

Epilepsia

Supporting Information

Genome-wide decrease in DNA methylation in adults with epilepsy treated with modified ketogenic diet: A prospective study.

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Table S1 Mean percentage change in seizure frequency after 12 weeks of dietary treatment (n = 49)

Mean percentage change in seizure frequency*	Number of patients (%)
Seizure freedom	0 (0%)
90 – 99.9% seizure reduction	1 (2.0%)
50 – 89.9% seizure reduction	8 (16.3%)
25 – 49.9% seizure reduction	11 (22.4%)
<25% seizure reduction	29 (59.2%)

*Mean percentage change in seizure frequency is calculated comparing the seizure frequency in week 5-12 of the intervention period to the seizure frequency in week 1-12 of the baseline period.

Table S2 Differentially methylated CpGs (sorted alphabetically by gene name and ascending by cgID for CpGs with no gene annotation) across all time points (n = 47)

cgID	Gene	Full gene name	Chr	Position	Gene context	CpG context	Mean beta			Δ beta			P-value	FDR
							B	4W	12W	4W-B	12W-B	12W-4W		
cg17828988	ANXA11	Annexin A11	10	81951504	5'UTR	OpenSea	0.725	0.699	0.696	-0.026	-0.029	-0.003	4.0E-06	0.038
cg14237301	APOB48R	Apolipoprotein B48 receptor	16	28506477	Body	N_Shelf	0.675	0.647	0.652	-0.028	-0.023	0.005	5.6E-06	0.043
cg18019618	ARHGEF28	Rho guanine nucleotide exchange factor 28	5	72964090	5'UTR	OpenSea	0.600	0.573	0.570	-0.027	-0.030	-0.003	2.7E-06	0.032
cg07380641	B4GALT5	Beta-1.4-galactosyltransferase 5	20	48295033	Body	OpenSea	0.509	0.477	0.478	-0.032	-0.031	0.001	1.2E-06	0.023
cg10077346	BCKDHB	Branched chain keto acid dehydrogenase E1 subunit beta	6	80920458	Body	OpenSea	0.748	0.716	0.728	-0.032	-0.020	0.012	2.1E-06	0.029
cg07397033	BLNK	B cell linker	10	98031201	5'UTR; 1stExon	OpenSea	0.573	0.555	0.547	-0.019	-0.027	-0.008	3.5E-06	0.035
cg04871807	C5orf27	NA	5	95186505	TSS1500	OpenSea	0.536	0.508	0.506	-0.028	-0.030	-0.002	3.3E-08	0.003
cg14928764	CD93	CD93 molecule	20	23064608	Body	OpenSea	0.821	0.799	0.796	-0.023	-0.026	-0.003	1.1E-07	0.004
cg20601482	CERS6	Ceramide synthase 6	2	169337576	Body	OpenSea	0.737	0.711	0.714	-0.026	-0.023	0.003	8.7E-07	0.019
cg08077617	CES1	Carboxylesterase 1	16	55868196	TSS1500	S_Shore	0.639	0.602	0.605	-0.037	-0.034	0.003	1.3E-06	0.024
cg02554361	CIITA	Class II major histocompatibility complex transactivator	16	11001757	Body	Island	0.912	0.902	0.902	-0.010	-0.009	0.001	4.5E-06	0.040
cg04075184	CLASP1	Cytoplasmic linker associated protein 1	2	122290763	Body	S_Shelf	0.744	0.732	0.718	-0.012	-0.025	-0.014	1.4E-06	0.025
