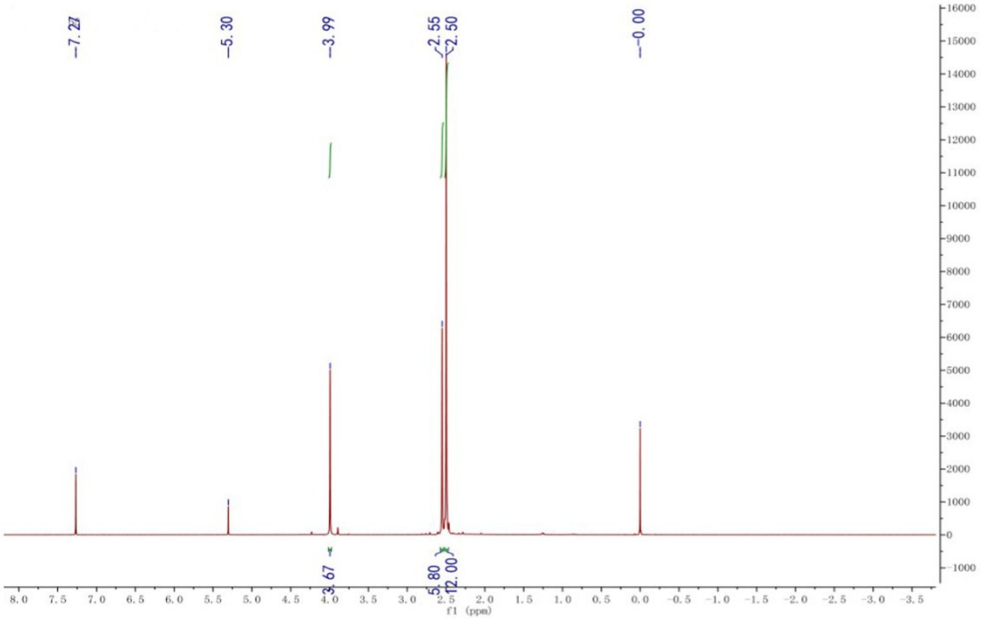

Figure S1 ^{1}H-NMR map of DTMP

Uniport	Accession	Protein names	(N2a/APP) / (N2a/WT)	(DTMP) / (N2a/APP)
mitochondrial function				
O35658	C1QBP_MOUSE	Complement component 1 Q subcomponent-binding protein, mitochondrial GN=C1qbp	0.701	1.434
P56394	COX17_MOUSE	Cytochrome c oxidase copper chaperone GN=Cox17	0.606	1.509
Q9CYN9	RENR_MOUSE	Renin receptor GN=Atp6ap2	1.275	0.684
Q60575	KIF1B_MOUSE	Kinesin-like protein KIF1B GN=Kif1b	1.267	0.739
Q99KR7	PPIF_MOUSE	Peptidyl-prolyl cis-trans isomerase F, mitochondrial GN=Ppif	0.591	1.402
Q8VEA4	MIA40_MOUSE	Mitochondrial intermembrane space import and assembly protein 40 GN=Chchd4	0.665	1.357
Q99JR1	SFXN1_MOUSE	Sideroflexin-1 GN=Sfxn1	1.288	0.735
P97478	COQ7_MOUSE	5-demethoxyubiquinone hydroxylase, mitochondrial GN=Coq7	1.265	0.552
Q80YD1	SUV3_MOUSE	ATP-dependent RNA helicase SUPV3L1, mitochondrial GN=Supv3l1	1.288	0.709
P36552	HEM6_MOUSE	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial GN=Cpox	1.265	0.658
Q9DCJ5	NDUA8_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 GN=Ndufa8	1.324	0.647
ATP bining				
Q9CYN9	RENR_MOUSE	Renin receptor GN=Atp6ap2	1.275	0.684
Q91Y97	ALDOB_MOUSE	Fructose-bisphosphate aldolase B GN=Aldob	1.428	0.794
Q60575	KIF1B_MOUSE	Kinesin-like protein KIF1B GN=Kif1b	1.267	0.739
Q99KR7	PPIF_MOUSE	Peptidyl-prolyl cis-trans isomerase F, mitochondrial GN=Ppif	0.591	1.402
O88708	ORC4_MOUSE	Origin recognition complex subunit 4 GN=Orc4	1.348	0.564
Q8VE99	CC115_MOUSE	Coiled-coil domain-containing protein 115 GN=Ccdc115	0.747	1.379
Q9Z129	RECQ1_MOUSE	ATP-dependent DNA helicase Q1 GN=Recql	1.542	0.623
Q80YD1	SUV3_MOUSE	ATP-dependent RNA helicase SUPV3L1, mitochondrial GN=Supv3l1	1.288	0.709
P36552	HEM6_MOUSE	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial GN=Cpox	1.265	0.658
Q9EQW7	KI13A_MOUSE	Kinesin-like protein KIF13A GN=Kif13a	1.32	0.736
GTPase function related				
Q62159	RHOC_MOUSE	Rho-related GTP-binding protein RhoC GN=Rhoc	2.005	0.456
Q8VEH3	ARL8A_MOUSE	ADP-ribosylation factor-like protein 8A GN=Arl8a	0.765	1.331
Q921J2	RHEB_MOUSE	GTP-binding protein Rheb GN=Rheb	0.776	1.296
Q9ESJ0	XPO4_MOUSE	Exportin-4 GN=Xpo4	0.764	1.365
Q9CQE5	RGS10_MOUSE	Regulator of G-protein signaling 10 GN=Rgs10	1.351	0.731
Q3UIA2	RHG17_MOUSE	Rho GTPase-activating protein 17 GN=Arhgap17	1.259	1.28
