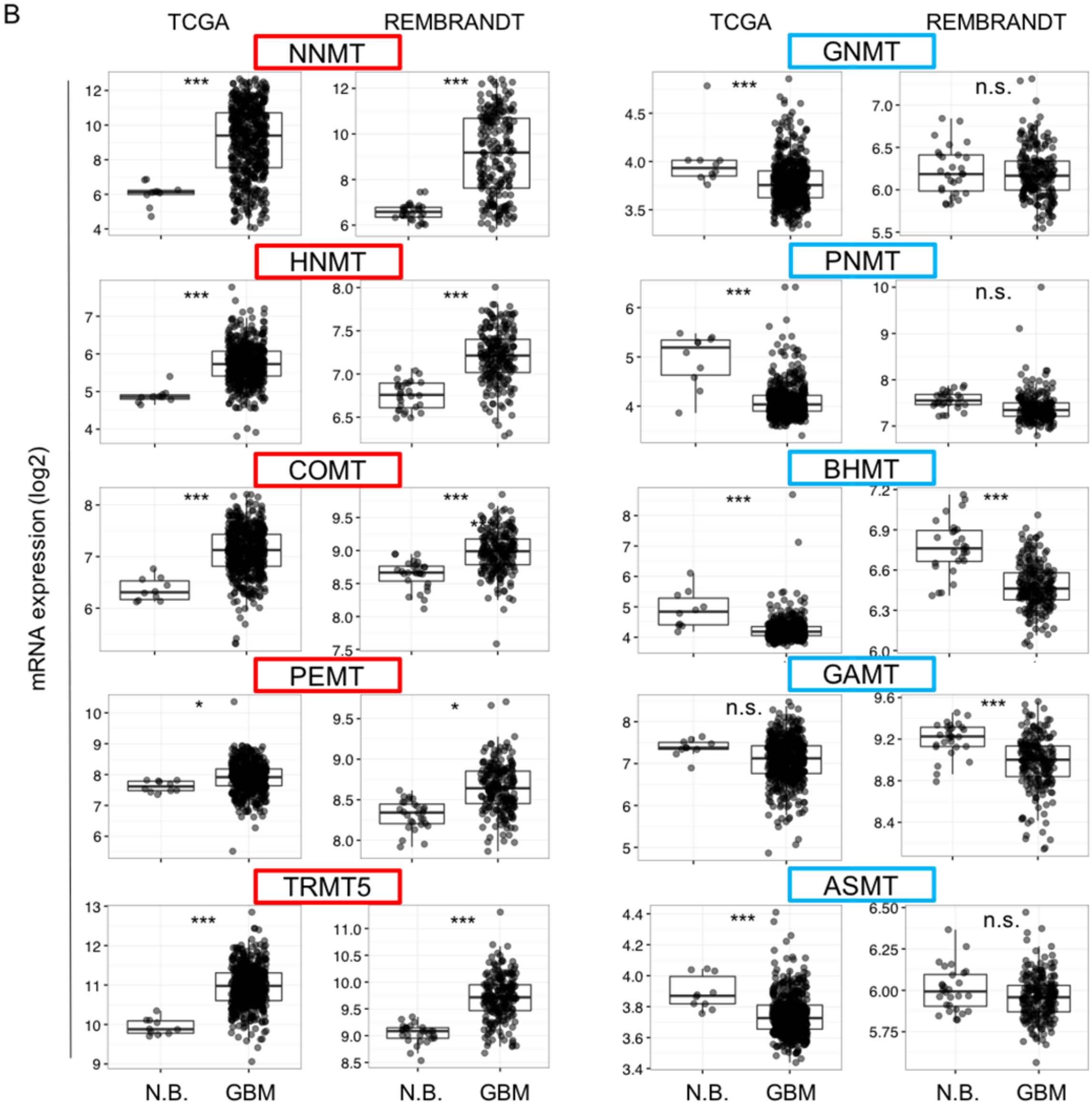
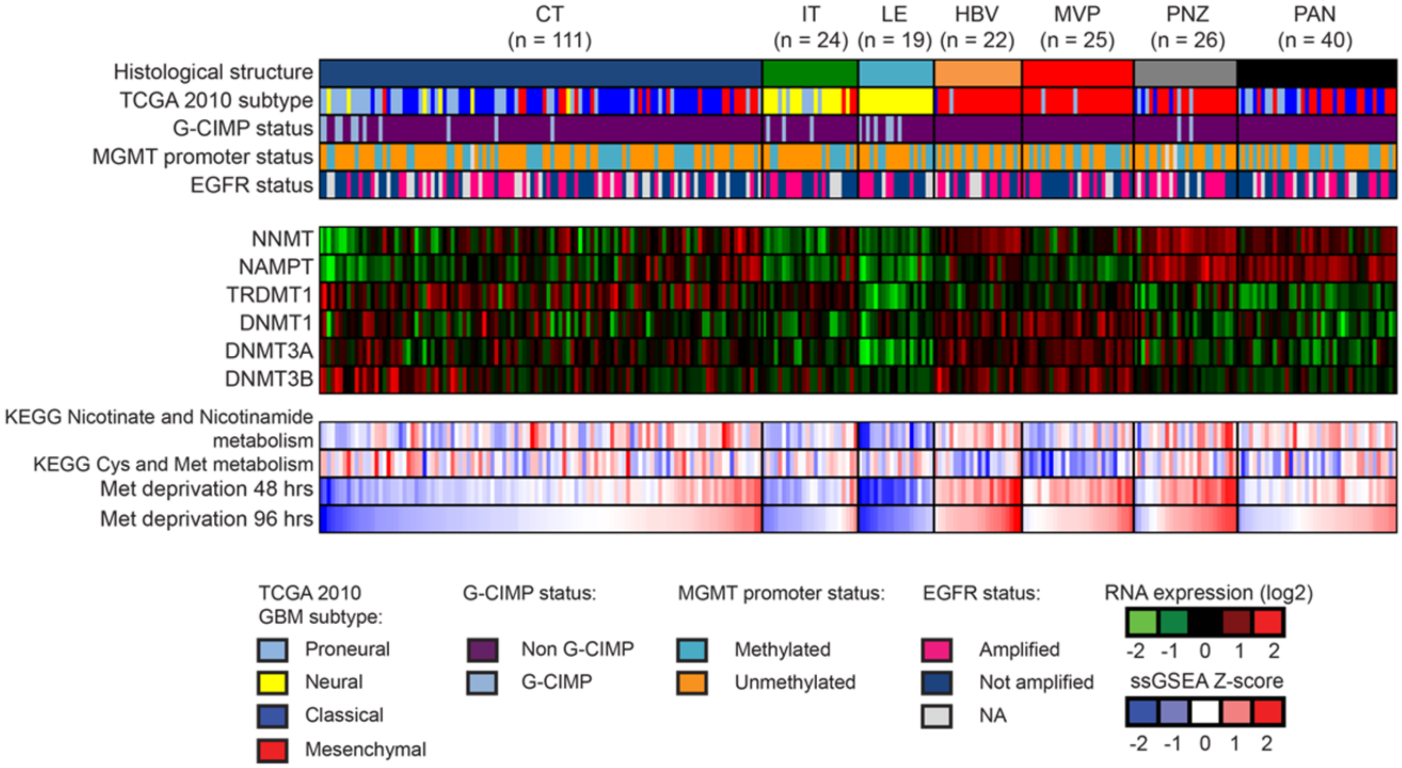
SUPPLEMENTAL FIGURES

A

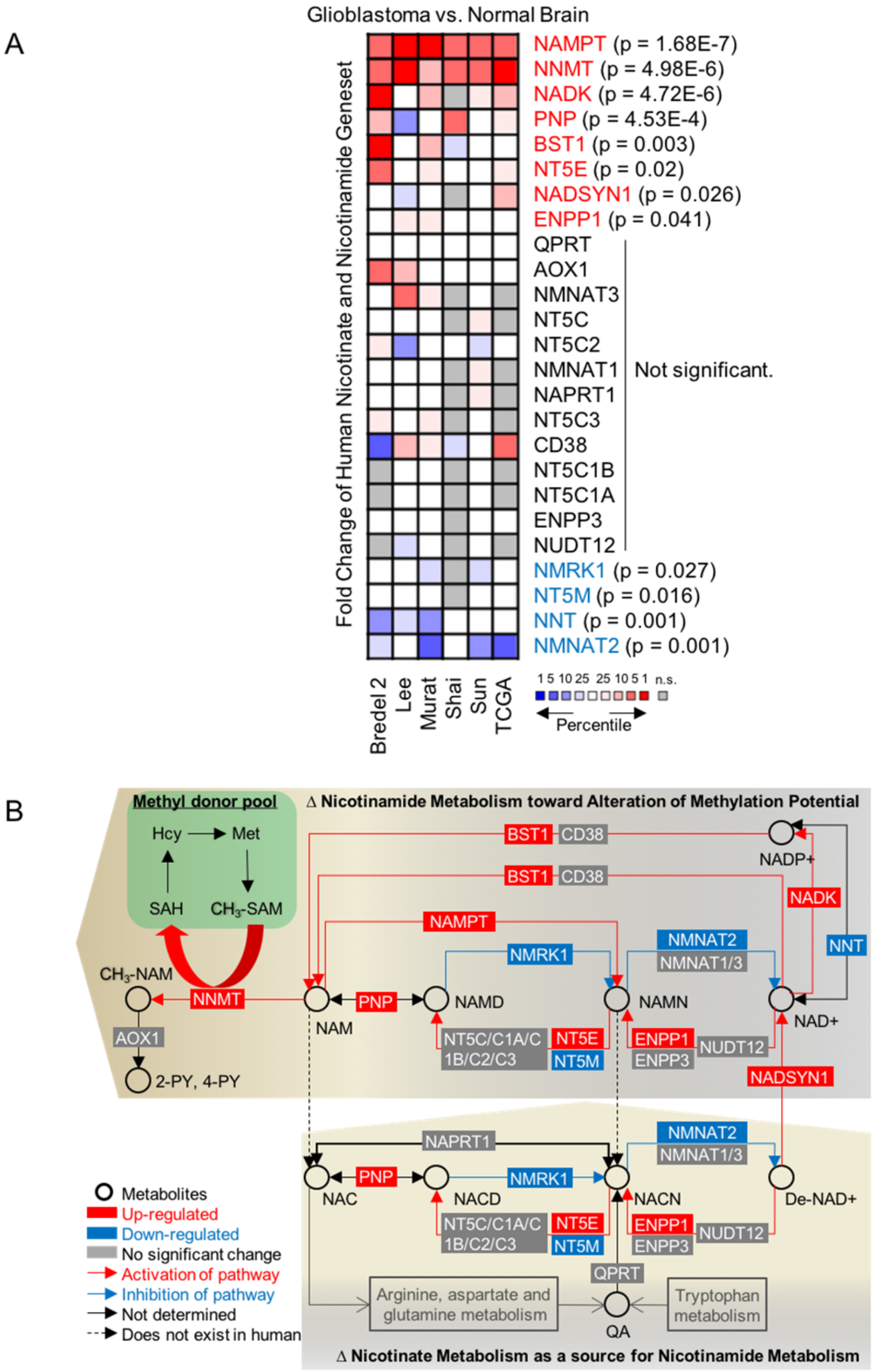
Symbol	SAM-dependent Unique Methyltransferases	GBM vs. Normal		Patient Survival Relevance		Functions of Product in Brain	Diseases Associated	Ref.
		TCGA	REMB.	TCGA	REMB.			
NNMT	Nicotinamide N-methyltransferase	UP	UP	YES	YES	Neurotoxin	Parkinson and Cancers	36,37
HNMT	Histamine N-methyltransferase	UP	UP	NO	NO	Enriched in Mast Cell	Parkinson	38
COMT	Catechol O-methyltransferase	UP	UP	NO	NO	Degradation of Dopamine	Parkinson	39
PEMT	Phosphatidylethanolamine N-methyltransferase	UP	UP	NO	NO	unknown	Obesity and Alzheimer	40,41
TRMT5	TRNA N-methyltransferase	UP	UP	NO	NO	unknown	Mitochondrial disorder	42
GNMT	Glycine N-methyltransferase	DOWN	N.S	NO	NO	Sarcosine	Liver Cancer	43
PNMT	Phenylethanolamine N-methyltransferase	DOWN	N.S.	NO	NO	Adrenaline Synthesis	Alzheimer	44
BHMT	Betaine-homocysteine S-methyltransferase	DOWN	DOWN	NO	NO	Neuroprotective	Hyperhomocysteinemia	45
GAMT	Guanidinoacetate N-methyltransferase	N.S.	DOWN	NO	NO	Neurologic Syndrome	Muscular Hypotonia	46
ASMT	Acetylserotonin O-methyltransferase	DOWN	N.S.	YES	YES	Melatonine Synthesis	Autism	47
CARNMT1	Carnosine N-methyltransferase	N/A	N.S.	N/A	NO	unknown	unknown	N/A



Supplemental Figure 1. Clinical relevance of natural product methyltransferases (NPMTs) in brain disorders. (A) Table summarizing characteristics of 11 NPMTs using data derived from the TCGA GBM and Rembrandt datasets for relative expression levels and survival. In addition, published studies of the 11 NPMTs are summarized. (B) The expression levels of 10 NPMTs in glioblastoma versus non-tumor brain are displayed in a heatmap, ranked by significance and expression levels. *, $p<0.05$; **, $p<0.01$; ***, $p<0.001$.

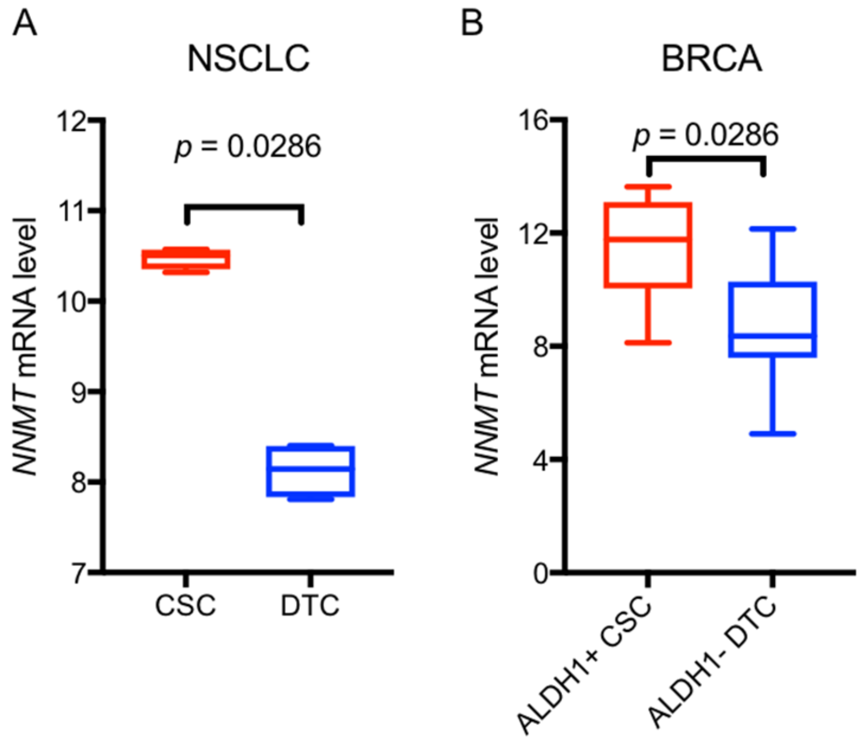


Supplemental Figure 2. Anatomical distribution of methyltransferase and metabolic signatures within glioblastomas. The Ivy GAP dataset was downloaded and interrogated by histological structure for *NNMT*, *NAMPT*, *DNMT* mRNA expression and selected gene expression signatures. The results are displayed on a heatmap. The sample size of each histological region as indicated on the figure.

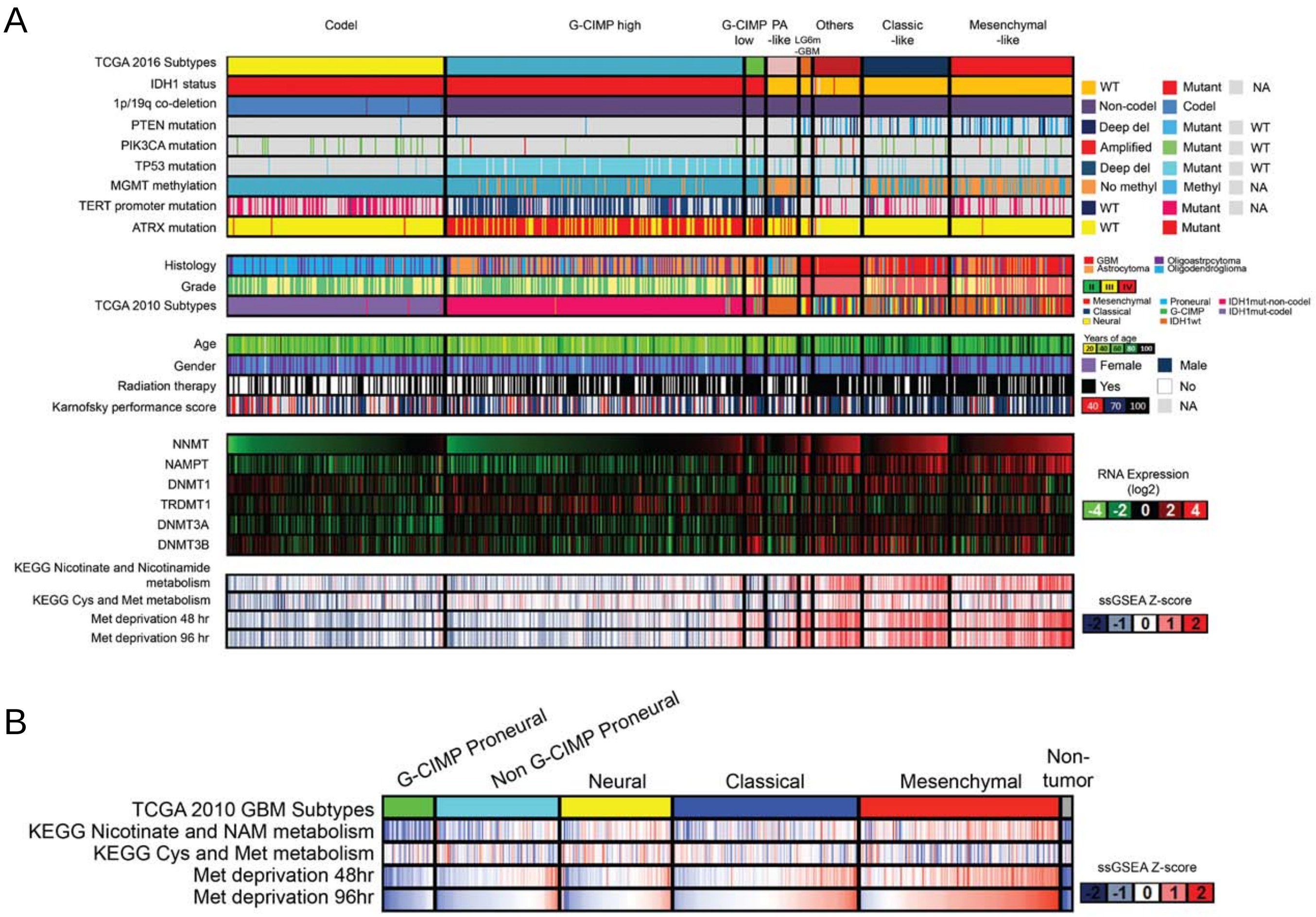


Supplemental Figure 3. Altered expression of nicotinamide and nicotinate metabolism-related enzymes in glioblastoma. (A) Heatmap (fold change of expression) of whole 25 enzymes in the KEGG nicotinate and nicotinamide metabolism gene set were analyzed in indicated glioblastoma expression datasets with Oncomine.

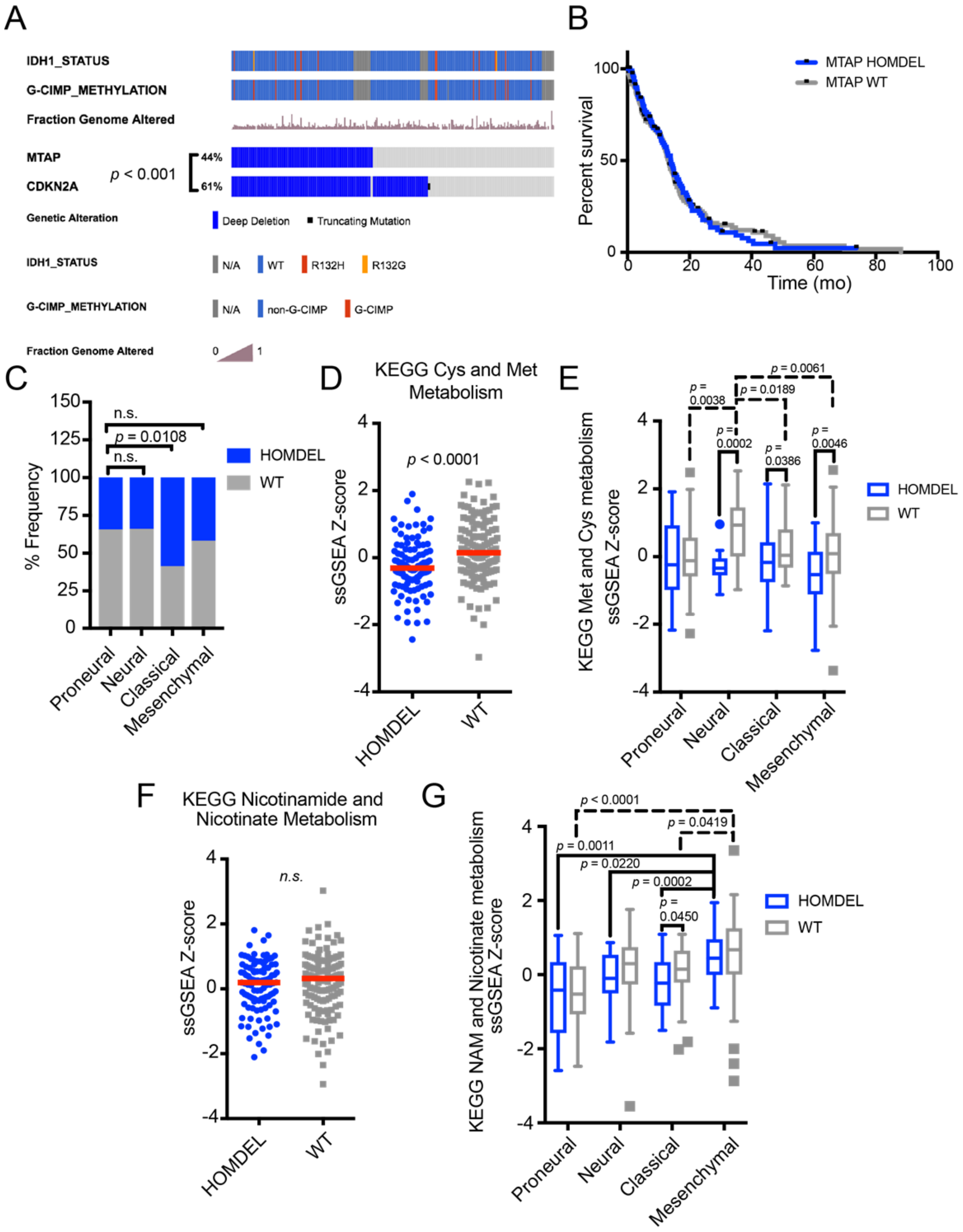
Color bar intensity indicates percentile of fold change in glioblastoma relative to normal brain. (B) Nicotinamide and nicotinate and methionine salvage pathways are displayed with the relative expression levels in glioblastoma specimens in the TCGA GBM dataset indicated.



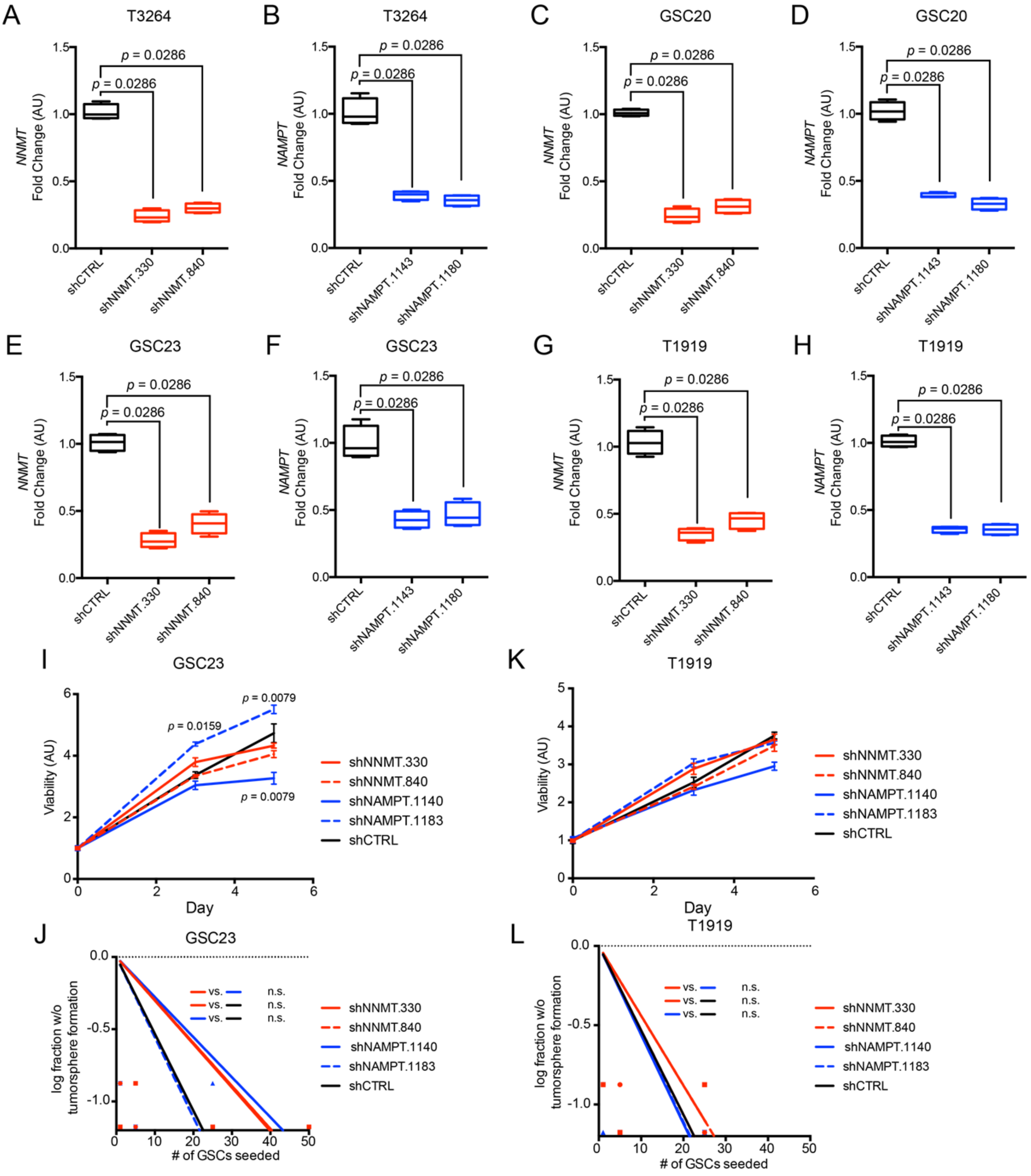
Supplementary Figure 4. *NNMT* mRNA expression is up-regulated in cancer stem cells in NSCLC and BRCA. A and B. *NNMT* mRNA expression levels from respective transcriptome array datasets (30, 35).