cg08813944	CPSF4L	Cleavage and polyadenylation specific factor 4 like	17	71258589	TSS1500	OpenSea	0.746	0.721	0.715	-0.025	-0.031	-0.006	2.8E-06	0.033
cg19393755	CPSF4L	Cleavage and polyadenylation specific factor 4 like	17	71258101	TSS200	OpenSea	0.707	0.689	0.680	-0.018	-0.027	-0.009	4.4E-06	0.040
cg22911054	CPT1A	Carnitine palmitoyltransferase 1A	11	68603379	5'UTR	N_Shelf	0.770	0.745	0.728	-0.025	-0.042	-0.017	2.0E-10	0.000
cg11095122	CSGALNACT1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	8	19540734	TSS1500	OpenSea	0.673	0.642	0.653	-0.031	-0.019	0.012	3.8E-06	0.037
cg06070496	DLGAP1	DLG associated protein 1	18	3706638	Body	OpenSea	0.634	0.610	0.601	-0.024	-0.033	-0.009	1.9E-06	0.028
cg12359298	DTD1	D-tyrosyl-tRNA deacylase 1	20	18735103	3'UTR	OpenSea	0.683	0.656	0.653	-0.026	-0.029	-0.003	4.0E-07	0.012
cg15546194	DZIP1L	DAZ interacting zinc finger protein 1 like	3	137800724	Body	OpenSea	0.685	0.664	0.666	-0.021	-0.018	0.002	3.0E-06	0.034
cg07019857	EFNA5	Ephrin A5	5	106822849	Body	OpenSea	0.707	0.715	0.679	0.008	-0.028	-0.037	1.7E-06	0.028
cg18518074	EHD1	EH domain containing 1	11	64642316	Body	N_Shelf	0.495	0.464	0.467	-0.031	-0.027	0.003	1.0E-06	0.021
cg03457142	EIF4E3	Eukaryotic translation initiation factor 4E family member 3	3	71804859	TSS1500	S_Shore	0.498	0.484	0.478	-0.014	-0.019	-0.006	2.6E-06	0.032
cg23752007	ELMO1	Engulfment and cell motility 1	7	37429500	5'UTR	OpenSea	0.742	0.717	0.720	-0.025	-0.022	0.003	1.9E-06	0.028
cg02314596	FOXN3	Forkhead box N3	14	89852725	Body	OpenSea	0.744	0.720	0.727	-0.024	-0.017	0.007	1.8E-07	0.006
cg02479755	FTO	Fat mass and obesity-associated protein	16	54097517	Body	OpenSea	0.830	0.808	0.804	-0.022	-0.026	-0.004	3.7E-07	0.011
cg03702011	GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	1	230193513	TSS200	OpenSea	0.732	0.701	0.708	-0.031	-0.024	0.007	5.2E-07	0.015
cg20703242	GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	1	230279135	Body	OpenSea	0.510	0.490	0.487	-0.020	-0.023	-0.003	4.3E-06	0.040
cg06783533	GNAO1	G protein subunit alpha o1	16	56388908	Body	OpenSea	0.843	0.822	0.820	-0.021	-0.023	-0.002	4.9E-06	0.041
cg27246571	HAL	Histidine ammonia-lyase	12	96389588	Body	Island	0.720	0.693	0.694	-0.028	-0.026	0.001	1.0E-06	0.021
cg17439422	HEPN1	Hepatocellular carcinoma down-regulated 1	11	124788656	TSS1500	N_Shelf	0.836	0.820	0.818	-0.017	-0.019	-0.002	2.5E-08	0.002
cg06865026	IMPA2	Inositol monophosphatase 2	18	12015910	Body	OpenSea	0.850	0.820	0.831	-0.029	-0.019	0.010	1.1E-08	0.002

