYAA, DEDD, FURIN, GDNF, IGHMBP2, INHA, LCK, MCF2L, MITF, MX1, MYO18A, NAI1, NET1, NLRP12, NOS3, NOTCH1, PCBP4, PEG10, PIM3, PLA2G6, PLEKHG5, PRKCZ, PRUNE2, RAC1, RASSF5, SART1, SFN, SMAD3, TERT, TNFRSF19, TNFSF12-TNFSF13, TNFSF13, VAV2, ZBTB16 |
| | GO:0012502 | induction of programmed cell death | | | |
| | GO:0042981 | regulation of apoptosis | | | |
| | GO:0043067 | regulation of programmed cell death | | | |
| | GO:0010941 | regulation of cell death | | | |
| | GO:0043065 | positive regulation of apoptosis | | | |
| | GO:0043068 | positive regulation of programmed cell death | | | |
| | GO:0010942 | positive regulation of cell death | | | |
| | GO:0043066 | negative regulation of apoptosis | | | |
| | GO:0043069 | negative regulation of programmed cell death | | | |
| | GO:0060548 | negative regulation of cell death | | | |
| | GO:0006916 | anti-apoptosis | | | |
| | GO:0006915 | apoptosis | | | |
| | GO:0008219 | cell death | | | |
| GO:0016265 | death | | | | |
| GO:0012501 | programmed cell death | | | | |
| Cluster 5 | GO:0008629 | induction of apoptosis by intracellular signals | 8 | 3.38E-02 | ABL1, BBC3, BRSK1, CDKN1A, FOXN3, PCBP4, SART1, SFN |
| | GO:0008630 | DNA damage response, signal transduction resulting in induction of apoptosis | | | |
| | GO:0042770 | DNA damage response, signal transduction | | | |
| Cluster 6 | GO:0001778 | plasma membrane repair | 8 | 4.52E-02 | DYSF, F8, GRHL3, MYH10, NOTCH1, PABPC4, SMAD3, SYT17 |
| | GO:0007009 | plasma membrane organization | | | |
| | GO:0042060 | wound healing | | | |

Table S8: Gene ontology analysis for 5mC-specific peaks at gene bodies

| Cluster | GO ID | GO Term | Count | P Value | Genes |
|-----------|------------|---|-------|----------|--|
| Cluster 1 | GO:0007156 | homophilic cell adhesion | 90 | 6.45E-15 | ACTN1, AJAP1, APBA1, APOA4, ARVCF, C21ORF29, CD4, CD58, CDH20, CDH3, CDH4, CDH5, CELSR1, CELSR2, CELSR3, CLSTN1, CNTNAP1, CNTNAP3, COL18A1, COL22A1, COL27A1, COL6A1, COL6A2, DCHS1, DSCAML1, FAT3, FBLN7, FCGBP, FLRT1, HAPLN4, HAS1, ISLR, LAMA1, LAMC3, MAG, MAGI1, NID1, NINJ2, NLGN4Y, NPHP4, NRXN1, NRXN2, NRXN3, PCDH8, PCDHA1, PCDHA10, PCDHA11, PCDHA12, PCDHA13, PCDHA2, PCDHA3, PCDHA4, PCDHA5, PCDHA6, PCDHA7, PCDHA8, PCDHA9, PCDHGA1, PCDHGA10, PCDHGA11, PCDHGA12, PCDHGA2, PCDHGA3, PCDHGA4, PCDHGA5, PCDHGA6, PCDHGA7, PCDHGA8, PCDHGA9, PCDHGB1, PCDHGB2, PCDHGB3, PCDHGB4, PCDHGB5, PCDHGB6, PCDHGB7, PKD1, PTPRF, PTPRS, RADIL, SCARB1, SCRIB, SDK1, TECTA, TGFB111, THBS2, TMEM8B, TNN, TNXA, TNXB |
