

**Additional file1: Table S1** List of 216 CpG sites and characteristics that were significantly associated with gestational age at birth

CpG	Selection Probability	p-value	CHR	Mapinfo	Annotated Genes	CpG location relative to gene	Relation to CpG island
cg03564730	83	1.57E-05	2	310099	<i>ALKAL2;</i> <i>ACP1;</i> <i>SH3YL1</i>		S_Shore
cg01195858	82	0.0002997	20	42839569	<i>C20orf111</i>	TSS200	Island
cg20118857	81	5.15E-07	17	48228624	<i>PPP1R9B</i>	TSS1500	Island
cg02733604	80	7.44E-05	7	569418	<i>PDGFA;</i> <i>PRKAR1B;</i> <i>FLJ44511</i>		N_Shore
cg17966227	79	4.64E-06	1	113738233	<i>LRIG2;</i> <i>MAGI3;</i> <i>SLC16A</i>		N_Shelf
cg19102771	79	2.95E-05	2	223166909	<i>CCDC140</i>	5'UTR	N_Shore
cg11408933	78	1.72E-05	5	141191429	<i>PCDH1;</i> <i>LOC719080;</i> <i>BC127870</i>		
cg14341558	78	8.73E-06	20	46131144	<i>NCOA3</i>	5'UTR	S_Shore
cg06155606	77	0.0002644	11	6704862	<i>MRPL17</i>	TSS1500	Island
cg16250330	77	4.26E-05	1	184943561	<i>FAM129A</i>	1stExon; 5'UTR	Island
cg22911867	77	0.0001613	11	126173548	<i>DCPS</i>	TSS200	Island
cg01740172	76	1.33E-05	3	18485840	<i>SATB1</i>		Island
cg18018245	76	0.0001234	1	167906535	<i>BRP44;</i> <i>DCAF6</i>	TSS1500; Body	Island
cg13153394	75	2.09E-05	3	45209196	<i>CDCP1;</i> <i>TMEM158</i>		
cg01432087	74	0.0001164	11	67242162	<i>TMEM134;</i> <i>AIP</i>		
cg05147765	74	6.19E-05	17	66555864	<i>FAM20A</i>	Body; TSS1500	
cg02827082	72	3.87E-05	18	7012277	<i>LAMA1</i>	Body	S_Shore

cg04699462	71	0.0004236	7	101328918	<i>MYL10;</i> <i>COL26A1;</i> <i>CUX1</i>			N_Shelf
cg08706837	71	1.12E-05	1	37940090	<i>ZC3H12A</i>	TSS200		Island
cg26282283	71	7.68E-05	7	2704368	<i>TTYH3</i>	3'UTR		S_Shelf
cg27431625	71	9.62E-05	2	107679531	<i>ST6GAL2</i>			
cg02698622	70	4.40E-05	2	242698811	<i>D2HGDH</i>	Body		
cg04391722	70	6.76E-05	8	81397601	<i>ZBTB10</i>	TSS1500		N_Shore
cg04829993	70	0.0001496	10	71561459	<i>COL13A1</i>	TSS200		Island
cg08418172	70	0.0001391	19	55791495	<i>HSPBP1</i>	5'UTR; 1stExon		Island
cg13548607	70	7.55E-05	12	91396741	<i>EPYC</i>	5'UTR		
cg18088494	70	0.0001289	1	16494143	<i>EPHA2;</i> <i>ARHGEF19</i>			Island
cg00991871	69	0.0001335	1	214358938	<i>SMYD2;</i> <i>PROX1;</i> <i>PTPN14</i>			N_Shore
cg05628381	69	0.0001386	19	982985	<i>WDR18</i>	TSS1500		Island
cg14795268	69	0.0001217	1	1341852	<i>MRPL20</i>	Body		N_Shore
cg25388264	69	6.85E-05	5	1168528	<i>BC032469;</i> <i>SLC6A19;</i> <i>SLC12A7;</i> <i>SLC6A18;</i> <i>TERT</i>			N_Shelf
cg07813142	68	9.16E-05	2	171573223	<i>SP5</i>	Body		Island
cg15664075	68	0.0002314	19	11456960	<i>CCDC159;</i> <i>TMEM205</i>	TSS1500; 5'UTR; 1stExon		Island
cg27109657	68	0.0001124	16	86909402	<i>AK125749;</i> <i>BC041439</i>			N_Shelf
cg03948415	67	6.30E-05	12	54718738	<i>COPZ1</i>	TSS200		
cg05081629	67	0.0001833	8	100906015	<i>COX6C</i>	TSS200		S_Shore

