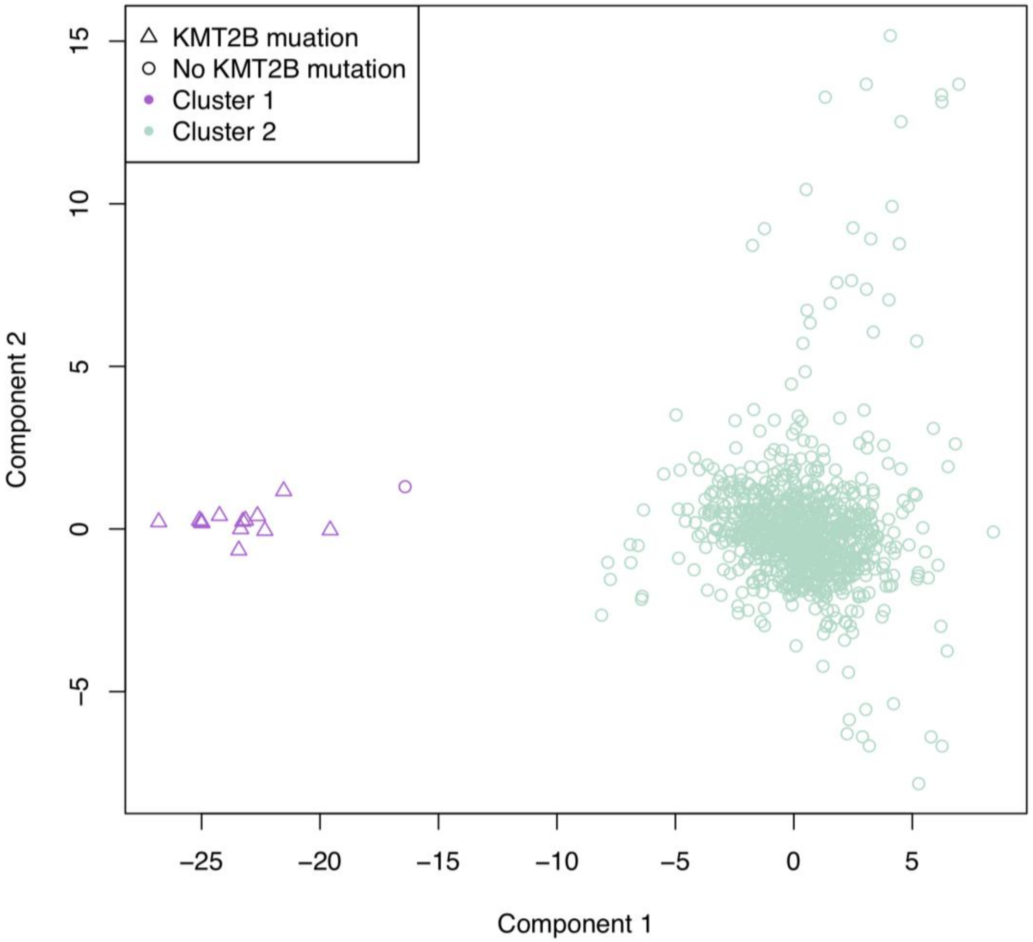
Supplementary Material for

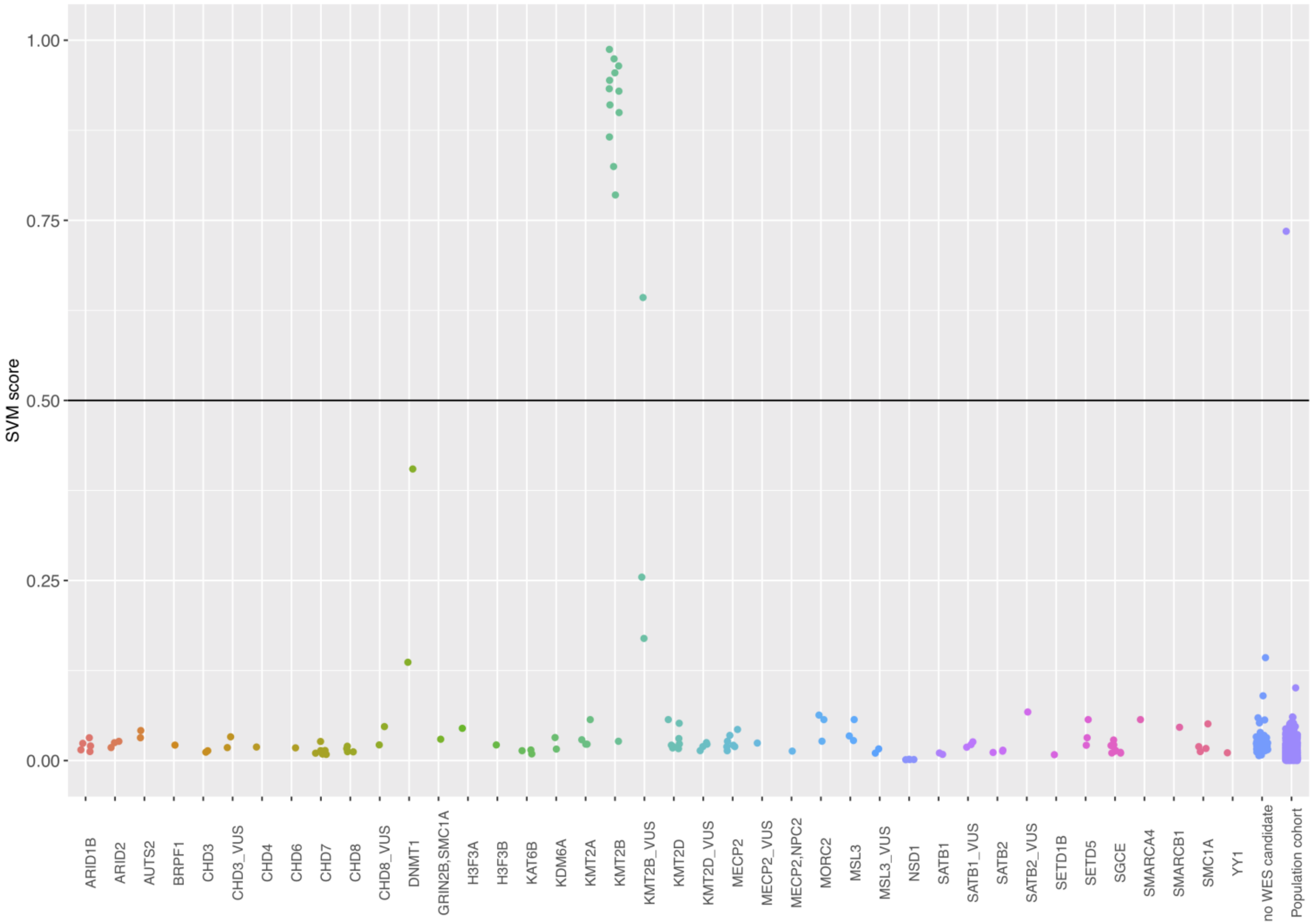
Blood DNA methylation yields accurate biomarker of *KMT2B*-related dystonia and predicts onset

Mirza-Schreiber at al (2021)

Content Page



Supplementary Figure 1. Kmeans Clustering applied on the *KMT2B* episignature (113 CpG-sites) of patients with pathogenic *KMT2B* mutation (triangles) and individuals without known *KMT2B* mutations (circles), i.e., individuals with *SGCE* mutation and individuals from the general population. Kmeans revealed two distinct clusters. One cluster (purple) contained all patients with pathogenic *KMT2B* mutation as well as the sample (purple circle) from the general population cohort (KORA) with an SVM score of 0.81, i.e., well above 0.5. The other cluster (green) contained all other samples.