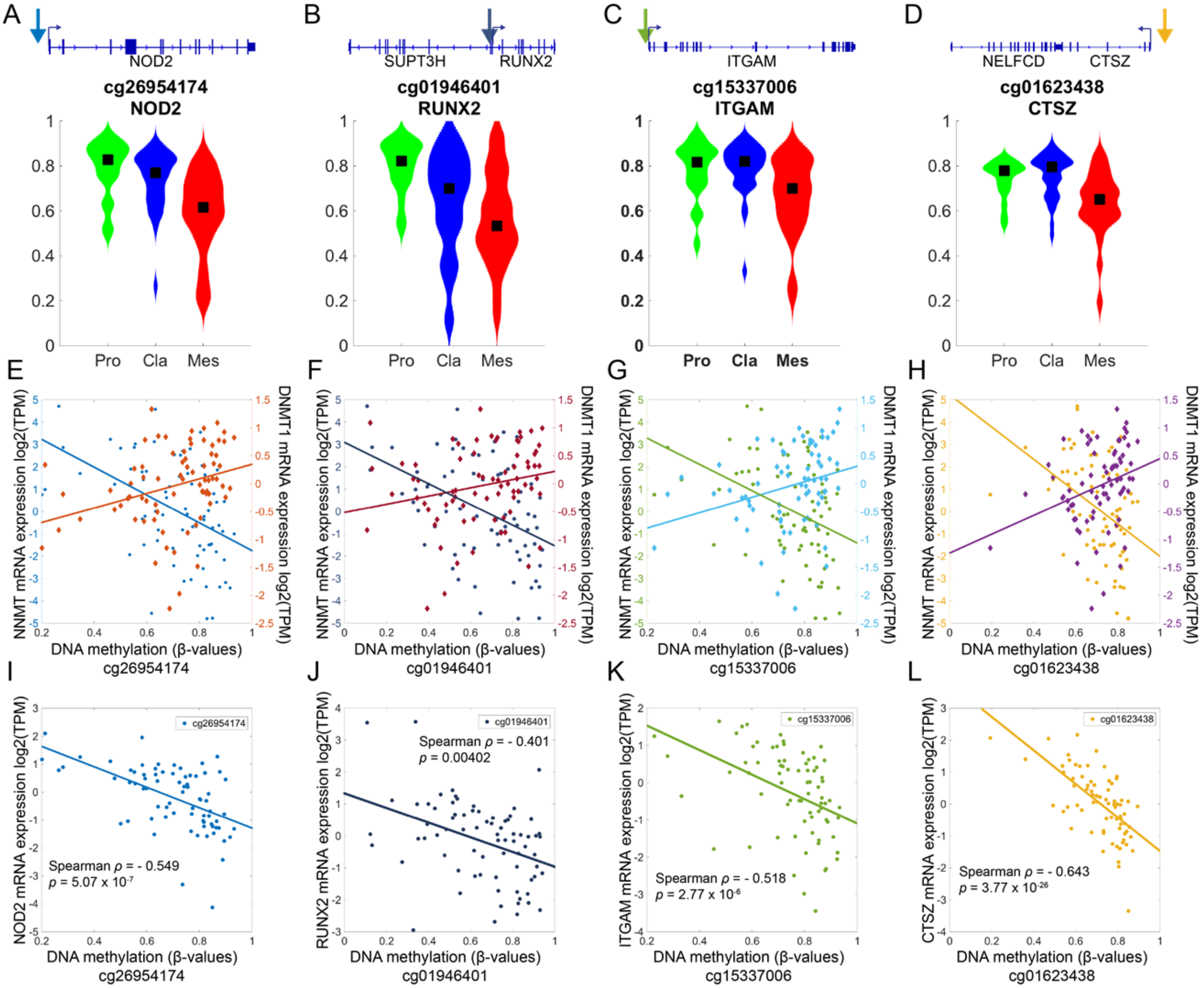
Supplemental Figure 5. **Intratumoral distribution of methyltransferase and metabolic signatures within gliomas.** (A, B) The expression levels of *NNMT*, *NAMPT*, and *DNMTs* mRNA and metabolic signatures are displayed with molecular and patient characteristics from as indicated from the (A) TCGA GBMLGG RNAseq dataset grouped by TCGA 2016 pan-glioma subtypes (Codel, n = 167; G-CIMP high, n = 236; G-CIMP low, n = 17; PA-like, n = 11; Others, n = 39; Classical-like, n = 69; Mesenchymal-like, n = 98) (6) or (B) TCGA GBM U133A microarray dataset grouped by TCGA 2010 GBM molecular subtypes (G-CIMP Proneural, n = 41; Non-G-CIMP Proneural, n = 97; Neural, n = 84; Classical, n = 145; Mesenchymal, n = 156; Non-tumor, n = 10) (4).



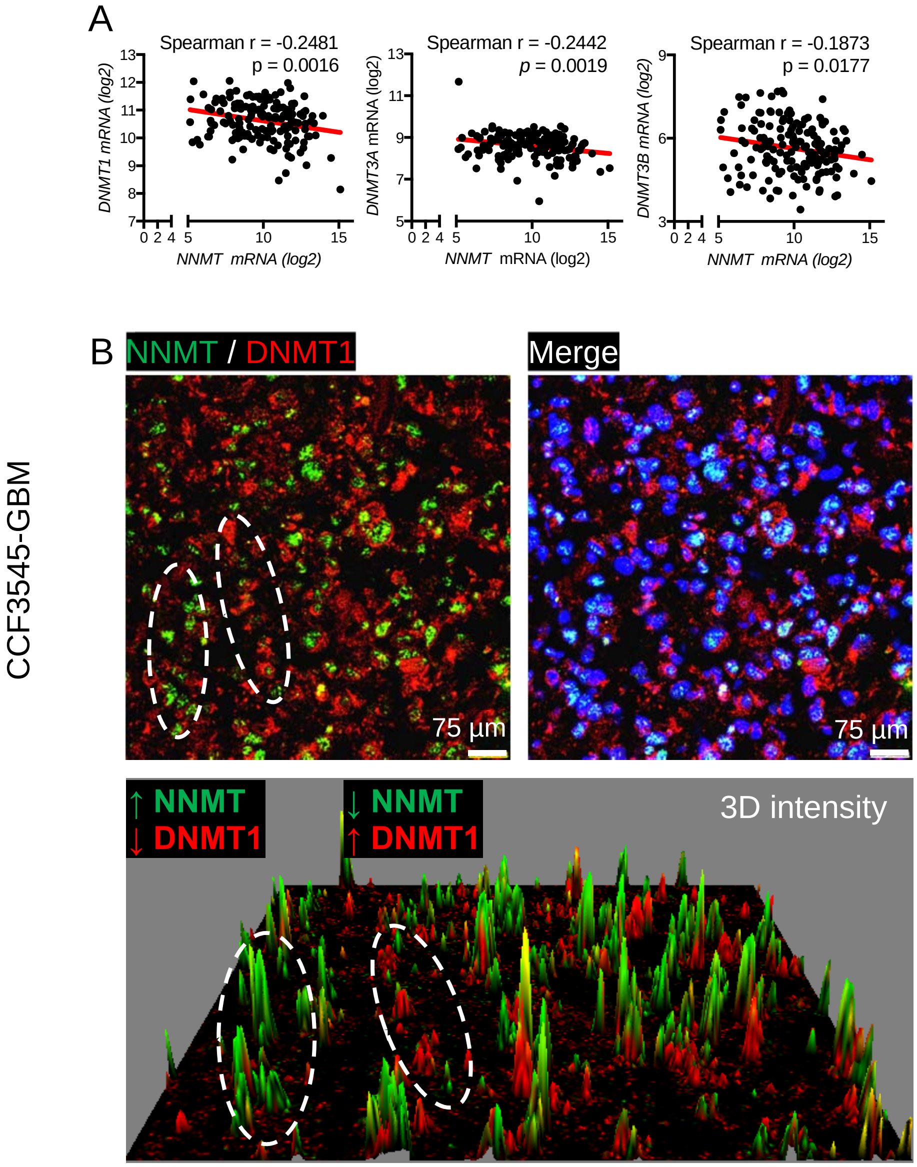
Supplementary Figure 6. *MTAP* genotype and nicotinamide metabolism in glioblastomas. (A) *MTAP* and *CDKN2A* copy number status in TCGA GBM dataset (n = 281). Copy number status and clinical tracks visualized on cBioportal. (B) Kaplan-Meier survival curve of GBM patients stratified by *MTAP* copy number status in TCGA GBM dataset. HOMDEL: homologous deletion (n = 123); WT: wild type (n =158). (C) Frequency of tumor specimens with homologous deletion or wild type copy number of *MTAP* in TCGA GBM specimens by molecular subtype. Significance of difference of distribution tested with Fisher exact test on sample counts. (D) Transcriptional signature scores of KEGG Methionine and Cysteine metabolism in TCGA GBM tumors with wild type or *MTAP* homozygous deletion. (E) KEGG Methionine and Cysteine metabolism signatures analyzed by *MTAP* genotype and by TCGA GBM molecular subtype. (F) Transcriptional signature scores of KEGG Nicotinamide and Nicotinate metabolism in TCGA GBM tumors with wild type or *MTAP* homozygous deletion. (G) KEGG Nicotinamide and Nicotinate metabolism signatures analyzed by *MTAP* genotype and by TCGA GBM molecular subtype.



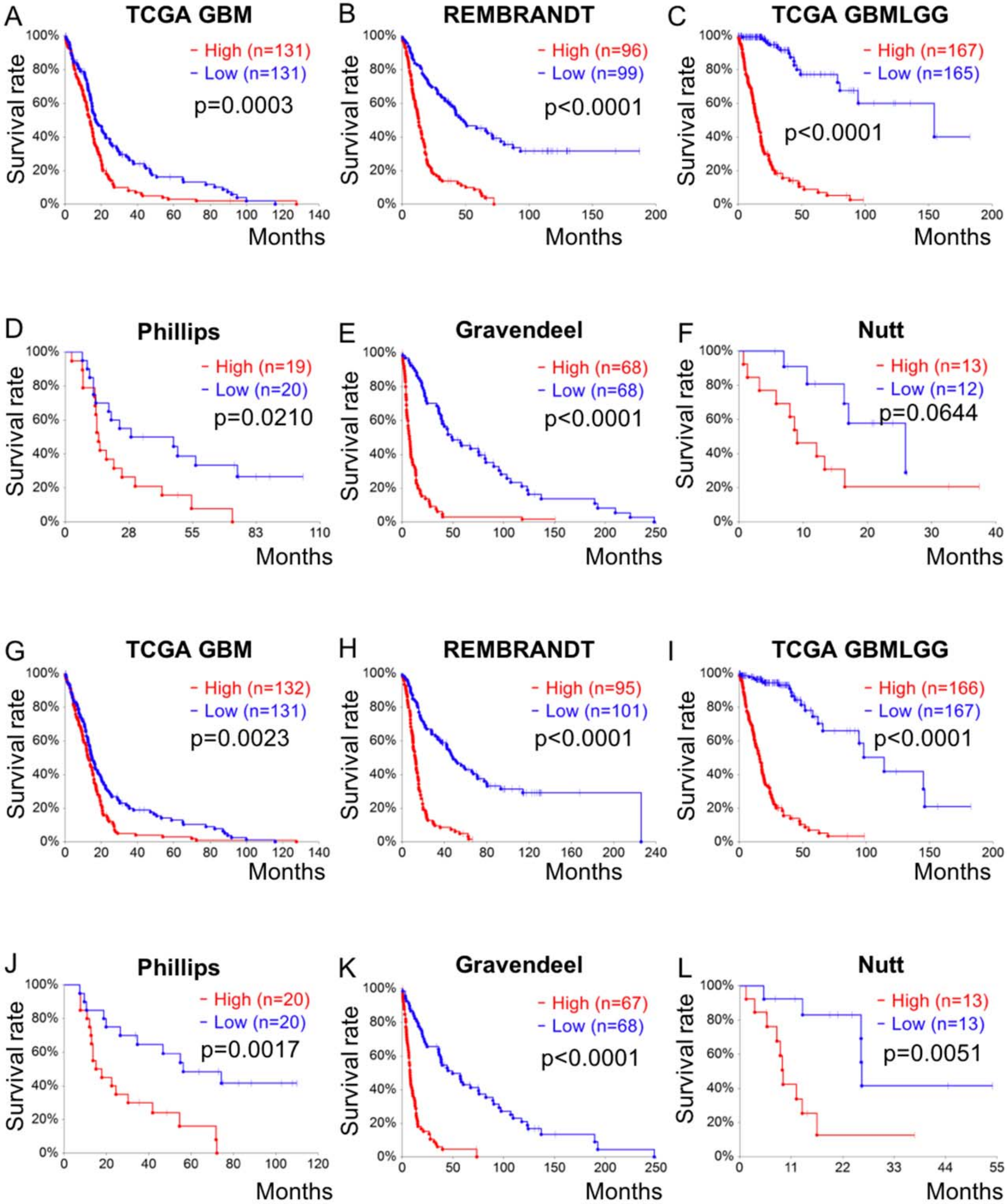
Supplemental Figure 7. ***NNMT*** **RNAi does not impede in vitro viability and self-renewal capacity in proneural GSCs.** (A-H) RT-PCR for *NNMT* or *NAMPT* knockdown efficiency in mesenchymal GSCs (T3264 and GSC20) or proneural GSCs (GSC20 and T1919) transduced with lentiviral shRNA clones targeting *NNMT* or *NAMPT* compared with non-targeting controls. For each condition, four technical replicates were analyzed. Mann-Whitney non-parametric test for differences in median was utilized to test for significance. (I-L) In vitro limiting dilution assay and cell viability assay of (I, J) GSC23 or (K, L) T3264 GSCs transduced with shCTRL, shNNMT.830, shNNMT.330, shNAMPT.1140, shNAMPT.1183 lentivirus. Nonparametric Mann-Whitney test was used to determine significance in differences between median of shNNMT and shNAMPT treated samples.



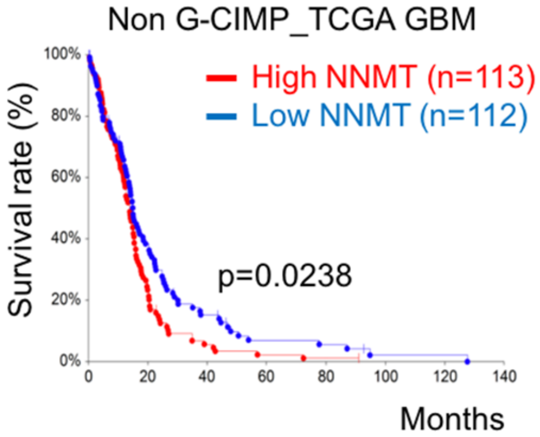
Supplemental Figure 8. Mesenchymal subtype genes correlation with *NNMT* and *DNMT1* mRNA expression and DNA methylation state. (A-D). Representative CpG probes annotated for mesenchymal subtype genes (*NOD2, RUNX2, ITGAM*, and *CTSZ*) and their DNA methylation state with significant anti-correlation with *NNMT* mRNA expression. (E-H). Correlation between *NNMT* or *DNMT1* mRNA expression and DNA methylation of CpG probes annotated for respective genes. (I-L). Correlation between respective gene mRNA expression and DNA methylation state of CpG probe.



Supplemental Figure 9. **Negative correlation between NNMT and DNMTs in mesenchymal glioblastoma.** (A) Correlative analysis of NNMT was performed with indicated DNMTs in of TCGA GBM database (n = 528). Spearman correlation coefficients were calculated with GraphPad Prism. (B) Representative image of patient glioblastoma tissue with NNMT and DNMT1 staining. Frozen glioblastoma section was stained with anti-NNMT, anti-DNMT1 antibodies, and DAPI. Scale bars: 75 µm. The 3D quantified peaks of NNMT and DNMT1 were visualized with ImageJ.



Supplemental Figure 10. **Kaplan-Meier survival curves of glioblastoma patients stratified by NNMT and NAMPT expression.** (A-L) Patient survival data based on expression of *NNMT* (A-F) and *NAMPT* (G-L) were evaluated by high versus low cut-off into different expression levels in the indicated databases using the top and bottom quartiles.



Supplemental Figure 11. **Kaplan-Meier survival curve based on NNMT mRNA expression in non-G-CIMP glioblastomas from the TCGA GBM microarray dataset.** NNMT expression levels were divided with the exclusion of G-CIMP patients, in TCGA GBM database. P-value represents log-rank p-value.

Supplementary Table 1. Metabolic gene expression differences between glioblastomas and non-tumor brain specimens in TCGA GBM dataset.

Supplementary Table 2. Correlation between *NNMT* mRNA expression and DNA methylation signatures in TCGA GBM dataset

Supplementary Table 3. Primers used for C/EBPβ ChIP-PCR and qMethyl-PCR

Supplemental Table 1: Metabolic gene expression fold changes - glioblastoma vs non-tumor in TCGA GBM dataset

Gene	Description	Fold change GBM vs NT	p-value	FDR-adjusted p-value
A1CF	APOBEC1 complementation factor	-0.05396	0.590164705	0.67709077
A4GALT	alpha 1,4-galactosyltransferase (globotriaosylceramide synthase)	-0.50653	4.73E-06	1.70E-05
A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	-0.01961	0.777790697	0.834872485
AACS	acetoacetyl-CoA synthetase	-1.74346	2.42E-29	6.16E-28
AADAC	arylacetamide deacetylase (esterase)	0.09560	0.617847199	0.698600309
AANAT	arylalkylamine N-acetyltransferase	-0.04109	0.41280092	0.504038601
AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-0.76500	3.81E-07	1.62E-06
AASS	aminoadipate-semialdehyde synthase	1.37036	7.34E-11	5.11E-10
ABAT	4-aminobutyrate aminotransferase	-0.41349	0.37681451	4.68E-01
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	2.83143	2.88E-15	2.91E-14
ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	0.03119	0.764332416	0.823469954
ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	-1.17749	2.13E-12	1.73E-11
ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	-0.69196	0.000249959	6.73E-04
ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	-0.36770	0.00280619	0.00609507
ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	-0.74635	0.000812193	1.97E-03
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	0.06202	0.598636658	0.682956412
ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7	-0.20289	0.048029657	0.079321115
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	-0.28415	0.575069646	0.662764507
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.04137	0.894381571	0.928640313
ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	-0.28834	6.17E-12	4.77E-11
ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	0.44581	0.013718913	2.56E-02
ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0.01715	0.857043577	0.898128655
ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	1.07976	1.22E-16	1.40E-15

ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	0.15617	0.064260539	0.10206381
ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-0.64823	9.50E-08	4.42E-07
ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0.51911	0.022931608	4.11E-02
ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	0.05053	0.715048658	0.782397159
ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	-0.14174	0.411822461	0.503448624
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.65029	0.000109353	3.12E-04
ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	1.26163	1.45E-08	7.51E-08
ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.38344	1.14E-09	6.97E-09
ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	-0.12052	0.251629152	0.334572966
ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-1.14648	3.06E-24	6.04E-23
ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0.04306	0.632554846	0.711274337
ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	0.06176	0.380605549	0.471236956
ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	0.08871	0.567117284	0.655745275
ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	1.03598	3.39E-11	2.45E-10
ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	0.52051	1.66E-08	8.55E-08
ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	0.70008	1.31E-07	5.97E-07
ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	0.44050	0.002420273	5.35E-03
ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	0.56797	5.25E-06	1.87E-05
ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	-0.29427	0.027976174	0.049200313
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	0.39647	0.050354031	0.082423305
ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	-0.11494	0.746556248	0.809034569
ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	-1.05833	5.46E-43	3.47E-41
ABCG5	ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1)	-0.29624	0.00392564	0.008261726
ABHD10	abhydrolase domain containing 10	-0.68925	1.38E-05	4.57E-05
ABHD11	abhydrolase domain containing 11	0.25680	0.181589456	0.250795764

ABHD14A	abhydrolase domain containing 14A	-1.37714	1.31E-10	8.83E-10
ABHD2	abhydrolase domain containing 2	0.41893	0.072707897	0.114283755
ABHD3	abhydrolase domain containing 3	1.40451	3.51E-13	3.05E-12
ABHD4	abhydrolase domain containing 4	1.35706	1.51E-12	1.23E-11
ABHD5	Abhydrolase domain containing 5	0.90148	5.21E-10	3.30E-09
ABHD6	abhydrolase domain containing 6	-0.81912	6.78E-05	0.000199225
ABHD8	abhydrolase domain containing 8	-1.08289	3.84E-15	3.87E-14
ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	-0.32221	1.10E-07	5.11E-07
ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	-0.09087	0.536131318	0.626410902
ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	0.51036	0.000257201	0.00068892
ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0.05894	0.660873704	0.737407377
ACACA	acetyl-Coenzyme A carboxylase alpha	-0.46648	0.000119124	3.38E-04
ACACB	acetyl-Coenzyme A carboxylase beta	-0.29504	0.141590176	0.203573428
ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	0.24116	0.014233481	0.026474536
ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	0.63240	0.001717416	3.91E-03
ACADL	acyl-Coenzyme A dehydrogenase, long chain	-0.01177	0.939507793	0.958089295
ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	0.90666	3.41E-10	2.20E-09
ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	0.04604	0.645790394	0.723356403
ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	-0.15767	0.136901962	0.198376114
ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	0.73119	4.05E-05	1.24E-04
ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	0.19290	0.158075324	0.2223994
ACAT2	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	0.16597	0.492484693	0.583802554
ACBD3	acyl-Coenzyme A binding domain containing 3	0.60316	1.25E-05	4.16E-05
ACBD4	acyl-Coenzyme A binding domain containing 4	-0.34283	0.002328176	0.005161595
ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-0.01515	0.813756838	0.864802746

ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	0.00967	0.91985272	0.943998273
ACHE	acetylcholinesterase (Yt blood group)	-0.14931	0.075898263	0.118601974
ACLY	ATP citrate lyase	0.55352	0.009734532	0.018865875
ACN9	ACN9 homolog (S. cerevisiae)	1.10243	0.000349546	9.18E-04
ACO1	aconitase 1, soluble	0.65689	5.32E-05	1.60E-04
ACO2	aconitase 2, mitochondrial	-0.58947	1.43E-07	6.50E-07
ACOT11	acyl-CoA thioesterase 11	0.13330	0.135589413	0.19661432
ACOT7	acyl-CoA thioesterase 7	-2.31509	9.66E-26	2.07E-24
ACOT8	Acyl-CoA thioesterase 8	-0.90327	1.43E-10	9.56E-10
ACOT9	acyl-CoA thioesterase 9	1.03727	2.08E-07	9.33E-07
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	0.26181	0.000948833	0.002264058
ACOX2	acyl-Coenzyme A oxidase 2, branched chain	1.17133	0.000207877	5.67E-04
ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	0.43945	0.000422579	0.001091902
ACOXL	acyl-Coenzyme A oxidase-like	-0.15136	0.002715126	0.005916595
ACSBG1	acyl-CoA synthetase bubblegum family member 1	-1.63704	4.28E-07	1.80E-06
ACSBG2	acyl-CoA synthetase bubblegum family member 2	0.15642	0.046891717	0.077757636
ACSF2	acyl-CoA synthetase family member 2	0.05921	0.761575987	0.820935303
ACSL1	acyl-CoA synthetase long-chain family member 1	0.30075	0.329722498	0.420266983
ACSL3	acyl-CoA synthetase long-chain family member 3	-0.76128	0.001028885	2.44E-03
ACSL4	Acyl-CoA synthetase long-chain family member 4	0.07562	0.711131098	0.779369015
ACSL5	acyl-CoA synthetase long-chain family member 5	0.08580	0.694589543	0.764951539
ACSL6	acyl-CoA synthetase long-chain family member 6	-1.73102	9.54E-21	1.44E-19
ACSM1	acyl-CoA synthetase medium-chain family member 1	-0.40313	8.10E-09	4.37E-08
ACSM3	acyl-CoA synthetase medium-chain family member 3	0.00707	0.958403696	0.971303447
ACSM5	acyl-CoA synthetase medium-chain family member 5	0.09499	0.665873971	0.740953356

ACSS3	acyl-CoA synthetase short-chain family member 3	1.17486	0.004355798	9.08E-03
ACYP1	acylphosphatase 1, erythrocyte (common) type	-0.75722	0.00034516	9.09E-04
ACYP2	acylphosphatase 2, muscle type	-0.92474	0.00103328	2.45E-03
ADA	adenosine deaminase	0.40218	0.079616618	0.123914684
ADCY1	adenylate cyclase 1 (brain)	-0.17486	0.019337136	0.035163145
ADCY10	testicular soluble adenylyl cyclase	-0.03436	0.610097896	0.692921241
ADCY2	adenylate cyclase 2 (brain)	-2.13307	4.07E-68	5.92E-66
ADCY3	adenylate cyclase 3	-0.35684	0.001427399	0.003297615
ADCY6	adenylate cyclase 6	0.14379	0.248612392	0.330778137
ADCY7	adenylate cyclase 7	0.76544	0.000491977	1.26E-03
ADCY8	adenylate cyclase 8 (brain)	0.21515	0.483962891	0.575714779
ADCY9	Adenylate cyclase 9	-0.30645	0.00022561	0.000612371
ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	-0.04647	0.537020426	0.626729349
ADH1B	Alcohol dehydrogenase 1B (class I), beta polypeptide	-0.00237	0.992505814	0.995393773
ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.08825	0.546638807	0.635401197
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	0.64237	1.02E-06	4.14E-06
ADH6	alcohol dehydrogenase 6 (class V)	-0.11296	0.072741357	0.114283755
ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0.21518	0.34122537	0.431949675
ADI1	acireductone dioxygenase 1	0.39194	0.09543326	0.143928648
ADK	adenosine kinase	0.38138	0.035392341	6.03E-02
ADO	2-aminoethanethiol (cysteamine) dioxygenase	-0.59105	0.000183022	5.03E-04
ADPGK	ADP-dependent glucokinase	0.59154	0.000175757	4.85E-04
ADSL	adenylosuccinate lyase	0.54818	0.003376079	0.007186982
ADSS	Adenylosuccinate synthase	-0.17420	0.391392318	0.482290782
AGA	aspartylglucosaminidase	1.48114	1.13E-10	7.65E-10

AGK	acylglycerol kinase	-0.17502	0.226215633	0.305455617
AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	0.73757	0.000284991	0.000759354
AGMAT	agmatine ureohydrolase (agmatinase)	-0.09565	0.141361139	0.203387966
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	-0.23196	0.140848444	0.20279383
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	0.11344	0.454808139	0.547115353
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	-0.63460	7.55E-08	3.61E-07
AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	-0.93731	3.41E-09	1.98E-08
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.12014	7.01E-08	3.36E-07
AGPS	alkylglycerone phosphate synthase	0.86655	6.56E-06	2.30E-05
AGXT	alanine-glyoxylate aminotransferase	-0.08116	0.186003656	0.255849414
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	-4.20223	4.09E-09	2.34E-08
AHCY	S-adenosylhomocysteine hydrolase	0.81495	1.79E-05	5.81E-05
AHCYL1	S-adenosylhomocysteine hydrolase-like 1	0.09411	0.73786475	0.801752558
AHCYL2	S-adenosylhomocysteine hydrolase-like 2	0.15668	0.456828857	0.548572396
AK1	adenylate kinase 1	-0.56265	0.006913277	1.39E-02
AK2	adenylate kinase 2	1.47406	2.50E-13	2.21E-12
AK5	adenylate kinase 5	-4.96120	7.97E-34	2.66E-32
AKR1A1	Aldo-keto reductase family 1, member A1 (aldehyde reductase)	0.59916	1.78E-05	5.80E-05
AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	0.31000	0.044178213	0.073739168
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	0.24595	0.551732633	0.640955681
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-2.06104	8.17E-05	2.36E-04
AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	-2.01310	0.000163259	4.53E-04
AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	-0.74890	0.172889283	0.239757103
AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	-0.32144	3.84E-05	0.000117435
AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	-0.01977	0.786348881	0.841393302

AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	0.33049	0.029544502	0.051424633
AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	0.11540	0.36131743	0.45287197
ALAD	aminolevulinate, delta-, dehydratase	-0.31333	0.007048837	0.014049299
ALAS1	aminolevulinate, delta-, synthase 1	-0.46903	0.000793098	1.93E-03
ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	-0.20162	0.163280823	0.228328796
ALDH18A1	aldehyde dehydrogenase 18 family, member A1	0.64467	0.001754499	3.99E-03
ALDH1A1	aldehyde dehydrogenase 1 family, member A1	-0.89020	0.082786915	1.28E-01
ALDH1A2	aldehyde dehydrogenase 1 family, member A2	-0.84158	7.18E-09	3.92E-08
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-0.40621	0.365058526	0.456997527
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	0.23251	0.019568534	0.035552126
ALDH1L1	aldehyde dehydrogenase 1 family, member L1	0.05931	0.824514723	0.87304085
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	-1.19323	6.99E-07	2.91E-06
ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	-0.01382	0.939099971	0.958089295
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	0.82998	2.96E-06	1.12E-05
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	0.34153	0.056997326	0.092110941
ALDH3B2	aldehyde dehydrogenase 3 family, member B2	-0.09684	0.243897559	0.325570412
ALDH4A1	aldehyde dehydrogenase 4 family, member A1	-0.05234	0.822375743	0.872138699
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	-1.39706	8.20E-09	4.41E-08
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	-0.98414	0.000355749	9.31E-04
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	0.53409	0.060048106	0.096048622
ALDH8A1	aldehyde dehydrogenase 8 family, member A1	-0.56564	0.000141574	0.000397542
ALDH9A1	aldehyde dehydrogenase 9 family, member A1	0.49917	0.000121316	3.44E-04
ALDOA	aldolase A, fructose-bisphosphate	-0.60650	6.30E-06	2.22E-05
ALDOB	aldolase B, fructose-bisphosphate	-0.16283	0.000177223	0.000488867
ALDOC	aldolase C, fructose-bisphosphate	-2.01043	7.22E-06	2.51E-05