Table S2 (continued)

cgID	Gene	Full gene name	Chr	Position	Gene context	CpG context	Mean beta			Δ beta			P-value	FDR
							B	4W	12W	4W-B	12W-B	12W-4W		
cg00416922	INPP1	Inositol polyphosphate-1-phosphatase	2	191207560	TSS1500	N_Shore	0.712	0.691	0.691	-0.021	-0.021	0.000	1.8E-06	0.028
cg11555067	INPP4A	Inositol polyphosphate-4-phosphatase type I A	2	99081350	5'UTR	OpenSea	0.291	0.262	0.275	-0.029	-0.017	0.013	2.1E-06	0.029
cg10967866	INPP5A	Inositol polyphosphate-5-phosphatase A	10	134362164	Body	S_Shore	0.744	0.712	0.716	-0.032	-0.028	0.004	8.3E-08	0.004
cg19137806	INPP5A	Inositol polyphosphate-5-phosphatase A	10	134362170	Body	S_Shore	0.709	0.677	0.678	-0.031	-0.030	0.001	4.5E-08	0.003
cg05993525	KCNQ1	Potassium voltage-gated channel subfamily Q member 1	11	2769184	Body	OpenSea	0.567	0.534	0.539	-0.033	-0.027	0.005	1.0E-06	0.021
cg08376310	KCNQ1	Potassium voltage-gated channel subfamily Q member 1	11	2858621	Body	OpenSea	0.902	0.887	0.886	-0.016	-0.016	0.000	5.4E-09	0.001
cg21214508	KIAA1267	KAT8 regulatory NSL complex subunit 1	17	44248233	1stExon	OpenSea	0.865	0.849	0.851	-0.017	-0.015	0.002	2.1E-06	0.029
cg04460609	LDB2	LIM domain binding 2	4	16532808	Body	OpenSea	0.514	0.490	0.481	-0.024	-0.033	-0.009	4.1E-08	0.003
cg24133663	LEPREL1	Prolyl 3-hydroxylase 2	3	189679585	Body	OpenSea	0.088	0.088	0.075	-0.001	-0.013	-0.012	6.3E-07	0.016
cg09954473	LOC101927156	NA	2	182245509	Body	OpenSea	0.826	0.805	0.810	-0.021	-0.017	0.005	4.7E-06	0.040
cg01164919	LOC101927588	NA	8	125214930	Body	OpenSea	0.855	0.847	0.833	-0.008	-0.022	-0.014	2.6E-06	0.032
cg04232816	LOC285033	NA	2	96905390	TSS1500	OpenSea	0.703	0.682	0.674	-0.022	-0.029	-0.008	6.4E-06	0.049
cg18394235	LTBP1	Latent transforming growth factor beta binding protein 1	2	33359059	TSS1500; Body	OpenSea	0.686	0.663	0.659	-0.023	-0.027	-0.004	5.3E-06	0.042
cg06022811	LY86;LY86-AS1	Lymphocyte antigen 86;NA	6	6599919	Body	OpenSea	0.725	0.698	0.697	-0.027	-0.028	-0.001	4.7E-06	0.040
cg09427959	MED13L	Mediator complex subunit 13 like	12	116520303	Body	OpenSea	0.813	0.800	0.791	-0.013	-0.023	-0.010	3.6E-06	0.036
cg14728609	MIR3134;SUSD1	NA; Sushi domain containing 1	9	114933506	Body	N_Shelf	0.679	0.659	0.656	-0.020	-0.023	-0.003	1.3E-06	0.024