Q6ZPE2	MTMR5_MOUSE	Myotubularin-related protein 5 GN=Sbf1	1.348	0.758
Q91VW5	GOGA4_MOUSE	Golgin subfamily A member 4 GN=Golga4	1.473	0.365
Q9R0Z9	RHG07_MOUSE	Rho GTPase-activating protein 7 GN=Dlc1	1.26	0.567
Q8R5A6	TB22A_MOUSE	TBC1 domain family member 22A GN=Tbc1d22a	1.494	0.593
Q9CPR7	SIKE1_MOUSE	Suppressor of IKBKE 1 GN=Sike1	1.319	0.473
Q80TE4	SI1L2_MOUSE	Signal-induced proliferation-associated 1-like protein 2 GN=Sipa1l2	1.425	0.641
A2A8U2	TM201_MOUSE	Transmembrane protein 201 GN=Tmem201	1.408	0.782
RNA binding				
P09405	NUCL_MOUSE	Nucleolin GN=Ncl	0.766	1.409
Q61937	NPM_MOUSE	Nucleophosmin GN=Npm1	0.743	1.277
Q9JKP5	MBNL1_MOUSE	Muscleblind-like protein 1 GN=Mbnl1	0.734	1.286
Q920Q6	MSI2H_MOUSE	RNA-binding protein Musashi homolog 2 GN=Msi2	1.351	0.771
Q9D7B1	DUS2L_MOUSE	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like GN=Dus2	1.298	0.606
O54836	ZMAT3_MOUSE	Zinc finger matrin-type protein 3 GN=Zmat3	1.254	0.715
Q9JHI7	EXOS9_MOUSE	Exosome complex component RRP45 GN=Exosc9	1.39	0.694
Q9D823	RL37_MOUSE	60S ribosomal protein L37 GN=Rpl37	1.303	0.566
Q4FZF3	DDX49_MOUSE	Probable ATP-dependent RNA helicase DDX49 GN=Ddx49	1.325	0.62
Q8VC70	RBMS2_MOUSE	RNA-binding motif, single-stranded-interacting protein 2 GN=Rbms2	1.254	0.648
DNA binding				
P09602	HMGN2_MOUSE	Non-histone chromosomal protein HMG-17 GN=Hmgn2	1.33	0.639
Q64127	TIF1A_MOUSE	Transcription intermediary factor 1-alpha GN=Trim24	1.255	0.583
Q62187	TTF1_MOUSE	Transcription termination factor 1 GN=Ttf1	1.411	0.685
O88559	MEN1_MOUSE	Menin GN=Men1	1.447	0.753
P45481	CBP_MOUSE	CREB-binding protein GN=Crebbp	1.306	0.58
O08811	ERCC2_MOUSE	General transcription and DNA repair factor IIH helicase subunit XPD GN=Ercc2	1.328	0.791
Q9Z104	HM20B_MOUSE	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related GN=Hmg20b	1.297	0.439
O88708	ORC4_MOUSE	Origin recognition complex subunit 4 GN=Orc4	1.348	0.564
Q9Z129	RECQ1_MOUSE	ATP-dependent DNA helicase Q1 GN=Recql	1.542	0.623
Q62311	TAF6_MOUSE	Transcription initiation factor TFIID subunit 6 GN=Taf6	0.764	1.255
Q8BMQ2	TF3C4_MOUSE	General transcription factor 3C polypeptide 4 GN=Gtf3c4	1.25	1.317
Q4G0F8	UBN1_MOUSE	Ubinuclein-1 GN=Ubn1	1.43	0.752
Q80YD1	SUV3_MOUSE	ATP-dependent RNA helicase SUPV3L1, mitochondrial GN=Supv3l1	1.288	0.709
Q9QXE7	TBL1X_MOUSE	F-box-like/WD repeat-containing protein TBL1X GN=Tbl1x	1.304	0.547