Supplementary Figure 2. Probability scores of an alternative SVM classifier for disease-causing *KMT2B* variants. To generate a SVM classifier with fully unbiased testing, the EWAS was performed with a set of only ten dystonia cases with pathogenic/likely pathogenic variants in *KMT2B*, leaving three (instead of one) KMT2B-deficient cases for later testing of the classifier. EWAS controls were the same as before, i.e., 8 dystonia patients with WES-diagnosed causative variants in *SGCE* which does not influence the epigenetic machinery. Due to the smaller EWAS case set, we adapted the cut-off to a FDR adjusted *p*-value ≤ 0.005 and abs(*logFC*) ≥ 1.5. This resulted in 184 CpG sites which included 63 (56%) of the 113 CpG sites in the original classifier. For training the alternative classifier, we used the EWAS samples and, as further controls, included a randomly sampled subset of 36 out of 72 WES-diagnosed ID/DD patients instead of non-KMT2B dystonia patients. These ID/DD patients had defects of the epigenetic machinery; see Suppl.Table 1c). Negative (SVM score < 0.5) and positive classifications did not differ between the alternative and the original classifier, including the three KMT2B-deficient samples in the alternative classifier's test set.

Supplementary Table 1a. Samples with disease-causing variants (bold) and variants of uncertain significance (VUS) in KMT2B

Gene	Transcript number (RefSeq)	Associated clinical syndrome (OMIM)	Sequencing mode	cDNA variant	Predicted protein change	Variant type	Variant inheritance	Zygosity	Significance of variant (ACMG)	Dystonia - age of onset [yr]	Dystonia - category
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	**c.3632G>A**	p.Gly1211Glu	missense	de novo	heterozygous	**likely pathogenic**	13	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	**c.6866delC**	p.Pro2289Argfs*36	loss-of-function	unknown	heterozygous	**pathogenic**	6	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.6406delC**	p.Leu2136Serfs*17	loss-of-function	de novo	heterozygous	**pathogenic**	7	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.3700G>A**	p.Glu1234Lys	missense	de novo	heterozygous	**likely pathogenic**	17	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.7050-2A>G**	p.Phe2321Serfs*93	loss-of-function	de novo	heterozygous	**pathogenic**	11	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.1633C>T**	p.Arg545*	loss-of-function	de novo	heterozygous	**pathogenic**	3	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.4847C>T**	p.Ala1616Val	missense	de novo	heterozygous	**likely pathogenic**	6	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	**c.2428C>T**	p.Gln810*	loss-of-function	from symptomatic father	heterozygous	**pathogenic**	4	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	**c.424C>T**	p.Arg142*	loss-of-function	unknown	heterozygous	**pathogenic**	2	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.521dupC**	p.Thr176Aspfs*8	loss-of-function	de novo	heterozygous	**pathogenic**	7	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.17_23dup**	p.Ser9Argfs*109	loss-of-function	de novo	heterozygous	**pathogenic**	5	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	**c.4549C>T**	p.Arg1517*	loss-of-function	de novo	heterozygous	**pathogenic**	3	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	**c.3335-9_3363del**	p.?	loss-of-function	unknown	heterozygous	**pathogenic**	5	complex
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	c.4622C>T	p.Ala1541Val	missense	unknown	heterozygous	VUS	43	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	c.5336G>A	p.Arg1779Gln	missense	unknown	heterozygous	VUS	7	isolated
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	solo	c.364-2A>G	p.?	loss-of-function	unknown	heterozygous	VUS	20	combined (+ parkinsonism)
KMT2B	NM_014727.1	Dystonia 28, childhood-onset (617284)	trio	c.7693C>G	p.Arg2565Gly	missense	from asymptomatic father	heterozygous	VUS	6	isolated

Supplementary Table 1b. Samples used in the EWAS, and for constructing (training) and testing the classifier

