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, TGFBI
	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, NAIF1, 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, TGFB1I1, 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, CHRFAM7A, CHRNA10, CHRNA4, CHRNA7, CHRNB2, CLCN7, GABRB3, GABRD, Genes, GRIN2B, GRIN3B, HEPHL1, JPH1, JPH2, JPH3, KCNA5, KCNC1, KCNC4, KCND1, KCND2, KCND3, KCNF1, KCNG1, KCNG2, KCNG4, KCNJ12, KCNJ14, KCNJ4, KCNK3, KCNN1, KCNQ1, KCNQ2, KCNV2, KCTD15, LOC153328, MFI2, MPST, MYO1C, NEDD4L, NFATC1, NOX5, OCA2, PKD1, POM121, POM121C, RGPD4, RGPD8, RYR1, RYR2, SCARA5, SCARB1, SCN4A, SLC12A4, SLC12A7, SLC19A1, SLC20A2, SLC25A24, SLC25A29, SLC25A6, SLC26A1, SLC2A5, SLC39A3, SLC41A3, SLC45A4, SLC47A2, SLC5A10, SLC9A3, SLCO3A1, SRI, SV2C, TRPM5, TRPV3
	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, CHRNB2, 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, TGFB1I1, 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			