Table S1 118 differentially expressed proteins after treated by DTMP in N2a/APPswe cells.

Uniport	Accession	Protein names	(N2a/APP) / (N2a/WT)	(DTMP) / (N2a/APP)
nucleotide binding				
Q62159	RHOC_MOUSE	Rho-related GTP-binding protein RhoC GN=Rhoc	2.005	0.456
P70303	PYRG2_MOUSE	CTP synthase 2 GN=Ctps2	1.691	1.405
P51855	GSHB_MOUSE	Glutathione synthetase GN=Gss	1.34	0.607
Q8VEH3	ARL8A_MOUSE	ADP-ribosylation factor-like protein 8A GN=Arl8a	0.765	1.331
Q91YH5	ATLA3_MOUSE	Atlastin-3 GN=Atl3	1.32	0.562
Q920Q6	MSI2H_MOUSE	RNA-binding protein Musashi homolog 2 GN=Msi2	1.351	0.771
Q9CQ37	UBE2T_MOUSE	Ubiquitin-conjugating enzyme E2 T GN=Ube2t	0.773	1.264
Q60575	KIF1B_MOUSE	Kinesin-like protein KIF1B GN=Kif1b	1.267	0.739
O08811	ERCC2_MOUSE	General transcription and DNA repair factor IIH helicase subunit XPD GN=Ercc2	1.328	0.791
O88708	ORC4_MOUSE	Origin recognition complex subunit 4 GN=Orc4	1.348	0.564
Q9Z129	RECQ1_MOUSE	ATP-dependent DNA helicase Q1 GN=Recql	1.542	0.623
Q80YD1	SUV3_MOUSE	ATP-dependent RNA helicase SUPV3L1, mitochondrial GN=Supv3l1	1.288	0.709
Q4FZF3	DDX49_MOUSE	Probable ATP-dependent RNA helicase DDX49 GN=Ddx49	1.325	0.62
Q91VJ4	STK38_MOUSE	Serine/threonine-protein kinase 38 GN=Stk38	1.374	0.718
Q8VC70	RBMS2_MOUSE	RNA-binding motif, single-stranded-interacting protein 2 GN=Rbms2	1.254	0.648
Q9EQW7	KI13A_MOUSE	Kinesin-like protein KIF13A GN=Kif13a	1.32	0.736
others				
P0DP27	CALM2_MOUSE	Calmodulin-2 GN=Calm2	0.76	1.336
C0HKE4	H2A1E_MOUSE	Histone H2A type 1-E GN=Hist1h2ae	1.457	0.647
Q68FL4	SAHH3_MOUSE	Putative adenosylhomocysteinase 3 GN=Ahcyl2	1.499	0.606
Q62446	FKBP3_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP3 GN=Fkbp3	0.748	1.25
Q9CQI6	COTL1_MOUSE	Coactosin-like protein GN=Cotl1 PE=1 SV=3	0.725	1.273
Q9WTJ4	FIZ1_MOUSE	Flt3-interacting zinc finger protein 1 GN=Fiz1	0.791	0.597
P16125	LDHB_MOUSE	L-lactate dehydrogenase B chain GN=Ldhb	0.779	0.439
Q99K41	EMIL1_MOUSE	EMILIN-1 GN=Emilin1	1.3	0.721
Q0VG62	CH059_MOUSE	Uncharacterized protein C8orf59 homolog	1.556	0.771
Q9D0R8	LSM12_MOUSE	Protein LSM12 homolog GN=Lsm12	1.277	0.674
Q4KML4	ABRAL_MOUSE	Costars family protein ABRACL GN=Abracl	1.428	0.748
Q8K2C7	OS9_MOUSE	Protein OS-9 GN=Os9	1.275	0.541
P19639	GSTM3_MOUSE	Glutathione S-transferase Mu 3 GN=Gstm3	1.255	0.707