Age	Sex	Gene	Use in EWAS	Classifier
19	male	-	-	Training
20	female	-	-	Training
40	female	-	-	Training
11	female	-	-	Training
1	male	-	-	Training
11	female	-	-	Training
9	female	-	-	Training
49	female	-	-	Training
68	male	-	-	Training
26	female	-	-	Training
60	male	-	-	Training
5	female	-	-	Training
3	female	-	-	Training
41	female	-	-	Training
2	male	-	-	Training
14	male	-	-	Training
30	male	-	-	Training
8	female	-	-	Training
9	female	-	-	Training
4	female	-	-	Training
7	female	-	-	Training
25	female	-	-	Training
28	female	-	-	Training
3	male	-	-	Training
21	female	-	-	Training
17	female	AUTS2	-	Training
48	female	CHD8	-	Training
44	female	CHD8	-	Training
42	male	DNMT1	-	Training
6	female	KMT2B	Case	Training
13	female	KMT2B	Case	Training
20	male	KMT2B	Case	Training
12	male	KMT2B	Case	Training
11	female	KMT2B	Case	Training
continued...				
21	male	KMT2B	Case	Training
33	female	KMT2B	Case	Training
57	male	KMT2B	Case	Training
4	female	MECP2	-	Training
10	female	MORC2	-	Training
7	female	SGCE	Control	Training
7	male	SGCE	Control	Training
16	female	SGCE	Control	Training
20	male	SGCE	Control	Training
34	male	SGCE	Control	Training
50	male	SGCE	Control	Training
23	male	SGCE	Control	Training
31	male	-	-	Test
18	male	-	-	Test
5	male	-	-	Test
6	male	-	-	Test
3	female	-	-	Test
6	male	-	-	Test
11	female	-	-	Test
24	female	-	-	Test
1	female	-	-	Test
43	male	BRPF1	-	Test
8	female	CHD4	-	Test
53	female	DNMT1	-	Test
17	male	KMT2B	Case	Test
32	male	KMT2B	Case	Test
18	female	KMT2B	Case	Test
31	male	KMT2B	-	Test
19	female	SGCE	Control	Test
45	female	YY1	-	Test
Assesement of samples with variants of unknown significance in KMT2B				
31	female	KMT2B_VUS	-	diagnostic application of the classifier
60	male	KMT2B_VUS	-	diagnostic application of the classifier
53	female	KMT2B_VUS	-	diagnostic application of the classifier
8	male	KMT2B_VUS	-	diagnostic application of the classifier

Supplementary Table 1c. Patient samples used for independent validation of the SVM classifier. Patients had verified or suspected WES-diagnosed monogenic disorders, with the majority of them affecting the epigenetic machinery.

