Table 1: Genes with increased methylation in epilepsy and decreased methylation during adenosine treatment.

Gene; name	Accession #	Probes	KA-N $CH_3\downarrow$	KA-N $CH_3\uparrow$	Ado-KA $CH_3\downarrow$	Ado-KA $CH_3\uparrow$	KA $CH_3\uparrow$	Ado $CH_3\downarrow$
Adra2b; adrenoceptor alpha 2B	NM_138505	19	0	6	6	0	32%	32%
Alg14; UDP-N-acetylglucosaminyltransferase subunit	NM_001014176	20	0	5	5	0	25%	25%
B4galt2; UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide2	NM_001107965	20	0	7	9	0	35%	45%
Cald1; caldesmon 1	NM_013146	19	0	5	8	0	26%	42%
Cd14; Cluster of Differentiation 14 molecule	NM_021744	18	0	5	8	0	28%	44%
Chst12; carbohydrate (chondroitin 4) sulfotransferase 12	NM_001037775	18	0	8	9	0	44%	50%
Coq6; coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	NM_001011983	20	0	5	6	0	25%	30%
Ctbp2; C-terminal binding protein 2	NM_053335	20	0	5	8	0	25%	40%
Ctnnbl1; catenin, beta like 1	NM_001024870	18	0	5	5	1	28%	28%
Cul3; cullin 3	NM_001106923	20	0	5	5	1	25%	25%
Dbh; dopamine beta-hydroxylase (dopamine beta-monooxygenase)	NM_013158	20	0	6	17	0	30%	85%
Dnajc28; DnaJ (Hsp40) homolog, subfamily C, member 28	NM_001014124	20	0	6	5	0	30%	25%
Fam83a; family with sequence similarity 83, member A	NM_001130576	20	0	7	17	0	35%	85%
Fcgr2a; Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_053843	19	0	5	9	0	26%	47%
Ggt6; gamma-glutamyltransferase 6	NM_001002820	19	0	9	15	0	47%	79%
Gjb3; gap junction protein, beta 3	NM_019240	15	0	4	7	1	27%	47%
Gnb3; guanine nucleotide binding protein (G protein), beta polypeptide 3	NM_021858	20	0	7	10	0	35%	50%
Gpr20; G protein-coupled receptor 20	NM_022216	20	0	5	7	1	25%	35%
Gpr56; G protein-coupled receptor 56	NM_152242	20	0	5	18	0	25%	90%
H19; imprinted maternally expressed transcript (non-protein coding)	NR_027324	20	0	9	15	0	45%	75%
Hmha1; histocompatibility (minor) HA-1	NM_001108067	20	0	8	14	0	40%	70%
Kcna5; potassium voltage-gated channel, shaker-related subfamily, member 5	NM_012972	18	0	6	6	0	33%	33%
Kcnd1; potassium voltage-gated channel, Shal-related subfamily, member1	NM_001105748	20	0	8	14	0	40%	70%
Kcnj13; potassium inwardly-rectifying channel, subfamily J, member 13	NM_053608	20	1	6	9	0	30%	45%
Kntc1; kinetochore associated 1	NM_001107140	20	0	5	9	0	25%	45%
Krt17; keratin 17	NM_212545	20	0	13	16	0	65%	80%
Lamb2; laminin, beta 2	NM_012974	19	0	11	11	0	58%	58%
Lhb; luteinizing hormone beta polypeptide	NM_012858	11	0	5	3	0	45%	27%
LOC500797; gene conserved in amniota	NM_001109284	20	1	8	9	0	40%	45%
Matn1; matrilin 1, cartilage matrix protein	NM_001006979	19	0	5	7	2	26%	37%
Mrgprd; MAS-related GPR, member D	NM_001001506	17	0	6	8	0	35%	47%
Ndrg4; NDRG family member 4	NM_031967	20	0	9	6	0	45%	30%
Nudt5; nudix (nucleoside diphosphate linked moiety X)-type motif 5	NM_001007733	20	1	7	6	3	35%	30%
Olr804; olfactory receptor 804	NM_001000852	20	0	6	11	0	30%	55%
Otop2; otopetrin 2	NM_001105851	20	0	7	5	0	35%	25%
Pak7; p21 protein (Cdc42/Rac)-activated kinase 7	NM_001107781	20	0	5	6	0	25%	30%
Pold1; polymerase (DNA directed), delta 1, catalytic subunit	NM_021662	20	0	5	15	0	25%	75%
Polr1e; polymerase (RNA) I polypeptide E	NM_001107938	17	0	8	8	0	47%	47%
Prima1; proline rich membrane anchor 1	NM_001108721	20	0	7	7	0	35%	35%
Ptgds; prostaglandin D2 synthase 21kDa (brain)	NM_013015	20	0	5	11	0	25%	55%