Q8VCH8	UBXN4_MOUSE	UBX domain-containing protein 4 GN=Ubxn4	1.329	0.665
Q3U2C5	RN149_MOUSE	E3 ubiquitin-protein ligase RNF149 GN=Rnf149	1.314	0.661
Q9Z0V7	TI17B_MOUSE	Mitochondrial import inner membrane translocase subunit Tim17-B GN=Timm17b	0.781	1.455
Q8BMZ5	SEN34_MOUSE	tRNA-splicing endonuclease subunit Sen34 GN=Tsen34	1.266	0.759
Q8BWR2	PITH1_MOUSE	PITH domain-containing protein 1 GN=Pithd1	1.406	0.597
Q9JHJ5	5HT3B_MOUSE	5-hydroxytryptamine receptor 3B GN=Htr3b	1.345	0.507
Q8CHU3	EPN2_MOUSE	Epsin-2 GN=Epn2	1.257	0.559
P01900	HA12_MOUSE	H-2 class I histocompatibility antigen, D-D alpha chain GN=H2-D1	1.361	0.572
Q9ESN9	JIP3_MOUSE	C-Jun-amino-terminal kinase-interacting protein 3 GN=Mapk8ip3	1.266	0.737
Q3URS9	CCD51_MOUSE	Coiled-coil domain-containing protein 51 GN=Ccdc51	1.273	0.47
P02802	MT1_MOUSE	Metallothionein-1 GN=Mt1	1.735	1.257
O88413	TULP3_MOUSE	Tubby-related protein 3 GN=Tulp3	1.257	0.706
Q8CDA1	SAC2_MOUSE	Phosphatidylinositide phosphatase SAC2 GN=Inpp5f	0.673	1.561
A6X935	ITIH4_MOUSE	Inter alpha-trypsin inhibitor, heavy chain 4 GN=Itih4	0.757	1.278
Q8K371	AMOL2_MOUSE	Angiomotin-like protein 2 GN=Amotl2	1.324	0.51
Q6DID5	MUM1_MOUSE	PWWP domain-containing protein MUM1 GN=Mum1	1.26	0.744
Q9WVQ5	MTNB_MOUSE	Methylthioribulose-1-phosphate dehydratase GN=Apip	1.362	0.67
Q3UMB9	WASC4_MOUSE	WASH complex subunit 4 GN=Washc4	1.329	0.793
Q9CX53	GEMI6_MOUSE	Gem-associated protein 6 GN=Gemin6	1.27	0.524
Q91ZV3	DCBD2_MOUSE	Discoidin, CUB and LCCL domain-containing protein 2 GN=Dcbld2	1.452	0.631
Q5XKN4	JAGN1_MOUSE	Protein jagunal homolog 1 GN=Jagn1	1.257	0.643
Q05793	PGBM_MOUSE	Basement membrane-specific heparan sulfate proteoglycan core protein GN=Hspg2	1.256	0.65
A2AI08	TPRN_MOUSE	Taperin GN=Tprn	1.377	0.456
Q8R1S0	COQ6_MOUSE	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial GN=Coq6	1.287	0.771
Q9R1X4	TIM_MOUSE	Protein timeless homolog GN=Timeless	1.315	0.794
A6H5Y3	METH_MOUSE	Methionine synthase GN=Mtr	1.461	0.772
Q8K207	CA021_MOUSE	Uncharacterized protein C1orf21 homolog	1.283	0.475
P29699	FETUA_MOUSE	Alpha-2-HS-glycoprotein GN=Ahsg	0.72	1.695
Q99LC2	CSTF1_MOUSE	Cleavage stimulation factor subunit 1 GN=Cstf1	1.395	0.775
Q8R1U1	COG4_MOUSE	Conserved oligomeric Golgi complex subunit 4 GN=Cog4	1.552	0.625

Table S2 118 differentially expressed proteins after treated by DTMP in N2aAPP cells.