cg06690899	67	4.69E-05	11	6285281	<i>CCKBR</i>	Body	S_Shelf
cg09154794	67	0.0004376	1	28239160	<i>RPA2</i>	Body	N_Shore
cg13013671	67	4.32E-05	5	114632084	<i>CCDC112</i>	Body; TSS200	Island
cg13315970	67	0.0002774	6	86159197	<i>NT5E</i>	TSS200	N_Shore
cg14218275	67	2.78E-05	10	11047435	<i>CUGBP2</i>	Body	
cg24738650	67	3.01E-05	1	113465464	<i>AFARP1; SLC16A1</i>	TSS1500; Body	
cg24918705	67	0.0002123	5	140501321	<i>PCDHB4</i>	TSS1500	N_Shore
cg26627405	67	0.000212	10	112104964	<i>SMNDC1; MXI1; DUSP5</i>		
cg02902477	66	0.0006042	6	26197071	<i>HIST1H3D</i>	Body	Island
cg03593076	66	2.02E-05	18	55866456	<i>NEDD4L</i>	5'UTR; Body	S_Shelf
cg07148818	66	0.0001527	17	8028835	<i>HES7</i>	TSS1500	Island
cg15000794	66	0.0002513	7	86849844	<i>C7orf23</i>	TSS1500	Island
cg16434546	66	0.000628	5	64063849	<i>SFRS12IP1; SDCCAG10</i>	Body; TSS1500	N_Shore
cg19508967	66	0.0003228	5	1840347	<i>NDUFS6; IRX4; MRPL36</i>		
cg25024993	66	0.0001504	5	140248610	<i>PCDHA7; PCDHA6; PCDHA11</i>	Body; 1stExon	N_Shore
cg27602786	66	0.0002672	16	30934666	<i>NCRNA00095; FBXL19</i>	TSS200; TSS1500	Island
cg00955096	65	0.0002403	6	125475363	<i>TPD52L1</i>	Body; TSS200	Island
cg12814529	65	0.0003409	12	103890083	<i>C12orf42</i>	TSS1500	S_Shore

cg18753664	65	0.000238	12	124515061	<i>ZNF664;</i> <i>CCDC92;</i> <i>DNAH10</i>		
cg19882663	65	0.0001381	3	180308459	<i>TTC14;</i> <i>CCDC39</i>		
cg21851142	65	0.0001891	6	132129008	<i>ENPP1</i>	TSS200	Island
cg23992410	65	0.0002046	1	214160848	<i>PROX1</i>	TSS1500	Island
cg07615781	64	0.0002507	11	71350888	<i>FAM86C1;</i> <i>KRTAP5-11;</i> <i>KRTAP5-10</i>		Island
cg09553448	64	0.0003427	9	134000424	<i>NUP214</i>	TSS1500	N_Shore
cg10454162	64	0.0001126	3	113955940	<i>ZNF80</i>	5'UTR; 1stExon	
cg19718882	64	0.0003895	11	32458714	<i>WIT1</i>	Body	N_Shore
cg24389632	64	7.46E-05	10	38146246	<i>ZNF248</i>	5'UTR; 1stExon	N_Shore
cg26892368	64	0.0004097	10	97416665	<i>ALDH18A1</i>	TSS200	Island
cg06308084	63	0.0006912	22	50493570	<i>TTLL8</i>	TSS1500	N_Shelf
cg08792584	63	0.0002955	11	43899178	<i>ALKBH3;</i> <i>HSD17B12</i>		N_Shelf
cg11523059	63	0.0001731	6	46921096	<i>GPR116</i>	5'UTR	
cg12794421	63	0.0002839	8	19171191	<i>SH2D4A</i>	TSS200	Island
cg16505550	63	0.0002262	1	57045708	<i>PPAP2B</i>	TSS1500	S_Shore
cg17120366	63	0.0002029	10	28571322	<i>MPP7</i>	TSS1500	
cg21497602	63	0.0002786	12	12715811	<i>DUSP16</i>	TSS1500	S_Shore
cg25965499	63	0.0006054	19	1885691	<i>FAM108A1</i>	TSS200	S_Shore
cg10220068	62	0.0002956	5	179770007	<i>GFPT2</i>	Body	
cg11454936	62	0.0002332	6	167184995	<i>RPS6KA2</i>	Body	
cg14537800	62	4.45E-05	4	15964950	<i>FGFBP2</i>	TSS200	