| | GO:0016337 | cell-cell adhesion | | | |
| | GO:0007155 | cell adhesion | | | |
| | GO:0022610 | biological adhesion | | | |
| Cluster 2 | GO:0030001 | metal ion transport | 81 | 4.21E-04 | ACCN1, ADD2, ATP5F1, CACNA1A, CACNA1H, CACNA1I, CACNA2D4, CALHM1, CAMK2G, CELSR3, CHRFB7A, CHRFB7B, CHRFB7C, CHRFB7D, CHRFB7E, CHRFB7F, CHRFB7G, CHRFB7H, CHRFB7I, CHRFB7J, CHRFB7K, CHRFB7L, CHRFB7M, CHRFB7N, CHRFB7O, CHRFB7P, CHRFB7Q, CHRFB7R, CHRFB7S, CHRFB7T, CHRFB7U, CHRFB7V, CHRFB7W, CHRFB7X, CHRFB7Y, CHRFB7Z, CHRFB7AA, CHRFB7AB, CHRFB7AC, CHRFB7AD, CHRFB7AE, CHRFB7AF, CHRFB7AG, CHRFB7AH, CHRFB7AI, CHRFB7AJ, CHRFB7AK, CHRFB7AL, CHRFB7AM, CHRFB7AN, CHRFB7AO, CHRFB7AP, CHRFB7AQ, CHRFB7AR, CHRFB7AS, CHRFB7AT, CHRFB7AU, CHRFB7AV, CHRFB7AW, CHRFB7AX, CHRFB7AY, CHRFB7AZ, CHRFB7BA, CHRFB7BB, CHRFB7BC, CHRFB7BD, CHRFB7BE, CHRFB7BF, CHRFB7BG, CHRFB7BH, CHRFB7BI, CHRFB7BJ, CHRFB7BK, CHRFB7BL, CHRFB7BM, CHRFB7BN, CHRFB7BO, CHRFB7BP, CHRFB7BQ, CHRFB7BR, CHRFB7BS, CHRFB7BT, CHRFB7BU, CHRFB7BV, CHRFB7BW, CHRFB7BX, CHRFB7BY, CHRFB7BZ, CHRFB7CA, CHRFB7CB, CHRFB7CC, CHRFB7CD, CHRFB7CE, CHRFB7CF, CHRFB7CG, CHRFB7CH, CHRFB7CI, CHRFB7CJ, CHRFB7CK, CHRFB7CL, CHRFB7CM, CHRFB7CN, CHRFB7CO, CHRFB7CP, CHRFB7CQ, CHRFB7CR, CHRFB7CS, CHRFB7CT, CHRFB7CU, CHRFB7CV, CHRFB7CW, CHRFB7CX, CHRFB7CY, CHRFB7CZ, CHRFB7DA, CHRFB7DB, CHRFB7DC, CHRFB7DD, CHRFB7DE, CHRFB7DF, CHRFB7DG, CHRFB7DH, CHRFB7DI, CHRFB7DJ, CHRFB7DK, CHRFB7DL, CHRFB7DM, CHRFB7DN, CHRFB7DO, CHRFB7DP, CHRFB7DQ, CHRFB7DR, CHRFB7DS, CHRFB7DT, CHRFB7DU, CHRFB7DV, CHRFB7DW, CHRFB7DX, CHRFB7DY, CHRFB7DZ, CHRFB7EA, CHRFB7EB, CHRFB7EC, CHRFB7ED, CHRFB7EE, CHRFB7EF, CHRFB7EG, CHRFB7EH, CHRFB7EI, CHRFB7EJ, CHRFB7EK, CHRFB7EL, CHRFB7EM, CHRFB7EN, CHRFB7EO, CHRFB7EP, CHRFB7EQ, CHRFB7ER, CHRFB7ES, CHRFB7ET, CHRFB7EU, CHRFB7EV, CHRFB7EW, CHRFB7EX, CHRFB7EY, CHRFB7EZ, CHRFB7FA, CHRFB7FB, CHRFB7FC, CHRFB7FD, CHRFB7FE, CHRFB7FF, CHRFB7FG, CHRFB7FH, CHRFB7FI, CHRFB7FJ, CHRFB7FK, CHRFB7FL, CHRFB7FM, CHRFB7FN, CHRFB7FO, CHRFB7FP, CHRFB7FQ, CHRFB7FR, CHRFB7FS, CHRFB7FT, CHRFB7FU, CHRFB7FV, CHRFB7FW, CHRFB7FX, CHRFB7FY, CHRFB7FZ, CHRFB7GA, CHRFB7GB, CHRFB7GC, CHRFB7GD, CHRFB7GE, CHRFB7GF, CHRFB7GG, CHRFB7GH, CHRFB7GI, CHRFB7GJ, CHRFB7GK, CHRFB7GL, CHRFB7GM, CHRFB7GN, CHRFB7GO, CHRFB7GP, CHRFB7GQ, CHRFB7GR, CHRFB7GS, CHRFB7GT, CHRFB7GU, CHRFB7GV, CHRFB7GW, CHRFB7GX, CHRFB7GY, CHRFB7GZ, CHRFB7HA, CHRFB7HB, CHRFB7HC, CHRFB7HD, CHRFB7HE, CHRFB7HF, CHRFB7HG, CHRFB7HH, CHRFB7HI, CHRFB7HJ, CHRFB7HK, CHRFB7HL, CHRFB7HM, CHRFB7HN, CHRFB7HO, CHRFB7HP, CHRFB7HQ, CHRFB7HR, CHRFB7HS, CHRFB7HT, CHRFB7HU, CHRFB7HV, CHRFB7HW, CHRFB7HX, CHRFB7HY, CHRFB7HZ, CHRFB7IA, CHRFB7IB, CHRFB7IC, CHRFB7ID, CHRFB7IE, CHRFB7IF, CHRFB7IG, CHRFB7IH, CHRFB7IJ, CHRFB7IK, CHRFB7IL, CHRFB7IM, CHRFB7IN, CHRFB7IO, CHRFB7IP, CHRFB7IQ, CHRFB7IR, CHRFB7IS, CHRFB7IT, CHRFB7IU, CHRFB7IV, CHRFB7IW, CHRFB7IX, CHRFB7IY, CHRFB7IZ, CHRFB7JA, CHRFB7JB, CHRFB7JC, CHRFB7JD, CHRFB7JE, CHRFB7JF, CHRFB7JG, CHRFB7JH, CHRFB7JI, CHRFB7JJ, CHRFB7JK, CHRFB7JL, CHRFB7JM, CHRFB7JN, CHRFB7JO, CHRFB7JP, CHRFB7JQ, CHRFB7JR, CHRFB7JS, CHRFB7JT, CHRFB7JU, CHRFB7JV, CHRFB7JW, CHRFB7JX, CHRFB7JY, CHRFB7JZ, CHRFB7KA, CHRFB7KB, CHRFB7KC, CHRFB7KD, CHRFB7KE, CHRFB7KF, CHRFB7KG, CHRFB7KH, CHRFB7KI, CHRFB7KJ, CHRFB7KK, CHRFB7KL, CHRFB7KM, CHRFB7KN, CHRFB7KO, CHRFB7KP, CHRFB7KQ, CHRFB7KR, CHRFB7KS, CHRFB7KT, CHRFB7KU, CHRFB7KV, CHRFB7KW, CHRFB7KX, CHRFB7KY, CHRFB7KZ, CHRFB7LA, CHRFB7LB, CHRFB7LC, CHRFB7LD, CHRFB7LE, CHRFB7LF, CHRFB7LG, CHRFB7LH, CHRFB7LI, CHRFB7LJ, CHRFB7LK, CHRFB7LL, CHRFB7LM, CHRFB7LN, CHRFB7LO, CHRFB7LP, CHRFB7LQ, CHRFB7LR, CHRFB7LS, CHRFB7LT, CHRFB7LU, CHRFB7LV, CHRFB7LW, CHRFB7LX, CHRFB7LY, CHRFB7LZ, CHRFB7MA, CHRFB7MB, CHRFB7MC, CHRFB7MD, CHRFB7ME, CHRFB7MF, CHRFB7MG, CHRFB7MH, CHRFB7MI, CHRFB7MJ, CHRFB7MK, CHRFB7ML, CHRFB7MN, CHRFB7MO, CHRFB7MP, CHRFB7MQ, CHRFB7MR, CHRFB7MS, CHRFB7MT, CHRFB7MU, CHRFB7MV, CHRFB7MW, CHRFB7MX, CHRFB7MY, CHRFB7MZ, CHRFB7NA, CHRFB7NB, CHRFB7NC, CHRFB7ND, CHRFB7NE, CHRFB7NF, CHRFB7NG, CHRFB7NH, CHRFB7NI, CHRFB7NJ, CHRFB7NK, CHRFB7NL, CHRFB7NM, CHRFB7NO, CHRFB7NP, CHRFB7NQ, CHRFB7NR, CHRFB7NS, CHRFB7NT, CHRFB7NU, CHRFB7NV, CHRFB7NW, CHRFB7NX, CHRFB7NY, CHRFB7NZ, CHRFB7OA, CHRFB7OB, CHRFB7OC, CHRFB7OD, CHRFB7OE, CHRFB7OF, CHRFB7OG, CHRFB7OH, CHRFB7OI, CHRFB7OJ, CHRFB7OK, CHRFB7OL, CHRFB7OM, CHRFB7ON, CHRFB7OO, CHRFB7OP, CHRFB7OQ, CHRFB7OR, CHRFB7OS, CHRFB7OT, CHRFB7OU, CHRFB7OV, CHRFB7OW, CHRFB7OX, CHRFB7OY, CHRFB7OZ, CHRFB7PA, CHRFB7PB, CHRFB7PC, CHRFB7PD, CHRFB7PE, CHRFB7PF, CHRFB7PG, CHRFB7PH, CHRFB7PI, CHRFB7PJ, CHRFB7PK, CHRFB7PL, CHRFB7PM, CHRFB7PN, CHRFB7PO, CHRFB7PP, CHRFB7PQ, CHRFB7PR, CHRFB7PS, CHRFB7PT, CHRFB7PU, CHRFB7PV, CHRFB7PW, CHRFB7PX, CHRFB7PY, CHRFB7PZ, CHRFB7QA, CHRFB7QB, CHRFB7QC, CHRFB7QD, CHRFB7QE, CHRFB7QF, CHRFB7QG, CHRFB7QH, CHRFB7QI, CHRFB7QJ, CHRFB7QK, CHRFB7QL, CHRFB7QM, CHRFB7QN, CHRFB7QO, CHRFB7QP, CHRFB7QQ, CHRFB7QR, CHRFB7QS, CHRFB7QT, CHRFB7QU, CHRFB7QV, CHRFB7QW, CHRFB7QX, CHRFB7QY, CHRFB7QZ, CHRFB7RA, CHRFB7RB, CHRFB7RC, CHRFB7RD, CHRFB7RE, CHRFB7RF, CHRFB7RG, CHRFB7RH, CHRFB7RI, CHRFB7RJ, CHRFB7RK, CHRFB7RL, CHRFB7RM, CHRFB7RN, CHRFB7RO, CHRFB7RP, CHRFB7RQ, CHRFB7RR, CHRFB7RS, CHRFB7RT, CHRFB7RU, CHRFB7RV, CHRFB7RW, CHRFB7RX, CHRFB7RY, CHRFB7RZ, CHRFB7SA, CHRFB7SB, CHRFB7SC, CHRFB7SD, CHRFB7SE, CHRFB7SF, CHRFB7SG, CHRFB7SH, CHRFB7SI, CHRFB7SJ, CHRFB7SK, CHRFB7SL, CHRFB7SM, CHRFB7SN, CHRFB7SO, CHRFB7SP, CHRFB7SQ, CHRFB7SR, CHRFB7SS, CHRFB7ST, CHRFB7SU, CHRFB7SV, CHRFB7SW, CHRFB7SX, CHRFB7SY, CHRFB7SZ, CHRFB7TA, CHRFB7TB, CHRFB7TC, CHRFB7TD, CHRFB7TE, CHRFB7TF, CHRFB7TG, CHRFB7TH, CHRFB7TI, CHRFB7TJ, CHRFB7TK, CHRFB7TL, CHRFB7TM, CHRFB7TN, CHRFB7TO, CHRFB7TP, CHRFB7TQ, CHRFB7TR, CHRFB7TS, CHRFB7TT, CHRFB7TU, CHRFB7TV, CHRFB7TW, CHRFB7TX, CHRFB7TY, CHRFB7TZ, CHRFB7UA, CHRFB7UB, CHRFB7UC, CHRFB7UD, CHRFB7UE, CHRFB7UF, CHRFB7UG, CHRFB7UH, CHRFB7UI, CHRFB7UJ, CHRFB7UK, CHRFB7UL, CHRFB7UM, CHRFB7UN, CHRFB7UO, CHRFB7UP, CHRFB7UQ, CHRFB7UR, CHRFB7US, CHRFB7UT, CHRFB7UU, CHRFB7UV, CHRFB7UW, CHRFB7UX, CHRFB7UY, CHRFB7UZ, CHRFB7VA, CHRFB7VB, CHRFB7VC, CHRFB7VD, CHRFB7VE, CHRFB7VF, CHRFB7VG, CHRFB7VH, CHRFB7VI, CHRFB7VJ, CHRFB7VK, CHRFB7VL, CHRFB7VM, CHRFB7VN, CHRFB7VO, CHRFB7VP, CHRFB7VQ, CHRFB7VR, CHRFB7VS, CHRFB7VT, CHRFB7VU, CHRFB7VV, CHRFB7VW, CHRFB7VX, CHRFB7VY, CHRFB7VZ, CHRFB7WA, CHRFB7WB, CHRFB7WC, CHRFB7WD, CHRFB7WE, CHRFB7WF, CHRFB7WG, CHRFB7WH, CHRFB7WI, CHRFB7WJ, CHRFB7WK, CHRFB7WL, CHRFB7WM, CHRFB7WN, CHRFB7WO, CHRFB7WP, CHRFB7WQ, CHRFB7WR, CHRFB7WS, CHRFB7WT, CHRFB7WU, CHRFB7WV, CHRFB7WW, CHRFB7WX, CHRFB7WY, CHRFB7WZ, CHRFB7XA, CHRFB7XB, CHRFB7XC, CHRFB7XD, CHRFB7XE, CHRFB7XF, CHRFB7XG, CHRFB7XH, CHRFB7XI, CHRFB7XJ, CHRFB7XK, CHRFB7XL, CHRFB7XM, CHRFB7XN, CHRFB7XO, CHRFB7XP, CHRFB7XQ, CHRFB7XR, CHRFB7XS, CHRFB7XT, CHRFB7XU, CHRFB7XV, CHRFB7XW, CHRFB7XX, CHRFB7XY, CHRFB7XZ, CHRFB7YA, CHRFB7YB, CHRFB7YC, CHRFB7YD, CHRFB7YE, CHRFB7YF, CHRFB7YG, CHRFB7YH, CHRFB7YI, CHRFB7YJ, CHRFB7YK, CHRFB7YL, CHRFB7YM, CHRFB7YN, CHRFB7YO, CHRFB7YP, CHRFB7YQ, CHRFB7YR, CHRFB7YS, CHRFB7YT, CHRFB7YU, CHRFB7YV, CHRFB7YW, CHRFB7YX, CHRFB7YY, CHRFB7YZ, CHRFB7ZA, CHRFB7ZB, CHRFB7ZC, CHRFB7ZD, CHRFB7ZE, CHRFB7ZF, CHRFB7ZG, CHRFB7ZH, CHRFB7ZI, CHRFB7ZJ, CHRFB7ZK, CHRFB7ZL, CHRFB7ZM, CHRFB7ZN, CHRFB7ZO, CHRFB7ZP, CHRFB7ZQ, CHRFB7ZR, CHRFB7ZS, CHRFB7ZT, CHRFB7ZU, CHRFB7ZV, CHRFB7ZW, CHRFB7ZX, CHRFB7ZY, CHRFB7ZZ |
| | GO:0006812 | cation transport | | | |
| | GO:0006816 | calcium ion transport | | | |
| | GO:0006811 | ion transport | | | |
| | GO:0006813 | potassium ion transport | | | |
| | GO:0015674 | di-, tri-valent inorganic cation transport | | | |
| | GO:0055085 | transmembrane transport | | | |
| | GO:0015672 | monovalent inorganic cation transport | | | |
| Cluster 3 | GO:0030182 | neuron differentiation | 70 | 3.49E-03 | AGRN, ANK1, ARPC4, BCL11B, BCL6, BRSK2, CACNA1A, CCNL2, CDH4, CELSR2, CELSR3, CHRNB2, COL18A1, COX10, CUX1, CYFIP1, DAPK3, DNAH17, DNAH5, DSCAML1, EPHA2, EPHB2, FGD3, Genes, GLI2, GLI3, GNAT1, IDUA, IGSF9, JAG2, JAK2, LAMA1, LHX2, LHX5, LINGO1, LRP5, LRP8, MAP1S, MAP7, MAPK8IP3, MC1R, MYH6, NCK2, NFATC1, NGFR, NOTCH1, NOTCH3, NR2E1, NRXN1, NRXN3, NTNG2, PCNT, PDGFB, PDGFRB, RPS27A, RTN1, RUNX3, SALL3, SCARB1, SCRIB, SHROOM3, STMN3, TNN, TP73, TSC2, TSGA10, TUBB2B, TUBB3, ULK1, USH1G, WNT7A |
| | GO:0000902 | cell morphogenesis | | | |
| | GO:0032989 | cellular component morphogenesis | | | |
| | GO:0048812 | neuron projection morphogenesis | | | |
| | GO:0032990 | cell part morphogenesis | | | |
| | GO:0031175 | neuron projection development | | | |