cg13617154	NAT8	N-acetyltransferase 8	2	73868507	Body	OpenSea	0.792	0.768	0.770	-0.024	-0.022	0.002	2.7E-09	0.001
cg26879421	NET1	Neuroepithelial cell transforming 1	10	5455710	Body	S_Shore	0.720	0.699	0.698	-0.021	-0.022	0.000	4.5E-06	0.040
cg22069247	NMUR1	Neuromedin U receptor 1	2	232393256	Body	N_Shore	0.665	0.627	0.638	-0.039	-0.027	0.011	2.1E-08	0.002
cg05262369	NUCKS1	Nuclear casein kinase and cyclin dependent kinase substrate 1	1	205716365	Body	N_Shore	0.738	0.709	0.713	-0.030	-0.025	0.005	7.0E-08	0.003
cg14499189	PDE4D	Phosphodiesterase 4D	5	59492401	5'UTR	OpenSea	0.806	0.787	0.783	-0.019	-0.023	-0.003	2.4E-06	0.031
cg23987137	PDE4D	Phosphodiesterase 4D	5	58653624	Body	OpenSea	0.800	0.777	0.778	-0.023	-0.022	0.001	1.1E-06	0.021
cg17075888	PDK4	Pyruvat dehydrogenase kinase 4	7	95225339	Body	N_Shore	0.595	0.594	0.568	-0.001	-0.027	-0.026	1.8E-06	0.028
cg07599432	PDZD8	PDZ domain containing 8	10	119126318	Body	OpenSea	0.770	0.740	0.740	-0.029	-0.029	0.000	8.2E-07	0.019
cg12368246	PLAGL1	PLAG1 like zinc finger 1	6	144286757	5'UTR	OpenSea	0.824	0.802	0.805	-0.022	-0.019	0.003	2.1E-06	0.029
cg16615151	PLCXD2	Phosphatidylinositol specific phospholipase C X domain containing 2	3	111409324	Body	OpenSea	0.545	0.510	0.514	-0.035	-0.030	0.004	1.0E-07	0.004
cg26683198	PPAP2B	Phospholipid phosphatase 3	1	57039392	Body	OpenSea	0.519	0.493	0.498	-0.026	-0.021	0.005	3.5E-06	0.035
cg15438481	PRKCA	Protein kinase C alpha	17	64499496	Body	OpenSea	0.877	0.867	0.859	-0.009	-0.017	-0.008	3.2E-06	0.034
cg02641339	PSTPIP2	Proline-serine-threonine phosphatase interacting protein 2	18	43635048	Body	OpenSea	0.609	0.589	0.570	-0.020	-0.039	-0.019	1.7E-06	0.028
cg03189652	PTH2R	Parathyroid hormone 2 receptor	2	209224422	TSS200	N_Shore	0.763	0.740	0.735	-0.022	-0.028	-0.006	5.3E-06	0.042
cg08047233	RERE	Arginine-glutamic acid dipeptide repeats	1	8578167	Body	OpenSea	0.696	0.671	0.666	-0.026	-0.031	-0.005	4.9E-06	0.041
cg07268595	RNF166	Ring finger protein 166	16	88766501	Body; 5'UTR	S_Shore	0.584	0.561	0.555	-0.023	-0.029	-0.006	5.8E-06	0.044
cg04161193	RNF19A	Ring finger protein 19A	8	101338327	5'UTR	OpenSea	0.551	0.525	0.526	-0.026	-0.025	0.001	3.4E-06	0.035
cg21882620	SLC22A23	Solute carrier family 22 member 23	6	3379971	Body	OpenSea	0.752	0.736	0.718	-0.017	-0.035	-0.018	8.5E-07	0.019