Term	percent	-LOG10(P-value)
macromolecular complex subunit organization	8.33	5.49
macromolecular complex assembly	7.84	5.27
response to metal ion	2.94	3.53
cellular macromolecular complex subunit organization	5.39	3.39
chromatin organization	5.88	3.10
ossification	3.43	2.93
regulation of nuclear mRNA splicing, via spliceosome	1.47	2.75
chromosome organization	6.37	2.73
bone development	3.43	2.69
response to copper ion	1.47	2.60
cellular macromolecular complex assembly	4.41	2.53
response to inorganic substance	2.94	2.44
protein complex assembly	4.41	2.41
protein complex biogenesis	4.41	2.41
regulation of mRNA processing	1.47	2.38
ribonucleoprotein complex biogenesis	3.43	2.37
aging	2.45	2.33
regulation of RNA splicing	1.47	2.28
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	1.96	2.10
RNA splicing, via transesterification reactions	1.96	2.10
nuclear mRNA splicing, via spliceosome	1.96	2.10
negative regulation of growth	2.45	2.10
nucleobase, nucleoside, nucleotide and nucleic acid transport	2.45	2.03
RNA processing	5.88	2.02
spliceosome assembly	1.47	1.93
chromatin modification	3.92	1.79
microtubule-based transport	1.47	1.78
cofactor biosynthetic process	2.45	1.73
positive regulation of molecular function	4.41	1.68
nitric oxide mediated signal transduction	0.98	1.66
RNA splicing	3.43	1.61
mRNA processing	3.92	1.57
detoxification of copper ion	0.98	1.48
negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.90	1.48
chromatin assembly or disassembly	2.45	1.48
coenzyme biosynthetic process	1.96	1.47
negative regulation of nitrogen compound metabolic process	4.90	1.46
RNA transport	1.96	1.43
nucleic acid transport	1.96	1.43
establishment of RNA localization	1.96	1.43
RNA localization	1.96	1.42
forebrain development	2.94	1.41
skeletal system development	3.92	1.40
protein localization	7.35	1.39
cell aging	1.47	1.39
proteasomal protein catabolic process	1.47	1.36
proteasomal ubiquitin-dependent protein catabolic process	1.47	1.36
regulation of alternative nuclear mRNA splicing, via spliceosome	0.98	1.36
L-glutamate import	0.98	1.36
chordate embryonic development	4.90	1.34
protein oligomerization	1.96	1.34
stem cell differentiation	1.47	1.34
embryonic morphogenesis	4.41	1.33
nucleosome assembly	1.96	1.32
embryonic development ending in birth or egg hatching	4.90	1.32
chromatin assembly	1.96	1.29
mRNA metabolic process	3.92	1.29
cytoskeleton-dependent intracellular transport	1.47	1.29
protein-DNA complex assembly	1.96	1.28
nucleosome organization	1.96	1.28
amino acid import	0.98	1.26
L-amino acid import	0.98	1.26
ribonucleoprotein complex assembly	1.47	1.26
chromatin remodeling	1.47	1.24
hemopoiesis	3.43	1.21
transcription initiation	1.47	1.20
positive regulation of Wnt receptor signaling pathway	0.98	1.19
N-terminal protein amino acid modification	0.98	1.19
regulation of vesicle-mediated transport	1.96	1.19
regulation of growth	3.43	1.18
positive regulation of catalytic activity	3.43	1.15
cellular zinc ion homeostasis	0.98	1.12
vesicle transport along microtubule	0.98	1.12
exocrine system development	1.47	1.12
di-, tri-valent inorganic cation homeostasis	2.45	1.10
histone modification	1.96	1.08
regulation of cell growth	1.96	1.08
zinc ion homeostasis	0.98	1.07
microtubule-based process	2.94	1.06
covalent chromatin modification	1.96	1.04
myeloid cell differentiation	1.96	1.04
nucleocytoplasmic transport	1.96	1.04
hemopoietic or lymphoid organ development	3.43	1.03
nuclear transport	1.96	1.02
urea metabolic process	0.98	1.02
urea cycle	0.98	1.02
ubiquinone biosynthetic process	0.98	1.02
ubiquinone metabolic process	0.98	1.02
negative regulation of cell growth	1.47	1.02
protein amino acid acylation	1.47	1.00
erythrocyte differentiation	1.47	1.00

Table S3 The biological processes of differential expression of proteins in 208 differential proteins in N2a/APPswe cells are annotated using Gene Ontology (GO).