Gene	Variant.classification	Age	Sex
ARID1B	likely pathogenic/pathogenic	4	female
ARID1B	likely pathogenic/pathogenic	6	female
ARID1B	likely pathogenic/pathogenic	30	female
ARID1B	likely pathogenic/pathogenic	4	male
ARID1B	likely pathogenic/pathogenic	17	male
ARID2	likely pathogenic/pathogenic	53	male
ARID2	likely pathogenic/pathogenic	29	male
ARID2	likely pathogenic/pathogenic	5	male
AUTS2	likely pathogenic/pathogenic	18	female
CHD3	likely pathogenic/pathogenic	6	male
CHD3	likely pathogenic/pathogenic	14	male
CHD3	variant of uncertain significance	34	male
CHD3	variant of uncertain significance	6	female
CHD6	likely pathogenic/pathogenic	6	female
CHD7	likely pathogenic/pathogenic	26	male
CHD7	likely pathogenic/pathogenic	4	male
CHD7	likely pathogenic/pathogenic	3	female
CHD7	likely pathogenic/pathogenic	2	male
CHD7	likely pathogenic/pathogenic	15	male
CHD7	likely pathogenic/pathogenic	3	male
CHD8	likely pathogenic/pathogenic	6	female
CHD8	likely pathogenic/pathogenic	10	male
CHD8	variant of uncertain significance	18	male
CHD8	variant of uncertain significance	42	female
GRIN2B,SMC1A	likely pathogenic/pathogenic	5	male
H3F3A	likely pathogenic/pathogenic	36	male
H3F3B	likely pathogenic/pathogenic	37	female
KAT6B	likely pathogenic/pathogenic	7	male
KAT6B	likely pathogenic/pathogenic	2	male
KAT6B	likely pathogenic/pathogenic	17	female
KDM6A	likely pathogenic/pathogenic	3	male
KDM6A	likely pathogenic/pathogenic	6	male
KMT2A	likely pathogenic/pathogenic	8	female
KMT2A	likely pathogenic/pathogenic	5	male
KMT2A	likely pathogenic/pathogenic	11	female
KMT2A	likely pathogenic/pathogenic	7	male
KMT2D	likely pathogenic/pathogenic	8	female
KMT2D	likely pathogenic/pathogenic	6	male
KMT2D	likely pathogenic/pathogenic	4	female
KMT2D	likely pathogenic/pathogenic	3	male
KMT2D	likely pathogenic/pathogenic	2	female
KMT2D	likely pathogenic/pathogenic	33	male
KMT2D	likely pathogenic/pathogenic	17	male
KMT2D	likely pathogenic/pathogenic	18	male
KMT2D	likely pathogenic/pathogenic	0	female
KMT2D	variant of uncertain significance	51	male
KMT2D	variant of uncertain significance	3	female
KMT2D	variant of uncertain significance	23	male
KMT2D	variant of uncertain significance	1	male
MECP2	likely pathogenic/pathogenic	20	female
MECP2	likely pathogenic/pathogenic	6	male
MECP2	likely pathogenic/pathogenic	13	female
MECP2	likely pathogenic/pathogenic	5	female
MECP2	likely pathogenic/pathogenic	2	female
MECP2	likely pathogenic/pathogenic	2	female
MECP2	variant of uncertain significance	5	female
MECP2,NPC2	likely pathogenic/pathogenic	6	male
MORC2	likely pathogenic/pathogenic	NA	male
MORC2	likely pathogenic/pathogenic	11	male
MSL3	likely pathogenic/pathogenic	3	female
MSL3	likely pathogenic/pathogenic	20	männlich
MSL3	likely pathogenic/pathogenic	30	male
MSL3	variant of uncertain significance	34	female
MSL3	variant of uncertain significance	7	male
NSD1	likely pathogenic/pathogenic	17	male
NSD1	likely pathogenic/pathogenic	4	male
NSD1	likely pathogenic/pathogenic	4	female
NSD1	likely pathogenic/pathogenic	7	male
SATB1	likely pathogenic/pathogenic	38	male
SATB1	likely pathogenic/pathogenic	2	female
SATB1	variant of uncertain significance	35	female
SATB1	variant of uncertain significance	8	male
SATB1	variant of uncertain significance	6	female
SATB2	likely pathogenic/pathogenic	8	female
SATB2	likely pathogenic/pathogenic	19	male
SATB2	likely pathogenic/pathogenic	6	female
SATB2	variant of uncertain significance	7	male
SETD1B	likely pathogenic/pathogenic	23	male
SETD5	likely pathogenic/pathogenic	7	male
SETD5	likely pathogenic/pathogenic	16	male
SETD5	likely pathogenic/pathogenic	6	female
SMARCA4	likely pathogenic/pathogenic	6	female
SMARCB1	likely pathogenic/pathogenic	4	female
SMC1A	likely pathogenic/pathogenic	15	female
SMC1A	likely pathogenic/pathogenic	3	female
SMC1A	likely pathogenic/pathogenic	2	female
SMC1A	likely pathogenic/pathogenic	2	female
-	-	23	female
-	-	9	male
-	-	4	male
-	-	4	female
-	-	15	male
-	-	6	male
-	-	16	male
-	-	8	male
-	-	8	female
-	-	12	female
-	-	6	male
-	-	18	female
-	-	3	female
-	-	8	male
-	-	15	male
-	-	10	male
-	-	6	male
-	-	4	female
-	-	14	female
-	-	3	female
-	-	6	female
-	-	2	female
-	-	10	male

Supplemetary Table 2. The 113 significant CpG sites with abs(logFC) > 1 used in the SVM classifier.