Table S2 (continued)

cgID	Gene	Full gene name	Chr	Position	Gene context	CpG context	Mean beta			Δ beta			P-value	FDR
							B	4W	12W	4W-B	12W-B	12W-4W		
cg03492107	SNTB1	Syntrophin beta 1	8	121715913	Body	OpenSea	0.644	0.612	0.613	-0.032	-0.031	0.001	2.5E-07	0.009
cg15835363	STARD9	StAR related lipid transfer domain containing 9	15	42894942	Body	OpenSea	0.759	0.727	0.731	-0.032	-0.028	0.004	1.9E-08	0.002
cg14957855	SWT1	SWT1. RNA endoribonuclease homolog	1	185234541	Body	OpenSea	0.857	0.833	0.865	-0.025	0.007	0.032	2.6E-06	0.032
cg02949436	TCF25	Transcription factor 25	16	89940853	Body	S_Shore	0.068	0.058	0.059	-0.010	-0.009	0.000	2.9E-06	0.033
cg19933954	TCFL5	Transcription factor like 5	20	61494242	TSS1500	S_Shore	0.630	0.588	0.591	-0.042	-0.039	0.003	3.4E-06	0.035
cg22744398	TEC	Tec protein tyrosine kinase	4	48226070	Body	OpenSea	0.650	0.622	0.612	-0.027	-0.038	-0.010	5.9E-07	0.016
cg27549551	TM4SF20	Transmembrane 4 L six family member 20	2	228245419	TSS1500	OpenSea	0.783	0.765	0.752	-0.018	-0.031	-0.012	3.2E-07	0.010
cg10288625	TMEM45A	Transmembrane protein 45A	3	100289748	Body	OpenSea	0.824	0.805	0.823	-0.019	-0.001	0.018	1.9E-06	0.028
cg25124205	TPD52L1	Tumor protein D52 like 1	6	125519976	5'UTR; Body	OpenSea	0.730	0.698	0.676	-0.032	-0.053	-0.022	9.2E-09	0.002
cg23999170	TSPAN2	Tetraspanin 2	1	115628111	Body	N_Shelf	0.715	0.688	0.687	-0.027	-0.028	-0.002	1.5E-06	0.026
cg11166303	TSSC1	EARP complex and GARP complex interacting protein 1	2	3320529	Body	N_Shore	0.650	0.624	0.620	-0.026	-0.030	-0.004	2.3E-06	0.031
cg06096446	TULP4	Tubby like protein 4	6	158744008	Body	OpenSea	0.700	0.686	0.680	-0.014	-0.020	-0.005	5.2E-06	0.042
cg20347155	ZEB2	Zinc finger E-box binding homeobox 2	2	145218951	Body	OpenSea	0.634	0.597	0.604	-0.037	-0.030	0.007	3.4E-06	0.035
cg00095930	NA	NA	12	109569116	NA	OpenSea	0.455	0.431	0.425	-0.024	-0.030	-0.006	6.5E-08	0.003
cg01119319	NA	NA	7	38356808	NA	OpenSea	0.596	0.552	0.558	-0.044	-0.038	0.006	1.2E-07	0.004
cg02146228	NA	NA	14	75401904	NA	OpenSea	0.528	0.511	0.503	-0.017	-0.025	-0.009	5.8E-08	0.003