ALG12	asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-mannosyltransferase)	0.34303	0.002421994	0.005346268
ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	0.06753	0.665802864	0.740953356
ALG3	asparagine-linked glycosylation 3 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	1.05688	3.29E-10	2.13E-09
ALG5	Asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)	0.74020	5.52E-05	0.000165413
ALG6	asparagine-linked glycosylation 6 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	2.06048	1.22E-17	1.46E-16
ALG8	asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	1.09939	3.89E-13	3.35E-12
ALOX12	arachidonate 12-lipoxygenase	0.02228	0.788022194	0.8427402
ALOX12B	arachidonate 12-lipoxygenase, 12R type	-0.42717	2.31E-06	8.80E-06
ALOX15	arachidonate 15-lipoxygenase	-0.24005	6.48E-06	2.28E-05
ALOX15B	arachidonate 15-lipoxygenase, type B	0.40360	0.086126027	1.32E-01
ALOX5	arachidonate 5-lipoxygenase	0.15275	0.279828867	0.365377063
ALOX5AP	arachidonate 5-lipoxygenase-activating protein	1.33301	0.00564404	1.15E-02
ALOXE3	arachidonate lipoxygenase 3	-0.28370	8.28E-07	3.39E-06
AMACR	alpha-methylacyl-CoA racemase	-0.24378	3.48E-05	0.000107058
AMD1	adenosylmethionine decarboxylase 1	-0.32413	0.063442425	0.101001135
AMDHD2	amidohydrolase domain containing 2	0.31930	0.014510584	0.02696528
AMPD1	adenosine monophosphate deaminase 1 (isoform M)	-0.31001	0.000889197	0.002131767
AMPD2	adenosine monophosphate deaminase 2 (isoform L)	-1.01242	8.49E-11	5.85E-10
AMPD3	adenosine monophosphate deaminase (isoform E)	-0.15787	0.302634392	0.390886734
AMT	aminomethyltransferase	-0.36228	0.139778365	0.201658853
ANKH	Ankylosis, progressive homolog (mouse)	-1.20708	4.66E-17	5.42E-16
AOAH	acyloxyacyl hydrolase (neutrophil)	0.41050	0.076918569	0.119827932
AOC2	amine oxidase, copper containing 2 (retina-specific)	-0.13510	0.042232962	0.070899763
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	-0.07142	0.776088514	0.833485446
AOX1	aldehyde oxidase 1	0.02449	0.898296584	0.93079016

APEH	N-acylaminoacyl-peptide hydrolase	0.52647	0.001029395	0.002444814
APRT	adenine phosphoribosyltransferase	1.18730	5.01E-10	3.19E-09
AQP1	aquaporin 1 (Colton blood group)	3.91324	6.74E-09	3.72E-08
AQP2	aquaporin 2 (collecting duct)	-0.17115	0.029086274	0.050801027
AQP3	aquaporin 3 (Gill blood group)	-0.55027	0.005439329	0.011102566
AQP4	aquaporin 4	0.00371	0.994521722	0.995393773
AQP5	aquaporin 5	-0.14358	0.138388348	0.199959852
AQP6	aquaporin 6, kidney specific	-0.08751	0.210838519	0.286329131
AQP7	aquaporin 7	-0.02457	0.740688509	0.80396142
AQP8	aquaporin 8	-0.12188	0.076058556	0.11876117
AQP9	aquaporin 9	0.30557	0.405530608	0.496952216
ARG1	Arginase, liver	-0.23886	0.041781102	0.070329306
ARG2	arginase, type II	-0.51146	0.007350078	1.46E-02
ARSA	Arylsulfatase A	0.21446	0.137332355	0.198858033
ARSB	arylsulfatase B	0.44529	6.34E-05	1.87E-04
ARSD	arylsulfatase D	-0.10407	0.139437207	0.201332275
ARSE	arylsulfatase E (chondrodysplasia punctata 1)	0.46898	0.028392687	0.049846574
ARSF	arylsulfatase F	0.26149	0.360182916	0.452007327
ARSJ	arylsulfatase family, member J	1.41263	0.000174614	4.83E-04
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	0.29261	0.051579082	0.084022656
ASL	argininosuccinate lyase	0.40688	0.074735833	0.116875345
ASMT	acetylserotonin O-methyltransferase	-0.14760	0.000446008	0.001144867
ASMTL	acetylserotonin O-methyltransferase-like	-0.53155	0.004974081	0.010223657
ASNA1	ArsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	0.10692	0.573086279	0.66122838
ASNS	Asparagine synthetase	-0.69836	0.003494806	7.41E-03

ASNSD1	asparagine synthetase domain containing 1	0.37213	0.003341858	0.007129064
ASPA	aspartoacylase (Canavan disease)	-1.66483	8.03E-05	0.000233698
ASRGL1	asparaginase like 1	-1.38248	1.27E-06	5.07E-06
ASS1	argininosuccinate synthetase 1	-1.93850	3.41E-05	1.06E-04
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	0.35070	0.031500394	0.054271441
ATP10A	ATPase, class V, type 10A	-0.50345	1.32E-05	4.37E-05
ATP10B	ATPase, class V, type 10B	-0.61712	0.014026515	0.026137402
ATP10D	ATPase, class V, type 10D	1.92948	1.37E-16	1.56E-15
ATP11A	ATPase, class VI, type 11A	-0.07503	0.517476088	0.607406979
ATP11B	ATPase, class VI, type 11B	0.61103	0.002740856	0.005959531
ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	-0.17662	0.141954099	0.203664561
ATP13A1	ATPase type 13A1	0.51540	0.002567061	0.005641984
ATP13A2	ATPase type 13A2	-1.96480	2.04E-21	3.21E-20
ATP13A3	ATPase type 13A3	0.80804	7.27E-07	3.01E-06
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-0.25342	0.176589948	0.244056672
ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-1.84760	0.00473031	9.80E-03
ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-3.19608	1.05E-34	3.67E-33
ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.96882	8.77E-11	6.03E-10
ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	-0.69087	0.186787935	2.56E-01
ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	0.47936	0.001092723	2.57E-03
ATP1B4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	-0.06986	0.172341721	0.2391609
ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-0.07779	0.19657006	0.268386119
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-0.50076	0.010904946	0.020875476
ATP2A3	ATPase, Ca++ transporting, ubiquitous	-0.01046	0.899199151	0.93079016
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-1.23496	3.20E-07	1.38E-06

ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	-2.49173	7.68E-29	1.90E-27
ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	-0.51830	2.83E-21	4.39E-20
ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-0.63086	0.013047487	0.024560687
ATP2C1	ATPase, Ca++-sequestering	-0.66167	3.99E-06	1.46E-05
ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	-0.45576	1.40E-05	4.63E-05
ATP4A	ATPase, H+/K+ exchanging, gastric, alpha polypeptide	-0.11854	0.117221327	0.172439188
ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	-0.14316	0.07353904	0.115180946
ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	-0.33674	0.000369031	9.63E-04
ATP5B	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	-0.44866	0.000656136	1.62E-03
ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	-0.66409	8.03E-06	2.77E-05
ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-0.31498	0.049143995	0.080702539
ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0.59936	4.60E-09	2.61E-08
ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	0.21532	0.045596473	0.075919435
ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.40379	0.023780713	0.042483471
ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	0.24754	0.000386173	0.001002668
ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3	-0.22486	0.227716416	0.306587731
ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	-0.37075	0.000494235	0.001260703
ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	-0.00087	0.994216108	0.995393773
ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	-0.13572	0.226274549	0.305455617
ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	0.35531	0.019804947	0.035917447
ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	0.03963	0.746201872	0.809034569
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-0.13853	0.218736625	0.296066284
ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	0.11976	0.512901455	0.605179926
ATP5SL	ATP5S-like	-0.00085	0.994904155	0.995393773
ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	-0.58654	1.08E-05	3.62E-05

ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	-0.49406	0.002869195	6.21E-03
ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit A1	-2.00044	5.41E-32	1.67E-30
ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit A2	0.10969	0.351376081	0.44360354
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit A4	-0.02979	0.846095685	0.890420552
ATP6V0B	ATPase, H+ transporting, lysosomal V0 subunit B	-0.32023	0.060764327	0.096990014
ATP6V0C	ATPase, H+ transporting, lysosomal V0 subunit C	-1.20395	6.22E-22	1.02E-20
ATP6V0D1	ATPase, H+ transporting, lysosomal V0 subunit D1	-1.30795	2.66E-18	3.38E-17
ATP6V0E1	ATPase, H+ transporting, lysosomal V0 subunit E	1.33774	2.13E-17	2.51E-16
ATP6V0E2	ATPase, H+ transporting, lysosomal V0 subunit E2	-0.62010	0.053123054	8.64E-02
ATP6V1A	ATPase, H+ transporting, lysosomal V1 subunit A	-1.87254	1.01E-22	1.75E-21
ATP6V1B1	ATPase, H+ transporting, lysosomal V1 subunit B1	-0.00976	0.941983171	0.959925707
ATP6V1B2	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.75608	8.16E-23	1.44E-21
ATP6V1C1	ATPase, H+ transporting, lysosomal V1 subunit C1	-0.95528	1.47E-06	5.80E-06
ATP6V1D	ATPase, H+ transporting, lysosomal V1 subunit D	-1.01567	7.83E-13	6.57E-12
ATP6V1E1	ATPase, H+ transporting, lysosomal V1 subunit E1	-1.42565	3.99E-23	7.19E-22
ATP6V1F	ATPase, H+ transporting, lysosomal V1 subunit F	-0.18215	0.216863433	0.293726422
ATP6V1G1	ATPase, H+ transporting, lysosomal V1 subunit G1	0.47973	6.61E-05	0.000194366
ATP6V1G2	ATPase, H+ transporting, lysosomal V1 subunit G2	-4.19070	9.61E-19	1.25E-17
ATP6V1H	ATPase, H+ transporting, lysosomal V1 subunit H	-1.96535	2.77E-44	1.94E-42
ATP7A	ATPase, Cu++ transporting, alpha polypeptide	0.82537	4.07E-08	2.01E-07
ATP7B	ATPase, Cu++ transporting, beta polypeptide	-0.11159	0.434508159	0.526119766
ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-2.32999	2.58E-22	4.41E-21
ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	-3.93400	1.07E-77	1.81E-75
ATP8B1	ATPase, class I, type 8B, member 1	0.91987	3.46E-05	1.07E-04
ATP8B2	ATPase, class I, type 8B, member 2	0.31545	0.001559272	0.003568911

ATP8B3	ATPase, class I, type 8B, member 3	-0.18184	0.002126829	0.004745698
ATP8B4	ATPase, class I, type 8B, member 4	0.41218	0.018045652	0.032962094
ATP9A	ATPase, class II, type 9A	-1.04137	4.08E-11	2.92E-10
ATP9B	ATPase, class II, type 9B	0.06795	0.57108781	0.659296716
AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	-1.32256	1.84E-17	2.17E-16
B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	0.22440	0.351522529	0.44360354
B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	-0.33399	6.04E-08	2.93E-07
B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-1.95708	4.78E-12	3.71E-11
B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	-0.11960	0.396543968	0.487114131
B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	0.07945	0.096989988	0.145843673
B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-1.87913	2.78E-07	1.21E-06
B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0.03621	0.766030365	0.82442548
B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-1.85724	7.03E-14	6.41E-13
B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	-0.13312	0.574486176	0.66246761
B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	-0.19881	0.080343764	0.124876813
B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	-0.72622	8.12E-14	7.37E-13
B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-0.04184	0.611372443	0.693593849
B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	-1.00375	0.000350759	9.20E-04
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	-0.00137	0.982999698	0.989815941
B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	-0.33303	0.005614385	0.01144839
B4GALT3	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	0.01966	0.890049069	0.925086788
B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	0.96513	3.48E-09	2.02E-08
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	0.43190	0.0293394	0.051111397
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	-1.30391	2.07E-14	1.99E-13
B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	0.29747	0.01145455	0.021804401

BAAT	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	-0.38031	8.60E-06	2.95E-05
BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	0.87071	0.108507309	1.61E-01
BCAT1	branched chain aminotransferase 1, cytosolic	1.32682	0.000253734	6.81E-04
BCAT2	branched chain aminotransferase 2, mitochondrial	0.22996	0.037646169	0.063876301
BCHE	butyrylcholinesterase	2.68293	5.03E-08	2.45E-07
BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	-0.26512	0.072612148	0.11425735
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	0.42541	0.026133356	0.046279715
BCMO1	beta carotene 15, 15 monooxygenase 1	0.35049	0.038600749	6.53E-02
BDH1	3-hydroxybutyrate dehydrogenase, type 1	-1.19122	8.25E-07	3.38E-06
BDH2	3-hydroxybutyrate dehydrogenase, type 2	0.68015	0.001759713	0.003992741
BEST1	Bestrophin 1	-0.85059	3.42E-05	0.000105578
BEST2	Bestrophin 2	0.16920	0.014844718	0.027535868
BHMT	Betaine-homocysteine methyltransferase	-0.66070	1.17E-08	6.10E-08
BHMT2	betaine-homocysteine methyltransferase 2	-0.38275	0.084290968	0.129919286
BLVRA	Biliverdin reductase A	0.50316	0.002273164	5.05E-03
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.15225	0.556508591	0.645397585
BPGM	2,3-bisphosphoglycerate mutase	0.94370	4.30E-06	1.56E-05
BPHL	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	0.09317	0.577190919	0.664832373
BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	0.05251	0.596062351	0.681853386
BST1	bone marrow stromal cell antigen 1	0.54181	0.004753279	0.009840546
BTD	biotinidase	0.55273	0.000295699	7.87E-04
C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	0.52486	0.003785311	7.98E-03
CA1	carbonic anhydrase I	-0.17334	0.009498427	0.018461093
CA10	carbonic anhydrase X	-2.69514	2.58E-07	1.13E-06
CA11	carbonic anhydrase XI	-3.81380	8.54E-31	2.41E-29

CA12	carbonic anhydrase XII	2.17838	3.37E-06	1.26E-05
CA14	carbonic anhydrase XIV	0.15856	0.663291848	0.738888946
CA2	carbonic anhydrase II	0.81860	0.041789376	7.03E-02
CA3	carbonic anhydrase III, muscle specific	1.83280	0.001688626	3.85E-03
CA4	carbonic anhydrase IV	-2.37409	1.10E-22	1.89E-21
CA5A	carbonic anhydrase VA, mitochondrial	0.01288	0.912703974	0.941414094
CA5B	carbonic anhydrase VB, mitochondrial	-0.07553	0.422061916	0.512269777
CA6	carbonic anhydrase VI	-0.24735	0.019833185	0.035936601
CA7	carbonic anhydrase VII	-0.90282	1.51E-29	3.93E-28
CA8	carbonic anhydrase VIII	-0.06016	0.819225705	0.869251492
CA9	carbonic anhydrase IX	0.72868	0.060779772	9.70E-02
CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.22902	7.22E-09	3.94E-08
CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit	-0.39014	3.10E-12	2.46E-11
CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	-0.29489	1.60E-08	8.28E-08
CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	-0.95930	5.60E-14	5.15E-13
CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	-0.16596	0.002228584	0.004957015
CACNA1F	calcium channel, voltage-dependent, alpha 1F subunit	-0.20777	0.021081478	0.037928004
CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	-0.34800	1.51E-06	5.94E-06
CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	-0.34811	8.12E-05	0.000235089
CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	-0.41707	5.42E-10	3.43E-09
CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	-0.39398	3.47E-11	2.49E-10
CACNA2D1	calcium channel, voltage-dependent, alpha2/delta subunit 1	-0.45605	1.06E-08	5.61E-08
CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	-1.76696	7.65E-10	4.75E-09
CACNA2D3	calcium channel, voltage-dependent, alpha2/delta subunit 3	-3.88905	5.78E-46	4.19E-44
CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-1.21405	2.98E-36	1.16E-34

CACNB2	calcium channel, voltage-dependent, beta 2 subunit	-3.40538	2.91E-34	1.00E-32
CACNB3	calcium channel, voltage-dependent, beta 3 subunit	-2.44416	2.08E-42	1.24E-40
CACNB4	calcium channel, voltage-dependent, beta 4 subunit	-2.86692	2.43E-27	5.55E-26
CACNG1	calcium channel, voltage-dependent, gamma subunit 1	-0.44732	5.92E-05	1.76E-04
CACNG2	calcium channel, voltage-dependent, gamma subunit 2	-1.52495	1.33E-36	5.53E-35
CACNG3	calcium channel, voltage-dependent, gamma subunit 3	-5.70142	6.19E-95	6.29E-92
CACNG4	calcium channel, voltage-dependent, gamma subunit 4	0.04502	0.832053462	0.880106497
CACNG5	calcium channel, voltage-dependent, gamma subunit 5	-0.20581	0.000565248	0.001423656
CAD	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	1.19493	2.97E-12	2.37E-11
CANT1	calcium activated nucleotidase 1	0.67456	8.41E-06	2.89E-05
CAT	Catalase	0.86945	5.50E-05	1.65E-04
CATSPERB	cation channel, sperm-associated, beta	-0.01499	0.837716084	0.885175052
CBR1	carbonyl reductase 1	0.20264	0.536899074	0.626729349
CBR3	carbonyl reductase 3	0.44472	0.084912657	0.130481807
CBR4	carbonyl reductase 4	0.38704	0.058722336	0.094224553
CBS	cystathionine-beta-synthase	0.50929	0.099041096	0.148495554
CCBL1	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase)	-0.30648	0.069592139	0.109680345
CCBL2	cysteine conjugate-beta lyase 2	0.31566	0.087162535	0.133234161
CDA	cytidine deaminase	0.35196	0.046381578	0.077037376
CDADC1	cytidine and dCMP deaminase domain containing 1	-0.15920	0.099045731	0.148495554
CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	-0.20763	0.081214881	0.125845925
CDO1	cysteine dioxygenase, type I	0.21571	0.642021749	0.720723477
CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	-1.23975	1.44E-14	1.40E-13
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.55042	0.000526169	0.001333792
CECR1	cat eye syndrome chromosome region, candidate 1	0.35128	0.339293759	0.430576911

CEL	carboxyl ester lipase (bile salt-stimulated lipase)	0.10341	0.523639828	0.613225674
CEPT1	choline/ethanolamine phosphotransferase 1	0.70628	1.52E-07	6.87E-07
CERK	ceramide kinase	-0.58935	0.00124029	2.90E-03
CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	0.12683	0.775199513	0.833411216
CES2	carboxylesterase 2 (intestine, liver)	-0.23474	0.090001507	0.136955886
CES3	carboxylesterase 3 (brain)	-0.30198	0.000504343	1.28E-03
CFTR	Cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	-0.09566	0.080748378	0.125314086
CH25H	cholesterol 25-hydroxylase	-0.96487	0.0473073	0.078299834
CHAT	choline acetyltransferase	-0.01739	0.817272635	0.868085301
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	3.01506	8.08E-05	2.34E-04
CHI3L2	chitinase 3-like 2	3.64596	2.78E-08	1.41E-07
CHIA	chitinase, acidic	-0.17409	0.0508663	0.083127965
CHIT1	chitinase 1	-0.10241	0.671054076	0.744273288
CHKA	choline kinase alpha	-0.24697	0.132877075	0.193232541
CHPF	chondroitin polymerizing factor	0.64314	0.001049934	2.48E-03
CHPF2	chondroitin sulfate glucuronyltransferase	0.82116	2.23E-05	7.12E-05
CHPT1	choline phosphotransferase 1	0.31270	0.15229355	0.21575804
CHRNA1	Cholinergic receptor, nicotinic, alpha 1 (muscle)	0.36250	0.161536706	0.226173639
CHRNA10	Cholinergic receptor, nicotinic, alpha 10	-0.00320	0.953963536	0.969219324
CHRNA2	Cholinergic receptor, nicotinic, alpha 2 (neuronal)	-0.23502	0.003423202	0.007272068
CHRNA3	Cholinergic receptor, nicotinic, alpha 3	-0.49503	1.10E-08	5.81E-08
CHRNA4	Cholinergic receptor, nicotinic, alpha 4	-0.08133	0.148926879	0.212320017
CHRNA5	Cholinergic receptor, nicotinic, alpha 5	0.20913	0.194274284	0.265429852
CHRNA6	Cholinergic receptor, nicotinic, alpha 6	-0.10569	0.192366114	0.263176521
CHRNA9	Cholinergic receptor, nicotinic, alpha 9	1.32097	0.003295922	7.05E-03

CHRNB1	Cholinergic receptor, nicotinic, beta 1 (muscle)	0.37600	0.023811971	0.042501965
CHRNB2	Cholinergic receptor, nicotinic, beta 2 (neuronal)	0.01913	0.831351099	0.879821335
CHRNB3	Cholinergic receptor, nicotinic, beta 3	0.07206	0.150469855	0.213770242
CHRNB4	Cholinergic receptor, nicotinic, beta 4	-0.13219	0.010637687	0.020421546
CHRND	Cholinergic receptor, nicotinic, delta	-0.21544	0.000632045	0.00157084
CHRNE	Cholinergic receptor, nicotinic, epsilon	0.04917	0.39166851	0.482290782
CHRNG	Cholinergic receptor, nicotinic, gamma	-0.00096	0.989345232	0.993744494
CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-3.00517	7.93E-20	1.10E-18
CHST10	carbohydrate sulfotransferase 10	-0.23679	0.244721234	0.326455557
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	0.68074	0.006215601	1.26E-02
CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	0.64911	3.33E-05	1.03E-04
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	-0.12830	0.682390257	0.754260947
CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	0.34397	0.155027531	0.218565166
CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	0.08718	0.456083051	0.548324567
CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	-0.14525	0.073288592	0.114965824
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	0.78138	0.018097247	0.033026664
CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	-0.14028	0.424969307	0.515490813
CHSY1	carbohydrate (chondroitin) synthase 1	1.58782	2.13E-14	2.04E-13
CKB	creatine kinase, brain	-1.18438	0.001222559	2.86E-03
CKM	creatine kinase, muscle	-0.17965	0.013175687	0.024719081
CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	-0.51794	0.007063691	0.014065116
CLC	Charcot-Leyden crystal protein	-0.22444	0.158728194	0.223163499
CLCA1	chloride channel calcium activated 1	0.09609	0.284118568	0.369790685
CLCA2	chloride channel calcium activated 2	-0.00515	0.981999929	0.989299235
CLCA4	chloride channel calcium activated 4	-0.93291	2.92E-06	1.10E-05

CLCC1	chloride channel CLIC-like 1	0.82528	4.90E-11	3.47E-10
CLCN1	chloride channel 1	-0.41435	2.48E-08	1.26E-07
CLCN2	chloride channel 2	0.22547	0.076705141	1.20E-01
CLCN3	chloride channel 3	-0.04275	0.840704581	0.886939671
CLCN4	chloride channel 4-2	-1.39724	9.71E-28	2.27E-26
CLCN5	chloride channel 5	0.05150	0.659347271	0.736512639
CLCN6	chloride channel 6	-1.18163	2.98E-08	1.50E-07
CLCN7	chloride channel 7	-0.20763	0.023627325	0.042246572
CLCNKB	chloride channel Kb	-0.23322	0.000591142	0.001480038
CLIC1	chloride intracellular channel 1	2.27955	3.05E-16	3.37E-15
CLIC2	chloride intracellular channel 2	0.50283	0.023528151	4.21E-02
CLIC3	chloride intracellular channel 3	0.20176	0.391524117	0.482290782
CLIC4	chloride intracellular channel 4 (mitochondrial)	2.07129	2.15E-10	1.41E-09
CLIC5	chloride intracellular channel 5	-0.43757	0.064134039	0.102022302
CMAS	Cytidine monophosphate N-acetylneuraminic acid synthetase	-1.71620	2.05E-18	2.62E-17
CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	0.22802	0.111048588	0.16395191
CNGA1	cyclic nucleotide gated channel alpha 1	-0.11486	0.129759514	0.188969264
CNGA3	cyclic nucleotide gated channel alpha 3	2.03139	5.87E-06	2.09E-05
CNGB1	cyclic nucleotide gated channel beta 1	-0.56777	3.08E-21	4.74E-20
CNGB3	cyclic nucleotide gated channel beta 3	-0.66834	3.02E-16	3.35E-15
CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	-0.88305	0.000662415	1.64E-03
COASY	Coenzyme A synthase	0.00260	0.9840368	0.990132417
COMT	catechol-O-methyltransferase	0.74200	3.86E-07	1.64E-06
COQ10B	Coenzyme Q10 homolog B (S. cerevisiae)	-0.25050	0.089627632	0.136489121
COQ2	coenzyme Q2 homolog, prenyltransferase (yeast)	1.20049	2.40E-13	2.14E-12

COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	-0.50703	0.001371557	0.003190361
COQ4	coenzyme Q4 homolog (S. cerevisiae)	0.25755	0.053399887	0.086780152
COQ6	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	-0.02054	0.884399108	0.920155265
COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	0.48754	0.004492562	0.009338833
COQ9	coenzyme Q9 homolog (S. cerevisiae)	0.12126	0.476179484	0.568785482
COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	-0.36810	0.001068876	2.52E-03
COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	-0.84040	1.70E-06	6.62E-06
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-0.03779	0.786029518	0.841393302
COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	-0.25136	0.245011037	0.326627829
COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	-0.16626	0.335795203	0.427203785
COX4I1	cytochrome c oxidase subunit IV isoform 1	-0.44020	0.000384397	9.99E-04
COX5A	cytochrome c oxidase subunit Va	-0.43732	0.000227794	6.17E-04
COX5B	Cytochrome c oxidase subunit Vb	-0.47915	0.00109302	0.002571887
COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	-0.55296	6.80E-06	2.38E-05
COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	-0.37005	0.000204329	0.000559087
COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	-0.26464	0.031564638	0.054290109
COX6C	cytochrome c oxidase subunit VIc	-0.52207	9.20E-08	4.29E-07
COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	-2.60210	6.75E-09	3.72E-08
COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	0.05136	0.752089118	0.812863996
COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	-0.58929	0.000231205	0.000624223
COX7B	cytochrome c oxidase subunit VIIb	0.06625	0.682493178	0.754260947
COX7C	cytochrome c oxidase subunit VIIc	-0.26978	0.00109498	0.00257352
COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	0.07303	0.514793554	0.606710316
CP	ceruloplasmin (ferroxidase)	1.07013	0.000654832	1.62E-03
CPOX	coproporphyrinogen oxidase	0.16201	0.306038264	0.394281237

CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	0.54306	0.096949417	1.46E-01
CPT1A	carnitine palmitoyltransferase 1A (liver)	-0.23147	0.009448497	0.018381621
CPT2	carnitine palmitoyltransferase II	0.88991	9.48E-16	1.01E-14
CRAT	carnitine acetyltransferase	-0.23091	0.088120805	0.134597743
CROT	carnitine O-octanoyltransferase	1.25620	3.97E-08	1.97E-07
CRYL1	crystallin, lambda 1	0.02561	0.922392027	0.94596999
CRYM	crystallin, mu	-5.16424	5.39E-24	1.02E-22
CRYZ	crystallin, zeta (quinone reductase)	1.12616	3.64E-06	1.34E-05
CRYZL1	crystallin, zeta (quinone reductase)-like 1	-1.13996	3.95E-10	2.52E-09
CS	citrate synthase	-0.37073	0.006923046	1.39E-02
CSAD	cysteine sulfinic acid decarboxylase	0.31026	0.259832497	0.344354281
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	-1.28267	0.000191954	5.27E-04
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	0.50890	0.003221073	0.006893096
CTBS	chitobiase, di-N-acetyl-	1.38893	1.16E-08	6.07E-08
CTH	cystathionase (cystathionine gamma-lyase)	0.50069	0.026190796	4.63E-02
CTNS	Cystinosis, nephropathic	0.84346	4.43E-08	2.17E-07
CTPS2	CTP synthase II	0.66351	1.19E-05	3.97E-05
CUBN	cubilin (intrinsic factor-cobalamin receptor)	0.12809	0.282793061	0.368739109
CYB561	cytochrome b-561	-1.07715	7.36E-09	4.00E-08
CYB5A	cytochrome b5 type A (microsomal)	0.73066	0.002960364	0.00638898
CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	0.15115	0.366566622	0.458603042
CYB5R1	cytochrome b5 reductase 1	0.01388	0.951273662	0.967453404
CYB5R2	cytochrome b5 reductase 2	-0.53525	0.100782018	0.150322702
CYB5R3	cytochrome b5 reductase 3	-0.14723	0.269706718	0.353875304
CYB5R4	cytochrome b5 reductase 4	0.72403	0.000825146	2.00E-03