Cpg	Chr	Position	Gene	on_to_CpG_	logFC	p.mod	q.mod
cg05038268	chr11	66885281	KDM2A	Island	3.14	1.98E-12	1.30E-06
cg17594860	chr1	19615358	AKR7A3	Island	2.04	1.06E-10	2.79E-05
cg05339727	chr2	165812079	SLC38A11	OpenSea	1.63	1.28E-10	2.79E-05
cg17181653	chr6	144417537	SF3B5	S_Shore	2.52	2.54E-10	3.16E-05
cg15574301	chr5	131607097	PDLIM4	Island	1.48	2.68E-10	3.16E-05
cg01203153	chr5	180643432	-	N_Shore	1.87	3.08E-10	3.16E-05
cg06961054	chr5	56204405	SETD9	N_Shore	2.28	4.20E-10	3.16E-05
cg20454887	chr2	54935920	-	OpenSea	1.93	4.48E-10	3.16E-05
cg03318695	chr6	72130799	C6orf155	S_Shore	1.85	4.61E-10	3.16E-05
cg09191232	chr4	108642411	PAPSS1	S_Shore	1.68	4.84E-10	3.16E-05
cg06409153	chr17	67323953	ABCA5	S_Shore	2	6.04E-10	3.49E-05
cg00054210	chr8	65711644	CYP7B1	Island	1.69	6.49E-10	3.49E-05
cg19476597	chr18	47794792	-	Island	1.91	7.24E-10	3.49E-05
cg15242449	chr6	17016484	-	OpenSea	1.95	7.48E-10	3.49E-05
cg19362196	chr1	26233615	STMN1	Island	1.36	8.72E-10	3.76E-05
cg14624145	chr17	37024169	-	N_Shore	2.5	9.20E-10	3.76E-05
cg04181892	chr2	54936027	-	OpenSea	2.09	1.19E-09	4.57E-05
cg04569429	chr17	37024625	LASP1	N_Shore	2.02	1.41E-09	5.11E-05
cg17583667	chr1	36039356	TFAP2E	Island	1.23	1.53E-09	5.28E-05
cg04274288	chr6	27648004	-	Island	1.9	1.62E-09	5.29E-05
cg05210364	chr6	34665139	C6orf106	S_Shore	1.39	1.95E-09	6.06E-05
cg11659317	chr2	43863985	PLEKHH2	N_Shore	1.64	2.10E-09	6.23E-05
cg27519958	chr1	161735129	ATF6	OpenSea	2.26	2.63E-09	7.38E-05
cg06645921	chr12	8025394	SLC2A14	Island	2.44	2.71E-09	7.38E-05
cg02763617	chr5	64331196	-	N_Shore	1.17	2.88E-09	7.42E-05
cg17566592	chr6	144417471	SF3B5	S_Shore	2.63	2.95E-09	7.42E-05
cg05628616	chr12	80794579	-	OpenSea	1.19	3.15E-09	7.52E-05
cg07957656	chr3	169684124	SEC62	N_Shore	1.31	3.25E-09	7.52E-05
cg12602555	chr13	50069501	PHF11	N_Shore	1.73	3.33E-09	7.52E-05
cg09512891	chr6	103780468	-	OpenSea	2.16	3.57E-09	7.55E-05
cg11917363	chr7	89975528	GTPBP10	N_Shore	1.1	3.58E-09	7.55E-05
cg03309722	chr2	74681805	INO80B	N_Shore	1.02	4.08E-09	8.02E-05
cg24499405	chr2	178030171	-	OpenSea	1.3	4.11E-09	8.02E-05
cg24777351	chr2	165811816	SLC38A11	OpenSea	1.39	4.18E-09	8.02E-05
cg13126552	chr3	52351599	DNAH1	OpenSea	1.3	4.29E-09	8.02E-05
cg02109484	chr2	74875253	C2orf65	Island	1.22	4.45E-09	8.09E-05
cg23525438	chr6	17016226	-	OpenSea	2.14	4.94E-09	8.74E-05