cg05303899	NA	NA	2	9919494	NA	OpenSea	0.692	0.674	0.673	-0.018	-0.019	-0.001	5.0E-06	0.041
cg05329280	NA	NA	20	5192635	NA	OpenSea	0.726	0.699	0.697	-0.028	-0.030	-0.002	6.9E-07	0.017
cg05999592	NA	NA	11	72925008	NA	N_Shelf	0.630	0.608	0.608	-0.022	-0.022	0.000	4.5E-06	0.040
cg07418291	NA	NA	15	58553346	NA	OpenSea	0.757	0.733	0.738	-0.024	-0.019	0.005	2.5E-06	0.032
cg08698943	NA	NA	10	3509758	NA	OpenSea	0.412	0.390	0.391	-0.023	-0.021	0.001	1.6E-06	0.027
cg10042645	NA	NA	11	2308589	NA	OpenSea	0.651	0.622	0.625	-0.029	-0.027	0.003	2.8E-06	0.032
cg10629173	NA	NA	10	5576434	NA	OpenSea	0.772	0.745	0.745	-0.027	-0.026	0.000	3.4E-06	0.035
cg12582317	NA	NA	17	55822272	NA	OpenSea	0.770	0.748	0.748	-0.022	-0.022	0.000	4.3E-06	0.040
cg14165660	NA	NA	10	112889349	NA	OpenSea	0.811	0.789	0.792	-0.023	-0.019	0.004	7.3E-08	0.003
cg15256315	NA	NA	8	135791732	NA	OpenSea	0.317	0.283	0.294	-0.035	-0.024	0.011	5.4E-06	0.042
cg15295322	NA	NA	3	178689645	NA	OpenSea	0.769	0.752	0.748	-0.016	-0.021	-0.004	4.6E-06	0.040
cg16797699	NA	NA	12	109569084	NA	OpenSea	0.708	0.682	0.682	-0.026	-0.026	0.000	3.2E-07	0.010
cg19815228	NA	NA	10	134232489	NA	OpenSea	0.615	0.581	0.575	-0.034	-0.040	-0.006	4.1E-06	0.038
cg20025086	NA	NA	12	109569130	NA	OpenSea	0.502	0.481	0.476	-0.021	-0.025	-0.005	7.5E-07	0.018
cg21156054	NA	NA	21	40225493	NA	OpenSea	0.464	0.453	0.439	-0.011	-0.025	-0.014	3.1E-06	0.034
cg22768761	NA	NA	15	58551412	NA	OpenSea	0.877	0.858	0.863	-0.019	-0.014	0.005	1.7E-06	0.028
cg26129664	NA	NA	10	134232399	NA	OpenSea	0.464	0.429	0.426	-0.034	-0.038	-0.003	2.6E-08	0.002
cg26645302	NA	NA	14	22891244	NA	OpenSea	0.254	0.231	0.217	-0.023	-0.037	-0.014	3.8E-06	0.037
cg26835531	NA	NA	18	47980832	NA	OpenSea	0.822	0.811	0.798	-0.011	-0.024	-0.013	2.6E-06	0.032

Abbreviations: 4W, 4 weeks of dietary treatment; 12W, 12 weeks of dietary treatment; B, Baseline; Chr, Chromosome; FDR, False discovery rate; NA, No information available. FDR <0.05. The beta value is defined as the ratio of methylated versus unmethylated allele ($\beta = M/(M + U + 100)$). The beta values are between 0 and 1 and can be interpreted as 0 being unmethylated and 1 being methylated.