CYBA	cytochrome b-245, alpha polypeptide	1.59796	1.56E-07	7.04E-07
CYBB	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	1.15024	8.42E-05	2.43E-04
CYBRD1	cytochrome b reductase 1	2.04399	1.06E-09	6.53E-09
CYC1	cytochrome c-1	0.09153	0.598145466	0.682956412
CYCS	cytochrome c, somatic	-0.07457	0.565020334	0.653777085
CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	-0.14962	0.133318855	0.193736406
CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	-0.18406	0.000443127	0.00114035
CYP11B2	cytochrome P450, family 11, subfamily B, polypeptide 2	-0.23649	0.001351072	0.003146311
CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	-0.13321	0.168138606	0.233933255
CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	0.42977	0.023025281	0.04127901
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	-0.37840	4.12E-08	2.03E-07
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	0.02119	0.790326919	0.844413769
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	-0.27507	0.596938973	0.682168034
CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	1.49212	9.98E-28	2.31E-26
CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-0.01735	0.839755531	0.886408616
CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	0.01494	0.910359368	0.939472384
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-0.77213	0.000368022	0.000961682
CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	-2.64829	2.31E-30	6.19E-29
CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	0.54806	0.005863255	1.19E-02
CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	0.52085	0.123664311	1.81E-01
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	-0.78746	3.94E-14	3.68E-13
CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	-0.30091	4.96E-05	0.000149348
CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7	-0.29077	0.000331778	0.000875981
CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	-0.14702	0.006946983	0.013873493
CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	-0.27139	0.003688628	0.007797474

CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	-0.18778	0.002003251	0.004485252
CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	-0.18545	0.000968035	0.002307169
CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	-0.04688	0.303330944	0.391289219
CYP2D6	Cytochrome P450, family 2, subfamily D, polypeptide 6	-0.13855	0.04242438	0.071162346
CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	-0.57749	3.92E-12	3.07E-11
CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	-0.11815	0.029798416	0.051777931
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	-0.93898	0.006940806	1.39E-02
CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	0.14485	0.106800067	0.158369465
CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	-0.28178	2.86E-05	8.98E-05
CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	0.30224	0.189426197	2.60E-01
CYP3A4	Cytochrome P450, family 3, subfamily A, polypeptide 4	-0.16597	0.003151116	0.006750495
CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	-0.01627	0.667723235	0.74179308
CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	0.09685	0.484737847	0.57596262
CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	-0.03438	0.705102096	0.774431422
CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	-4.24774	2.89E-24	5.76E-23
CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	-0.07933	0.149828002	0.213156283
CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22	-0.03784	0.375683501	0.467706404
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	-0.24979	0.36040582	0.45200804
CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	0.07686	0.606883174	0.68965539
CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	-0.30400	0.005164051	0.010572523
CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	-0.02666	0.858418846	0.899091878
CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	0.15164	0.642418724	0.720771118
CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	-0.21446	0.000770324	0.001875531
CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	0.22303	0.262250722	0.347106587
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	-0.02671	0.587960546	0.67570593

CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	-0.32173	0.024798889	0.044070054
DAD1	defender against cell death	0.63155	1.92E-05	6.20E-05
DAGLA	diacylglycerol lipase, alpha	-0.65891	1.86E-10	1.23E-09
DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	-0.30300	0.004875941	0.010053537
DAO	D-amino-acid oxidase	-0.01363	0.908780424	0.938319249
DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	-0.16869	0.009440008	0.018381621
DBT	dihydrolipoamide branched chain transacylase E2	0.21710	0.104755154	0.155791681
DCK	deoxycytidine kinase	0.25105	0.186183664	0.255883852
DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	0.25166	0.253776859	3.37E-01
DCTD	dCMP deaminase	0.53395	0.006475125	1.31E-02
DCXR	dicarbonyl/L-xylulose reductase	-0.43104	0.014146168	0.026336226
DDAH1	dimethylarginine dimethylaminohydrolase 1	-0.94256	0.00057733	1.45E-03
DDAH2	dimethylarginine dimethylaminohydrolase 2	0.84733	3.81E-06	1.40E-05
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-0.07526	0.543605309	0.632960821
DDHD2	DDHD domain containing 2	-1.71964	2.89E-19	3.90E-18
DDO	D-aspartate oxidase	0.37228	0.001999324	0.004481395
DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1.05124	2.44E-14	2.29E-13
DDT	D-dopachrome tautomerase	-0.13198	0.459995932	0.551690981
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	0.88696	8.03E-12	6.12E-11
DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	0.22823	0.096602447	0.14547613
DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	0.70006	1.81E-07	8.14E-07
DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	1.63236	7.79E-19	1.02E-17
DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	-0.30716	0.025749971	0.045680358
DGKA	diacylglycerol kinase, alpha 80kDa	-0.46019	5.97E-05	1.77E-04
DGKB	diacylglycerol kinase, beta 90kDa	-2.68422	1.39E-13	1.25E-12

DGKD	diacylglycerol kinase, delta 130kDa	0.20595	0.213005713	0.289056113
DGKE	diacylglycerol kinase, epsilon 64kDa	-0.26065	9.45E-05	0.00027147
DGKG	diacylglycerol kinase, gamma 90kDa	-0.42222	0.125331378	0.183202136
DGKI	diacylglycerol kinase, iota	-1.38808	8.71E-08	4.09E-07
DGKQ	diacylglycerol kinase, theta 110kDa	-0.06678	0.48299496	0.574899739
DGKZ	diacylglycerol kinase, zeta 104kDa	-2.57525	9.72E-39	4.59E-37
DGUOK	deoxyguanosine kinase	0.24166	0.128263138	0.186923986
DHCR24	24-dehydrocholesterol reductase	-1.81612	1.92E-06	7.45E-06
DHCR7	7-dehydrocholesterol reductase	-0.19742	0.385575335	0.476230889
DHDDS	dehydrodolichyl diphosphate synthase	-0.54488	5.80E-06	2.06E-05
DHFR	dihydrofolate reductase	1.88222	1.55E-15	1.58E-14
DHODH	dihydroorotate dehydrogenase	0.42592	9.65E-08	4.48E-07
DHRS1	dehydrogenase/reductase (SDR family) member 1	0.31286	0.095403777	0.143928648
DHRS11	dehydrogenase/reductase (SDR family) member 11	-0.97829	4.81E-08	2.34E-07
DHRS12	dehydrogenase/reductase (SDR family) member 12	-0.08515	0.320996571	0.41068976
DHRS2	dehydrogenase/reductase (SDR family) member 2	-0.17246	0.351815818	0.443698237
DHRS3	dehydrogenase/reductase (SDR family) member 3	0.68148	0.012712686	0.02396391
DHRS7	dehydrogenase/reductase (SDR family) member 7	-0.05682	0.625009572	0.70474326
DHRS7B	dehydrogenase/reductase (SDR family) member 7B	0.20490	0.16736675	0.233052468
DHRS9	dehydrogenase/reductase (SDR family) member 9	-1.63032	1.81E-06	7.02E-06
DHTKD1	dehydrogenase E1 and transketolase domain containing 1	0.50673	0.002715289	0.005916595
DIO1	deiodinase, iodothyronine, type I	-0.13578	0.100454234	0.150164307
DIO2	deiodinase, iodothyronine, type II	-2.05630	8.91E-15	8.75E-14
DIO3	deiodinase, iodothyronine, type III	-0.16006	0.072898701	0.114442516
DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	-0.00670	0.957978223	0.971303447

DLD	dihydrolipoamide dehydrogenase	0.28575	0.046490631	7.72E-02
DOLK	dolichol kinase	0.48483	0.002335103	0.005171312
DOLPP1	dolichyl pyrophosphate phosphatase 1	0.28236	0.031393987	0.054133992
DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	0.43151	0.004978564	0.010223657
DPEP1	dipeptidase 1 (renal)	0.32430	0.088656268	0.135313959
DPEP2	dipeptidase 2	0.32095	0.051419205	0.083896664
DPEP3	dipeptidase 3	-0.26742	0.025838883	0.045798126
DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	0.60057	8.04E-05	2.34E-04
DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	0.39177	0.011733681	0.022293994
DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	0.90154	0.000327881	0.000866816
DPYD	dihydropyrimidine dehydrogenase	3.34244	4.46E-14	4.14E-13
DPYS	dihydropyrimidinase	-0.28963	0.000109665	0.000312254
DPYSL2	dihydropyrimidinase-like 2	-0.52219	0.057392728	9.25E-02
DPYSL3	dihydropyrimidinase-like 3	2.05704	1.99E-09	1.18E-08
DPYSL4	dihydropyrimidinase-like 4	-0.17308	0.085071182	0.130580203
DSE	dermatan sulfate epimerase	2.10256	5.86E-10	3.69E-09
DTYMK	deoxythymidylate kinase (thymidylate kinase)	2.04475	2.41E-17	2.81E-16
DUOX1	dual oxidase 1	-0.11129	0.33917574	0.430576911
DUOX2	dual oxidase 2	-0.10511	0.093051045	0.140858357
DUT	deoxyuridine triphosphatase	0.43038	0.001467498	0.0033711
EBP	emopamil binding protein (sterol isomerase)	-0.28919	0.243562696	0.325337031
ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	0.13658	0.288874506	0.374781028
ECHDC1	enoyl Coenzyme A hydratase domain containing 1	0.22512	0.130408997	0.189779164
ECHDC2	enoyl Coenzyme A hydratase domain containing 2	-0.03100	0.926648225	0.948100574
ECHDC3	enoyl Coenzyme A hydratase domain containing 3	-0.07770	0.717505361	0.784241074

ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-0.63027	1.20E-06	4.80E-06
EDEM1	ER degradation enhancer, mannosidase alpha-like 1	0.12360	0.488181268	0.579376834
EDEM2	ER degradation enhancer, mannosidase alpha-like 2	1.43875	7.58E-13	6.40E-12
EDEM3	ER degradation enhancer, mannosidase alpha-like 3	0.47194	0.000441014	1.14E-03
EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	0.23339	0.251798421	0.334579209
ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0.63737	0.000268977	0.000718567
ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	0.97798	0.043995546	7.35E-02
ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-2.50790	7.02E-24	1.31E-22
ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	-0.10748	0.385576018	0.476230889
ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	0.57577	0.003069113	6.60E-03
ENO1	enolase 1, (alpha)	0.41252	0.093903562	1.42E-01
ENO2	enolase 2 (gamma, neuronal)	-2.30847	7.25E-12	5.56E-11
ENO3	enolase 3 (beta, muscle)	0.36599	0.009954952	0.019256345
ENOPH1	enolase-phosphatase 1	-0.08059	0.600029325	0.684161312
ENOSF1	enolase superfamily member 1	0.32107	0.326163462	0.416514019
ENOX1	ecto-NOX disulfide-thiol exchanger 1	-0.77527	9.79E-05	2.80E-04
ENOX2	ecto-NOX disulfide-thiol exchanger 2	0.24031	0.00311408	0.006678189
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	0.07724	0.404157393	0.495568142
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-2.35813	8.82E-06	3.00E-05
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-0.20053	0.000557646	0.001408316
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	-0.96194	0.012418786	2.35E-02
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	1.76709	6.11E-11	4.31E-10
ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	-0.18859	0.006202626	0.012547203
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	-3.33805	3.58E-31	1.04E-29
ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	-1.01593	5.64E-14	5.16E-13

ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	0.27988	0.029896064	0.051903243
ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	-1.88569	8.77E-29	2.15E-27
ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	0.15580	0.159361524	0.223899086
EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	-0.83763	0.004813846	9.95E-03
EPHX2	epoxide hydrolase 2, cytoplasmic	-0.20804	0.336276885	0.427549036
EPX	eosinophil peroxidase	-0.18167	0.007314686	0.014550642
ESD	esterase D/formylglutathione hydrolase	0.12512	0.355188557	0.447396739
ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	0.59175	0.000837241	2.02E-03
ETFB	electron-transfer-flavoprotein, beta polypeptide	-0.38884	0.032165499	5.51E-02
ETFDH	electron-transferring-flavoprotein dehydrogenase	0.09773	0.494705242	0.585751751
ETNK1	ethanolamine kinase 1	0.70754	0.000664197	0.00164072
ETNK2	ethanolamine kinase 2	0.07114	0.722687402	0.787758773
EXT1	exostoses (multiple) 1	-0.09357	0.51821301	0.607920975
EXT2	exostoses (multiple) 2	0.56228	2.52E-05	8.01E-05
EXTL1	exostoses (multiple)-like 1	-0.99316	3.10E-26	6.77E-25
EXTL2	exostoses (multiple)-like 2	-0.05479	0.721363825	0.786766446
EXTL3	exostoses (multiple)-like 3	-0.07514	0.6736494	0.746337455
FA2H	fatty acid 2-hydroxylase	-2.00749	2.77E-06	1.05E-05
FAAH	fatty acid amide hydrolase	-1.58234	1.67E-30	4.60E-29
FADS1	fatty acid desaturase 1	-0.07781	0.733969454	0.797946471
FADS2	fatty acid desaturase 2	0.37232	0.149610987	0.212996595
FADS3	fatty acid desaturase 3	-0.49864	0.007601157	1.50E-02
FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	0.72121	0.001872036	4.22E-03
FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	-0.31748	0.048368	0.079685692
FAR2	fatty acyl CoA reductase 2	-1.00162	9.09E-05	2.62E-04

FASN	fatty acid synthase	-0.71769	1.21E-09	7.36E-09
FBP1	fructose-1,6-bisphosphatase 1	0.63232	0.018924902	0.034475203
FBP2	fructose-1,6-bisphosphatase 2	-0.14842	0.057165717	0.092309693
FDFT1	farnesyl-diphosphate farnesyltransferase 1	-0.92634	1.38E-06	5.47E-06
FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	0.12700	0.267973483	0.352843323
FDX1	ferredoxin 1	0.85766	1.48E-09	8.95E-09
FDXR	ferredoxin reductase	0.90520	8.66E-06	2.96E-05
FECH	ferrochelatase (protoporphyria)	0.00352	0.98083412	0.988614658
FH	fumarate hydratase	0.01953	0.908686309	0.938319249
FHIT	Fragile histidine triad gene	-0.70440	0.000253292	0.000681142
FIG4	FIG4 homolog (S. cerevisiae)	-1.31146	6.76E-16	7.31E-15
FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	0.72245	4.91E-06	1.76E-05
FLVCR2	Feline leukemia virus subgroup C cellular receptor family, member 2	0.98463	9.98E-09	5.31E-08
FMO1	flavin containing monooxygenase 1	0.09297	0.727324991	0.791569436
FMO2	flavin containing monooxygenase 2	-0.00286	0.993670898	0.995393773
FMO3	flavin containing monooxygenase 3	0.26092	0.269155332	3.54E-01
FMO4	flavin containing monooxygenase 4	0.40512	0.020342406	3.67E-02
FMO5	flavin containing monooxygenase 5	0.05599	0.615906972	0.697182001
FN3K	fructosamine 3 kinase	-0.15988	0.003362678	0.007165958
FN3KRP	fructosamine-3-kinase-related protein	-0.37990	0.000483271	0.001235837
FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	-0.83519	0.001775479	0.004019543
FOLR1	folate receptor 1 (adult)	0.05946	0.791385387	0.845003409
FOLR2	folate receptor 2 (fetal)	0.33703	0.386141769	0.476640083
FOLR3	folate receptor 3 (gamma)	0.00693	0.938602607	0.958089295
FOXRED2	FAD-dependent oxidoreductase domain containing 2	-0.90490	1.16E-08	6.07E-08

FPGS	folylpolyglutamate synthase	0.15007	0.165771662	0.231465515
FPGT	fucose-1-phosphate guanylyltransferase	1.86765	4.40E-22	7.27E-21
FTCD	formiminotransferase cyclodeaminase	-0.33882	3.46E-06	1.29E-05
FUCA1	fucosidase, alpha-L- 1, tissue	0.29843	0.263648793	3.48E-01
FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	-0.88285	6.35E-12	4.89E-11
FUT2	fucosyltransferase 2 (secretor status included)	-0.08746	0.312523698	0.402127012
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	-0.25170	0.001453685	3.35E-03
FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	0.36183	0.001415123	3.27E-03
FUT5	fucosyltransferase 5 (alpha (1,3) fucosyltransferase)	0.09827	0.219199041	0.296494777
FUT6	Fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	-0.05676	0.351460877	0.44360354
FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	-0.28453	8.69E-06	2.97E-05
FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	0.19943	0.369742215	0.46172354
FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	-0.62272	2.11E-21	3.30E-20
FXN	frataxin	0.28488	0.057905974	0.093061538
G6PC	glucose-6-phosphatase, catalytic subunit	-0.14414	0.003984135	0.008367508
G6PC2	glucose-6-phosphatase, catalytic, 2	0.03900	0.56422271	0.653225951
G6PC3	glucose 6 phosphatase, catalytic, 3	0.72508	2.95E-05	9.27E-05
G6PD	glucose-6-phosphate dehydrogenase	0.13056	0.529274221	0.619110754
GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	1.18627	5.88E-10	3.69E-09
GABRA1	Gamma-aminobutyric acid (GABA) A receptor, alpha 1	-5.66710	1.46E-36	5.94E-35
GABRA2	Gamma-aminobutyric acid (GABA) A receptor, alpha 2	-4.27750	5.71E-31	1.63E-29
GABRA3	Gamma-aminobutyric acid (GABA) A receptor, alpha 3	-2.18568	2.71E-23	4.92E-22
GABRA4	Gamma-aminobutyric acid (GABA) A receptor, alpha 4	-2.62901	3.80E-44	2.57E-42
GABRA5	Gamma-aminobutyric acid (GABA) A receptor, alpha 5	-1.74617	2.40E-79	4.43E-77
GABRA6	Gamma-aminobutyric acid (GABA) A receptor, alpha 6	-0.00772	0.923635234	0.94596999

GABRB1	Gamma-aminobutyric acid (GABA) A receptor, beta 1	-3.77312	3.95E-09	2.27E-08
GABRB2	Gamma-aminobutyric acid (GABA) A receptor, beta 2	-1.19893	2.98E-33	9.62E-32
GABRB3	Gamma-aminobutyric acid (GABA) A receptor, beta 3	-2.23651	2.11E-41	1.23E-39
GABRD	Gamma-aminobutyric acid (GABA) A receptor, delta	-2.01095	2.53E-66	3.43E-64
GABRE	Gamma-aminobutyric acid (GABA) A receptor, epsilon	-0.18954	0.467323523	0.559522215
GABRG2	Gamma-aminobutyric acid (GABA) A receptor, gamma 2	-4.55138	1.26E-62	1.42E-60
GABRG3	Gamma-aminobutyric acid (GABA) A receptor, gamma 3	-0.33788	1.94E-08	9.97E-08
GABRP	Gamma-aminobutyric acid (GABA) A receptor, pi	0.00314	0.985969041	0.991332869
GABRQ	Gamma-aminobutyric acid (GABA) receptor, theta	-0.07484	0.245588932	0.327183682
GABRR1	Gamma-aminobutyric acid (GABA) receptor, rho 1	0.02524	0.861441871	0.900880311
GABRR2	Gamma-aminobutyric acid (GABA) receptor, rho 2	-0.36773	3.59E-06	1.33E-05
GAD1	glutamate decarboxylase 1 (brain, 67kDa)	-0.39226	0.157634144	0.221932282
GAD2	Glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	-1.26881	9.92E-43	6.11E-41
GAL3ST1	galactose-3-O-sulfotransferase 1	-0.36262	0.153325897	0.216767419
GAL3ST4	galactose-3-O-sulfotransferase 4	1.36568	4.33E-11	3.09E-10
GALC	galactosylceramidase	0.06995	0.718920995	0.785366138
GALE	UDP-galactose-4-epimerase	0.29311	0.028580835	0.050133596
GALK1	galactokinase 1	0.33587	0.004377886	9.12E-03
GALK2	galactokinase 2	0.00063	0.996810823	0.996810823
GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)	0.49965	0.002586868	5.68E-03
GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	1.51217	4.34E-23	7.74E-22
GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	1.51751	8.34E-08	3.94E-07
GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	-0.84623	3.60E-07	1.54E-06
GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	0.30600	0.228244439	0.30704973
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	-1.83610	1.05E-12	8.74E-12

GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	0.98466	2.06E-06	7.95E-06
GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	0.30932	0.140136654	0.20191199
GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	0.08265	0.725689051	0.790212019
GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	0.93972	1.66E-06	6.49E-06
GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	-0.21829	0.006180156	0.012514199
GALT	galactose-1-phosphate uridylyltransferase	-0.62272	0.000100764	0.00028812
GAMT	guanidinoacetate N-methyltransferase	-0.29586	0.073486171	0.115180946
GANAB	glucosidase, alpha; neutral AB	1.21064	1.17E-12	9.69E-12
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.15431	0.185901164	0.255849414
GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	-0.25934	4.18E-05	0.000126953
GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	0.89957	9.75E-10	6.01E-09
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	1.06838	0.018008849	3.29E-02
GBA3	glucosidase, beta, acid 3 (cytosolic)	-0.04625	0.593973366	0.680258573
GBE1	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	2.17123	8.52E-22	1.37E-20
GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	-0.09922	0.603173713	0.686975999
GCDH	glutaryl-Coenzyme A dehydrogenase	0.46736	0.007322614	0.014552173
GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	0.28929	0.376443524	0.468079317
GCK	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	-0.38211	0.042808283	0.071747106
GCLC	glutamate-cysteine ligase, catalytic subunit	0.21145	0.384292333	0.475222818
GCLM	glutamate-cysteine ligase, modifier subunit	0.84563	0.001384691	3.21E-03
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	0.06618	0.7062416	0.775264132
GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.08701	0.353131251	0.445081112
GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	-0.08641	0.669911518	0.743411635
GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	-0.20869	0.004191055	0.008783933
GDE1	glycerophosphodiester phosphodiesterase 1	-0.76488	0.000761967	1.86E-03

GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	0.46703	0.086376769	0.132231906
GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	0.19538	0.167304218	0.233052468
GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	-0.94954	1.90E-10	1.25E-09
GFOD1	glucose-fructose oxidoreductase domain containing 1	-3.11290	1.14E-43	7.50E-42
GFOD2	glucose-fructose oxidoreductase domain containing 2	-0.53341	3.11E-07	1.34E-06
GFPT1	glutamine-fructose-6-phosphate transaminase 1	0.17567	0.412559265	0.504038601
GFPT2	glutamine-fructose-6-phosphate transaminase 2	0.59143	0.163300575	0.228328796
GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	1.29603	5.18E-06	1.85E-05
GGPS1	geranylgeranyl diphosphate synthase 1	0.35106	0.004231868	8.84E-03
GGT1	gamma-glutamyltransferase 1	0.15485	0.274875333	0.359833581
GGT5	gamma-glutamyltransferase 5	0.89432	9.15E-05	2.63E-04
GGTLC1	gamma-glutamyltransferase-like activity 4	-0.00595	0.965498847	0.976391243
GK	glycerol kinase	0.22142	0.084250933	0.129919286
GK2	glycerol kinase 2	-0.07144	0.276545436	0.361786919
GLA	galactosidase, alpha	1.20941	1.20E-12	9.89E-12
GLB1	galactosidase, beta 1	1.07015	5.91E-10	3.70E-09
GLB1L	galactosidase, beta 1-like	0.39896	0.005690397	1.16E-02
GLB1L2	galactosidase, beta 2-like	0.46189	0.070708738	0.111348462
GLCE	glucuronic acid epimerase	-0.33261	0.106060236	0.157387197
GLDC	glycine dehydrogenase (decarboxylating)	0.70334	0.083578219	1.29E-01
GLO1	glyoxalase I	0.02195	0.838609904	0.885659187
GLOD4	glyoxalase domain containing 4	0.38628	0.020449253	0.036888492
GLRA1	Glycine receptor, alpha 1 (startle disease/hyperekplexia)	-0.10132	0.066844976	0.105755515
GLRA2	Glycine receptor, alpha 2	-0.51961	6.25E-08	3.02E-07
GLRA3	Glycine receptor, alpha 3	-0.25322	6.23E-06	2.21E-05

GLRB	Glycine receptor, beta	-1.92984	1.50E-11	1.12E-10
GLRX	glutaredoxin (thioltransferase)	0.22562	0.356248829	0.448176899
GLRX2	glutaredoxin 2	-0.79050	1.01E-05	3.40E-05
GLRX3	glutaredoxin 3	0.36998	0.049649454	0.08146678
GLRX5	glutaredoxin 5	-0.65305	1.23E-07	5.64E-07
GLS	glutaminase	-2.67429	3.80E-39	1.84E-37
GLS2	glutaminase 2 (liver, mitochondrial)	-2.80946	5.86E-57	5.41E-55
GLT25D1	glycosyltransferase 25 domain containing 1	1.16293	3.57E-12	2.81E-11
GLT25D2	glycosyltransferase 25 domain containing 2	0.11628	0.78314501	0.839290356
GLT8D1	glycosyltransferase 8 domain containing 1	0.80952	6.95E-09	3.82E-08
GLT8D2	glycosyltransferase 8 domain containing 2	-0.18273	0.494101256	0.585377537
GLTP	glycolipid transfer protein	0.60746	0.001264128	0.002953992
GLUD1	glutamate dehydrogenase 1	-0.81596	7.49E-06	2.59E-05
GLUD2	glutamate dehydrogenase 2	-0.63559	1.08E-06	4.36E-06
GLUL	glutamate-ammonia ligase (glutamine synthetase)	0.05764	0.852959264	0.894770993
GLYAT	glycine-N-acyltransferase	-0.13126	0.006374655	0.012869587
GMDS	GDP-mannose 4,6-dehydratase	0.07214	0.633547348	0.71199655
GMPPA	GDP-mannose pyrophosphorylase A	0.96287	2.16E-09	1.28E-08
GMPPB	GDP-mannose pyrophosphorylase B	0.41245	0.002932252	0.006335035
GMPR	guanosine monophosphate reductase	0.46636	0.144121721	2.06E-01
GMPR2	guanosine monophosphate reductase 2	-0.01785	0.914451451	0.941997042
GMPS	guanine monphosphate synthetase	0.80380	1.86E-05	6.04E-05
GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	-0.20064	0.34012399	0.431361243
GNMT	glycine N-methyltransferase	-0.21273	0.005030634	0.010320161
GNPAT	glyceronephosphate O-acyltransferase	0.50764	3.56E-06	1.32E-05

GNPDA1	glucosamine-6-phosphate deaminase 1	0.68056	3.57E-06	1.32E-05
GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	-0.53968	3.21E-09	1.87E-08
GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	1.68638	1.70E-11	1.27E-10
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	-2.92616	2.63E-36	1.05E-34
GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	-1.05027	1.13E-14	1.10E-13
GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	0.06155	0.822970165	0.872314048
GPD1L	glycerol-3-phosphate dehydrogenase 1-like	-1.26758	2.21E-08	1.13E-07
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.07575	0.459242301	0.551144981
GPHN	gephyrin	-1.12511	2.07E-06	7.97E-06
GPI	glucose phosphate isomerase	-0.70794	0.001065624	2.52E-03
GPLD1	glycosylphosphatidylinositol specific phospholipase D1	-0.31936	9.44E-10	5.83E-09
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	0.07785	0.265874129	0.350533142
GPX1	glutathione peroxidase 1	0.87178	2.78E-07	1.21E-06
GPX2	glutathione peroxidase 2 (gastrointestinal)	0.01993	0.957261876	0.971303447
GPX3	glutathione peroxidase 3 (plasma)	1.06643	0.026449548	4.67E-02
GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	-0.15315	0.185839902	0.255849414
GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	-0.15989	0.000229772	0.000621178
GPX7	glutathione peroxidase 7	2.19836	1.76E-16	2.00E-15
GRHPR	glyoxylate reductase/hydroxypyruvate reductase	0.02606	0.859237977	0.899091878
GRIA1	Glutamate receptor, ionotropic, AMPA 1	-1.61828	5.85E-05	1.74E-04
GRIA2	Glutamate receptor, ionotropic, AMPA 2	-2.45557	3.56E-05	1.09E-04
GRIA3	Glutamate receptor, ionotrophic, AMPA 3	-1.63811	3.35E-06	1.25E-05
GRIA4	Glutamate receptor, ionotrophic, AMPA 4	0.19729	0.419701737	0.509889092
GRID2	Glutamate receptor, ionotropic, delta 2	-0.28829	0.008358405	0.016386342
GRIK1	Glutamate receptor, ionotropic, kainate 1	-0.54528	0.027563927	4.85E-02