cg15630459	62	0.0001165	5	175223225	<i>CPLX2</i>	TSS1500	N_Shore
cg15664909	62	0.0003183	17	685709	<i>GLOD4; RNMTL1</i>	TSS200; 1stExon	Island
cg18314121	62	9.11E-05	1	225726360	<i>ENAH</i>	Body	
cg27597392	62	4.42E-05	12	12753718	<i>CREBL2; DUSP16</i>		
cg00911376	61	0.0005774	16	84274417	<i>KCNG4</i>	TSS1500	S_Shelf
cg01084379	61	0.0006116	5	179160712	<i>MAML1</i>	Body	S_Shore
cg01900371	61	4.16E-05	2	27256120	<i>TMEM214</i>	Body	Island
cg11718315	61	0.0002811	15	65579480	<i>PARP16</i>	TSS1500	Island
cg15090899	61	0.0001347	6	167178260	<i>RPS6KA2</i>	Body	
cg16540921	61	0.0004033	16	86588494	<i>MTHFSD</i>	Body; 5'UTR	Island
cg17973394	61	0.0006905	15	25684267	<i>UBE3A</i>	TSS200	Island
cg07754138	60	0.0002435	22	46973496	<i>CELSR1; GRAMD4; CERK</i>		Island
cg08199544	60	0.0006667	5	140418	<i>PLEKHG4B</i>	5'UTR; 1stExon	
cg12851526	60	8.67E-05	7	100609034	<i>MUC3A; AK057259; AK096803; MUC3B</i>		Island
cg18320379	60	0.0003056	11	75947361	<i>WNT11; UVRAG; PRKRIR</i>		Island
cg18608017	60	0.0003267	10	73158072	<i>CDH23</i>	5'UTR	S_Shore
cg24323328	60	0.0002215	12	1099998	<i>ERC1</i>	TSS1500	Island
cg00118365	59	0.0003418	5	140779112	<i>PCDHGA4; PCDHGB5; PCDHGA6</i>	Body; 1stExon	Island

cg00646621	59	0.0003368	2	235949598	<i>SH3BP4</i>	Body	N_Shore
cg05194808	59	0.0001778	21	47405786	<i>COL6A1</i>	Body	N_Shore
cg06715928	59	0.0004612	10	112257500	<i>DUSP5</i>	TSS200	Island
cg10744200	59	0.0003013	4	24844162	<i>CCDC149</i>	Body	
cg12392225	59	0.0005448	2	3464066	<i>TTC15</i>	Body	S_Shelf
cg16637873	59	0.0004348	12	6982822	<i>SPSB2</i>	TSS1500	Island
cg16767964	59	0.0001994	14	21167096	<i>RNASE4</i>	5'UTR	
cg18643199	59	0.0005881	10	82363313	<i>SH2D4B</i>	Body	
cg20547031	59	0.0006331	7	31381526	<i>NEUROD6</i>	TSS1500	
cg22745781	59	0.0002844	7	16461244	<i>ISPD</i>	TSS1500	Island
cg00783553	58	0.0004489	1	7023495	<i>CAMTA1</i>	Body	S_Shore
cg05198596	58	0.0001313	12	113591127	<i>CCDC42B</i>	Body	Island
cg09960435	58	0.0003222	19	44323775	<i>LYPD5</i>	5'UTR	N_Shore
cg18317951	58	0.0003042	8	96145702	<i>PLEKHF2</i>	TSS1500	N_Shore
cg20002523	58	0.000247	1	54665230	<i>CYB5RL;</i> <i>MRPL37</i>	5'UTR; TSS1500	N_Shore
cg21752383	58	0.0004731	5	140739976	<i>PCDHGA4;</i> <i>PCDHGA2;</i> <i>PCDHGB2</i>	Body; 1stExon	N_Shore
cg22534374	58	0.0006553	1	201511610	<i>RPS10P7;</i> <i>CSRP1;</i> <i>PHLDA3</i>		S_Shelf
cg25403084	58	0.0004747	7	6048832	<i>PMS2;</i> <i>AIMP2</i>	TSS200	Island
cg05155578	57	0.0008234	6	88032202	<i>GJB7;</i> <i>C6orf162</i>	5'UTR; TSS200	Island
cg05645292	57	0.0004194	3	59795625	<i>FHIT</i>	Body	
cg16857548	57	0.0004433	18	3011965	<i>LPIN2</i>	TSS200	N_Shore
cg17046855	57	0.0001871	7	6749638	<i>ZNF12;</i> <i>PMS2CL</i>		S_Shelf