Table S3 Differentially methylated CpGs (sorted alphabetically by gene name and ascending by cgID for CpGs with no gene annotation) from baseline to 4 weeks of dietary treatment (n=56)

cgID	Gene	Full gene name	Chr	Position	Gene context	CpG context	Mean beta			Δ beta		FDR
							B	4W	12W	4W-B	P-value	
cg17951488	AGAP7	NA	10	230193513	TSS1500	N_Shore	0.891	0.872	0.879	-0.019	1.8E-06	0.044
cg10077346	BCKDHB	Branched chain keto acid dehydrogenase E1 subunit beta	6	2308589	Body	OpenSea	0.748	0.716	0.728	-0.032	5.8E-07	0.022
cg04871807	C5orf27	NA	5	23064608	TSS1500	OpenSea	0.536	0.508	0.506	-0.028	1.4E-06	0.036
cg14928764	CD93	CD93 molecule	20	112889349	Body	OpenSea	0.821	0.799	0.796	-0.023	1.4E-06	0.036
cg20601482	CERS6	Ceramide synthase 6	2	58553346	Body	OpenSea	0.737	0.711	0.714	-0.026	6.6E-07	0.023
cg12359298	DTD1	D-tyrosyl-tRNA deacylase 1	20	95186505	3'UTR	OpenSea	0.683	0.656	0.653	-0.026	1.5E-06	0.036
cg23752007	ELMO1	Engulfment and cell motility 1	7	2769184	5'UTR	OpenSea	0.742	0.717	0.720	-0.025	2.2E-06	0.050
cg02314596	FOXN3	Forkhead box N3	14	18735103	Body	OpenSea	0.744	0.720	0.727	-0.024	7.6E-08	0.007
cg03702011	GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	1	135791732	TSS200	OpenSea	0.732	0.701	0.708	-0.031	2.6E-07	0.014
cg27246571	HAL	Histidine ammonia-lyase	12	109569116	Body	Island	0.720	0.693	0.694	-0.028	5.0E-07	0.021
cg17439422	HEPN1	Hepatocellular carcinoma down-regulated 1	11	38356808	TSS1500	N_Shelf	0.836	0.820	0.818	-0.017	1.1E-07	0.007
cg06865026	IMPA2	Inositol monophosphatase 2	18	73868507	Body	OpenSea	0.850	0.820	0.831	-0.029	1.9E-09	0.001
cg11555067	INPP4A	Inositol polyphosphate-4-phosphatase type I A	2	205716365	5'UTR	OpenSea	0.291	0.262	0.275	-0.029	3.3E-07	0.017
cg10967866	INPP5A	Inositol polyphosphate-5-phosphatase A	10	134232399	Body	S_Shore	0.744	0.712	0.716	-0.032	1.0E-07	0.007
cg19137806	INPP5A	Inositol polyphosphate-5-phosphatase A	10	96389588	Body	S_Shore	0.709	0.677	0.678	-0.031	9.8E-08	0.007
cg05993525	KCNQ1	Potassium voltage-gated channel subfamily Q member 1	11	134362164	Body	OpenSea	0.567	0.534	0.539	-0.033	9.0E-07	0.026
cg08376310	KCNQ1	Potassium voltage-gated channel subfamily Q member 1	11	99081350	Body	OpenSea	0.902	0.887	0.886	-0.016	4.8E-08	0.006
cg13617154	NAT8	N-acetyltransferase 8	2	12015910	Body	OpenSea	0.792	0.768	0.770	-0.024	1.3E-08	0.003
cg22069247	NMUR1	Neuromedin U receptor 1	2	121715913	Body	N_Shore	0.665	0.627	0.638	-0.039	9.9E-09	0.003
cg05262369	NUCKS1	Nuclear casein kinase and cyclin dependent kinase substrate 1	1	89852725	Body	N_Shore	0.738	0.709	0.713	-0.030	9.7E-08	0.007
cg16615151	PLCXD2	Phosphatidylinositol specific phospholipase C X domain containing 2	3	2858621	Body	OpenSea	0.545	0.510	0.514	-0.035	1.1E-07	0.007
cg03492107	SNTB1	Syntrophin beta 1	8	80920458	Body	OpenSea	0.644	0.612	0.613	-0.032	6.4E-07	0.023
cg15835363	STARD9	StAR related lipid transfer domain containing 9	15	55822272	Body	OpenSea	0.759	0.727	0.731	-0.032	2.8E-08	0.005
cg00095930	NA	NA	12	134362170	NA	OpenSea	0.455	0.431	0.425	-0.024	7.8E-07	0.025
cg01119319	NA	NA	7	42894942	NA	OpenSea	0.596	0.552	0.558	-0.044	7.9E-08	0.007
cg07418291	NA	NA	15	232393256	NA	OpenSea	0.757	0.733	0.738	-0.024	7.2E-07	0.024
cg10042645	NA	NA	11	51487759	NA	OpenSea	0.651	0.622	0.625	-0.029	8.3E-07	0.025
cg12582317	NA	NA	17	37429500	NA	OpenSea	0.770	0.748	0.748	-0.022	1.5E-06	0.036
cg14165660	NA	NA	10	109569084	NA	OpenSea	0.811	0.789	0.792	-0.023	4.8E-08	0.006
cg15256315	NA	NA	8	111409324	NA	OpenSea	0.317	0.283	0.294	-0.035	1.3E-06	0.035
cg16797699	NA	NA	12	169337576	NA	OpenSea	0.708	0.682	0.682	-0.026	5.4E-07	0.022
cg22768761	NA	NA	15	58551412	NA	OpenSea	0.877	0.858	0.863	-0.019	4.0E-07	0.018
cg26129664	NA	NA	10	124788656	NA	OpenSea	0.464	0.429	0.426	-0.034	4.1E-07	0.018