GRIK2	Glutamate receptor, ionotropic, kainate 2	-0.52739	0.017259955	3.18E-02
GRIK3	Glutamate receptor, ionotropic, kainate 3	-0.15983	0.013972733	0.02606107
GRIK4	Glutamate receptor, ionotropic, kainate 4	-0.56794	2.29E-07	1.02E-06
GRIK5	Glutamate receptor, ionotropic, kainate 5	-0.69869	6.26E-09	3.49E-08
GRIN1	Glutamate receptor, ionotropic, N-methyl D-aspartate 1	-2.01450	7.49E-92	3.80E-89
GRIN2A	Glutamate receptor, ionotropic, N-methyl D-aspartate 2A	-3.04695	3.62E-86	1.05E-83
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	-0.67062	6.50E-40	3.22E-38
GRIN2C	Glutamate receptor, ionotropic, N-methyl D-aspartate 2C	-0.36309	3.69E-08	1.83E-07
GRIN2D	Glutamate receptor, ionotropic, N-methyl D-aspartate 2D	-0.08827	0.12316811	0.180404011
GSR	glutathione reductase	0.23734	0.264052579	0.348583697
GSS	glutathione synthetase	0.13005	0.33400394	0.425190989
GSTA1	glutathione S-transferase A1	0.26266	0.026917364	0.047420278
GSTA3	glutathione S-transferase A3	-0.05879	0.443067521	0.534573454
GSTA4	glutathione S-transferase A4	-0.61725	0.007765532	1.53E-02
GSTCD	glutathione S-transferase, C-terminal domain containing	0.08954	0.292264343	0.378695608
GSTK1	glutathione S-transferase kappa 1	1.51057	3.47E-13	3.03E-12
GSTM1	glutathione S-transferase M1	-0.36328	0.118578048	0.174308873
GSTM2	glutathione S-transferase M2 (muscle)	-0.44391	0.066643531	0.105518924
GSTM3	glutathione S-transferase M3 (brain)	-0.46982	0.152585565	0.216021207
GSTM4	glutathione S-transferase M4	0.13915	0.410160068	0.502020119
GSTM5	glutathione S-transferase M5	-2.31917	3.24E-09	1.89E-08
GSTO1	glutathione S-transferase omega 1	-0.58032	0.010010238	0.019319956
GSTP1	glutathione S-transferase pi	1.05925	1.15E-07	5.32E-07
GSTT1	glutathione S-transferase theta 1	-0.58343	0.206473415	0.280588538
GSTT2	glutathione S-transferase theta 2	0.20141	0.619455773	0.699640882

GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	0.58327	0.006987067	0.01393985
GTDC1	glycosyltransferase-like domain containing 1	-0.45505	3.70E-12	2.91E-11
GUCY1A2	guanylate cyclase 1, soluble, alpha 2	-0.04332	0.655959338	0.733131025
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-1.95722	4.61E-08	2.25E-07
GUCY1B3	guanylate cyclase 1, soluble, beta 3	-3.18454	5.61E-24	1.06E-22
GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	-0.02312	0.774667304	0.833279698
GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	-0.00734	0.916909395	0.943836354
GUCY2F	guanylate cyclase 2F, retinal	-0.03209	0.515792276	0.606805027
GUK1	guanylate kinase 1	-0.42919	0.0007742	0.001882714
GUSB	glucuronidase, beta	1.77966	1.52E-18	1.96E-17
GYG1	glycogenin 1	0.55347	0.00087685	2.11E-03
GYG2	glycogenin 2	0.84964	0.00480744	9.94E-03
GYS1	glycogen synthase 1 (muscle)	1.21844	5.83E-07	2.43E-06
GYS2	glycogen synthase 2 (liver)	-0.00902	0.846184213	0.890420552
H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0.29113	0.0008802	0.002117689
HAAO	3-hydroxyanthranilate 3,4-dioxygenase	-0.06889	0.507428908	0.600118074
HADH	hydroxyacyl-Coenzyme A dehydrogenase	0.65391	6.19E-05	1.83E-04
HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	0.49802	3.59E-06	1.33E-05
HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	0.54760	4.93E-07	2.07E-06
HAGH	hydroxyacylglutathione hydrolase	-1.38332	1.70E-19	2.34E-18
HAL	histidine ammonia-lyase	0.00935	0.923032395	0.94596999
HAO1	hydroxyacid oxidase (glycolate oxidase) 1	-0.10695	0.04833316	0.079685692
HAO2	hydroxyacid oxidase 2 (long chain)	-0.36900	2.22E-10	1.45E-09
HAS1	hyaluronan synthase 1	-0.37866	0.000724472	0.001776661
HAS2	hyaluronan synthase 2	1.28731	5.83E-05	1.74E-04

HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	-0.09786	0.554984201	0.643997078
HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	-0.46688	2.13E-07	9.50E-07
HCN4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	-0.00979	0.898006045	0.93079016
HDC	Histidine decarboxylase	0.01964	0.819211293	0.869251492
HEPH	hephaestin	-0.57707	0.01137148	2.17E-02
HEXA	hexosaminidase A (alpha polypeptide)	0.71157	2.54E-07	1.12E-06
HEXB	hexosaminidase B (beta polypeptide)	1.14930	7.96E-09	4.30E-08
HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)	-0.02238	0.883618052	0.919813364
HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	-0.17391	0.419849651	0.509889092
HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	0.60207	0.000256048	6.87E-04
HK1	hexokinase 1	-1.61989	6.30E-20	8.89E-19
HK2	hexokinase 2	1.48315	1.42E-15	1.47E-14
HK3	hexokinase 3 (white cell)	0.46555	0.010675909	2.05E-02
HKDC1	hexokinase domain containing 1	-0.08160	0.36293533	0.454619548
HLCS	holocarboxylase synthetase (biotin-(proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)) ligase)	0.26576	0.000554458	0.001402006
HMBS	hydroxymethylbilane synthase	1.16522	1.17E-11	8.80E-11
HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	0.46501	0.002851972	0.006181299
HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-1.06241	2.12E-06	8.14E-06
HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	-1.03090	6.66E-06	2.34E-05
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	-0.08079	0.543972484	0.633025793
HMOX1	heme oxygenase (decycling) 1	2.45895	5.74E-09	3.23E-08
HMOX2	heme oxygenase (decycling) 2	-0.88955	2.38E-14	2.26E-13
HNMT	histamine N-methyltransferase	0.84551	3.41E-07	1.46E-06
HPD	4-hydroxyphenylpyruvate dioxygenase	0.14278	0.404030878	0.495568142
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-0.04134	0.859289483	0.899091878

HPRT1	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	-1.95668	2.47E-12	1.99E-11
HPSE	heparanase	1.45469	2.56E-07	1.12E-06
HPSE2	heparanase 2	-0.35655	0.001294003	0.00302033
HS2ST1	heparan sulfate 2-O-sulfotransferase 1	0.48700	0.005333557	1.09E-02
HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0.35303	0.009797811	0.018970428
HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-4.21407	1.16E-33	3.81E-32
HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	1.08667	0.015411507	2.85E-02
HS3ST3B1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	0.11040	0.038871575	0.065745351
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	-0.21326	4.64E-05	0.000140397
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	-0.88527	0.000636089	1.58E-03
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	0.00155	0.987523027	0.992404505
HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	0.30458	0.048146181	0.079449015
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	1.38370	7.74E-21	1.17E-19
HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	0.93004	3.32E-06	1.24E-05
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-0.15456	0.319494078	0.409282584
HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	0.15798	0.357255494	0.44916538
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	0.01858	0.868599242	0.906500133
HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	0.13382	0.373752943	0.466159345
HSD17B4	Hydroxysteroid (17-beta) dehydrogenase 4	0.26882	0.029072838	0.050801027
HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	-1.43804	0.000404246	1.05E-03
HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	0.67800	4.68E-05	1.41E-04
HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	0.20928	0.417885314	0.508410905
HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	-0.10368	0.107526348	0.159330223
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	-0.34239	3.13E-08	1.57E-07
HSDL2	hydroxysteroid dehydrogenase like 2	0.76426	0.0022014	0.004901912

HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	-0.30090	0.011128236	0.021242914
HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	-0.39457	3.20E-10	2.08E-09
HYAL1	hyaluronoglucosaminidase 1	-0.10307	0.613741695	0.6955055
HYAL2	hyaluronoglucosaminidase 2	0.95995	2.58E-09	1.52E-08
HYAL3	hyaluronoglucosaminidase 3	-0.42214	2.65E-05	8.40E-05
HYAL4	hyaluronoglucosaminidase 4	-0.18898	0.000881878	0.002119218
HYI	hydroxypyruvate isomerase homolog (E. coli)	0.17836	0.165658729	0.231465515
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	2.20172	6.01E-35	2.18E-33
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.25323	0.145241866	0.207502961
IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	-0.96883	1.21E-07	5.56E-07
IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	-0.41818	0.002837799	0.006157146
IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	-0.43095	8.15E-06	2.80E-05
IDI1	isopentenyl-diphosphate delta isomerase 1	-1.43057	7.65E-11	5.29E-10
IDO1	indoleamine 2,3-dioxygenase 1	0.35129	0.26934902	0.353738086
IDS	iduronate 2-sulfatase (Hunter syndrome)	-1.72687	5.05E-20	7.18E-19
IDUA	iduronidase, alpha-L-	-0.22428	0.000970366	0.002310017
ILVBL	ilvB (bacterial acetolactate synthase)-like	0.78870	7.91E-06	2.73E-05
IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	-0.14861	0.413733571	0.504874159
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	0.90202	0.009119808	1.78E-02
IMPAD1	inositol monophosphatase domain containing 1	0.66952	0.000501934	1.28E-03
IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	-0.18941	0.215103808	0.291537361
IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	0.80977	1.12E-07	5.16E-07
INPP1	inositol polyphosphate-1-phosphatase	-0.67920	0.000169438	4.69E-04
INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	-1.41089	1.81E-76	2.83E-74
INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-1.08708	6.05E-09	3.38E-08

INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	-2.00631	3.89E-25	8.00E-24
INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	0.15675	0.056015202	0.090667918
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	0.52670	0.004839168	9.99E-03
INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	-0.25666	0.119011425	0.174819528
INPP5F	inositol polyphosphate-5-phosphatase F	-3.15406	9.55E-24	1.77E-22
INPP5J	inositol polyphosphate-5-phosphatase J	-0.71010	7.45E-16	7.97E-15
INPP5K	inositol polyphosphate-5-phosphatase K	-0.30003	0.001766327	0.004003281
INPPL1	inositol polyphosphate phosphatase-like 1	0.81584	1.39E-07	6.33E-07
IP6K1	inositol hexaphosphate kinase 1	-1.04030	4.33E-13	3.72E-12
IP6K2	inositol hexaphosphate kinase 2	-0.25806	0.089522913	0.136431845
IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	0.00648	0.947082935	0.964156037
ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-0.43137	0.009354577	0.0182513
ISYNA1	myo-inositol 1-phosphate synthase A1	0.39049	0.100564935	0.150219334
ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	0.86107	4.44E-12	3.46E-11
ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	-0.26509	0.000517129	0.001312513
ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	-3.12958	3.13E-61	3.35E-59
ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	0.01493	0.967569533	0.97766842
ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	0.59507	0.001385776	3.21E-03
ITPR1	Inositol 1,4,5-triphosphate receptor, type 1	-2.91978	6.14E-35	2.19E-33
ITPR2	inositol 1,4,5-triphosphate receptor, type 2	0.67063	0.004881572	1.01E-02
ITPR3	inositol 1,4,5-triphosphate receptor, type 3	0.26286	0.283368021	0.369050087
IVD	isovaleryl Coenzyme A dehydrogenase	0.35484	0.03063758	0.053054685
KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1	-0.44459	5.57E-05	0.000166738
KCNA10	potassium voltage-gated channel, shaker-related subfamily, member 10	-0.14790	0.011022759	0.021067886
KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2	-0.15176	0.012718672	0.02396391

KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	-0.93160	1.98E-19	2.69E-18
KCNA4	potassium voltage-gated channel, shaker-related subfamily, member 4	-0.78476	7.78E-20	1.09E-18
KCNA5	potassium voltage-gated channel, shaker-related subfamily, member 5	-0.79231	2.08E-09	1.23E-08
KCNA6	potassium voltage-gated channel, shaker-related, subfamily, member 6	-0.89896	7.89E-08	3.76E-07
KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-2.07847	1.57E-58	1.59E-56
KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	-2.41845	3.23E-90	1.31E-87
KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	-0.02612	0.759858318	0.81995327
KCNB1	potassium voltage gated channel, Shab-related subfamily, member 1	-3.23375	9.51E-18	1.14E-16
KCNB2	potassium voltage gated channel, Shab-related subfamily, member 2	-0.84950	3.45E-36	1.32E-34
KCNC1	potassium voltage gated channel, Shaw-related subfamily, member 1	-2.76458	5.68E-56	4.82E-54
KCNC2	potassium voltage gated channel, Shaw-related subfamily, member 2	-0.29215	0.000275096	0.000733949
KCNC3	potassium voltage gated channel, Shaw-related subfamily, member 3	-0.06848	0.285452347	0.371051548
KCNC4	potassium voltage gated channel, Shaw-related subfamily, member 4	-0.44974	6.91E-10	4.31E-09
KCND1	potassium voltage-gated channel, Shal-related family, member 1	0.02547	0.851098105	0.893804593
KCND2	potassium voltage-gated channel, Shal-related family, member 2	0.24568	0.660480825	0.737373705
KCND3	potassium voltage-gated channel, Shal-related family, member 3	-0.55821	2.30E-05	7.34E-05
KCNE1	potassium voltage-gated channel, Isk-related subfamily, member 1	-0.05259	0.408231028	0.499960048
KCNE1L	potassium voltage-gated channel, Isk-related family, member 1-like	0.06873	0.855540277	0.89701567
KCNE2	potassium voltage-gated channel, Isk-related subfamily, gene 2	-0.18520	0.007507751	0.014876469
KCNE4	potassium voltage-gated channel, Isk-related subfamily, gene 4	1.19251	0.000431462	1.11E-03
KCNF1	potassium voltage-gated channel, subfamily F, member 1	-1.11329	0.003732729	7.88E-03
KCNG1	potassium voltage-gated channel, subfamily G, member 1	-1.11382	8.24E-13	6.86E-12
KCNG2	potassium voltage-gated channel, subfamily G, member 2	0.00132	0.980090908	0.988355563
KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member 1	-0.79705	1.06E-20	1.58E-19
KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0.15136	0.453491051	0.545853942

KCNH4	potassium voltage-gated channel, subfamily H (eag-related), member 4	-0.20849	0.001689531	0.003850691
KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	-0.27819	7.02E-06	2.45E-05
KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	-0.18302	0.00034893	0.000917691
KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	-0.32180	0.150762403	0.214011235
KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	-0.40262	1.46E-06	5.76E-06
KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	-0.37494	7.95E-05	0.000232289
KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	0.09336	0.102345506	0.152431073
KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	-0.06821	0.716781257	0.783871057
KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	0.19989	0.764875475	0.823618559
KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	-0.48344	0.082669394	0.127904778
KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	-1.92447	2.62E-86	8.87E-84
KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	-2.37350	1.89E-63	2.40E-61
KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	-0.08618	0.138222074	0.199861647
KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6	-3.07847	8.55E-37	3.70E-35
KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	0.92662	0.002541321	0.005591456
KCNJ9	potassium inwardly-rectifying channel, subfamily J, member 9	-0.82050	5.39E-28	1.27E-26
KCNK1	potassium channel, subfamily K, member 1	-4.32543	1.99E-21	3.16E-20
KCNK10	potassium channel, subfamily K, member 10	-1.52620	1.43E-12	1.17E-11
KCNK12	potassium channel, subfamily K, member 12	-2.23950	3.41E-41	1.88E-39
KCNK13	potassium channel, subfamily K, member 13	-0.08858	0.067999907	0.107415549
KCNK15	potassium channel, subfamily K, member 15	-0.25489	0.002096076	0.004682772
KCNK2	potassium channel, subfamily K, member 2	-0.22918	0.170629612	0.236946722
KCNK3	potassium channel, subfamily K, member 3	-2.40622	7.09E-19	9.42E-18
KCNK5	potassium channel, subfamily K, member 5	0.04482	0.720198966	0.786339687
KCNK7	potassium channel, subfamily K, member 7	-0.02237	0.743145263	0.806197609

KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	-2.66763	9.00E-25	1.83E-23
KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	1.08487	0.001197176	2.81E-03
KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	-0.71975	2.12E-05	6.80E-05
KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	0.42859	0.001650166	3.77E-03
KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	-1.29424	3.52E-07	1.51E-06
KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	-1.98934	5.32E-63	6.36E-61
KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	-0.23799	0.617225752	0.698286007
KCNN3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	0.09771	0.793739408	0.846183648
KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	-0.18739	0.442252911	0.533907463
KCNQ1	potassium voltage-gated channel, subfamily Q, member 1	-0.07934	0.315736865	0.405235509
KCNQ2	potassium voltage-gated channel, subfamily Q, member 2	0.62003	0.105321459	1.56E-01
KCNQ3	potassium voltage-gated channel, subfamily Q, member 3	-0.94338	6.85E-22	1.11E-20
KCNQ4	potassium voltage-gated channel, subfamily Q, member 4	-0.20279	0.001443394	0.003330784
KCNS1	K+ voltage-gated channel, subfamily S, 1	-1.92274	2.13E-38	9.63E-37
KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	-0.52672	0.096263937	0.145073821
KCNV1	potassium channel, subfamily V, member 1	-3.01472	8.74E-86	2.22E-83
KCNV2	potassium channel, subfamily V, member 2	-0.06303	0.14187948	0.203664561
KCTD12	potassium channel tetramerisation domain containing 12	0.79157	0.014534525	2.70E-02
KCTD13	potassium channel tetramerisation domain containing 13	-1.27877	9.10E-08	4.25E-07
KCTD14	potassium channel tetramerisation domain containing 14	0.69269	0.012029389	2.28E-02
KCTD15	potassium channel tetramerisation domain containing 15	-0.26276	0.064707277	0.102613022
KCTD17	potassium channel tetramerisation domain containing 17	-0.73722	1.82E-10	1.21E-09
KCTD2	potassium channel tetramerisation domain containing 2	-0.73204	8.52E-08	4.02E-07
KCTD20	potassium channel tetramerisation domain containing 20	0.21680	0.188851419	0.259065409
KCTD3	potassium channel tetramerisation domain containing 3	1.42068	1.52E-10	1.01E-09

KCTD5	potassium channel tetramerisation domain containing 5	1.13431	4.49E-11	3.19E-10
KCTD7	potassium channel tetramerisation domain containing 7	0.02008	0.914659203	0.941997042
KCTD9	potassium channel tetramerisation domain containing 9	0.94226	2.53E-05	8.03E-05
KDSR	3-ketodihydrosphingosine reductase	0.15520	0.036646936	0.062293663
KHK	ketohexokinase (fructokinase)	-0.23629	0.005145867	0.010545915
KL	klotho	-0.47839	0.006722034	0.01350385
KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.41289	0.154180419	0.217824039
KYNU	kynureninase (L-kynurenine hydrolase)	0.75758	0.002599243	5.70E-03
L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.12178	0.268232839	0.352956221
LALBA	lactalbumin, alpha-	-0.02687	0.663275018	0.738888946
LARGE	like-glycosyltransferase	-1.27385	2.86E-58	2.77E-56
LBR	Lamin B receptor	1.96324	7.59E-26	1.64E-24
LCAT	lecithin-cholesterol acyltransferase	0.42962	0.001504161	3.45E-03
LCT	lactase	-0.15733	0.017902008	0.03275858
LDHA	lactate dehydrogenase A	0.44362	0.030126261	5.22E-02
LDHAL6B	lactate dehydrogenase A-like 6B	-0.03719	0.418132333	0.508410905
LDHB	lactate dehydrogenase B	-0.30871	0.01780874	3.26E-02
LDHC	lactate dehydrogenase C	-0.29625	0.002697649	0.005896879
LGSN	lens protein with glutamine synthetase domain	0.03275	0.824356225	0.87304085
LIAS	lipoic acid synthetase	-0.48229	0.011026184	0.021067886
LIPA	Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	0.22113	0.337936332	0.429390352
LIPC	lipase, hepatic	-0.14539	0.100656677	0.15024598
LIPE	lipase, hormone-sensitive	-0.16693	0.000752057	0.001839869
LIPF	lipase, gastric	-0.17140	0.004976395	0.010223657
LIPG	lipase, endothelial	0.80934	0.006059931	0.01228299

LIPT1	lipoyltransferase 1	0.59527	0.001877227	0.00422636
LNPEP	leucyl/cystinyl aminopeptidase	0.23509	0.041297479	0.069616729
LPCAT1	lysophosphatidylcholine acyltransferase 1	0.83819	2.69E-05	8.50E-05
LPCAT3	membrane bound O-acyltransferase domain containing 5	0.36736	0.000222461	6.05E-04
LPCAT4	lysophosphatidylcholine acyltransferase 4	-2.14540	4.97E-54	4.04E-52
LPGAT1	lysophosphatidylglycerol acyltransferase 1	-0.03063	0.887667237	0.923083117
LPIN1	lipin 1	-0.92926	7.64E-06	2.64E-05
LPIN2	lipin 2	-0.30966	0.057850462	0.093045878
LPL	lipoprotein lipase	2.68992	8.24E-08	3.90E-07
LPO	lactoperoxidase	-0.10497	0.198642054	0.270851305
LPPR2	lipid phosphate phosphatase-related protein type 2	-0.86795	1.55E-11	1.16E-10
LPPR4	plasticity related gene 1	-2.70484	1.51E-09	9.06E-09
LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	-0.13496	0.150257548	0.213617899
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	-0.48985	1.58E-05	5.18E-05
LTA4H	leukotriene A4 hydrolase	0.09972	0.498608034	0.590029181
LTC4S	leukotriene C4 synthase	0.03321	0.875626303	0.912428639
LYPLA1	lysophospholipase I	1.83428	8.94E-20	1.24E-18
LYPLA2	lysophospholipase II	-0.10059	0.359265553	0.45113457
LYZ	lysozyme (renal amyloidosis)	2.86656	6.83E-08	3.28E-07
LYZL6	lysozyme-like 6	-0.07305	0.236904021	0.317276597
MAGT1	magnesium transporter 1	1.90516	4.06E-22	6.76E-21
MAN1A1	mannosidase, alpha, class 1A, member 1	-0.43814	0.092747171	0.140502979
MAN1A2	mannosidase, alpha, class 1A, member 2	0.21928	0.047334233	0.078299834
MAN1B1	mannosidase, alpha, class 1B, member 1	0.48323	0.00094266	0.002251972
MAN1C1	mannosidase, alpha, class 1C, member 1	0.23961	0.579221161	0.666793104

MAN2A1	mannosidase, alpha, class 2A, member 1	0.49541	0.057844954	0.093045878
MAN2A2	mannosidase, alpha, class 2A, member 2	-1.17704	3.94E-16	4.29E-15
MAN2B1	mannosidase, alpha, class 2B, member 1	1.95900	2.88E-20	4.18E-19
MAN2B2	mannosidase, alpha, class 2B, member 2	-0.61823	0.002726183	0.005933971
MAN2C1	mannosidase, alpha, class 2C, member 1	0.10657	0.542697036	0.632265372
MANBA	mannosidase, beta A, lysosomal	0.85597	2.50E-07	1.10E-06
MANEA	mannosidase, endo-alpha	1.04027	3.43E-08	1.71E-07
MAOA	monoamine oxidase A	-0.16534	0.588440779	0.675875765
MAOB	Monoamine oxidase B	-0.02749	0.960238068	0.972421759
MAT1A	methionine adenosyltransferase I, alpha	-0.19044	0.008054893	0.015821833
MAT2A	methionine adenosyltransferase II, alpha	0.79406	1.34E-05	4.42E-05
MAT2B	methionine adenosyltransferase II, beta	-0.23967	0.127492123	0.186200781
MBOAT2	membrane bound O-acyltransferase domain containing 2	-0.39848	0.099989723	0.149579917
MBOAT7	membrane bound O-acyltransferase domain containing 7	-1.44586	1.65E-35	6.10E-34
MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	-0.77975	8.82E-07	3.59E-06
MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	0.12862	0.444424519	0.535575013
MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.54293	2.98E-05	9.33E-05
MCOLN1	Mucolipin 1	0.24395	0.190053161	0.260187257
MCOLN3	Mucolipin 3	0.04720	0.707152411	0.775845036
MDH1	malate dehydrogenase 1, NAD (soluble)	-1.69076	5.06E-32	1.58E-30
MDH2	malate dehydrogenase 2, NAD (mitochondrial)	-0.56291	1.97E-05	6.32E-05
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	-1.98483	3.00E-06	1.13E-05
ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	0.12769	0.433354142	0.525035144
ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	-1.33421	7.49E-13	6.34E-12
MECR	mitochondrial trans-2-enoyl-CoA reductase	-0.58637	4.26E-07	1.80E-06

MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.21395	0.04971863	8.15E-02
MFSD1	Major Facilitator Superfamily Domain Containing 1	1.46952	7.60E-18	9.20E-17
MFSD10	Major Facilitator Superfamily Domain Containing 10	0.77311	5.64E-07	2.36E-06
MFSD11	Major Facilitator Superfamily Domain Containing 11	0.48733	0.000544222	1.38E-03
MFSD5	Major Facilitator Superfamily Domain Containing 5	0.56444	0.000144042	4.03E-04
MFSD7	Major Facilitator Superfamily Domain Containing 7	-0.07832	0.292666258	0.378974842
MFSD9	Major Facilitator Superfamily Domain Containing 9	0.23033	0.033070091	0.056592168
MGAM	maltase-glucoamylase (alpha-glucosidase)	0.12376	0.295069441	0.381843523
MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.01793	1.75E-09	1.05E-08
MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	0.76133	4.03E-06	1.47E-05
MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	-0.99456	1.90E-25	3.95E-24
MGAT4A	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	1.18585	2.26E-06	8.65E-06
MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	0.26293	0.229784523	0.308554778
MGAT4C	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	-0.39698	0.066595888	0.105518924
MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-0.61450	3.12E-11	2.26E-10
MGLL	monoglyceride lipase	-1.24578	1.84E-05	5.96E-05
MGST2	microsomal glutathione S-transferase 2	1.01221	2.85E-05	8.98E-05
MGST3	microsomal glutathione S-transferase 3	-1.19996	1.79E-15	1.82E-14
MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1	0.49475	0.019951552	0.036086748
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-2.61621	7.74E-21	1.17E-19
MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	-0.40472	0.089085193	0.135866615
MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	0.46399	0.017278721	0.031760976
MIP	Major intrinsic protein of lens fiber	-0.27598	3.13E-05	9.73E-05
MLYCD	malonyl-CoA decarboxylase	-0.02711	0.792627186	0.845441274
MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	-0.40612	0.012575488	0.023738131

MMADHC	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	0.58952	0.000160911	4.48E-04
MME	membrane metallo-endopeptidase	0.10544	0.713683529	0.78149974
MOCOS	molybdenum cofactor sulfurase	0.44220	0.109424532	1.62E-01
MOCS1	molybdenum cofactor synthesis 1	0.00859	0.939709815	0.958089295
MOCS2	molybdenum cofactor synthesis 2	-0.22138	0.239211942	0.320156601
MOCS3	molybdenum cofactor synthesis 3	-0.16046	0.116007199	0.17090046
MOGAT2	monoacylglycerol O-acyltransferase 2	-0.21082	0.0053667	0.010965327
MPI	mannose phosphate isomerase	-0.10272	0.460239992	0.551690981
MPO	myeloperoxidase	-0.15011	0.001831412	0.004141557
MPST	mercaptopyruvate sulfurtransferase	1.05133	3.33E-08	1.67E-07
MSRA	methionine sulfoxide reductase A	-0.52928	0.008724984	1.71E-02
MSRB2	methionine sulfoxide reductase B2	-0.93580	6.76E-08	3.26E-07
MTAP	methylthioadenosine phosphorylase	0.06083	0.439584891	0.531633601
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	0.55571	0.000228429	6.18E-04
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	2.82918	9.04E-22	1.45E-20
MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	-0.12096	0.560358645	0.649122009
MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	-0.34116	3.03E-07	1.31E-06
MTHFS	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	0.65878	0.000221115	6.02E-04
MTHFSD	methenyltetrahydrofolate synthetase domain containing	0.44144	3.20E-06	1.20E-05
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	0.41498	0.024109191	0.042919426
MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0.20457	0.101405708	0.151142085
MTTP	microsomal triglyceride transfer protein	0.51820	0.098242403	1.48E-01
MUT	methylmalonyl Coenzyme A mutase	0.05189	0.703275151	0.772842369
MVD	mevalonate (diphospho) decarboxylase	-0.02299	0.782821208	0.839290356
MVK	mevalonate kinase (mevalonic aciduria)	-0.39220	3.01E-05	9.40E-05

NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	-0.08554	0.560330591	0.649122009
NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	0.13246	0.145767599	0.207961774
NADK	NAD kinase	0.21464	0.055903207	0.090558741
NADSYN1	NAD synthetase 1	0.76968	1.08E-06	4.36E-06
NAGA	N-acetylgalactosaminidase, alpha-	1.10654	2.37E-11	1.72E-10
NAGK	N-acetylglucosamine kinase	0.38233	0.010722583	0.020545723
NAGLU	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)	0.49309	3.80E-09	2.19E-08
NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.24825	3.30E-16	3.63E-15
NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	0.41950	0.013464952	0.0251833
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.56509	8.04E-08	3.82E-07
NAT10	N-acetyltransferase 10	0.30055	0.024780913	0.044070054
NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	-0.13918	0.378817171	0.469594701
NAT6	N-acetyltransferase 6	-0.40577	0.000231892	0.000625247
NAT8	N-acetyltransferase 8	-0.10212	0.175802806	0.243134085
NAT8B	N-acetyltransferase 8B	-0.07033	0.213130897	0.289056113
NAT9	N-acetyltransferase 9	0.63421	2.36E-05	7.51E-05
NDOR1	NADPH dependent diflavin oxidoreductase 1	-0.15713	0.06727927	0.106359841
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-0.20399	0.015532919	0.02873378
NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	-0.62875	9.31E-06	3.16E-05
NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	-1.78911	6.76E-29	1.70E-27
NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	-0.29322	0.037731738	0.063923853
NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	-0.33107	0.006929947	0.013866716
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	-0.64991	2.40E-07	1.06E-06
NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	-0.00855	0.957793675	0.971303447
NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	0.08880	0.594264252	0.680258573

NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	-0.51224	0.002629183	0.005759838
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	-0.38831	0.004569108	0.00948825
NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	1.14748	0.000155676	4.35E-04
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	-0.02652	0.783619417	0.839356309
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	-0.20477	0.184880166	0.254821273
NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	0.38255	0.030862524	0.053353325
NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	-0.83192	7.40E-09	4.01E-08
NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	0.02357	0.882866881	0.919502239
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	-0.57405	5.82E-05	1.73E-04
NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-0.48095	0.000422689	0.001091902
NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	-0.06746	0.642905756	0.720919692
NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	-0.14364	0.258363242	0.342630444
NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	0.11079	0.402047653	0.493576617
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	-0.27281	0.022819842	0.040982985
NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 12kDa	-0.20569	0.069595497	0.109680345
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	0.11647	0.451504233	0.543784422
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	-0.11375	0.486425174	0.577629894
NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	0.10744	0.340644524	0.431752068
NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	-0.95072	2.44E-16	2.74E-15
NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	0.01449	0.894113431	0.928640313
NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	-0.08574	0.44209661	0.533907463
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	-0.54530	2.12E-07	9.49E-07
NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	-0.53794	4.52E-06	1.63E-05
NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	-0.35471	0.012562692	0.023736015
NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	-0.16486	0.332956811	0.424123557

NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	0.29212	0.023995509	0.042754487
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	-0.06810	0.689405485	0.760478215
NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	0.04237	0.782596026	0.839290356
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	-0.75292	6.41E-09	3.56E-08
NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	0.01348	0.919212527	0.943998273
NEU1	sialidase 1 (lysosomal sialidase)	0.82919	0.000115248	3.28E-04
NEU2	sialidase 2 (cytosolic sialidase)	-0.06603	0.312800888	0.402229098
NEU3	sialidase 3 (membrane sialidase)	-0.18054	0.000299256	0.000795277
NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	-0.44406	0.003382121	0.007192313
NIT1	nitrilase 1	-0.07067	0.567729639	0.655792248
NIT2	nitrilase family, member 2	0.08992	0.682656243	0.754260947
NME1	non-metastatic cells 1, protein (NM23A) expressed in	0.30660	0.104894732	0.155885227
NME3	non-metastatic cells 3, protein expressed in	0.44118	0.030689715	0.053099736
NME4	non-metastatic cells 4, protein expressed in	1.18873	9.40E-12	7.11E-11
NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	-1.30391	8.05E-05	2.34E-04
NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	1.00642	2.15E-11	1.58E-10
NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	0.37573	0.043178213	0.072247989
NMNAT2	nicotinamide nucleotide adenylyltransferase 2	-4.30971	1.27E-25	2.66E-24
NNMT	nicotinamide N-methyltransferase	3.03010	3.96E-06	1.45E-05
NNT	nicotinamide nucleotide transhydrogenase	-0.09042	0.644444764	0.722247081
NOS1	nitric oxide synthase 1 (neuronal)	-0.24996	7.44E-05	0.000217539
NOS2	Nitric oxide synthase 2 (inducible, hepatocytes)	0.20085	0.269801634	0.353875304
NOS3	nitric oxide synthase 3 (endothelial cell)	0.08810	0.153315655	0.216767419
NOX1	NADPH oxidase 1	-0.24499	0.019898925	3.60E-02
NOX3	NADPH oxidase 3	0.00740	0.898740978	0.93079016

NOX4	NADPH oxidase 4	1.47808	7.75E-07	3.20E-06
NOX5	NADPH oxidase, EF-hand calcium binding domain 5	-0.41949	2.07E-06	7.97E-06
NPC1	Niemann-Pick disease, type C1	0.13473	0.202070006	0.274972103
NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	-0.13338	0.028362375	0.049836394
NPC2	Niemann-Pick disease, type C2	1.86888	5.79E-13	4.95E-12
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	2.25179	2.22E-11	1.63E-10
NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	-0.21966	0.092027144	0.13951617
NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	-0.00446	0.972290968	0.981463525
NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	0.07793	0.732798928	0.797100171
NQO1	NAD(P)H dehydrogenase, quinone 1	-0.18290	0.626043658	0.705513723
NQO2	NAD(P)H dehydrogenase, quinone 2	-0.34172	0.093715202	0.141652792
NSDHL	NAD(P) dependent steroid dehydrogenase-like	0.02804	0.845012749	0.890109284
NT5C2	5'-nucleotidase, cytosolic II	0.15272	0.313597931	0.402999111
NT5DC2	5'-nucleotidase domain containing 2	2.15092	3.76E-13	3.25E-12
NT5DC3	5'-nucleotidase domain containing 3	-1.83193	1.48E-14	1.43E-13
NT5E	5'-nucleotidase, ecto (CD73)	0.91142	0.029166572	5.09E-02
NT5M	5',3'-nucleotidase, mitochondrial	-0.20068	0.166496812	0.232318475
NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	1.82887	9.19E-17	1.06E-15
NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	-1.67641	6.30E-06	2.22E-05
NUDT13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	0.04358	0.620383514	0.700299658
NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	0.24597	0.169092883	0.234973228
NUDT18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	-0.32034	0.009601915	0.018627474
NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-0.34502	0.174799081	0.242075295
NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.74217	0.000844012	0.002037858
NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	-0.38855	0.015784343	2.92E-02

NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-0.23823	0.282947865	0.368739109
NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0.00845	0.965825278	0.976391243
NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-0.18971	0.003497081	0.00741352
NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	-0.12839	0.278603157	0.364010424
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	1.20188	0.001456606	3.35E-03
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.48085	0.01837905	3.35E-02
OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	1.48042	1.45E-05	4.78E-05
OASL	2'-5'-oligoadenylate synthetase-like	0.43601	0.091249973	1.39E-01
OAT	ornithine aminotransferase (gyrate atrophy)	-1.14752	6.95E-11	4.87E-10
OCA2	Oculocutaneous albinism II (pink-eye dilution homolog, mouse)	-1.48626	4.14E-24	7.93E-23
ODC1	ornithine decarboxylase 1	1.24521	5.62E-08	2.73E-07
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-0.12642	0.518842481	0.608308399
OGDHL	oxoglutarate dehydrogenase-like	-2.42233	3.12E-24	6.09E-23
OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0.36975	0.009602358	0.018627474
OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.09331	0.376012752	0.467829819
OLAH	oleoyl-ACP hydrolase	0.12036	0.058356107	0.093710873
ORAI2	ORAI calcium release-activated calcium modulator 2	-0.16687	0.414460754	0.505155104
ORAI3	ORAI calcium release-activated calcium modulator 3	0.77890	9.84E-06	3.33E-05
OTC	ornithine carbamoyltransferase	0.05667	0.220724958	0.298360265
OXA1L	oxidase (cytochrome c) assembly 1-like	0.52483	0.001193466	2.80E-03
OXCT1	3-oxoacid CoA transferase 1	-1.54641	1.03E-15	1.09E-14
OXCT2	3-oxoacid CoA transferase 2	-0.59061	1.27E-12	1.04E-11
OXSM	3-oxoacyl-ACP synthase, mitochondrial	1.03865	9.27E-09	4.95E-08
P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	-0.28885	0.000307562	0.000816285
P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	-0.19035	0.001047024	0.002480886

P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3	-0.03372	0.430066249	0.521362364
P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	0.95612	2.07E-06	7.97E-06
P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-2.44764	1.59E-29	4.10E-28
P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	-0.27910	2.57E-05	8.16E-05
P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	0.49619	0.03767225	0.063876301
PAH	phenylalanine hydroxylase	-0.50834	0.000127173	0.000359586
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	1.56793	9.25E-09	4.95E-08
PAM	peptidylglycine alpha-amidating monooxygenase	0.37925	0.061369803	0.097854753
PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-0.35340	0.004210674	0.008815962
PANK3	pantothenate kinase 3	-0.26321	0.031175541	0.053848662
PANK4	pantothenate kinase 4	-0.50522	0.000618572	1.54E-03
PAOX	polyamine oxidase (exo-N4-amino)	-0.85030	3.93E-15	3.93E-14
PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-0.08601	0.538699345	0.628328037
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.01291	0.000148513	4.15E-04
PC	pyruvate carboxylase	-1.02542	8.66E-08	4.08E-07
PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	-0.28987	0.1892975	0.259502237
PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	-0.14628	0.142315651	0.203895503
PCCB	Propionyl Coenzyme A carboxylase, beta polypeptide	0.37687	0.049800229	0.081582486
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	-0.37567	0.097873267	0.147063083
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.66157	0.008092379	1.59E-02
PCTP	Phosphatidylcholine transfer protein	0.87072	4.06E-06	1.48E-05
PCYOX1	prenylcysteine oxidase 1	0.25050	0.228361629	0.30704973
PCYOX1L	prenylcysteine oxidase 1 like	-1.18576	9.86E-11	6.71E-10
PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	0.16423	0.144228281	0.206344894
PCYT1B	phosphate cytidylyltransferase 1, choline, beta	-0.26681	0.000262511	0.000702217

PCYT2	phosphate cytidylyltransferase 2, ethanolamine	-0.74598	8.74E-06	2.98E-05
PDE10A	phosphodiesterase 10A	0.06421	0.369161887	0.461282186
PDE11A	phosphodiesterase 11A	-0.03125	0.625013329	0.70474326
PDE12	2'-phosphodiesterase	-0.27748	3.74E-05	0.000114788
PDE1A	phosphodiesterase 1A, calmodulin-dependent	-3.25616	1.69E-28	4.05E-27
PDE1B	phosphodiesterase 1B, calmodulin-dependent	-0.95065	2.19E-30	5.94E-29
PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	-0.31442	0.037027208	0.062887481
PDE2A	phosphodiesterase 2A, cGMP-stimulated	-3.75366	3.99E-40	2.03E-38
PDE3A	phosphodiesterase 3A, cGMP-inhibited	-0.11700	0.058972422	0.094551211
PDE3B	phosphodiesterase 3B, cGMP-inhibited	-0.15506	0.205343898	0.279240231
PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	-0.31612	2.65E-06	1.01E-05
PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	0.54460	0.139861772	0.201658853
PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	-0.42022	2.37E-07	1.05E-06
PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	-0.04274	0.650289913	0.727995261
PDE5A	phosphodiesterase 5A, cGMP-specific	-0.03609	0.59213616	0.678969438
PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	-0.15328	0.040722421	0.068704301
PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)	0.00064	0.994654787	0.995393773
PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	-0.13279	0.01037787	0.019941597
PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	-0.14994	0.328585526	0.419343613
PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	-0.10363	0.227054549	0.306102055
PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	-0.20644	1.72E-05	5.61E-05
PDE7B	phosphodiesterase 7B	-0.17212	0.01325948	0.024844721
PDE8A	phosphodiesterase 8A	0.08901	0.654627946	0.732045442
PDE8B	phosphodiesterase 8B	-1.33875	0.000764042	1.86E-03
PDE9A	phosphodiesterase 9A	0.48756	0.031353428	0.054109948

PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	-0.82737	6.92E-11	4.87E-10
PDHA2	pyruvate dehydrogenase (lipoamide) alpha 2	-0.16106	0.006600828	0.013273475
PDHB	pyruvate dehydrogenase (lipoamide) beta	-0.27071	0.013671952	0.025546947
PDHX	pyruvate dehydrogenase complex, component X	-0.51453	0.000122768	3.48E-04
PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	0.57922	0.004398444	0.009152545
PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2	0.71908	3.13E-05	9.73E-05
PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	-0.62249	1.67E-05	5.46E-05
PECR	peroxisomal trans-2-enoyl-CoA reductase	0.28787	0.093356616	0.141215774
PEMT	phosphatidylethanolamine N-methyltransferase	0.28346	0.064497996	0.102360988
PFAS	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	0.32468	0.081127981	0.125807159
PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-0.06766	0.269298976	0.353738086
PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	0.16908	0.174302633	0.241552319
PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0.38226	0.144931698	0.207205445
PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0.10675	0.12534883	0.183202136
PFKL	phosphofructokinase, liver	0.23857	0.087077859	0.133204881
PFKM	phosphofructokinase, muscle	-0.96408	3.93E-07	1.67E-06
PFKP	phosphofructokinase, platelet	-1.54216	9.81E-11	6.69E-10
PGAM1	phosphoglycerate mutase 1 (brain)	-1.06060	1.61E-17	1.92E-16
PGAM2	phosphoglycerate mutase 2 (muscle)	0.36338	0.351025657	0.44360354
PGAP1	GPI deacylase	0.37087	0.151686265	0.215047543
PGD	phosphogluconate dehydrogenase	0.95800	4.18E-05	1.27E-04
PGK1	phosphoglycerate kinase 1	0.68988	0.010139075	1.95E-02
PGK2	phosphoglycerate kinase 2	-0.13817	0.021225123	0.038152675
PGLS	6-phosphogluconolactonase	1.23382	5.04E-18	6.22E-17
PGM1	phosphoglucomutase 1	0.32802	0.035952688	0.061164699

PGM3	phosphoglucomutase 3	0.92346	7.84E-07	3.23E-06
PGM5	phosphoglucomutase 5	-0.40923	1.00E-06	4.07E-06
PGS1	phosphatidylglycerophosphate synthase 1	-0.31262	0.011159892	0.021283358
PHGDH	phosphoglycerate dehydrogenase	0.02896	0.917835978	0.943998273
PHYH	phytanoyl-CoA 2-hydroxylase	-0.10580	0.662799857	0.738888946
PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	-0.73808	2.81E-13	2.46E-12
PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	-2.70169	2.63E-32	8.36E-31
PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	0.06357	0.689294549	0.760478215
PIGA	phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria)	0.43448	0.002315546	0.005139197
PIGB	phosphatidylinositol glycan anchor biosynthesis, class B	0.54170	0.017346981	0.031857644
PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	0.64852	0.001741853	3.96E-03
PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	0.76744	1.70E-06	6.62E-06
PIGG	phosphatidylinositol glycan anchor biosynthesis, class G	0.77475	1.01E-06	4.09E-06
PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	0.09225	0.601092185	0.68498902
PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	-0.03905	0.790417807	0.844413769
PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	0.21863	0.048622167	0.080039567
PIGN	phosphatidylinositol glycan anchor biosynthesis, class N	1.22847	7.78E-12	5.95E-11
PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	0.29490	0.013156081	0.024719081
PIGP	phosphatidylinositol glycan anchor biosynthesis, class P	-0.18816	0.319085737	0.40927527
PIGQ	phosphatidylinositol glycan anchor biosynthesis, class Q	-0.22021	0.005698709	0.011573901
PIGT	phosphatidylinositol glycan anchor biosynthesis, class T	0.76927	1.61E-07	7.24E-07
PIGV	phosphatidylinositol glycan anchor biosynthesis, class V	0.03718	0.801881108	0.853073936
PIGZ	phosphatidylinositol glycan anchor biosynthesis, class Z	-2.18856	3.68E-22	6.18E-21
PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	0.66247	0.001386253	3.21E-03
PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	-0.44972	0.13475085	0.195537815

PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	-0.13528	0.128222762	0.186923986
PIK3C3	phosphoinositide-3-kinase, class 3	0.46266	7.52E-11	5.22E-10
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	0.85115	0.001481008	0.003398296
PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	-0.61806	1.79E-08	9.21E-08
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	-0.13720	0.265457714	0.350211247
PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	0.15589	0.019194119	0.034934327
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-0.86548	0.002975751	6.42E-03
PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	-0.38293	0.000675722	0.001667163
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	-0.17581	0.314171107	4.03E-01
PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	0.01394	0.795129318	0.847221124
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5, p101	0.14334	0.08510515	0.130580203
PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	-1.22311	1.79E-09	1.07E-08
PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	-1.01768	1.23E-15	1.27E-14
PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	-1.17723	1.41E-06	5.59E-06
PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	-0.01131	0.934320504	0.954989233
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	-1.08829	3.96E-10	2.52E-09
PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	-1.56926	7.04E-18	8.58E-17
PIPOX	pipecolic acid oxidase	1.28281	0.009415777	1.84E-02
PISD	phosphatidylserine decarboxylase	-0.74980	2.33E-07	1.03E-06
PKD1	Polycystic kidney disease 1 (autosomal dominant)	-0.46682	3.00E-05	9.37E-05
PKD2	Polycystic kidney disease 2 (autosomal dominant)	0.74108	0.000157073	4.38E-04
PKD2L1	Polycystic kidney disease 2-like 1	-0.32245	0.000576824	0.001447241
PKLR	pyruvate kinase, liver and RBC	-0.08290	0.034299644	0.058548426
PLA1A	phospholipase A1 member A	-0.15650	0.394239768	0.48474789
PLA2G10	phospholipase A2, group X	-0.06362	0.615789303	0.697182001

PLA2G12A	phospholipase A2, group XIIA	0.78227	1.54E-06	6.03E-06
PLA2G15	phospholipase A2, group XV	-0.03776	0.791864208	0.845070832
PLA2G16	phospholipase A2, group XVI	-0.38234	0.157090385	0.221319994
PLA2G1B	phospholipase A2, group IB (pancreas)	0.01169	0.923573695	0.94596999
PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	2.10193	0.003653391	7.74E-03
PLA2G2D	phospholipase A2, group IID	0.14188	0.161198922	0.225911142
PLA2G2E	phospholipase A2, group IIE	-0.03928	0.511725457	0.604496138
PLA2G2F	phospholipase A2, group IIF	-0.22379	0.000565821	0.001423656
PLA2G3	phospholipase A2, group III	-0.43041	3.03E-06	1.14E-05
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1.67359	1.01E-05	3.40E-05
PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	-1.26748	1.92E-05	6.20E-05
PLA2G5	phospholipase A2, group V	0.76768	0.193699398	2.65E-01
PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	-0.84699	4.47E-15	4.45E-14
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.01551	0.952620582	0.968338822
PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	-1.29114	3.65E-19	4.88E-18
PLCB2	phospholipase C, beta 2	-0.11231	0.082159831	0.127213204
PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	0.19248	0.03185177	0.054691426
PLCB4	phospholipase C, beta 4	-1.13290	1.87E-05	6.05E-05
PLCD1	phospholipase C, delta 1	0.54688	0.016050332	0.029636989
PLCE1	Phospholipase C, epsilon 1	0.73639	0.00270044	0.005896879
PLCG1	phospholipase C, gamma 1	0.24594	0.083387064	0.128819074
PLCG2	Phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.63772	0.020578323	0.037055563
PLCH1	phospholipase C, eta 1	-0.42576	1.19E-15	1.24E-14
PLCH2	phospholipase C, eta 2	-0.56065	2.96E-10	1.93E-09
PLCL1	phospholipase C-like 1	-0.88286	0.000158615	4.42E-04

PLCL2	phospholipase C-like 2	-1.32164	3.71E-14	3.47E-13
PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	-0.74342	0.000701383	0.001724197
PLD1	phospholipase D1, phosphatidylcholine-specific	-0.05392	0.596328244	0.681853386
PLD2	phospholipase D2	0.20105	0.064184997	0.102023534
PLD3	phospholipase D family, member 3	-1.59763	1.08E-20	1.61E-19
PMM1	phosphomannomutase 1	-0.53546	0.003892455	0.008200375
PMM2	phosphomannomutase 2	0.80123	6.75E-06	2.36E-05
PMVK	phosphomevalonate kinase	-0.16589	0.297471257	0.384462216
PNLIP	pancreatic lipase	-0.34416	2.85E-05	8.98E-05
PNLIPRP1	pancreatic lipase-related protein 1	-0.27213	1.42E-09	8.58E-09
PNLIPRP2	pancreatic lipase-related protein 2	-0.15460	0.007620894	0.015042017
PNMT	phenylethanolamine N-methyltransferase	-0.84047	2.50E-13	2.21E-12
PNPLA2	patatin-like phospholipase domain containing 2	-0.23451	0.012130205	0.022982951
PNPLA3	patatin-like phospholipase domain containing 3	-0.37247	0.002905584	0.006284097
PNPLA4	patatin-like phospholipase domain containing 4	-0.53755	0.091265031	0.138567444
PNPLA6	patatin-like phospholipase domain containing 6	-0.71810	0.000683738	1.68E-03
PNPO	pyridoxamine 5'-phosphate oxidase	0.51863	0.00254084	0.005591456
POFUT1	protein O-fucosyltransferase 1	0.49794	4.20E-08	2.06E-07
POFUT2	protein O-fucosyltransferase 2	-0.00264	0.969083418	0.978711669
POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	0.56056	2.73E-05	8.63E-05
POMT1	protein-O-mannosyltransferase 1	-0.14300	0.416763398	0.507657273
POMT2	protein-O-mannosyltransferase 2	0.25380	0.008853141	0.017306188
PON1	paraoxonase 1	-0.19046	0.009985962	0.019297967
PON2	paraoxonase 2	0.73684	0.002128911	4.75E-03
PON3	paraoxonase 3	-0.10022	0.760914979	0.820657906

POR	P450 (cytochrome) oxidoreductase	0.60430	0.000105061	3.00E-04
PPA1	pyrophosphatase (inorganic) 1	-1.03747	1.03E-08	5.48E-08
PPA2	pyrophosphatase (inorganic) 2	0.15765	0.319878625	0.409517157
PPAP2A	phosphatidic acid phosphatase type 2A	0.17711	0.469934991	0.562317738
PPAP2B	phosphatidic acid phosphatase type 2B	-0.19573	0.480676192	0.572810492
PPAP2C	phosphatidic acid phosphatase type 2C	-0.17194	0.567366423	0.655745275
PPAT	phosphoribosyl pyrophosphate amidotransferase	0.54442	0.008033166	0.015794416
PPCDC	phosphopantothenoylcysteine decarboxylase	0.77991	1.62E-05	5.31E-05
PPCS	phosphopantothenoylcysteine synthetase	0.11863	0.521401828	0.610956725
PPOX	protoporphyrinogen oxidase	0.10654	0.515854208	0.606805027
PRDX1	peroxiredoxin 1	0.30629	0.047790341	7.90E-02
PRDX2	peroxiredoxin 2	0.09192	0.367312267	0.459253284
PRDX3	peroxiredoxin 3	0.00953	0.918488287	0.943998273
PRDX4	peroxiredoxin 4	2.17080	1.82E-26	4.12E-25
PRDX6	peroxiredoxin 6	0.60237	4.82E-05	1.45E-04
PRG2	plasticity-related gene 2	0.01444	0.852257049	0.894495911
PRODH	proline dehydrogenase (oxidase) 1	-1.23975	1.26E-05	4.20E-05
PRODH2	proline dehydrogenase (oxidase) 2	-0.25788	0.000849628	0.002048984
PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.10655	0.524949965	0.614406032
PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	0.09003	0.05683486	0.091921456
PRPS2	phosphoribosyl pyrophosphate synthetase 2	0.12807	0.627524352	0.706790586
PRPSAP1	Phosphoribosyl pyrophosphate synthetase-associated protein 1	-0.03844	0.759449533	0.819947372
PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	0.10595	0.540631224	0.63021977
PSPH	phosphoserine phosphatase	1.86375	4.18E-08	2.06E-07
PTDSS1	phosphatidylserine synthase 1	-0.41215	0.000444402	0.001142187

PTDSS2	phosphatidylserine synthase 2	0.07016	0.636809468	0.715267209
PTEN	phosphatase and tensin homolog	0.36901	0.031538322	0.054290109
PTER	phosphotriesterase related	-0.61616	0.041984257	0.070598838
PTGDS	prostaglandin D2 synthase 21kDa (brain)	-2.94405	3.79E-07	1.62E-06
PTGES	prostaglandin E synthase	-0.16638	0.377416407	0.468715672
PTGES2	prostaglandin E synthase 2	-1.01507	2.76E-18	3.48E-17
PTGES3	prostaglandin E synthase 3 (cytosolic)	0.40299	0.000916774	2.19E-03
PTGIS	prostaglandin I2 (prostacyclin) synthase	-0.06045	0.377883721	0.469009527
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1.50384	8.52E-05	0.000245749
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-0.05332	0.89877567	0.93079016
PTS	6-pyruvoyltetrahydropterin synthase	-0.66323	0.000576873	0.001447241
PYCR1	pyrroline-5-carboxylate reductase 1	0.30980	0.051544173	0.084022656
PYCRL	pyrroline-5-carboxylate reductase-like	0.07491	0.482737998	0.574899739
PYGB	phosphorylase, glycogen; brain	-0.18147	0.414135313	0.505061243
PYGL	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	2.78091	2.91E-18	3.65E-17
PYGM	phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	-1.55699	1.13E-09	6.94E-09
PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	0.00192	0.990606621	0.994520128
QDPR	quinoid dihydropteridine reductase	-1.41481	3.69E-10	2.37E-09
QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	0.37254	0.145750302	0.207961774
RBKS	ribokinase	-0.23523	0.200057591	0.27259858
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	0.05288	0.751322529	0.812467395
RDH14	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	-0.43489	0.000207328	5.67E-04
RDH16	retinol dehydrogenase 16 (all-trans)	-0.13316	0.161238105	0.225911142
RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	0.23750	0.137959549	0.199624031
RDH8	retinol dehydrogenase 8 (all-trans)	-0.26406	0.00014313	0.000401356

RENBP	renin binding protein	0.38424	0.032699223	0.056004651
RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.63021	0.000202055	5.54E-04
RFK	riboflavin kinase	-0.52162	0.000903323	2.16E-03
RHAG	Rh-associated glycoprotein	-0.07823	0.324534547	0.414694365
RHBG	Rh family, B glycoprotein	-0.37332	0.001452202	0.003346932
RHCG	Rh family, C glycoprotein	-0.41937	0.000351394	0.000920598
RPE	ribulose-5-phosphate-3-epimerase	0.41435	0.00156063	3.57E-03
RPE65	retinal pigment epithelium-specific protein 65kDa	1.29532	0.001995252	4.48E-03
RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	0.83417	8.43E-09	4.52E-08
RRM1	ribonucleotide reductase M1 polypeptide	1.45847	1.16E-10	7.81E-10
RRM2	ribonucleotide reductase M2 polypeptide	4.55601	1.61E-28	3.89E-27
RYR1	ryanodine receptor 1 (skeletal)	-0.76188	1.06E-08	5.61E-08
RYR2	ryanodine receptor 2 (cardiac)	-3.74688	4.38E-82	9.88E-80
RYR3	ryanodine receptor 3	-1.11150	0.031623783	5.43E-02
SARDH	sarcosine dehydrogenase	-0.17992	0.000140933	0.000396288
SAT1	spermidine/spermine N1-acetyltransferase 1	1.59802	2.70E-16	3.01E-15
SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	-0.66205	1.22E-08	6.32E-08
SCCPDH	saccharopine dehydrogenase (putative)	-0.13057	0.374151014	0.466369719
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-0.92460	9.78E-05	2.80E-04
SCD5	stearoyl-CoA desaturase 5	0.32119	0.154980508	0.218565166
SCLY	selenocysteine lyase	0.04641	0.593805196	0.680258573
SCN10A	sodium channel, voltage-gated, type X, alpha	-0.56716	7.85E-13	6.57E-12
SCN11A	sodium channel, voltage-gated, type XI, alpha	0.11798	0.042105848	0.070744784
SCN1A	sodium channel, voltage-gated, type I, alpha	-1.20185	0.001924462	4.33E-03
SCN1B	sodium channel, voltage-gated, type I, beta	-1.30614	9.31E-10	5.77E-09