cg18454916	57	0.0004311	8	74005562	<i>C8orf84</i>	TSS200	Island
cg20413202	57	0.000616	1	10056853	<i>RBP7</i>	TSS1500	N_Shore
cg21470142	57	0.0003724	8	41732895	<i>ANK1</i>	Body	N_Shore
cg21605452	57	0.0012944	3	176915282	<i>TBL1XR1</i>	TSS1500	N_Shore
cg24693982	57	0.0004843	6	144508735	<i>STX11</i>	3'UTR	S_Shore
cg00107629	56	0.0005711	11	46389307	<i>DGKZ</i>	Body	Island
cg00480331	56	0.0010039	3	187455371	<i>BCL6</i>	5'UTR; TSS1500	Island
cg03193847	56	0.000856	4	169637496	<i>PALLD</i>	Body	
cg05180182	56	0.0003354	10	3666755	<i>KLF6</i>		
cg05185021	56	0.000591	17	2324794	<i>METT10D</i>	Body	
cg05817664	56	0.0005699	1	212731921	<i>ATF3; FAM71A; NENF</i>		Island
cg16255150	56	0.0001496	14	73924775	<i>NUMB</i>	5'UTR	Island
cg21680208	56	0.002076	12	82752713	<i>CCDC59; C12orf26</i>	TSS1500; Body	Island
cg25538235	56	0.0002037	18	70211974	<i>CBLN2</i>	TSS1500	S_Shore
cg05838155	55	0.0003626	17	37557276	<i>FBXL20</i>	Body	N_Shore
cg06143663	55	0.0001909	16	11242115	<i>CLEC16A</i>	Body	
cg09409311	55	0.0003184	19	45457933	<i>CLPTM1</i>	TSS1500	N_Shore
cg10492152	55	0.0017821	6	52051113	<i>IL17A</i>	TSS200	
cg12116137	55	0.0003915	17	1576449	<i>PRPF8</i>	Body	
cg13408347	55	0.000483	12	91347805	<i>C12orf12</i>	1stExon	Island
cg17192533	55	0.0004368	4	160408494	<i>RAPGEF2</i>		
cg17353896	55	0.0005827	2	209116254	<i>IDH1</i>	Body	N_Shelf
cg17996591	55	0.0007001	3	88198870	<i>C3orf38</i>	TSS200	Island
cg20781212	55	0.0011189	22	35653362	<i>HMGXB4</i>	TSS200	Island
cg22242857	55	0.0010964	18	76751952	<i>SALL3</i>	Body	Island
cg27475652	55	0.0006154	8	24774727	<i>NEFM</i>	Body	S_Shelf
cg01477015	54	0.000599	16	28948319	<i>CD19</i>	Body	Island

cg01547733	54	0.0005774	6	153304507	<i>FBXO5</i>	1stExon; 5'UTR; TSS1500	Island
cg02337277	54	0.0004764	6	52795627	<i>GSTA3; GSTA4</i>		
cg04214430	54	0.0026281	13	50702707	<i>DLEU1; DLEU2</i>		N_Shore
cg04630171	54	0.0003781	12	121735002	<i>CAMKK2</i>	5'UTR	Island
cg05277991	54	0.0005186	3	69788295	<i>MITF</i>	TSS1500	N_Shore
cg07838205	54	0.0002758	1	110091179	<i>GNAI3</i>	TSS200	Island
cg08706141	54	0.0006592	22	20073403	<i>MIR1306; DGCR8</i>	TSS200; 5'UTR	Island
cg11004797	54	0.000431	5	61699868	<i>DIMT1L</i>	TSS200	Island
cg11190156	54	0.0003755	6	26104118	<i>HIST1H4C</i>	TSS200	N_Shore
cg13396152	54	0.0004113	1	62005072	<i>NFIA; TM2D1; PATJ</i>		
cg14642395	54	0.0003853	11	64322079	<i>SLC22A11</i>	TSS1500	
cg15041373	54	0.0008182	19	39577941	<i>PAPL</i>	Body	S_Shelf
cg15608402	54	0.0002754	11	3122933	<i>OSBPL5</i>	Body	
cg19504782	54	0.000245	11	2886232	<i>KCNQ1DN; KCNQ1; CDKN1C; SLC22A18AS</i>		S_Shore
cg22909759	54	0.0002247	14	65185328	<i>PLEKHG3</i>	5'UTR	
cg23081534	54	0.0005247	3	169540079	<i>LRRIQ4</i>	1stExon	
cg27558564	54	0.0001575	3	194325087	<i>TMEM44</i>	Body	
cg03200309	53	0.0006641	12	48722990	<i>H1FNT</i>	5'UTR; 1stExon	N_Shore
cg05150023	53	0.001313	5	42944267	<i>SEPP1; AK056817; LOC648987</i>		Island



cg06823965	53	0.0005732	7	101632645	<i>CUX1</i>	Body	
cg12150994	53	0.0006513	8	2130263	<i>MYOM2;</i> <i>KBTBD11;</i> <i>ARHGEF10</i>		Island
cg12878710	53	0.0012054	3	197517984	<i>LRCH3</i>	TSS200	Island
cg13954965	53	0.000952	2	133175192	<i>GPR39</i>	1stExon	Island
cg14495916	53	0.0010237	3	171800301	<i>FNDC3B</i>	5'UTR	
cg19353425	53	0.0004908	2	69968558	<i>ANXA4</i>	TSS1500	N_Shore
cg19547547	53	0.0009293	5	140166059	<i>PCDHA1</i>	1stExon	Island
cg19840226	53	0.0003743	15	78369626	<i>TBC1D2B</i>	Body	Island
cg21016177	53	0.0001445	17	74100207	<i>EXOC7</i>	TSS1500	S_Shore
cg25803423	53	0.0009276	14	23563820	<i>C14orf119;</i> <i>ACIN1</i>	TSS1500; Body	N_Shore
cg27139077	53	0.0006516	15	43622721	<i>ADAL;</i> <i>LCMT2</i>	TSS200; 5'UTR; 1stExon	Island
cg00307497	52	0.0005601	2	207976271	<i>KLF7</i>	Body	
cg01025774	52	0.0014409	5	42944457	<i>CCDC30</i>		Island
cg01814364	52	0.000246	19	15285108	<i>NOTCH3</i>	Body	Island
cg03068843	52	0.0009537	8	12985953	<i>DLC1</i>	Body	N_Shelf
cg03551406	52	0.0005365	16	56715756	<i>MT1X</i>	TSS1500	N_Shore
cg07934026	52	0.0012898	4	467794	<i>ZNF721;</i> <i>ABCA11P</i>	5'UTR; Body	Island
cg09095914	52	0.0006478	4	649881	<i>PDE6B</i>	Body	N_Shore
cg09204302	52	0.0004042	16	70713462	<i>MTSS1L</i>	Body	Island
cg09601629	52	0.0009597	19	15122224	<i>CCDC105</i>	Body	S_Shore
cg09680131	52	0.0003448	13	111100754	<i>COL4A2</i>	Body	
cg09962807	52	0.0002956	8	70747337	<i>SLCO5A1</i>	TSS200	Island
cg13214121	52	0.0014901	7	157549678	<i>PTPRN2</i>	Body	N_Shore