| | GO:0048858 | cell projection morphogenesis | | | |
| | GO:0048667 | cell morphogenesis involved in neuron differentiation | | | |
| | GO:0030030 | cell projection organization | | | |
| | GO:0000904 | cell morphogenesis involved in differentiation | | | |
| | GO:0007409 | axonogenesis | | | |
| | GO:0048666 | neuron development | | | |

| | | | | | |
|------------|--|--|----|----------|--|
| | GO:0007411 | axon guidance | | | |
| | GO:0006928 | cell motion | | | |
| Cluster 4 | GO:0022604 | regulation of cell morphogenesis | 51 | 6.76E-03 | ADD2, AGRN, ATP10A, BCL6, CACNA1A, CDC42EP4, CDH4, CENPF, CHRN2, CYFIP1, DLL1, EPHB2, FGD3, FGF23, Genes, GLI2, GLI3, HLX, LHX5, LINGO1, MAG, MBP, MID1, MID1IP1, MYH14, NCK2, NEDD4L, NF1, NGFR, NOTCH1, NOTCH3, NR2E1, PACSIN1, PBX1, PLXNB2, PML, PPARA, PRDM16, PRKCZ, PTPRF, RPS27A, RUNX1, SHROOM3, SIX2, SKI, SMAD6, SPTB, TBX3, TGFB111, TTC3, ULK1, WNT7A |
| | GO:0010769 | regulation of cell morphogenesis involved in differentiation | | | |
| | GO:0045664 | regulation of neuron differentiation | | | |
| | GO:0045596 | negative regulation of cell differentiation | | | |
| | GO:0051960 | regulation of nervous system development | | | |
| | GO:0060284 | regulation of cell development | | | |
| | GO:0010975 | regulation of neuron projection development | | | |
| | GO:0050767 | regulation of neurogenesis | | | |
| | GO:0031344 | regulation of cell projection organization | | | |
| | GO:0031345 | negative regulation of cell projection organization | | | |
| | GO:0050770 | regulation of axonogenesis | | | |
| | GO:0050771 | negative regulation of axonogenesis | | | |
| | GO:0051129 | negative regulation of cellular component organization | | | |
| | GO:0010721 | negative regulation of cell development | | | |
| | GO:0050768 | negative regulation of neurogenesis | | | |
| | GO:0010720 | positive regulation of cell development | | | |
| | GO:0050769 | positive regulation of neurogenesis | | | |
| | GO:0031346 | positive regulation of cell projection organization | | | |
| GO:0050772 | positive regulation of axonogenesis | | | | |
| GO:0051130 | positive regulation of cellular component organization | | | | |