Term	percent	-LOG10(P-value)
chromatin binding	3.43	2.11
RNA binding	7.84	2.10
nucleotide binding	18.14	2.08
DNA binding	15.20	1.90
purine nucleotide binding	14.71	1.41
enzyme activator activity	3.43	1.22
adenyl nucleotide binding	11.76	1.07
purine nucleoside binding	11.76	1.04
ribonucleotide binding	13.24	1.02
purine ribonucleotide binding	13.24	1.02
nucleoside binding	11.76	1.02

Table S4 The molecular function of differential expression of proteins in 208 differential proteins in N2aAPP cells are annotated using Gene Ontology (GO).

Term	percent	-LOG10(P-value)
cell cycle	8.76	7.71
cell division	4.94	5.69
protein localization	8.54	5.03
cell cycle process	5.39	4.43
cell cycle phase	4.49	3.69
establishment of protein localization	6.97	3.62
protein transport	6.74	3.32
mitotic cell cycle	3.60	3.29
negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.72	3.08
M phase	3.82	3.08
regulation of mRNA processing	0.90	3.05
negative regulation of nitrogen compound metabolic process	4.72	3.02
mitosis	2.92	2.84
nuclear division	2.92	2.84
M phase of mitotic cell cycle	2.92	2.76
organelle fission	2.92	2.71
negative regulation of RNA metabolic process	3.82	2.68
regulation of organelle organization	2.47	2.54
mRNA processing	3.37	2.54
negative regulation of macromolecule metabolic process	5.17	2.52
microtubule-based process	2.92	2.46
DNA metabolic process	4.49	2.41
mRNA metabolic process	3.60	2.38
intracellular transport	4.49	2.30
negative regulation of gene expression	4.27	2.19
regulation of nuclear mRNA splicing, via spliceosome	0.67	2.13
regulation of Ras GTPase activity	1.57	2.00
negative regulation of cellular biosynthetic process	4.27	1.99
macromolecular complex subunit organization	3.82	1.98
negative regulation of biosynthetic process	4.27	1.95
macromolecular complex assembly	3.60	1.95
negative regulation of transcription, DNA-dependent	3.37	1.94
regulation of vesicle-mediated transport	1.57	1.93
chromosome organization	4.04	1.92
RNA processing	4.27	1.92
protein complex assembly	2.70	1.81
protein complex biogenesis	2.70	1.81
negative regulation of macromolecule biosynthetic process	4.04	1.80
RNA splicing	2.47	1.76
cofactor biosynthetic process	1.57	1.74
embryonic development ending in birth or egg hatching	4.04	1.73
respiratory gaseous exchange	0.90	1.73
regulation of cell growth	1.57	1.72
regulation of GTPase activity	1.57	1.70
chromatin modification	2.70	1.70
regulation of RNA splicing	0.67	1.68
vesicle-mediated transport	4.27	1.66
positive regulation of cellular component organization	1.80	1.66
transcription	12.13	1.62
negative regulation of transcription	3.60	1.60
chromatin organization	3.15	1.53
myoblast differentiation	0.67	1.53
Golgi organization	0.67	1.53
proteasomal protein catabolic process	0.90	1.51
proteasomal ubiquitin-dependent protein catabolic process	0.90	1.51
regulation of endocytosis	1.12	1.51
positive regulation of organelle organization	1.12	1.51
response to metal ion	1.12	1.48
chordate embryonic development	3.82	1.48
stem cell differentiation	0.90	1.48
microtubule cytoskeleton organization	1.57	1.38
spliceosome assembly	0.67	1.35
negative regulation of RNA splicing	0.45	1.34
anterograde axon cargo transport	0.45	1.34
negative regulation of mRNA processing	0.45	1.34
negative regulation of nuclear mRNA splicing, via spliceosome	0.45	1.34
chromatin remodeling	0.90	1.34
regulation of mitotic metaphase/anaphase transition	0.67	1.29
response to drug	1.35	1.29
RNA splicing, via transesterification reactions	0.90	1.28
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	0.90	1.28
nuclear mRNA splicing, via spliceosome	0.90	1.28
cellular macromolecular complex subunit organization	2.47	1.25
coenzyme biosynthetic process	1.12	1.23
regulation of Rab protein signal transduction	0.90	1.23
regulation of Rab GTPase activity	0.90	1.23
response to inorganic substance	1.35	1.22
DNA replication	1.80	1.22
adult behavior	1.35	1.21
microtubule-based transport	0.67	1.20
response to DNA damage stimulus	2.70	1.17
nucleocytoplasmic transport	1.35	1.16
regulation of growth	2.47	1.15
ureteric bud development	0.90	1.15
cytoskeleton organization	2.92	1.15
mitochondrion organization	1.35	1.14
regulation of transcription from RNA polymerase II promoter	4.72	1.13
nuclear transport	1.35	1.13
pyrimidine nucleotide biosynthetic process	0.67	1.12
negative regulation of growth	1.12	1.10
cellular response to stress	3.37	1.09
developmental maturation	1.35	1.09
microtubule-based movement	1.35	1.09
chondrocyte differentiation	0.67	1.08
regulation of chromosome organization	0.67	1.08
negative regulation of transcription from RNA polymerase II promoter	2.25	1.07
myelination in the central nervous system	0.45	1.05
ensheathment of axons in the central nervous system	0.45	1.05
cell maturation	1.12	1.03
hexose metabolic process	1.80	1.03
ossification	1.35	1.02
stem cell development	0.67	1.02