cg16593941	52	0.000796	16	89351893	<i>ANKRD11</i>	Body	N_Shore
cg18887073	52	0.0010225	19	13001796	<i>GCDH</i>	TSS200	N_Shore
cg19477247	52	0.0002365	3	113955994	<i>ZNF80</i>	5'UTR; 1stExon	
cg20145426	52	0.0007946	1	30179925	<i>BC042538</i>		
cg22544231	52	0.0008891	12	132195441	<i>SFRS8</i>	TSS200	Island
cg22625548	52	0.001611	8	42698722	<i>THAP1</i>	TSS1500	Island
cg24644436	52	0.0009591	10	135202906	<i>PAOX</i>	Body; 3'UTR	N_Shore
cg25338902	52	0.0005156	3	15828883	<i>ANKRD28</i>	Body	
cg26167744	52	0.0003319	12	124068794	<i>TMED2</i>	TSS1500	N_Shore
cg00712686	51	0.0011502	17	46102784	<i>COPZ2; NFE2L1; CDK5RAP3</i>		Island
cg01190171	51	0.0011749	6	31126373	<i>CCHCR1; TCF19</i>	1stExon; TSS1500; 5'UTR	Island
cg03566107	51	0.0002816	18	70211962	<i>CBLN2</i>	TSS1500	S_Shore
cg06326971	51	0.0003866	16	57836692	<i>KIFC3</i>	TSS1500	Island
cg06996372	51	0.0008081	1	16271373	<i>ZBTB17</i>	Body	Island
cg11444704	51	0.0009176	5	159738916	<i>CCNJL</i>	Body	Island
cg12097080	51	0.0016491	14	88793139	<i>KCNK10</i>	1stExon; 5'UTR	Island
cg14834903	51	0.0004979	14	73712902	<i>PAPLN</i>	Body	Island
cg17366378	51	0.001068	15	45458906	<i>SHF; DUOX1</i>		Island
cg17725364	51	0.0004795	2	238280514	<i>COL6A3</i>	Body	Island
cg20494553	51	0.0001616	4	71554112	<i>UTP3</i>	TSS200	Island
cg21275702	51	0.0003956	20	18269109	<i>ZNF133</i>	TSS200	Island
cg21336650	51	0.0004861	17	78161706	<i>CARD14</i>	Body; 5'UTR; 1stExon	N_Shelf
cg23234828	51	0.000867	14	55818341	<i>FBXO34</i>	Body; Body	
cg24954670	51	0.0026624	3	50337092	<i>HYAL3; NAT6</i>	TSS200; TSS1500	S_Shore

cg02539518	50	0.0008797	2	113915155	<i>PSD4; IL1RN</i>		Island
cg02583334	50	0.0009703	3	180397599	<i>CCDC39</i>	TSS1500	Island
cg09728102	50	0.0004842	5	66124492	<i>MAST4</i>	TSS200; Body	
cg14474582	50	0.0004689	5	176924578	<i>PDLIM7</i>	1stExon; 5'UTR	Island
cg22548000	50	0.0004356	2	32391035	<i>SLC30A6</i>	Body	S_Shore
cg24797187	50	0.0008095	2	100175768	<i>AFF3</i>	Body	
cg24900963	50	0.0003984	16	28948266	<i>CD19</i>	Body	Island
cg25217428	50	0.0014714	1	168148809	<i>TIPRL</i>	Body	S_Shore