SCN2A	sodium channel, voltage-gated, type II, alpha 1	-4.09831	3.18E-41	1.80E-39
SCN2B	sodium channel, voltage-gated, type II, beta	-0.91010	3.67E-50	2.87E-48
SCN3A	sodium channel, voltage-gated, type III, alpha	-0.86383	0.12194247	1.79E-01
SCN3B	sodium channel, voltage-gated, type III, beta	-5.31927	5.60E-32	1.70E-30
SCN4A	sodium channel, voltage-gated, type IV, alpha	-0.29353	4.15E-05	0.000126305
SCN5A	sodium channel, voltage-gated, type V, alpha	-0.41145	5.25E-06	1.87E-05
SCN7A	sodium channel, voltage-gated, type VII, alpha	-0.07930	0.46528186	0.557406024
SCN8A	sodium channel, voltage-gated, type VIII, alpha	-1.85169	1.95E-79	3.96E-77
SCN9A	sodium channel, voltage-gated, type IX, alpha	0.16170	0.390000431	0.481110968
SCNN1A	sodium channel, nonvoltage-gated, type I, alpha	-0.49286	5.74E-09	3.23E-08
SCNN1B	sodium channel, nonvoltage-gated 1 beta	0.21336	0.109455932	0.161835571
SCNN1D	sodium channel, nonvoltage-gated 1, delta	-0.09498	0.091355359	0.138601078
SCNN1G	sodium channel, nonvoltage-gated 1 gamma	0.02648	0.681284709	0.753974858
SCP2	sterol carrier protein 2	1.35987	2.16E-31	6.36E-30
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-0.33946	0.007616553	0.015042017
SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-0.00473	0.960463794	0.972421759
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	0.58854	6.02E-05	1.78E-04
SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	0.53946	5.58E-09	3.15E-08
SDR39U1	short chain dehydrogenase/reductase family 39U, member 1	-0.03606	0.836792821	0.884659285
SDS	serine dehydratase	-0.47545	0.060684471	0.096990014
SEPHS1	selenophosphate synthetase 1	0.45268	0.017428006	0.031948724
SEPHS2	selenophosphate synthetase 2	-0.08709	0.517387425	0.607406979
SFXN1	Sideroflexin 1	0.62263	0.000164398	0.000455964
SFXN3	Sideroflexin 3	-0.98517	4.40E-09	2.50E-08
SGMS1	sphingomyelin synthase 1	0.16541	0.484556922	0.57596262

SGPL1	sphingosine-1-phosphate lyase 1	1.08001	4.34E-09	2.48E-08
SGPP1	sphingosine-1-phosphate phosphatase 1	0.10311	0.690232874	0.760978
SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	0.63859	2.51E-06	9.55E-06
SHMT1	serine hydroxymethyltransferase 1 (soluble)	0.23939	0.000696278	0.001713721
SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.24612	3.22E-07	1.39E-06
SI	sucrase-isomaltase (alpha-glucosidase)	-0.08959	0.076377262	0.119167286
SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	-0.26795	3.52E-05	0.000108141
SLC10A2	solute carrier family 10, member 2	-0.12359	0.086091524	0.13194741
SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0.63605	0.000373095	0.000972439
SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.69374	4.00E-05	1.22E-04
SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-0.03854	0.796934266	0.848652539
SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	-0.05630	0.267037772	0.351839139
SLC12A2	solute carrier family 12, member 2	0.12214	0.47213973	0.564623572
SLC12A3	solute carrier family 12, member 3	-0.05099	0.392671369	0.483232986
SLC12A4	solute carrier family 12, member 4	0.02435	0.619272989	0.699640882
SLC12A5	solute carrier family 12, member 5	-5.44219	3.26E-38	1.44E-36
SLC12A6	solute carrier family 12, member 6	-0.46863	1.25E-07	5.73E-07
SLC12A7	solute carrier family 12, member 7	0.19961	0.359177441	0.45113457
SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	-0.66683	0.004664512	0.009676482
SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.69030	1.93E-09	1.15E-08
SLC13A1	solute carrier family 13 (sodium/sulphate symporters), member 1	-0.06583	0.168229424	0.233933255
SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	-0.00798	0.918896831	0.943998273
SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-0.92653	2.66E-09	1.56E-08
SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	-1.30497	1.03E-15	1.09E-14
SLC14A1	solute carrier family 14 (urea transporter), member 1	0.50075	0.262723055	0.347505511

SLC14A2	solute carrier family 14 (urea transporter), member 2	-0.19213	0.029142458	0.050853894
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	-0.11311	0.057299257	0.092389675
SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	-0.16394	0.585659831	0.673442554
SLC15A3	solute carrier family 15, member 3	0.89216	5.74E-05	1.71E-04
SLC16A1	solute carrier family 16 (monocarboxylic acid transporters), member 1	2.15998	2.95E-20	4.26E-19
SLC16A10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0.56275	0.074185776	0.116104452
SLC16A2	solute carrier family 16 (monocarboxylic acid transporters), member 2	0.03501	0.863238085	0.902294615
SLC16A3	solute carrier family 16 (monocarboxylic acid transporters), member 3	0.60590	0.000471826	1.21E-03
SLC16A4	solute carrier family 16 (monocarboxylic acid transporters), member 4	2.26014	2.69E-11	1.95E-10
SLC16A5	solute carrier family 16 (monocarboxylic acid transporters), member 5	-0.01185	0.929665821	0.950709564
SLC16A6	solute carrier family 16 (monocarboxylic acid transporters), member 6	-0.10203	0.632291231	0.711274337
SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	-0.54076	0.017403289	3.19E-02
SLC16A8	solute carrier family 16 (monocarboxylic acid transporters), member 8	-0.39664	1.55E-06	6.07E-06
SLC17A1	solute carrier family 17 (sodium phosphate), member 1	0.01044	0.851158727	0.893804593
SLC17A2	solute carrier family 17 (sodium phosphate), member 2	-0.36562	7.75E-07	3.20E-06
SLC17A3	solute carrier family 17 (sodium phosphate), member 3	-0.02163	0.750555502	0.812467395
SLC17A4	solute carrier family 17 (sodium phosphate), member 4	-0.42716	2.83E-08	1.43E-07
SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	0.56513	0.002421315	0.005346268
SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	-3.44652	9.94E-23	1.74E-21
SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	-6.00159	9.65E-36	3.63E-34
SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	-0.00146	0.991829788	0.995256643
SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	-0.04866	0.51319734	0.605179926
SLC18A3	solute carrier family 18 (vesicular monoamine), member 3	-0.29929	0.003939704	0.008282749
SLC19A1	solute carrier family 19 (folate transporter), member 1	0.17490	0.006489593	0.013074754
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	1.06358	2.34E-07	1.04E-06

SLC19A3	solute carrier family 19 (sodium/hydrogen exchanger), member 3	-0.20798	0.043562609	0.072831236
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-1.43575	1.37E-06	5.42E-06
SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	-3.27877	8.66E-14	7.83E-13
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-0.41811	0.379290792	0.469895296
SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	-1.20487	5.12E-06	1.84E-05
SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	0.52089	0.007584547	0.015014005
SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	-1.44248	5.13E-34	1.74E-32
SLC1A7	solute carrier family 1 (glutamate transporter), member 7	-0.28310	1.18E-05	3.94E-05
SLC20A1	solute carrier family 20, member 1	-0.24939	0.305382492	0.393685863
SLC20A2	solute carrier family 20, member 2	0.34054	0.14217726	2.04E-01
SLC22A1	solute carrier family 22 (organic cation transporter), member 1	-0.30373	2.73E-09	1.60E-08
SLC22A11	solute carrier family 22 (organic anion/cation transporter), member 11	-0.10346	0.051203252	0.083611415
SLC22A13	solute carrier family 22 (organic cation transporter), member 13	-0.15780	0.013167507	0.024719081
SLC22A14	solute carrier family 22 (organic cation transporter), member 14	-0.09806	0.201799143	0.274787447
SLC22A17	solute carrier family 22 (organic cation transporter), member 17	-0.89495	5.93E-09	3.32E-08
SLC22A18	solute carrier family 22 (organic cation transporter), member 18	0.57677	0.048762559	0.080205731
SLC22A18AS	solute carrier family 22 (organic cation transporter), member 18 antisense	0.08519	0.472675743	0.564932266
SLC22A2	solute carrier family 22 (organic cation transporter), member 2	-0.31787	4.27E-06	1.55E-05
SLC22A3	solute carrier family 22 (organic cation transporter), member 3	-0.03823	0.751095681	0.812467395
SLC22A4	solute carrier family 22 (organic cation transporter), member 4	0.50788	0.060047184	0.096048622
SLC22A5	solute carrier family 22 (organic cation transporter), member 5	0.42247	0.028757802	0.050357116
SLC22A6	solute carrier family 22 (organic anion transporter), member 6	-0.25165	1.07E-05	3.60E-05
SLC22A7	solute carrier family 22 (organic anion transporter), member 7	-0.27998	2.71E-08	1.37E-07
SLC22A8	solute carrier family 22 (organic anion transporter), member 8	-0.49874	6.66E-09	3.69E-08
SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	-1.07456	9.05E-07	3.68E-06

SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	0.00825	0.869948234	0.907442155
SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	-1.46380	9.84E-37	4.17E-35
SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	-0.98318	0.012546154	2.37E-02
SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0.28795	0.023425601	0.04195969
SLC25A1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	0.79955	3.92E-05	1.20E-04
SLC25A10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	-0.20032	0.054778671	0.08894971
SLC25A11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	-0.51050	0.000731661	0.00179213
SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-1.62876	2.80E-22	4.74E-21
SLC25A13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	1.94952	3.48E-24	6.74E-23
SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	-1.40812	2.22E-20	3.28E-19
SLC25A15	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.06111	4.44E-06	1.61E-05
SLC25A16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	-0.14013	0.233404462	0.313002158
SLC25A17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	0.49827	0.000179646	0.000494879
SLC25A20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	1.07616	7.46E-06	2.59E-05
SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	-0.03916	0.667444491	0.74179308
SLC25A22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	-2.58043	3.88E-56	3.43E-54
SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	-0.98796	1.35E-06	5.36E-06
SLC25A24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	1.30085	2.84E-06	1.07E-05
SLC25A28	solute carrier family 25, member 28	-1.05173	7.09E-13	6.03E-12
SLC25A3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-0.33847	0.000414056	1.07E-03
SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	0.08441	0.023876404	0.042579587
SLC25A32	solute carrier family 25, member 32	0.11465	0.489679975	0.580816446
SLC25A36	solute carrier family 25, member 36	-0.39411	0.00686936	1.38E-02
SLC25A37	solute carrier family 25, member 37	0.06168	0.75732279	0.818085671
SLC25A38	solute carrier family 25, member 38	0.02867	0.842891424	0.888335026

SLC25A4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	-2.14164	1.21E-31	3.62E-30
SLC25A40	solute carrier family 25, member 40	-0.05317	0.667466579	0.74179308
SLC25A42	solute carrier family 25, member 42	-0.05463	0.271741963	0.356190464
SLC25A44	solute carrier family 25, member 44	-0.87978	8.90E-15	8.75E-14
SLC25A46	solute carrier family 25, member 46	-0.08932	0.590088591	0.67709077
SLC25A5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	0.32648	0.040269026	0.067995788
SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	-0.06085	0.707794898	0.776131083
SLC26A1	solute carrier family 26 (sulfate transporter), member 1	-0.15216	0.007827643	0.015405225
SLC26A10	solute carrier family 26, member 10	0.17345	0.476989828	0.569084695
SLC26A2	solute carrier family 26 (sulfate transporter), member 2	1.55134	8.88E-08	4.16E-07
SLC26A3	solute carrier family 26, member 3	-0.03860	0.456446037	0.54843664
SLC26A4	solute carrier family 26, member 4	-0.12226	0.284911381	0.370585309
SLC26A6	solute carrier family 26, member 6	0.17783	0.068849929	0.10867384
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	-1.16380	1.60E-10	1.06E-09
SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	1.38229	4.24E-06	1.54E-05
SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	-0.43920	0.045759768	0.076066729
SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	-0.08018	0.653106546	0.730746069
SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	-0.09975	0.141709401	0.203600856
SLC28A2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	-0.05215	0.277735476	0.363110111
SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	-0.10106	0.102893106	0.153134469
SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	0.36049	0.033211507	5.68E-02
SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	0.12502	0.417927272	0.508410905
SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	-0.48709	0.007382633	0.014642821
SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	0.12686	0.513117895	0.605179926
SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	2.33986	3.64E-10	2.34E-09

SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	-0.17687	0.003072484	0.006595946
SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	-0.04984	0.606055827	0.689100389
SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.32593	0.355801659	0.4478915
SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	0.03497	0.61111929	0.693593849
SLC2A5	solute carrier family 2 (facilitated glucose transporter), member 5	1.01315	0.005650667	1.15E-02
SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	-1.59946	5.45E-18	6.68E-17
SLC2A8	solute carrier family 2, (facilitated glucose transporter), member 8	-0.44748	0.000344022	0.000907131
SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	0.17845	0.110913472	0.163871431
SLC30A1	solute carrier family 30 (zinc transporter), member 1	0.06282	0.696808373	0.766564623
SLC30A10	solute carrier family 30, member 10	-0.67078	5.63E-05	0.000168255
SLC30A3	solute carrier family 30 (zinc transporter), member 3	-3.81993	9.53E-96	1.94E-92
SLC30A4	solute carrier family 30 (zinc transporter), member 4	0.12695	0.010016347	0.019319956
SLC30A5	solute carrier family 30 (zinc transporter), member 5	0.87253	6.90E-16	7.42E-15
SLC30A6	solute carrier family 30 (zinc transporter), member 6	-0.04953	0.319486914	0.409282584
SLC30A9	solute carrier family 30 (zinc transporter), member 9	-0.49447	5.93E-06	2.10E-05
SLC31A1	solute carrier family 31, member 1	0.80656	7.08E-07	2.94E-06
SLC31A2	solute carrier family 31, member 2	-0.39136	0.235717233	0.315895277
SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	1.20952	2.32E-14	2.22E-13
SLC34A1	solute carrier family 34 (sodium phosphate), member 1	-0.23843	8.30E-07	3.39E-06
SLC34A2	solute carrier family 34 (sodium phosphate), member 2	-0.05059	0.867665193	0.905990415
SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member 1	0.78751	8.08E-07	3.32E-06
SLC35A2	solute carrier family 35 (UDP-galactose transporter), member 2	0.47502	0.000600132	0.0015007
SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	0.86500	3.41E-07	1.46E-06
SLC35A5	solute carrier family 35, member A5	0.47541	0.004103222	8.61E-03
SLC35B1	solute carrier family 35, member B1	0.21594	0.062676017	0.099859203

SLC35C1	solute carrier family 35, member C1	-0.14962	0.174923049	0.242082068
SLC35C2	solute carrier family 35, member C2	0.45069	0.000502539	0.001278675
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	1.25450	1.31E-09	7.97E-09
SLC35D2	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D2	1.30926	1.54E-15	1.58E-14
SLC35E1	solute carrier family 35, member E1	0.33086	0.010254328	0.019722846
SLC35E3	solute carrier family 35, member E3	0.29849	0.329500285	0.420247227
SLC35F2	solute carrier family 35, member F2	1.33235	1.61E-06	6.30E-06
SLC35F5	solute carrier family 35, member F5	0.25180	0.04492173	0.074857276
SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	0.07702	0.695625775	0.765677965
SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-0.29300	0.039182691	0.066216467
SLC37A4	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	0.45459	0.000133974	3.78E-04
SLC38A1	solute carrier family 38, member 1	-1.27365	0.001984178	4.46E-03
SLC38A2	solute carrier family 38, member 2	0.30696	0.044770277	0.074666098
SLC38A3	solute carrier family 38, member 3	0.05046	0.776001048	0.833485446
SLC38A4	solute carrier family 38, member 4	0.04310	0.748808604	0.811043096
SLC38A6	solute carrier family 38, member 6	1.87298	5.54E-14	5.12E-13
SLC38A7	solute carrier family 38, member 7	-0.01225	0.936237021	0.956467269
SLC39A1	solute carrier family 39 (zinc transporter), member 1	1.28255	3.69E-16	4.03E-15
SLC39A14	solute carrier family 39 (zinc transporter), member 14	1.40960	1.30E-06	5.17E-06
SLC39A2	solute carrier family 39 (zinc transporter), member 2	-0.00439	0.957366639	0.971303447
SLC39A4	solute carrier family 39 (zinc transporter), member 4	-0.29799	0.381589168	0.472167241
SLC39A6	solute carrier family 39 (metal ion transporter), member 6	0.81879	8.75E-06	2.98E-05
SLC39A8	solute carrier family 39 (metal ion transporter), member 8	0.68584	0.004229798	8.84E-03
SLC39A9	solute carrier family 39 (zinc transporter), member 9	-0.08921	0.280323493	0.365787973
SLC3A1	solute carrier family 3, member 1	-0.89328	1.51E-18	1.96E-17

SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	1.11105	3.69E-09	2.13E-08
SLC41A3	solute carrier family 41, member 3	-1.13707	1.07E-15	1.12E-14
SLC43A1	solute carrier family 43, member 1	0.15600	0.167186305	0.233052468
SLC43A3	solute carrier family 43, member 3	1.55773	1.96E-11	1.44E-10
SLC44A1	solute carrier family 44, member 1	0.35453	0.239479393	0.320303688
SLC44A4	solute carrier family 44, member 4	0.00337	0.984288055	0.990132417
SLC45A2	solute carrier family 45, member 2	-0.12568	0.016359286	0.030180062
SLC46A3	solute carrier family 46, member 3	-0.08190	0.672232199	0.745173425
SLC47A1	solute carrier family 47, member 1	-0.21941	0.508024187	0.600472775
SLC4A1	solute carrier family 4 (anion exchanger), member 1	-0.38524	1.02E-05	3.44E-05
SLC4A10	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	-0.15037	7.05E-05	0.000206894
SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	-0.75576	6.99E-11	4.88E-10
SLC4A2	solute carrier family 4 (anion exchanger), member 2	1.50065	3.41E-12	2.70E-11
SLC4A3	solute carrier family 4 (anion exchanger), member 3	-1.67302	5.20E-09	2.94E-08
SLC4A4	solute carrier family 4 (anion exchanger), member 4	-0.40942	0.323396109	0.413499553
SLC4A5	solute carrier family 4 (anion exchanger), member 5	-0.06674	0.272865374	0.357432543
SLC4A7	solute carrier family 4 (anion exchanger), member 7	1.04663	2.40E-14	2.27E-13
SLC4A8	solute carrier family 4 (anion exchanger), member 8	-0.58479	0.001074877	2.54E-03
SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	-0.20261	0.099696858	0.149310973
SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	0.01471	0.841131179	0.886939671
SLC5A2	solute carrier family 5 (sodium/glucose cotransporter), member 2	-0.28862	4.80E-06	1.73E-05
SLC5A3	solute carrier family 5 (inositol transporters), member 3	0.31537	0.232533676	0.31204024
SLC5A4	solute carrier family 5, member 4a	0.00677	0.903867419	0.934195457
SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	-0.23404	0.003689705	0.007797474
SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	0.18928	0.227019019	0.306102055

SLC5A7	solute carrier family 5 (choline transporter), member 7	-0.31689	7.34E-05	0.000215023
SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	-2.01527	1.48E-05	4.88E-05
SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	-0.10302	0.375642511	0.467706404
SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	-0.58311	4.44E-07	1.87E-06
SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	-0.85811	1.83E-16	2.06E-15
SLC6A14	solute carrier family 6 (neurotransmitter transporter), member 14	-0.01919	0.926184754	0.948100574
SLC6A15	solute carrier family 6 (neurotransmitter transporter), member 15	-3.48869	1.39E-38	6.43E-37
SLC6A16	solute carrier family 6 (neurotransmitter transporter), member 16	-0.23170	0.045688179	0.076009876
SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	-0.06887	0.186280424	0.255883852
SLC6A20	solute carrier family 6 (neurotransmitter transporter), member 20	-0.47205	1.15E-05	3.87E-05
SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	-0.01480	0.873238818	0.910407445
SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	-0.27976	0.032028901	0.054949161
SLC6A5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	-0.12663	0.029625097	0.051520807
SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	-0.01562	0.7973076	0.848652539
SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	0.02816	0.686047705	0.757596407
SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0.37205	0.079663793	0.123914684
SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	0.27292	0.116484322	1.71E-01
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0.06715	0.443955223	0.53532679
SLC7A10	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10	-0.90245	1.87E-11	1.39E-10
SLC7A11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	-0.41656	0.229658751	0.308554778
SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-0.06652	0.476926328	0.569084695
SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	-0.52104	1.04E-25	2.21E-24
SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	-0.33595	0.240109602	0.320935451
SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-0.01670	0.914200376	0.941997042
SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	2.06926	2.60E-13	2.29E-12

SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	-0.33554	0.015024712	0.02784434
SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	0.25748	0.004237146	0.008844063
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	0.03090	0.516067827	0.606805027
SLC8A2	solute carrier family 8 (sodium/calcium exchanger), member 2	-4.03162	9.73E-94	6.59E-91
SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	-0.74571	2.96E-08	1.50E-07
SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-0.37014	9.63E-11	6.59E-10
SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	-0.14998	0.084608673	0.13021153
SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	0.11339	0.1549419	0.218565166
SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	-2.15860	3.86E-30	1.02E-28
SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), isoform 7	-0.27273	0.001305731	0.00304421
SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0.57010	6.49E-05	1.91E-04
SLCO1A2	solute carrier organic anion transporter family, member 1a2	-0.53131	0.000769849	0.001875531
SLCO1B1	solute carrier organic anion transporter family, member 1b1	-0.18539	0.001865665	0.004209652
SLCO1B3	solute carrier organic anion transporter family, member 1b3	-0.01173	0.902162457	0.932907566
SLCO1C1	solute carrier organic anion transporter family, member 1c1	-1.72654	0.00070382	1.73E-03
SLCO2A1	solute carrier organic anion transporter family, member 2a1	0.24493	0.370864292	0.462840458
SLCO2B1	solute carrier organic anion transporter family, member 2b1	0.63460	0.006495574	0.013074754
SLCO3A1	solute carrier organic anion transporter family, member 3a1	-0.82041	0.002997003	6.45E-03
SLCO4A1	solute carrier organic anion transporter family, member 4a1	0.08886	0.713844081	0.78149974
SLCO4C1	solute carrier organic anion transporter family, member 4C1	-0.28400	0.019588716	0.035557018
SLCO5A1	solute carrier organic anion transporter family, member 5A1	-0.13842	0.160988503	0.225872758
SLN	sarcolipin	-0.33322	0.631587575	0.710973167
SMOX	spermine oxidase	0.26370	0.091028762	0.138415462
SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	-0.21226	0.05534121	0.08971984
SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	0.28413	0.034505481	0.058850371

SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	-0.96384	2.87E-12	2.30E-11
SMPDL3A	Sphingomyelin phosphodiesterase, acid-like 3A	0.63198	0.013180267	0.024719081
SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	-0.09379	0.411763095	0.503448624
SMS	spermine synthase	0.93165	3.10E-05	9.66E-05
SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	2.59489	2.91E-26	6.44E-25
SOAT2	sterol O-acyltransferase 2	-0.09078	0.227322322	0.306259961
SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	-0.60887	3.52E-08	1.75E-07
SOD2	Superoxide dismutase 2, mitochondrial	2.58317	1.37E-10	9.19E-10
SOD3	superoxide dismutase 3, extracellular	-0.02608	0.919702	0.943998273
SORD	sorbitol dehydrogenase	0.83871	2.00E-05	6.44E-05
SPHK1	sphingosine kinase 1	0.76007	0.003063775	6.59E-03
SPHK2	sphingosine kinase 2	-0.39041	0.000325044	0.000860435
SPR	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	0.19014	0.302998914	0.391109074
SPTLC1	serine palmitoyltransferase, long chain base subunit 1	0.67814	1.95E-05	6.29E-05
SPTLC2	serine palmitoyltransferase, long chain base subunit 2	0.08534	0.581384695	0.668904971
SPTLC3	serine palmitoyltransferase, long chain base subunit 3	-0.31779	0.000559702	0.001411755
SQLE	Squalene epoxidase	-0.57008	0.011844612	2.25E-02
SQRDL	sulfide quinone reductase-like (yeast)	1.71442	2.69E-07	1.17E-06
SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	-0.97818	7.42E-06	2.58E-05
SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	-0.46241	1.98E-08	1.01E-07
SRD5A3	steroid 5 alpha-reductase 3	-0.15242	0.342467937	0.433252842
SRM	spermidine synthase	0.09027	0.611948577	0.693860266
SRR	serine racemase	0.35038	0.159740396	0.224276399
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	0.02606	0.899107289	0.93079016
ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	-0.26164	0.000608766	0.001520418

ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	0.02648	0.738939749	0.802491725
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	-0.35158	0.007702184	1.52E-02
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	0.37180	0.120096914	0.17615947
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	-0.06046	0.598444822	0.682956412
ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	0.31324	0.288851445	0.374781028
ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	0.31744	0.034642487	0.059034515
ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	-3.94159	2.42E-24	4.88E-23
ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	0.45855	0.084392787	0.129977679
ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-0.09320	0.18290195	0.252436975
ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	-1.04438	7.14E-19	9.42E-18
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0.30446	0.084848257	0.130481472
ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	-0.81951	0.030076161	0.052171361
STAR	steroidogenic acute regulatory protein	-0.96414	2.37E-20	3.47E-19
STARD13	StAR-related lipid transfer (START) domain containing 13	-1.39388	1.96E-11	1.44E-10
STARD3	StAR-related lipid transfer (START) domain containing 3	0.15711	0.051779755	0.084282019
STARD5	StAR-related lipid transfer (START) domain containing 5	0.26928	0.049022961	0.080568861
STARD7	StAR-related lipid transfer (START) domain containing 7	0.05203	0.604390378	0.687591291
STARD8	StAR-related lipid transfer (START) domain containing 8	0.09188	0.552051425	0.640959764
STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	0.09194	0.394379247	0.48474789
STS	steroid sulfatase (microsomal), isozyme S	-1.43511	1.46E-23	2.67E-22
SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	-0.53468	0.003322314	7.09E-03
SUCLG1	succinate-CoA ligase, alpha subunit	-0.16499	0.197487118	0.269457255
SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	2.10481	2.81E-26	6.27E-25
SULF1	sulfatase 1	0.68851	0.149285852	0.212682647
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	-0.92943	8.01E-05	2.34E-04

SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	-0.52143	0.001377882	3.20E-03
SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	-0.00397	0.977023242	0.985750993
SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	-0.00722	0.962068513	0.973561616
SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	-0.08739	0.441598967	0.533751903
SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	-0.03644	0.517027821	0.607406979
SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	-0.35066	0.000611089	0.001524348
SULT4A1	sulfotransferase family 4A, member 1	-3.32711	2.53E-46	1.90E-44
SUOX	sulfite oxidase	-0.52713	0.002485059	0.005479529
SV2A	Synaptic vesicle glycoprotein 2A	-2.43394	8.26E-12	6.27E-11
SV2B	Synaptic vesicle glycoprotein 2B	-5.95412	3.42E-40	1.83E-38
SV2C	Synaptic vesicle glycoprotein 2C	-2.66810	1.24E-30	3.47E-29
SYNJ1	synaptojanin 1	-1.99326	3.92E-40	2.03E-38
SYNJ2	synaptojanin 2	-0.33708	0.001849266	0.004177286
TALDO1	transaldolase 1	0.24327	0.059789374	0.095785498
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.86875	2.14E-12	1.73E-11
TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.30481	0.020528272	3.70E-02
TAT	tyrosine aminotransferase	-0.08309	0.133615586	0.194028919
TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	0.89509	0.000883417	2.12E-03
TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	1.30981	1.10E-06	4.41E-06
TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	-0.05037	0.604126242	0.687591291
TCN2	transcobalamin II; macrocytic anemia	0.66623	0.000375151	9.77E-04
TDO2	tryptophan 2,3-dioxygenase	0.84445	0.113382435	0.167154815
TF	transferrin	-1.34861	0.000310292	8.22E-04
TGDS	TDP-glucose 4,6-dehydratase	0.87801	3.22E-05	9.99E-05
TH	tyrosine hydroxylase	-0.01922	0.846824988	0.890633833