Abbreviations: 4W, 4 weeks of dietary treatment; 12W, 12 weeks of dietary treatment; B, Baseline; Chr, Chromosome; FDR, False discovery rate; NA, No information available. FDR <0.05. The beta value is defined as the ratio of methylated versus unmethylated allele ($\beta = M/(M + U + 100)$). The beta values are between 0 and 1 and can be interpreted as 0 being unmethylated and 1 being methylated.

Table S4 Differentially methylated CpGs (sorted alphabetically by gene name and ascending by cgID for CpGs with no gene annotation) from baseline to 12 weeks of dietary treatment (n= 49)

cgID	Gene	Full gene name	Chr	Position	Gene context	CpG context	Mean beta			Δ beta		
							B	4W	12W	12W-B	P-value	FDR
cg04871807	C5orf27	NA	5	95186505	TSS1500	OpenSea	0.536	0.508	0.506	-0.030	9.9E-08	0.013
cg14928764	CD93	CD93 molecule	20	23064608	Body	OpenSea	0.821	0.799	0.796	-0.026	5.9E-07	0.023
cg04075184	CLASP1	Cytoplasmic linker associated protein 1	2	122290763	Body	S_Shelf	0.744	0.732	0.718	-0.025	2.2E-07	0.015
cg19393755	CPSF4L	Cleavage and polyadenylation specific factor 4 like	17	71258101	TSS200	OpenSea	0.707	0.689	0.680	-0.027	1.6E-06	0.039
cg22911054	CPT1A	Carnitine palmitoyltransferase 1A	11	68603379	5'UTR	N_Shelf	0.770	0.745	0.728	-0.042	4.9E-11	0.000
cg03457142	EIF4E3	Eukaryotic translation initiation factor 4E family member 3	3	71804859	TSS1500	S_Shore	0.498	0.484	0.478	-0.019	5.1E-07	0.021
cg24170465	FAM198B	Family with sequence similarity 198 member B	4	159094277	TSS200	OpenSea	0.682	0.670	0.649	-0.033	1.4E-06	0.038
cg02479755	FTO	Fat mass and obesity-associated protein	16	54097517	Body	OpenSea	0.830	0.808	0.804	-0.026	4.1E-07	0.020
cg17439422	HEPN1	Hepatocellular carcinoma down-regulated 1	11	124788656	TSS1500	N_Shelf	0.836	0.820	0.818	-0.019	7.1E-07	0.026
cg08376310	KCNQ1	Potassium voltage-gated channel subfamily Q member 1	11	2858621	Body	OpenSea	0.902	0.887	0.886	-0.016	1.3E-07	0.014
cg04460609	LDB2	LIM domain binding 2	4	16532808	Body	OpenSea	0.514	0.490	0.481	-0.033	1.3E-08	0.003
cg24133663	LEPREL1	Prolyl 3-hydroxylase 2	3	189679585	Body	OpenSea	0.088	0.088	0.075	-0.013	7.8E-07	0.027
cg01164919	LOC101927588	NA	8	125214930	Body	OpenSea	0.855	0.847	0.833	-0.022	4.2E-07	0.020
cg09427959	MED13L	Mediator complex subunit 13 like	12	116520303	Body	OpenSea	0.813	0.800	0.791	-0.023	9.3E-07	0.029
cg14728609	MIR3134; SUSD1	NA; Sushi domain containing 1	9	114933506	Body	N_Shelf	0.679	0.659	0.656	-0.023	1.0E-06	0.031
cg13617154	NAT8	N-acetyltransferase 8	2	73868507	Body	OpenSea	0.792	0.768	0.770	-0.022	1.7E-07	0.015
cg17075888	PDK4	Pyruvate dehydrogenase kinase 4	7	95225339	Body	N_Shore	0.595	0.594	0.568	-0.027	1.6E-06	0.039
cg15438481	PRKCA	Protein kinase C alpha	17	64499496	Body	OpenSea	0.877	0.867	0.859	-0.017	1.3E-06	0.034
cg02641339	PSTPIP2	Proline-serine-threonine phosphatase interacting protein 2	18	43635048	Body	OpenSea	0.609	0.589	0.570	-0.039	3.2E-07	0.020
cg21882620	SLC22A23	Solute carrier family 22 member 23	6	3379971	Body	OpenSea	0.752	0.736	0.718	-0.035	1.6E-07	0.015
cg22744398	TEC	Tec protein tyrosine kinase	4	48226070	Body	OpenSea	0.650	0.622	0.612	-0.038	3.5E-07	0.020
cg27549551	TM4SF20	Transmembrane 4 L six family member 20	2	228245419	TSS1500	OpenSea	0.783	0.765	0.752	-0.031	9.1E-08	0.013
cg25124205	TPD52L1	Tumor protein D52 like 1	6	125519976	5'UTR. Body	OpenSea	0.730	0.698	0.676	-0.053	3.4E-09	0.001
cg06096446	TULP4	Tubby like protein 4	6	158744008	Body	OpenSea	0.700	0.686	0.680	-0.020	8.7E-07	0.029
cg00095930	NA	NA	12	109569116	NA	OpenSea	0.455	0.431	0.425	-0.030	1.8E-08	0.020
cg02146228	NA	NA	14	75401904	NA	OpenSea	0.528	0.511	0.503	-0.025	1.2E-06	0.003
cg14783355	NA	NA	5	10530621	NA	OpenSea	0.721	0.706	0.692	-0.029	5.2E-07	0.033
cg21156054	NA	NA	21	40225493	NA	OpenSea	0.464	0.453	0.439	-0.025	1.9E-07	0.021
cg26129664	NA	NA	10	134232399	NA	OpenSea	0.464	0.429	0.426	-0.038	1.1E-06	0.015
cg26645302	NA	NA	14	22891244	NA	OpenSea	0.254	0.231	0.217	-0.037	4.3E-07	0.033
cg26835531	NA	NA	18	47980832	NA	OpenSea	0.822	0.811	0.798	-0.024	9.9E-08	0.020

Abbreviations: 4W, 4 weeks of dietary treatment; 12W, 12 weeks of dietary treatment; B, Baseline; Chr, Chromosome; FDR, False discovery rate; NA, No information available. FDR <0.05. The beta value is defined as the ratio of methylated versus unmethylated allele ($\beta = M/(M + U + 100)$). The beta values are between 0 and 1 and can be interpreted as 0 being unmethylated and 1 being methylated.