Supplementary Table 2 continued...							
cg02483449	chr1	84326856	-	S_Shore	2	6.00E-09	0.000101
cg00830285	chr7	149119905	-	Island	1.76	6.02E-09	0.000101
cg06501295	chr6	147523200	-	N_Shelf	1.92	6.83E-09	0.000109
cg00327322	chr6	74355165	SLC17A5	OpenSea	1.58	7.03E-09	0.000109
cg19477945	chr3	179064461	MFN1	N_Shore	2.07	7.07E-09	0.000109
cg06482716	chr18	47794995	-	Island	1.79	7.19E-09	0.000109
cg16207110	chr17	37024401	-	N_Shore	1.63	7.78E-09	0.000116
cg05730038	chr17	8702698	MFSD6L	Island	1.76	8.08E-09	0.000117
cg23793686	chr15	68133972	-	S_Shore	1.35	8.97E-09	0.000124
cg06818777	chr17	48546620	CHAD	Island	1.69	9.06E-09	0.000124
cg02474731	chr2	150185860	LYPD6	N_Shore	1.18	9.21E-09	0.000124
cg05237828	chr17	67323976	ABCA5	S_Shore	1.99	9.32E-09	0.000124
cg10622551	chr4	2366555	ZFYVE28	Island	1.57	1.05E-08	0.000137
cg12301695	chr2	165812159	SLC38A11	OpenSea	1.56	1.20E-08	0.000152
cg04854089	chr11	46355137	DGKZ	Island	1.3	1.21E-08	0.000152
cg21073930	chr19	12984170	MAST1	Island	1.43	1.28E-08	0.000158
cg06330157	chr5	137225205	PKD2L2	Island	2.21	1.37E-08	0.000166
cg05090759	chr2	165812146	SLC38A11	OpenSea	1.4	1.40E-08	0.000167
cg07579404	chr6	150346721	RAET1L	OpenSea	1.16	1.46E-08	0.00017
cg03232933	chr21	18985641	BTG3	Island	1.49	1.52E-08	0.00017
cg09423283	chr6	146755301	GRM1	N_Shore	1.12	1.53E-08	0.00017
cg12273319	chr19	50861262	-	Island	2.22	1.54E-08	0.00017
cg08918020	chr20	30225706	COX4I2	Island	1.45	1.56E-08	0.00017
cg12251452	chr1	46805700	NSUN4	N_Shore	2.15	1.71E-08	0.000178
cg03847339	chr7	112580806	C7orf60	S_Shore	1.35	1.72E-08	0.000178
cg13607316	chr14	90421828	TDP1	N_Shore	1.76	1.78E-08	0.000182
cg07061500	chr6	159290520	-	N_Shore	1.78	1.81E-08	0.000183
cg22462010	chr8	124173385	-	Island	2.71	2.03E-08	0.000196
cg03749037	chr4	103682875	MANBA	S_Shore	1.23	2.03E-08	0.000196
cg10187674	chr17	67323922	ABCA5	S_Shore	1.92	2.05E-08	0.000196
cg26188543	chr3	148664839	-	OpenSea	1.28	2.07E-08	0.000196
cg02593403	chr10	102278918	SEC31B	N_Shore	1.05	2.15E-08	0.000199
cg09364688	chr1	36038877	TFAP2E	N_Shore	1.32	2.19E-08	0.000199
cg14853772	chr2	9613781	IAH1	N_Shore	1.2	2.19E-08	0.000199
cg14237604	chr3	179064487	MFN1	N_Shore	2.5	2.26E-08	0.000202
cg03552293	chr3	113160183	WDR52	N_Shore	1.41	2.32E-08	0.000203
cg05820491	chr20	35169594	MYL9	S_Shore	1.09	2.33E-08	0.000203
cg19025461	chr1	16163610	FLJ37453	N_Shore	1.34	2.44E-08	0.000206
cg16345520	chr14	60432168	LRRC9	OpenSea	1.79	2.44E-08	0.000206