**Additional file1: Table S2** Description of the genes that appeared in the biological pathways

GO: 0098742		GO:0007156	
Gene Name	Gene Symbol	Gene Name	Gene Symbol
<i>CDH23</i>	cadherin related 23	<i>CDH23</i>	cadherin related 23
<i>PCDHGB5</i>	protocadherin gamma subfamily B, 5	<i>PCDHGB5</i>	protocadherin gamma subfamily B, 5
<i>PCDHGB2</i>	protocadherin gamma subfamily B, 2	<i>PCDHGB2</i>	protocadherin gamma subfamily B, 2
<i>PCDHGA6</i>	protocadherin gamma subfamily A, 6	<i>PCDHGA6</i>	protocadherin gamma subfamily A, 6
<i>PCDHGA4</i>	protocadherin gamma subfamily A, 4	<i>PCDHGA4</i>	protocadherin gamma subfamily A, 4
<i>PCDHGA2</i>	protocadherin gamma subfamily A, 2	<i>PCDHGA2</i>	protocadherin gamma subfamily A, 2
<i>PCDHB4</i>	protocadherin beta 4	<i>PCDHB4</i>	protocadherin beta 4
<i>PCDHA11</i>	protocadherin alpha 11	<i>PCDHA11</i>	protocadherin alpha 11
<i>PCDHA7</i>	protocadherin alpha 7	<i>PCDHA7</i>	protocadherin alpha 7
<i>PCDHA6</i>	protocadherin alpha 6	<i>PCDHA6</i>	protocadherin alpha 6
<i>PCDHA1</i>	protocadherin alpha 1	<i>PCDHA1</i>	protocadherin alpha 1
<i>CELSR1</i>	cadherin EGF LAG seven-pass G-type receptor 1	<i>CELSR1</i>	cadherin EGF LAG seven-pass G-type receptor 1
<i>PCDH1</i>	protocadherin 1	<i>PCDH1</i>	protocadherin 1
<i>IL1RN</i>	interleukin 1 receptor antagonist		

**A**

**Additional file1: Table S3** Correlation between DNA methylation levels of pathway-related CpGs and expression levels of annotated genes in offspring umbilical cord blood (IoWBC, n=132)

Probe Name	Annotated Gene	CpG	Spearman coefficient (n=132)	p-value
A_23_P422044	<i>PCDHGA2</i>		0.0026	0.9760
A_24_P334529	<i>PCDHGA3</i>		-0.1210	0.1653
A_33_P3395651	<i>PCDHGA5</i>		-0.0152	0.8622
A_24_P308851	<i>PCDHGA7</i>		0.0005	0.9954
A_23_P390545	<i>PCDHGA8</i>		-0.0454	0.6036
A_23_P364414	<i>PCDHGA9</i>		-0.0844	0.3344
A_33_P3417611	<i>PCDHGA12</i>		0.0419	0.6322
A_23_P411772	<i>PCDHGB1</i>		-0.1014	0.2454
A_23_P395418	<i>PCDHGB2</i>	cg00118365	-0.1081	0.2154
A_23_P359588	<i>PCDHGB3</i>		0.0723	0.4082
A_23_P415470	<i>PCDHGB4</i>		-0.0453	0.6045
A_33_P3410981	<i>PCDHGB6</i>		-0.0496	0.5710
A_23_P218937	<i>PCDHGB7</i>		-0.0579	0.5080
A_33_P3422301	<i>PCDHGC3</i>		-0.0471	0.5905
A_32_P32856	<i>PCDHGC4</i>		-0.0515	0.5563
A_24_P34944	<i>PCDHGC5</i>		-0.0454	0.6039
A_33_P3246829	<i>IL1RN</i>	cg02539518	-0.1346	0.1224
A_33_P3246833	<i>IL1RN</i>		-0.0460	0.5995
A_21_P0012311	<i>CELSR1</i>		-0.0523	0.5497
A_23_P132378	<i>CELSR1</i>		-0.1445	0.0971
A_33_P3328653	<i>CELSR1</i>	cg07754138	-0.0109	0.9013
A_33_P3328659	<i>CELSR1</i>		-0.0688	0.4311
A_24_P234838	<i>PCDH1</i>	cg11408933	-0.0604	0.4901
A_33_P3349637	<i>PCDH1</i>		0.0854	0.3284
A_23_P217946	<i>CDH23</i>		-0.0224	0.7982
A_23_P307968	<i>CDH23</i>	cg18608017	-0.0652	0.4560
A_23_P364437	<i>CDH23</i>		0.1201	0.1685
A_33_P3403693	<i>PCDHA1</i>		0.0225	0.7968
A_33_P3391846	<i>PCDHA2</i>		-0.0506	0.5627
A_33_P3332521	<i>PCDHA3</i>		-0.0291	0.7398
A_33_P3318002	<i>PCDHA4</i>		-0.0376	0.6673
A_33_P3258546	<i>PCDHA5</i>		-0.0279	0.7498
A_33_P3352867	<i>PCDHA6</i>	cg19547547	-0.0112	0.8986
A_33_P3355608	<i>PCDHA7</i>		-0.0278	0.7510
A_33_P3250695	<i>PCDHA8</i>		-0.0684	0.4340
A_23_P323102	<i>PCDHA9</i>		-0.0592	0.4984
A_33_P3281299	<i>PCDHA10</i>		-0.0155	0.8595
A_24_P360206	<i>PCDHA11</i>		-0.0348	0.6910