THNSL1	threonine synthase-like 1 (S. cerevisiae)	-0.28060	0.054867096	0.089022192
THNSL2	threonine synthase-like 2 (S. cerevisiae)	-0.25887	0.341219362	0.431949675
THTPA	Thiamine triphosphatase	-0.92862	2.20E-06	8.41E-06
TK1	thymidine kinase 1, soluble	0.90305	0.000207681	5.67E-04
TK2	thymidine kinase 2, mitochondrial	0.08241	0.532004222	0.621946281
TKT	transketolase (Wernicke-Korsakoff syndrome)	0.06448	0.7212153	0.786766446
TKTL1	transketolase-like 1	0.29881	0.286013351	0.371543222
TM7SF2	transmembrane 7 superfamily member 2	-0.52710	0.016739309	0.030825195
TMCO3	Transmembrane and coiled-coil domains 3	0.46661	0.002644315	5.79E-03
TMEM104	Transmembrane protein 104	0.21348	0.050792377	0.083073935
TMLHE	trimethyllysine hydroxylase, epsilon	-0.07721	0.480125801	0.572490178
TPCN1	two pore segment channel 1	-0.47996	0.026555663	0.046864291
TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	0.20335	0.25261323	0.33544265
TPI1	triosephosphate isomerase 1	-0.05783	0.701909708	0.771759024
TPK1	thiamin pyrophosphokinase 1	-0.05221	0.808280679	0.859432333
TPMT	thiopurine S-methyltransferase	-0.31264	0.020138051	0.036391695
TPO	thyroid peroxidase	-0.14371	0.016591726	0.030581123
TREH	trehalase (brush-border membrane glycoprotein)	-0.23940	1.51E-05	4.96E-05
TRPA1	transient receptor potential cation channel, subfamily A, member 1	-0.01139	0.866166719	0.904890514
TRPC1	transient receptor potential cation channel, subfamily C, member 1	-0.21031	0.291881366	0.378440572
TRPC3	transient receptor potential cation channel, subfamily C, member 3	-0.20301	0.02563864	0.045522581
TRPC4	transient receptor potential cation channel, subfamily C, member 4	-0.09934	0.263359139	0.348120371
TRPC5	transient receptor potential cation channel, subfamily C, member 5	-0.10463	0.028906878	0.050574599
TRPC6	transient receptor potential cation channel, subfamily C, member 6	0.21096	0.099736499	0.149310973
TRPC7	transient receptor potential cation channel, subfamily C, member 7	-0.07287	0.246926367	0.328750035

TRPM1	transient receptor potential cation channel, subfamily M, member 1	-0.20477	4.05E-06	1.48E-05
TRPM2	transient receptor potential cation channel, subfamily M, member 2	-0.70922	5.61E-07	2.35E-06
TRPM3	transient receptor potential cation channel, subfamily M, member 3	0.07952	0.43612446	0.527762516
TRPM4	transient receptor potential cation channel, subfamily M, member 4	-0.00772	0.949184816	0.965812177
TRPM6	transient receptor potential cation channel, subfamily M, member 6	-0.08881	0.127750574	0.186444305
TRPM8	transient receptor potential cation channel, subfamily M, member 8	0.03342	0.723048633	0.787758773
TRPV1	transient receptor potential cation channel, subfamily V, member 1	-0.55719	0.000132045	0.000372844
TRPV2	transient receptor potential cation channel, subfamily V, member 2	-0.01153	0.942855678	0.960333463
TRPV4	transient receptor potential cation channel, subfamily V, member 4	-0.05778	0.307381342	0.395760778
TRPV5	transient receptor potential cation channel, subfamily V, member 5	-0.33621	1.70E-07	7.66E-07
TRPV6	transient receptor potential cation channel, subfamily V, member 6	-0.15938	0.028741982	0.050357116
TST	thiosulfate sulfurtransferase (rhodanese)	0.04359	0.847692257	0.891084983
TSTA3	tissue specific transplantation antigen P35B	0.09363	0.515836234	0.606805027
TTYH1	Tweety homolog 1 (Drosophila)	-1.03864	0.057306139	9.24E-02
TXNRD1	Thioredoxin reductase 1	0.76832	0.000197876	5.43E-04
TXNRD2	Thioredoxin reductase 2	-0.01011	0.900832017	0.932005847
TXNRD3	Thioredoxin reductase 3	0.69127	8.02E-07	3.30E-06
TYMP	Thymidine phosphorylase	0.47524	0.010103509	1.95E-02
TYMS	thymidylate synthetase	1.59478	5.05E-18	6.22E-17
TYR	tyrosinase (oculocutaneous albinism IA)	-0.52924	1.31E-07	5.99E-07
TYRP1	tyrosinase-related protein 1	-1.76530	4.00E-20	5.73E-19
UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	0.11604	0.544454545	0.633224308
UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	0.87681	1.22E-05	4.07E-05
UCK2	uridine-cytidine kinase 2	0.63935	0.011536221	0.021939324
UCKL1	uridine-cytidine kinase 1-like 1	0.73626	4.62E-05	1.40E-04

UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	-0.05827	0.378265305	0.469196684
UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	1.25726	1.33E-05	4.40E-05
UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	-0.29792	7.59E-08	3.62E-07
UEVLD	UEV and lactate/malate dehyrogenase domains	1.25191	2.27E-19	3.08E-18
UGCG	UDP-glucose ceramide glucosyltransferase	0.44786	0.03378607	5.77E-02
UGDH	UDP-glucose dehydrogenase	1.79910	1.90E-13	1.70E-12
UGP2	UDP-glucose pyrophosphorylase 2	-1.02967	1.12E-08	5.86E-08
UGT2A3	UDP glucuronosyltransferase 2 family, polypeptide A3	0.01678	0.692040226	0.762557062
UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	-0.09504	0.112613597	0.166141831
UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	-0.05337	0.668511205	0.742262851
UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	-0.19212	0.150850025	0.214011235
UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	0.02768	0.680352936	0.753353769
UGT8	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	-1.21600	0.026907159	0.047420278
UMPS	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	1.36977	4.50E-15	4.46E-14
UPB1	ureidopropionase, beta	-0.17617	0.013397394	0.02508002
UPP1	uridine phosphorylase 1	1.66437	3.42E-06	1.27E-05
UQCRB	ubiquinol-cytochrome c reductase binding protein	-0.22405	0.047166255	0.078149142
UQCRC1	ubiquinol-cytochrome c reductase core protein I	-0.43244	0.002074548	4.64E-03
UQCRC2	ubiquinol-cytochrome c reductase core protein II	-0.43058	0.008447305	0.016544673
UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	-0.49513	0.000819424	1.99E-03
UQCRH	ubiquinol-cytochrome c reductase hinge protein	-0.20467	0.183935796	0.253691637
UQCRQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	0.23392	0.080416968	0.124895107
UROD	uroporphyrinogen decarboxylase	0.72084	2.17E-05	6.94E-05
UROS	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	-1.92620	4.82E-18	6.01E-17
UST	uronyl-2-sulfotransferase	1.02737	0.000135474	3.81E-04

UXS1	UDP-glucuronate decarboxylase 1	-0.20520	0.261625342	0.346504443
VDAC1	voltage-dependent anion channel 1	-0.80523	6.43E-06	2.27E-05
VDAC2	voltage-dependent anion channel 2	-0.47359	0.000619195	1.54E-03
VDAC3	voltage-dependent anion channel 3	-0.39585	0.026461076	0.046737939
VKORC1	vitamin K epoxide reductase complex, subunit 1	1.02785	7.15E-09	3.92E-08
WWOX	WW domain containing oxidoreductase	-0.39627	0.042953914	0.071931883
XDH	xanthine dehydrogenase	-0.39372	1.15E-06	4.60E-06
XYLB	xylulokinase homolog (H. influenzae)	-0.04888	0.296344804	0.383249992
XYLT1	xylosyltransferase I	-1.23979	0.000461647	1.18E-03
XYLT2	xylosyltransferase II	0.18098	0.11954258	0.175472971

Supplemental Table 2: Correlation between NNMT mRNA expression and DNA methylation signatures in TCGA GBM dataset

Name	Description	Correlation (Spearman)	p-val	FDR-adj. p-val
MEISSNER_BRAIN_ICP_WITH_H3K4ME3	> Genes with intermediate-CpG-density promoters (ICP) bearing histone H3 trimethylation mark at K4 (H3K4me3) in brain.	-0.3996792	4.7172E-22	3.5923E-21
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation mark at K4 (H3K4me2) and trimethylation mark at K27 (H3K27me3) in neural precursor cells (NPC).	-0.242976	1.1401E-08	2.625E-08
CHENG_IMPRINTED_BY_ESTRADIOL	> Genes whose CpG islands became hypermethylated in breast progenitor cells pre-exposed to estradiol [PubChem=5757].	-0.2970832	2.0042E-12	7.0862E-12
BIOCARTA_CARM1_PATHWAY	> Transcription Regulation by Methyltransferase of CARM1	-0.1905648	8.5596E-06	1.6296E-05
ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN	> Genes whose DNA is hyper-methylated in hepatocellular carcinoma (HCC) compared to normal liver.	-0.1381521	0.00131642	0.0022089
MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing histone H3 trimethylation marks at k4 (H3K4me3) and K27 ((H3K27me3) in neural precursor cells (NPC).	-0.1339581	0.00184598	0.00299594
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	> Genes down-regulated in PaCa44 and CFPAC1 cells (pancreatic cancer) after treatment with decitabine [PubChem=451668], a DNA hypomethylating agent similar to azacitidine [PubChem=9444].	-0.1134212	0.00845924	0.01268886
SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_IN_CANCER	> Genes bearing the H3K27me3 mark in normal cells; their DNA is methylated in cancer cells.	-0.1091441	0.01130067	0.01649228
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3	> Genes whose promoters display higher histone H3 trimethylation mark at K9 (H3K9me3) in hepatocellular carcinoma (HCC) compared to normal liver. combined UP & DN	-0.097933	0.02310346	0.03090868
TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA	> Genes with hypermethylated DNA in all four esophageal squamous cell carcinoma (ESCC) lines analyzed.	-0.0565184	0.19055743	0.23006324
LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED	> X chromosome and imprinted genes up-regulated in HeLa cells (cervical cancer) after knockdown of the MBD (methyl-CpG binding domain) proteins by RNAi.	-0.0471601	0.27486237	0.30922017
LOPES_METHYLATED_IN_COLON_CANCER	> Genes methylated aberrantly in HCT116 and Colo320 (colon cancer) cells. combined UP & DN	-0.0342108	0.42841973	0.46101688
HATADA_METHYLATED_IN_LUNG_CANCER_DN	> Genes with unmethylated DNA in lung cancer samples.	-0.0299747	0.48780967	0.51928126
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	> Genes whose promoters display lower histone H3 trimethylation mark at K9 (H3K9me3) in hepatocellular carcinoma (HCC) compared to normal liver.	-0.0200015	0.64343751	0.66354493
LOPES_METHYLATED_IN_COLON_CANCER_UP	> Genes methylated aberrantly in HCT116 and Colo320 (colon cancer) cells.	-0.0170452	0.6932342	0.70030802
MEISSNER_NPC_HCP_WITH_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing the H3K27 tri-methylation (H3K27me3) mark in neural precursor cells (NPC).	0.01829202	0.6720553	0.68591211
MEISSNER_NPC_ICP_WITH_H3K4ME3	> Genes with intermediate-CpG-density promoters (ICP) bearing histone H3 trimethylation mark at K4 (H3K4me3) in neural precursor cells (NPC).	0.02333873	0.58909209	0.61389597
HATADA_METHYLATED_IN_LUNG_CANCER	> Genes with hypermethylated DNA in lung cancer samples. combined UP & DN	0.02788018	0.51873462	0.54632689
HATADA_METHYLATED_IN_LUNG_CANCER_UP	> Genes with hypermethylated DNA in lung cancer samples.	0.03450262	0.42448827	0.46101688
MEISSNER_NPC_HCP_WITH_H3K4ME2	> Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation mark at K4 (H3K4me2) in neural precursor cells (NPC).	0.03473874	0.42132325	0.46101688
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3	> Genes whose promoters display higher levels of histone H3 trimethylation mark at K27 (H3K27me3) in hepatocellular carcinoma (HCC) compared to normal liver. combined UP & DN	0.03527158	0.41423172	0.46077461
LOPES_METHYLATED_IN_COLON_CANCER_DN	> Genes un-methylated aberrantly in HCT116 and Colo320 (colon cancer) cells.	0.04756462	0.27076157	0.30810799
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	> Genes whose promoters display lower levels of histone H3 trimethylation mark at K27 (H3K27me3) in hepatocellular carcinoma (HCC) compared to normal liver.	0.05184132	0.22996032	0.26783614
WEBER_METHYLATED_ICP_IN_FIBROBLAST	> Germline-specific genes with intermediate-CpG-density promoters (ICP) that are methylated in primary fibroblasts.	0.05423292	0.20914433	0.24649153
MEISSNER_NPC_ICP_WITH_H3_UNMETHYLATED	> Genes with intermediate-CpG-density promoters (ICP) that have no histone H3 methylation marks in neural precursor cells (NPC).	0.05943197	0.16865917	0.20613898
WEBER_METHYLATED_ICP_IN_SPERM_DN	> Unmethylated germline-specific genes with intermediate-CpG-density promoters (ICP) in sperm.	0.06299763	0.14449073	0.17880728
WEBER_METHYLATED_HCP_IN_SPERM_DN	> Unmethylated germline-specific genes with high-CpG-density promoters (HCP) in sperm.	0.06395481	0.13847674	0.17353414
MEISSNER_BRAIN_HCP_WITH_H3_UNMETHYLATED	> Genes with high-CpG-density promoters (HCP) that have no histone H3 methylation marks in brain.	0.1056689	0.01420095	0.02037528
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP	> Genes whose promoters display higher levels of histone H3 trimethylation mark at K27 (H3K27me3) in hepatocellular carcinoma (HCC) compared to normal liver.	0.11621766	0.00696468	0.01060775
MEISSNER_BRAIN_HCP_WITH_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing the H3K27 tri-methylation (H3K27me3) mark in brain.	0.22437009	1.4459E-07	3.0456E-07
HOQUE_METHYLATED_IN_CANCER	> Genes whose DNA was methylated both in primary tumors and across a panel of cancer cell lines.	0.22678134	1.0529E-07	2.266E-07
SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1B	> Genes with some basal expression and partially methylated promoters, up-regulated by the combination of TSA and decitabine [PubChem=5562;451668] in RKO cells (colorectal cancer).	0.24930283	4.5763E-09	1.105E-08
SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER	> Genes bearing H3K27me3 mark or whose promoters are bound by the polycomb proteins SUZ12 or EED [GeneID=23512;8726]; their DNA is methylated de novo in cancer.	0.26258695	6.1961E-10	1.7039E-09
MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED	> Genes with high-CpG-density promoters (HCP) that have no histone H3 methylation marks in neural precursor cells (NPC).	0.33695959	9.4603E-16	3.9024E-15
WEBER_METHYLATED_IN_COLON_CANCER	> Genes identified as hypermethylated in SW48 cells (colon cancer).	0.29426463	3.2998E-12	1.0889E-11
SUZUKI_RESPONSE_TO_TSA	> Genes up-regulated by TSA alone [PubChem=5562], with non-hypermethylated promoters, in RKO cells (colorectal cancer).	0.35602785	1.6019E-17	7.5519E-17
HELLER_SILENCED_BY_METHYLATION	> Genes up-regulated in at least one of three multiple myeloma (MM) cell lines treated with the DNA hypomethylating agent decitabine (5-aza-2'-deoxycytidine) [PubChem=451668]. combined UP & DN	0.34908999	7.2973E-17	3.141E-16
MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing bivalent histone H3 dimethylation mark at K4 (H3K4me2) and trimethlation mark at K27 (H3K27me3) in brain.	0.41368884	1.1744E-23	1.057E-22
MISSIAGLIA_REGULATED_BY_METHYLATION	> Genes up-regulated in PaCa44 and CFPAC1 cells (pancreatic cancer) after treatment with decitabine [PubChem=451668], a DNA hypomethylating agent similar to azacitidine [PubChem=9444]. combined UP & DN	0.36836	9.8502E-19	5.4176E-18
SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A	> Genes basally silent, with hypermethylated promoters, up-regulated by the combination of TSA and decitabine [PubChem=5562;451668] in RKO cells (colorectal cancer).	0.39456864	1.738E-21	1.1471E-20
MCGARVEY_SILENCED_BY_METHYLATION_IN_COLON_CANCER	> Genes silenced in HCT116 cells (colon cancer) by methylation of CpG islands in their promoters.	0.350426	5.4653E-17	2.4594E-16
HELLER_SILENCED_BY_METHYLATION_DN	> Genes down-regulated in at least one of three multiple myeloma (MM) cell lines treated with the DNA hypomethylating agent decitabine (5-aza-2'-deoxycytidine) [PubChem=451668].	0.36596578	1.7089E-18	8.9043E-18
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	> Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	0.35712023	1.2574E-17	6.2241E-17
WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER	> Genes silenced by DNA methylation in bladder cancer cell lines.	0.46517187	3.0635E-30	3.7911E-29
LOPEZ_MBD_TARGETS	> Genes up-regulated in HeLa cells (cervical cancer) after simultaneus knockdown of all three MBD (methyl-CpG binding domain) proteins MeCP2, MBD1 and MBD2 [GeneID=4204;4152;8932] by RNAi.	0.45178479	2.0315E-28	2.0112E-27
HELLER_SILENCED_BY_METHYLATION_UP	> Genes up-regulated in at least one of three multiple myeloma (MM) cell lines treated with the DNA hypomethylating agent decitabine (5-aza-2'-deoxycytidine) [PubChem=451668].	0.55152437	3.8289E-44	9.4766E-43
NOUSHMEHR_GBM_SILENCED_BY_METHYLATION	> Top 50 most differentially hypermethylated and down-regulated genes in proneural G-CIMP (a CpG island methylator phenotype) GBM (glyoblastoma multiforme) tumors.	0.58057938	8.4068E-50	2.7742E-48
MISSIAGLIA_REGULATED_BY_METHYLATION_UP	> Genes up-regulated in PaCa44 and CFPAC1 cells (pancreatic cancer) after treatment with decitabine [PubChem=451668], a DNA hypomethylating agent similar to azacitidine [PubChem=9444].	0.63398856	7.965E-62	3.9427E-60

Supplementary Table 3

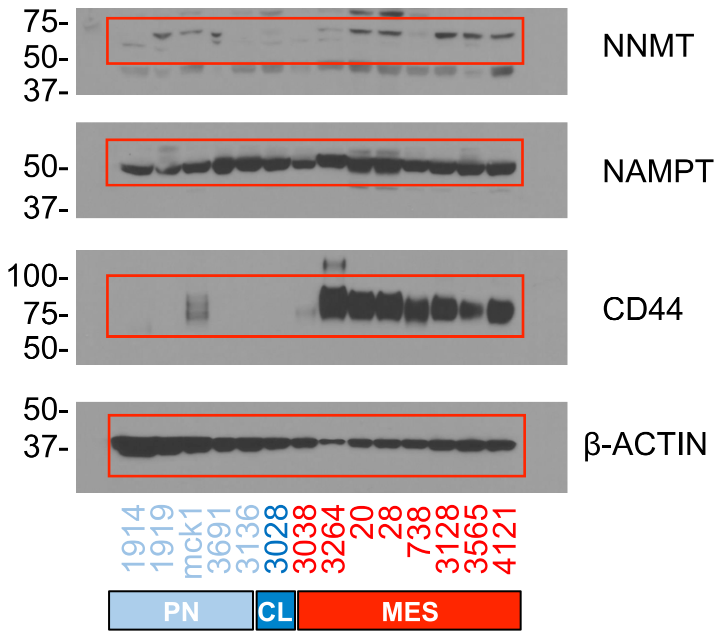
ChiP-PCR Primers

NNMT R1 FWD	CTTCTCCGGGAATTTCATCA
NNMT R1 REV	CTGCCCTCCTTCTCTTTCCT
NNMT R2 FWD	GTGGGAATGCACGAAAGAAT
NNMT R2 REV	CAGCTACTTGGGAGGCTGAG
NNMT R3 FWD	CTTGGCATCCTTCTCAAAGC
NNMT R3 REV	GACCATAAGGGCGTCACTGT
NAMPT R1 FWD	ACGCGCAGTTACTCACCTTT
NAMPT R1 REV	TCGGGAAAAGTCAAACCATC
NAMPT R2 FWD	CCAAGAGAACACAAGAGGAGGT
NAMPT R2 REV	TTGAAATCGAGCCAAGATCC
NAMPT R3 FWD	CAACGAGAACACCAGCTCAA
NAMPT R3 REV	GTATTGTCACGGTGGCTCCT
IL6 R1 FWD	TGCACTTTTCCCCCTAGTTG
IL6 R1 REV	GCCTCAGACATCTCCAGTCC
IL6 R2 FWD	AGAAGGACGCAGCACAAGAT
IL6 R2 REV	GAATGAAGAGGCTGGCTTTG
ASCL1 R1 FWD	CAAGAGAGCTTCACCCCAAG
ASCL1 R1 REV	CTCCATTCAGCTGGGTTTGT
ASCL1 R2 FWD	TTCACCCCAAGTCTTTCCAC
ASCL1 R2 REV	CTCCATTCAGCTGGGTTTGT

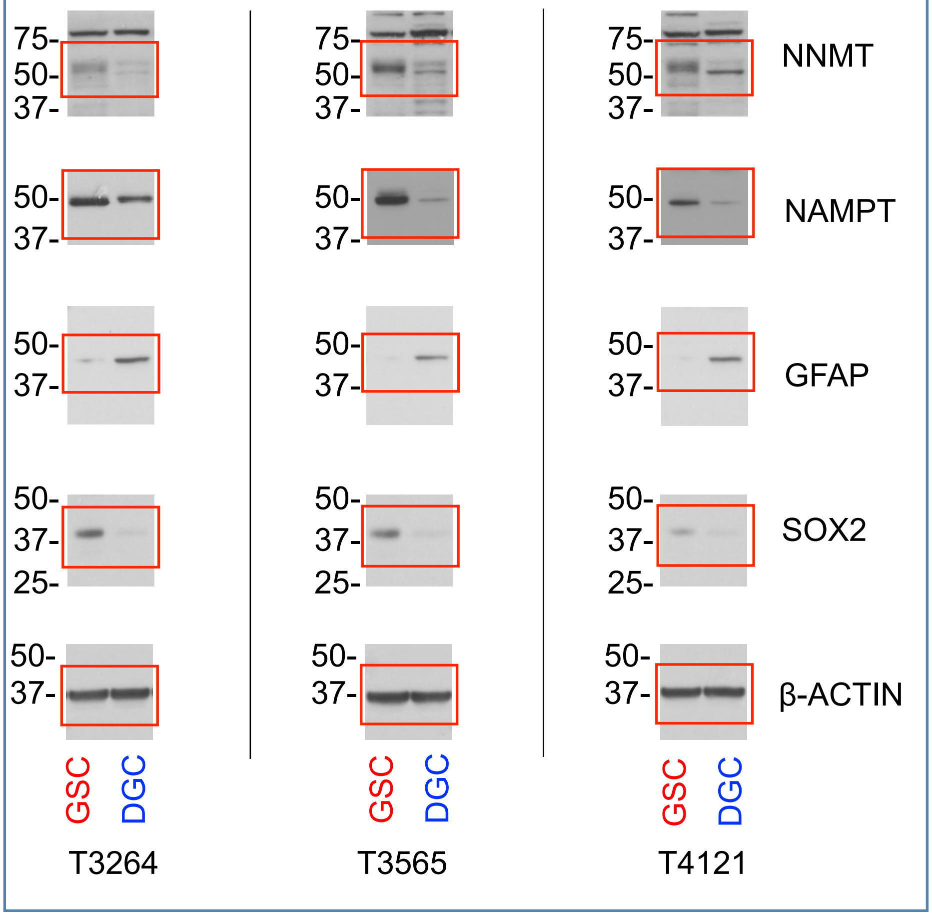
qMethyl PCR Primers

CTSZ_Reg1_F1	CCCAGGACGTGGTTTTGTAA
CTSZ_Reg1_R1	TTCCGGGAATGGTCATGG

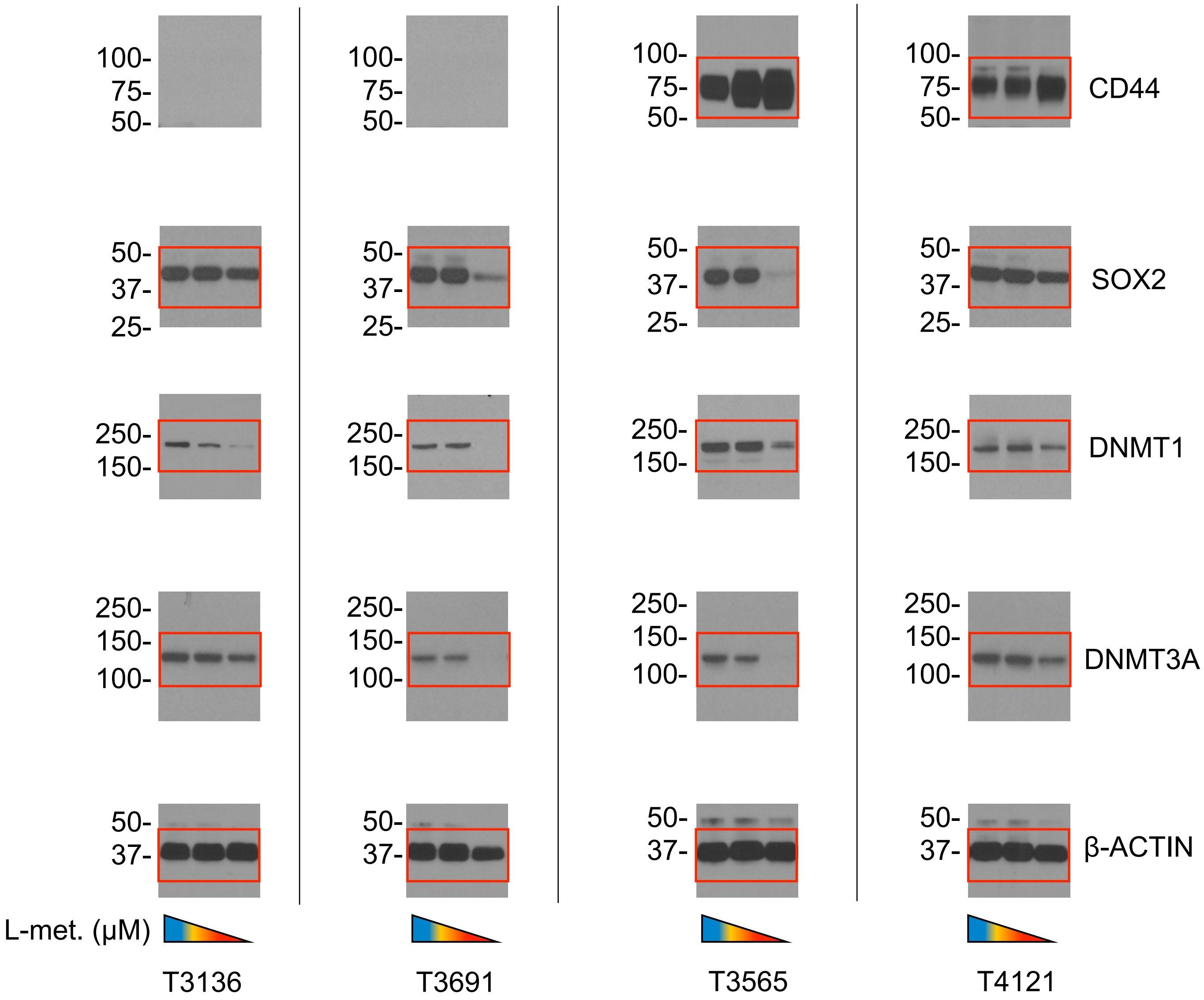
Full unedited gel for Figure 2I



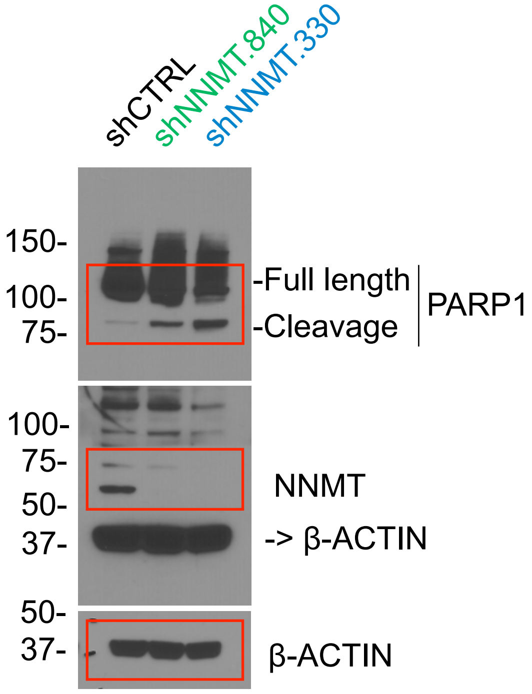
Full unedited gel for Figure 3A



Full unedited gel for Figure 4G



Full unedited gel for Figure 5D



Full unedited gel for Figure 6D