Supplementary Table 2 continued…							
cg20042692	chr2	55450874	C2orf63	Island	2.98	2.47E-08	0.000206
cg15294435	chr10	116391467	ABLIM1	Island	1.32	2.51E-08	0.000206
cg17788570	chr5	122180522	SNX24	N_Shore	1.61	2.53E-08	0.000206
cg03589001	chr15	79164714	MORF4L1	N_Shore	1.33	2.55E-08	0.000206
cg01315572	chr10	116391550	ABLIM1	Island	1.34	2.59E-08	0.000206
cg11182518	chr5	55117965	-	Island	1.35	2.62E-08	0.000206
cg01510388	chr8	65711658	CYP7B1	Island	1.81	2.76E-08	0.000215
cg16763089	chr20	5485284	LOC149837	OpenSea	2.06	2.90E-08	0.000223
cg05766251	chr17	37024760	LASP1	N_Shore	1.17	2.93E-08	0.000223
cg23579199	chr2	73497077	FBXO41	S_Shore	1.25	3.29E-08	0.000241
cg11966450	chr18	59992157	TNFRSF11A	Island	1.5	3.35E-08	0.000241
cg08894761	chr2	31806234	SRD5A2	Island	1.23	3.37E-08	0.000241
cg13876206	chr6	52861201	GSTA4	S_Shore	1.29	3.38E-08	0.000241
cg14769991	chr6	112688311	-	Island	1.57	3.39E-08	0.000241
cg26677783	chr3	169684118	SEC62	N_Shore	1.31	3.41E-08	0.000241
cg01907562	chr22	32072708	-	OpenSea	1.21	3.53E-08	0.000241
cg14076195	chr1	26233459	STMN1	Island	1.55	3.55E-08	0.000241
cg18304498	chr15	101389882	-	Island	2.09	3.58E-08	0.000241
cg23117796	chr15	101389700	-	N_Shore	2.06	3.68E-08	0.000241
cg13494481	chr15	101390350	-	S_Shore	1.15	3.69E-08	0.000241
cg16750440	chr10	105992436	C10orf79	S_Shore	1.24	3.71E-08	0.000241
cg16578742	chr5	35617687	SPEF2	N_Shore	1.28	3.73E-08	0.000241
cg02413092	chr7	156741538	NOM1	Island	1.3	3.76E-08	0.000241
cg01253612	chr9	77502715	TRPM6	S_Shore	1.25	3.83E-08	0.000241
cg03163459	chr5	76373719	ZBED3	Island	1.95	3.83E-08	0.000241
cg04988061	chr3	43731533	ABHD5	N_Shore	1.5	3.92E-08	0.000245
cg19275978	chr2	60983087	PAPOLG	N_Shore	1.32	4.00E-08	0.000247
cg02558611	chr5	118324627	DTWD2	S_Shore	1.28	4.08E-08	0.000247
cg01634275	chr6	144417437	SF3B5	S_Shore	3.01	4.17E-08	0.000247
cg10903903	chr6	27647843	-	Island	3.05	4.19E-08	0.000247
cg22757019	chr7	91808805	-	S_Shore	1.57	4.20E-08	0.000247
cg03252977	chr20	443540	TBC1D20	S_Shore	1.27	4.22E-08	0.000247
cg21757368	chr6	121656329	C6orf170	S_Shore	1.11	4.47E-08	0.000259
cg26158288	chr7	87563052	ADAM22	N_Shore	1.11	4.59E-08	0.000259
cg06797156	chr8	124173733	-	S_Shore	1.67	4.67E-08	0.000261
cg19791813	chr19	44555139	ZNF223	OpenSea	1.71	4.83E-08	0.000268
cg03727015	chr7	100231133	TFR2	Island	2.54	5.00E-08	0.000275