A_33_P3329274	<i>PCDHA12</i>		0.0269	0.7586
A_33_P3210934	<i>PCDHA13</i>		-0.0571	0.5141
A_24_P191931	<i>PCDHAC1</i>		0.0299	0.7330
A_23_P218942	<i>PCDHAC2</i>		-0.0413	0.6374
A_23_P422044	<i>PCDHGA2</i>		-0.0470	0.5913
A_24_P334529	<i>PCDHGA3</i>		0.0220	0.8012
A_33_P3395650	<i>PCDHGA5</i>		0.0004	0.9601
A_23_P435444	<i>PCDHGA7</i>		-0.0849	0.3313
A_23_P354734	<i>PCDHGA8</i>		-0.1481	0.0890
A_23_P364414	<i>PCDHGA9</i>		-0.1319	0.1301
A_24_P34944	<i>PCDHGA12</i>		0.0519	0.5528
A_23_P310972	<i>PCDHGB1</i>	<b>cg21752383</b>	0.0098	0.9105
A_23_P411772	<i>PCDHGB2</i>		0.0170	0.8463
A_23_P395418	<i>PCDHGB3</i>		0.0850	0.3309
<b>A_23_P359588</b>	<b><i>PCDHGB4</i></b>		<b>0.2726</b>	<b>0.0015</b>
A_23_P415470	<i>PCDHGB6</i>		-0.0198	0.8214
A_23_P370494	<i>PCDHGB7</i>		0.0325	0.7106
A_23_P218937	<i>PCDHGC3</i>		0.0443	0.6124
A_23_P303101	<i>PCDHGC4</i>		0.0617	0.4808
A_32_P32856	<i>PCDHGC5</i>		0.0031	0.9722
A_23_P81262	<i>PCDHB4</i>	cg24918705	-0.0125	0.8869
A_33_P3403693	<i>PCDHA1</i>		-0.0303	0.7294
A_33_P3391846	<i>PCDHA2</i>		-0.0781	0.3715
A_33_P3332521	<i>PCDHA3</i>		-0.1406	0.1064
<b>A_33_P3318002</b>	<b><i>PCDHA4</i></b>		<b>-0.2267</b>	<b>0.0087</b>
A_33_P3258546	<i>PCDHA5</i>		-0.0687	0.4319
A_33_P3352867	<i>PCDHA6</i>		-0.0634	0.4686
A_33_P3355608	<i>PCDHA7</i>		0.0263	0.7640
A_33_P3250695	<i>PCDHA8</i>	<b>cg25024993</b>	-0.1179	0.1767
A_23_P323102	<i>PCDHA9</i>		-0.0706	0.4194
A_33_P3281299	<i>PCDHA10</i>		-0.0101	0.9084
A_33_P3351904	<i>PCDHA11</i>		-0.0923	0.2907
A_33_P3329274	<i>PCDHA12</i>		0.0066	0.9395
A_33_P3210934	<i>PCDHA13</i>		-0.0975	0.2643
A_24_P191931	<i>PCDHAC1</i>		0.0043	0.9611
A_23_P218942	<i>PCDHAC2</i>		-0.0878	0.3151

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Note: Bolded mark represents significant correlation

**Additional file1: Table S4** Correlation between DNA methylation levels of pathway-related CpGs and expression levels of annotated genes in offspring umbilical cord blood (IoWBC, n=47)