Pycr1; pyrroline-5-carboxylate reductase 1	NM_001105857	19	0	5	14	0	26%	74%
Rassf7; Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	NM_001106317	20	0	5	7	0	25%	35%
RGD1305347; uncharacterized protein LOC362576	NM_001108674	20	0	5	12	0	25%	60%
RGD1563425; uncharacterized protein LOC498129	NM_001109059	17	0	5	5	0	29%	29%
Rps6kl1; ribosomal protein S6 kinase-like 1	NM_001106745	20	0	6	17	0	30%	85%
Rsrc2; arginine/serine-rich coiled-coil 2	NM_001014128	20	0	5	9	0	25%	45%
Selplg; selectin P ligand	NM_001013230	19	0	7	5	0	37%	26%
Slc16a10; solute carrier family 16, member 10 (aromatic amino acid transporter)	NM_138831	20	0	5	6	0	25%	30%
Slc24a6; solute carrier family 24 (sodium/lithium/calcium exchanger), member 6	NM_001017488	20	0	8	10	0	40%	50%
Slc46a2; solute carrier family 46, member 2	NM_001106652	20	0	5	10	0	25%	50%
Snrpn; small nuclear ribonucleoprotein polypeptide N	NM_031117	11	0	4	4	0	36%	36%
Stk35; serine/threonine kinase 35	NM_001107773	17	0	5	6	0	29%	35%
Sult1c2; sulfotransferase family, cytosolic, 1C, member 2	NM_133547	19	1	5	5	0	26%	26%
Sycn; syncollin	NM_139086	18	0	6	12	0	33%	67%
Tbxa2r; thromboxane A2 receptor	NM_017054	20	0	6	6	1	30%	30%
Tcirg1; T-cell, immune regulator 1	NM_199089	20	0	11	13	0	55%	65%
Tessp1; protease, serine, 41	NM_001135087	19	0	6	9	0	32%	47%
Tessp2; protease, serine, 42	NM_001106863	19	0	5	9	0	26%	47%
Tnni2; troponin I type 2 (skeletal, fast)	NM_017185	20	0	5	7	0	25%	35%
Tnxa; tenascin XA (pseudogene)	NR_024118	19	0	6	11	0	32%	58%
Txnip; thioredoxin interacting protein	NM_001008767	20	0	6	8	0	30%	40%
Tymp; thymidine phosphorylase	NM_001012122	20	0	5	5	1	25%	25%
Wisp1; WNT1 inducible signaling pathway protein 1	NM_031716	20	0	8	7	0	40%	35%
Znf524; zinc finger protein 524	NM_001108905	20	0	7	10	0	35%	50%
Znf541; zinc finger protein 541	NM_001107458	19	0	5	12	0	26%	63%
Znf710; zinc finger protein 710	NM_001134563	19	0	5	10	0	26%	53%

Table 1: Genes with increased methylation in epilepsy and decreased methylation during adenosine treatment. Individual targets from Fig. 6B that show increased methylation status (CH_3↑) in epilepsy (9 weeks after KA *vs.* naive control: 'KA-N') and decreased methylation status (CH_3↓) during adenosine treatment [(9 wk KA + 5 d Ado) *vs.* 9 wk KA: 'Ado-KA') are shown. For a complete list of targets please refer to Gene Expression Omnibus (tracking number 16742404). Column 1: gene symbols and names according to the HUGO Gene Nomenclature Committee; column 2: gene accession number according to the National Center for Biotechnology Information; column 3: number of different probes for each gene represented on the array; column 4: KA-N CH_3↓, number of probes with reduced methylation in epileptic *vs.* control rats; note that the majority of probes does not show reduced methylation in epilepsy; column 5: KA-N CH_3↑, number of probes with increased methylation in epilepsy; column 6: Ado-KA CH_3↓, number of probes with reduced methylation during adenosine treatment; column 7: Ado-KA CH_3↑, number of probes with increased methylation during adenosine treatment; note that the majority of probes does not show increased methylation during adenosine treatment; column 8: KA CH_3↑ percentage of probes with increased methylation in epilepsy; column 9: Ado CH_3↓ percentage of probes with reduced methylation during adenosine treatment.