

Table S4Functional enrichment of the eight methylated genes signature.

Go analysis							
ID	Descriptor	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:000486	serine-type endopeptidase	95/17354	0.032404	0.072666	0.032206	DDX28	1 hsa00380
GO:000486	endopeptidase	173/17354	0.05835	0.081622	0.036176	DDX28	1 hsa00970
GO:006113	endopeptidase	179/17354	0.060322	0.081622	0.036176	DDX28	1 hsa00650
GO:003041	peptidase	182/17354	0.061307	0.081622	0.036176	DDX28	1 hsa00410
GO:006113	peptidase	218/17354	0.073054	0.086752	0.03845	DDX28	1 hsa00640
GO:000485	enzyme inhibitor	395/17354	0.129046	0.129046	0.057195	DDX28	1 hsa00250
GO:000486	triglyceride	21/17354	0.00724	0.054553	0.024179	TMED8	1 hsa00280
GO:001921	deacetylase	57/17354	0.019549	0.058596	0.025971	TMED8	1 hsa04727
GO:001623	lipase activity	123/17354	0.041786	0.075612	0.033512	TMED8	1
GO:001717	serine hydrolase	277/17354	0.092042	0.097155	0.043061	TMED8	1
GO:005108	unfolded protein	113/17354	0.038444	0.075612	0.033512	LOC15117	1
GO:000821	heparin binding	160/17354	0.054067	0.081622	0.036176	LOC15117	1
GO:000553	glycosaminoglycan	213/17354	0.07143	0.086752	0.03845	LOC15117	1
GO:190166	sulfur compound	232/17354	0.077589	0.089345	0.039599	LOC15117	1
GO:007188	14-3-3 protein	25/17354	0.008614	0.054553	0.024179	EFNB2	1
GO:000806	N-acetyltransferase	84/17354	0.028697	0.072666	0.032206	EFNB2	1
GO:001646	acetyltransferase	101/17354	0.034421	0.072666	0.032206	EFNB2	1
GO:001646	N-acyltransferase	101/17354	0.034421	0.072666	0.032206	EFNB2	1
GO:001674	transferase	218/17354	0.073054	0.086752	0.03845	EFNB2	1
GO:001674	transferase	254/17354	0.084679	0.094641	0.041946	EFNB2	1
GO:000216	aminoacyl-tRNA	12/17354	0.004142	0.054553	0.024179	GHRHR	1
GO:000486	aminoacyl-tRNA	43/17354	0.014777	0.058596	0.025971	GHRHR	1
GO:000004	tRNA binding	52/17354	0.017847	0.058596	0.025971	GHRHR	1
GO:001655	amino acid	58/17354	0.019889	0.058596	0.025971	GHRHR	1
GO:014011	catalytic activity	121/17354	0.041118	0.075612	0.033512	GHRHR	1
GO:001687	ligase activity	171/17354	0.057693	0.081622	0.036176	GHRHR	1
GO:003146	carboxylic acid	184/17354	0.061963	0.081622	0.036176	GHRHR	1
GO:004317	organic acid	185/17354	0.06229	0.081622	0.036176	GHRHR	1
GO:014009	catalytic activity	364/17354	0.119449	0.122677	0.054372	GHRHR	1
GO:000848	transaminase	21/17354	0.00724	0.054553	0.024179	SLC29A3	1
GO:001674	transferase	23/17354	0.007927	0.054553	0.024179	SLC29A3	1
GO:003017	pyridoxal phosphate	53/17354	0.018188	0.058596	0.025971	SLC29A3	1
GO:007027	vitamin B6	53/17354	0.018188	0.058596	0.025971	SLC29A3	1
GO:005155	iron-sulfur	63/17354	0.021588	0.058596	0.025971	SLC29A3	1
GO:005154	metal cluster	63/17354	0.021588	0.058596	0.025971	SLC29A3	1
GO:001984	vitamin binding	133/17354	0.045118	0.077931	0.03454	SLC29A3	1
GO:004803	cofactor binding	265/17354	0.088206	0.095767	0.042445	SLC29A3	1
GO:005266	carboxylic acid	140/17354	0.000949	0.036059	0.015982	TMED8/GH	2

KEGG analysis

Descriptor	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
Tryptophan	40/7528	0.015858	0.025346	NA	EFNB2	1
Aminoacyl	66/7528	0.026075	0.0298	NA	GHRHR	1
Butanoate	28/7528	0.011118	0.025346	NA	SLC29A3	1
beta-Alani	31/7528	0.012305	0.025346	NA	SLC29A3	1
Propanoat	32/7528	0.0127	0.025346	NA	SLC29A3	1
Alanine, as	35/7528	0.013885	0.025346	NA	SLC29A3	1
Valine, leu	48/7528	0.019009	0.025346	NA	SLC29A3	1
GABAergic	89/7528	0.035055	0.035055	NA	SLC29A3	1