CpGs	Annotated Gene	Probe Name	Spearman coefficient	p-value
cg00118365	<i>PCDHGA12</i>	A_24_P34944	0.0488	0.7446
	<i>PCDHGA2</i>	A_23_P422044	0.0430	0.7740
	<i>PCDHGA3</i>	A_24_P334529	-0.0740	0.6210
	<i>PCDHGA5</i>	A_33_P3395650	-0.0599	0.6926
	<i>PCDHGA7</i>	A_23_P435444	0.0451	0.7661
	<i>PCDHGA8</i>	A_23_P354734	-0.1987	0.1807
	<i>PCDHGA9</i>	A_23_P364414	-0.1763	0.2357
	<i>PCDHGB1</i>	A_23_P310972	0.1969	0.1846
	<i>PCDHGB2</i>	A_23_P411772	-0.1482	0.3200
	<i>PCDHGB3</i>	A_23_P395418	-0.1805	0.2247
	<i>PCDHGB4</i>	A_23_P359588	0.2479	0.0968
	<i>PCDHGB6</i>	A_23_P415470	-0.1822	0.2309
	<i>PCDHGB7</i>	A_33_P3410981	-0.0016	0.9914
	<i>PCDHGC3</i>	A_23_P218937	-0.0631	0.6733
	<i>PCDHGC4</i>	A_33_P3422301	-0.0623	0.6773
<i>PCDHGC5</i>	A_32_P32856	0.0072	0.9619	
cg02539518	<i>IL1RN</i>	A_33_P3246833	0.0345	0.8181
	<i>IL1RN</i>	A_33_P3246829	-0.0636	0.6746
cg07754138	<i>CELSR1</i>	A_33_P3328653	-0.2306	0.1189
	<i>CELSR1</i>	A_23_P132378	-0.1649	0.2736
	<i>CELSR1</i>	A_33_P3328659	-0.0315	0.8338
cg11408933	<i>CELSR1</i>	A_21_P0012311	0.0117	0.9379
	<i>PCDH1</i>	A_24_P234838	-0.1272	0.3995
	<i>PCDH1</i>	A_33_P3349637	0.0576	0.7006
cg18608017	<i>CDH23</i>	A_23_P307968	-0.1460	0.3330
	<i>CDH23</i>	A_23_P364437	0.2781	0.0584
	<i>CDH23</i>	A_23_P217946	-0.1708	0.2510
cg19547547	<i>PCDHA1</i>	A_33_P3403693	-0.0076	0.9594
	<i>PCDHA10</i>	A_33_P3281299	0.0115	0.9394
	<i>PCDHA11</i>	A_24_P360206	0.1515	0.3094
	<i>PCDHA12</i>	A_33_P3329274	0.2201	0.1372
	<i>PCDHA13</i>	A_33_P3210934	-0.0392	0.7936
	<i>PCDHA2</i>	A_33_P3391846	0.0223	0.8832
	<i>PCDHA3</i>	A_33_P3332521	-0.0564	0.7064
	<i>PCDHA4</i>	A_33_P3318002	-0.0554	0.7115
<i>PCDHA5</i>	A_33_P3258546	0.0505	0.7389	
<i>PCDHA6</i>	A_33_P3352867	0.1323	0.3754	
<i>PCDHA7</i>	A_33_P3355608	-0.0931	0.5337	
<i>PCDHA8</i>	A_33_P3250695	-0.0559	0.7092	

	<i>PCDHA9</i>	A_23_P323102	0.0828	0.5842
	<i>PCDHAC1</i>	A_24_P191931	0.1362	0.3613
	<i>PCDHAC2</i>	A_23_P218942	-0.0538	0.7223
	<i>PCDHGA12</i>	A_24_P34944	-0.1514	0.3098
	<i>PCDHGA2</i>	A_23_P422044	-0.1736	0.2433
	<i>PCDHGA3</i>	A_24_P334529	-0.0347	0.8169
	<i>PCDHGA5</i>	A_33_P3395651	0.0162	0.9140
	<i>PCDHGA7</i>	A_24_P308851	-0.1599	0.2829
	<i>PCDHGA8</i>	A_23_P390545	-0.0471	0.7562
	<i>PCDHGA9</i>	A_23_P364414	-0.1811	0.2232
cg21752383	<i>PCDHGB1</i>	A_33_P3417611	-0.1632	0.2732
	<i>PCDHGB2</i>	A_23_P411772	0.0651	0.6637
	<i>PCDHGB3</i>	A_23_P395418	0.0888	0.5528
	<i>PCDHGB4</i>	A_23_P359588	0.2179	0.1458
	<i>PCDHGB6</i>	A_23_P415470	-0.0781	0.6100
	<i>PCDHGB7</i>	A_23_P370494	0.0751	0.6161
	<i>PCDHGC3</i>	A_23_P218937	0.0934	0.5322
	<i>PCDHGC4</i>	A_23_P303101	0.0500	0.7388
	<i>PCDHGC5</i>	A_32_P32856	-0.1001	0.5030
cg24918705	<i>PCDHB4</i>	A_23_P81262	-0.1207	0.4243
	<i>PCDHA1</i>	A_33_P3403693	-0.1162	0.4366
	<i>PCDHA10</i>	A_33_P3281299	-0.0452	0.7655
	<i>PCDHA11</i>	A_33_P3351904	-0.2163	0.1488
	<i>PCDHA12</i>	A_33_P3329274	-0.0532	0.7225
	<i>PCDHA13</i>	A_33_P3210934	-0.0488	0.7446
	<i>PCDHA2</i>	A_33_P3391846	-0.1619	0.2824
	<i>PCDHA3</i>	A_33_P3332521	-0.1732	0.2443
cg25024993	<i>PCDHA4</i>	A_33_P3318002	-0.1583	0.2879
	<i>PCDHA5</i>	A_33_P3258546	-0.1091	0.4705
	<i>PCDHA6</i>	A_33_P3352867	-0.0911	0.5424
	<i>PCDHA7</i>	A_33_P3355608	0.1131	0.4491
	<i>PCDHA8</i>	A_33_P3250695	-0.1745	0.2408
	<i>PCDHA9</i>	A_23_P323102	-0.0381	0.8018
	<i>PCDHAC1</i>	A_24_P191931	-0.1204	0.4203
	<i>PCDHAC2</i>	A_23_P218942	-0.1808	0.2293

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