Table SI. Compound heterozygous single nucleotide variant pairs identified.

Gene	**Chr**	**Position**	**Effect**	**Genotype**		**Depth of coverage in twin A**		**Variant frequency in twin A, %**	**Depth of coverage in twin B**		**Variant frequency in twin B, %**
				Ref	Alt	Ref	Alt		Ref	Alt	
MYH13	17	10355094	Missense	T	C	11	16	59	10	14	58
	17	10364477	Missense	C	T	12	8	40	11	10	48
SERPINH1	11	75571891	Missense	G	A	15	19	56	18	19	51
	11	75566641	Missense	G	A	22	14	39	22	18	45
MYO7A	11	77197505	Missense	A	G	19	20	51	17	15	47
	11	77157323	Missense	G	A	11	10	48	8	9	53
UGT1A1	2	233767132	Missense	A	G	15	20	57	18	23	56
	2	233772415	Missense	C	T	18	14	44	19	15	44
KRT36	17	41488264	Missense	C	A	18	28	61	14	15	52
	17	41489742	Missense	C	T	24	18	43	16	15	48
CHRNE	17	4900230	Other	A	G	19	12	39	15	14	48
	17	4898842	Missense	A	G	12	19	61	14	14	50
TECPR1	7	98243546	Missense	C	T	13	10	43	14	12	46

	7	98230972	Missense	G	T	14	14	50	16	15	48
TRIM10	6	30154437	Missense	G	A	18	16	47	18	25	58
	6	30156991	Missense	C	T	14	16	53	26	20	43

Alt; alternative allele, *MYH13*, myosin heavy chain 13; *SERPINH1*, serpin family H member 1; *MYO7A*, myosin VIIA; *UGT1A1*, UDP glucuronosyltransferase family 1 member A1; *KRT36*, keratin 36; *CHRNE*, cholinergic receptor nicotinic ε subunit; *TECPR1*, tectonin β-propeller repeat containing 1; *TRIM10*, tripartite motif containing 10.

Table SII. Significantly enriched Gene Ontology biological processes associated with differentially methylated regions.

Binomial rank	**ID**	**Description**	**Binomial raw P-value**	**Binomial false discovery rate (q-value)**	**Binomial fold enrichment**	**Binomial observed region hits**	**Binomial region set coverage**
1	GO:0007420	brain development	9.35×10^{-10}	1.21×10^{-5}	11.60	12	0.0543
2	GO:0060322	head development	1.66×10^{-9}	1.07×10^{-5}	11.00	12	0.0543
3	GO:0021879	forebrain neuron differentiation	1.46×10^{-8}	6.27×10^{-5}	69.40	5	0.0226
4	GO:0007417	central nervous system development	1.52×10^{-8}	4.92×10^{-5}	9.00	12	0.0543
5	GO:0021872	forebrain generation of neurons	4.23×10^{-8}	1.09×10^{-4}	55.90	5	0.0226
6	GO:0021884	forebrain neuron development	1.14×10^{-7}	2.45×10^{-4}	96.90	4	0.0181
7	GO:0030900	forebrain development	2.41×10^{-7}	4.45×10^{-4}	13.20	8	0.0362
8	GO:0030182	neuron differentiation	2.51×10^{-7}	4.05×10^{-4}	7.80	11	0.0498
9	GO:0021830	interneuron migration from the subpallium to the cortex	2.58×10^{-7}	3.71×10^{-4}	257.00	3	0.0136
10	GO:0001764	neuron migration	7.29×10^{-7}	9.42×10^{-4}	31.30	5	0.0226
11	GO:0022029	telencephalon cell migration	1.43×10^{-6}	1.68×10^{-3}	51.10	4	0.0181
12	GO:0021953	central nervous system	1.46×10^{-6}	1.57×10^{-3}	17.80	6	0.0271

		neuron differentiation					
13	GO:0021885	forebrain cell migration	1.78x10^{-6}	1.77x10^{-3}	48.30	4	0.0181
14	GO:0048663	neuron fate commitment	2.36x10^{-6}	2.18x10^{-3}	24.60	5	0.0226
15	GO:0021954	central nervous system neuron development	3.36x10^{-6}	2.89x10^{-3}	41.10	4	0.0181
16	GO:0021537	telencephalon development	5.13x10^{-6}	4.14x10^{-3}	14.20	6	0.0271
17	GO:0009887	animal organ morphogenesis	8.92x10^{-6}	6.78x10^{-3}	6.84	9	0.0407
18	GO:0021799	cerebral cortex radially oriented cell migration	1.24x10^{-5}	8.89x10^{-3}	70.30	3	0.0136
19	GO:0003002	regionalization	1.85x10^{-5}	1.26x10^{-2}	11.30	6	0.0271
20	GO:0021853	cerebral cortex GABAergic interneuron migration	2.80x10^{-5}	1.81x10^{-2}	266.00	2	0.0091
21	GO:0021894	cerebral cortex GABAergic interneuron development	3.40x10^{-5}	2.09x10^{-2}	241.00	2	0.0091
22	GO:0021795	cerebral cortex cell migration	3.55x10^{-5}	2.09x10^{-2}	49.20	3	0.0136
23	GO:0016477	cell migration	3.88x10^{-5}	2.18x10^{-2}	6.53	8	0.0362
24	GO:2000177	regulation of neural precursor cell proliferation	5.25x10^{-5}	2.83x10^{-2}	20.30	4	0.0181
25	GO:0008284	positive regulation of cell	5.52x10^{-5}	2.85x10^{-2}	6.21	8	0.0362

		proliferation					
26	GO:0007389	pattern specification process	6.20x10^{-5}	3.08x10^{-2}	9.09	6	0.0271
27	GO:0048732	gland development	6.42x10^{-5}	3.07x10^{-2}	9.03	6	0.0271
28	GO:0021800	cerebral cortex tangential migration	6.72x10^{-5}	3.10x10^{-2}	172.00	2	0.0091
29	GO:0045596	negative regulation of cell differentiation	7.26x10^{-5}	3.23x10^{-2}	7.08	7	0.0317
30	GO:0048870	cell motility	8.05x10^{-5}	3.46x10^{-2}	5.88	8	0.0362
31	GO:0045165	cell fate commitment	8.45x10^{-5}	3.52x10^{-2}	11.60	5	0.0226
32	GO:0050768	negative regulation of neurogenesis	8.58x10^{-5}	3.46x10^{-2}	11.50	5	0.0226
33	GO:0021892	cerebral cortex GABAergic interneuron differentiation	8.96x10^{-5}	3.51x10^{-2}	148.00	2	0.0091
34	GO:0051961	negative regulation of nervous system development	1.15x10^{-4}	4.36x10^{-2}	10.80	5	0.0226
35	GO:0050767	regulation of neurogenesis	1.25x10^{-4}	4.60x10^{-2}	6.48	7	0.0317