Table S5 The biological processes of differential expression of proteins in 449 differentially expressed proteins in DTMP-treated N2aAPP cells are annotated using Gene Ontology (GO).

Term	percent	-LOG10(P-value)
RNA binding	8.54	6.45
nucleotide binding	17.53	4.77
chromatin binding	3.15	4.35
DNA binding	14.61	4.20
purine nucleotide binding	14.16	3.10
ribonucleotide binding	13.71	3.10
purine ribonucleotide binding	13.71	3.10
double-stranded RNA binding	1.35	3.05
helicase activity	2.02	2.08
histone acetyltransferase activity	0.90	2.02
lysine N-acetyltransferase activity	0.90	2.02
ATP binding	10.34	1.88
Ras GTPase activator activity	1.35	1.83
adenyl nucleotide binding	10.79	1.81
adenyl ribonucleotide binding	10.34	1.80
protein transporter activity	1.35	1.80
purine nucleoside binding	10.79	1.75
DNA helicase activity	0.90	1.75
nucleoside binding	10.79	1.71
telomeric DNA binding	0.67	1.62
enzyme activator activity	2.70	1.62
GTP binding	3.37	1.55
RNA polymerase II carboxy-terminal domain kinase activity	0.67	1.55
GTPase activator activity	2.25	1.54
enzyme binding	2.47	1.48
guanyl ribonucleotide binding	3.37	1.47
guanyl nucleotide binding	3.37	1.47
peptidyl-prolyl cis-trans isomerase activity	0.90	1.37
transcription repressor activity	2.25	1.32
cis-trans isomerase activity	0.90	1.31
DNA-dependent ATPase activity	0.90	1.28
transcription factor binding	2.70	1.23
ATPase activity, coupled	2.25	1.20
diphosphoinositol-polyphosphate diphosphatase activity	0.45	1.18
structural constituent of myelin sheath	0.45	1.18
Ral GTPase binding	0.45	1.18
Rab GTPase activator activity	0.90	1.15
protein kinase binding	1.12	1.13
transcription corepressor activity	1.12	1.11
transition metal ion binding	15.51	1.05
zinc ion binding	12.81	1.05
P-P-bond-hydrolysis-driven transmembrane transporter activity	1.35	1.04
primary active transmembrane transporter activity	1.35	1.02
rRNA binding	0.67	1.00
ATPase activity	2.47	1.00

Table S6 The molecular function of differential expression of proteins in 449 differentially expressed proteins in DTMP-treated N2aAPP cells are annotated using Gene Ontology (GO)