

Suppl. Table 3. Association between GDM, maternal pre-pregnancy BMI and offspring DNA methylation degree

Differentially methylated CpGs		Model 1, n=186		Model 2, n=186		Model 3, n=175			
Gene name	Probe name	Association to GDM		Association to GDM		Association to GDM		Association to pre-preg. BMI	
		β (95% CI)	p-value	β (95% CI)	p-value	β (95% CI)	p-value	β (95% CI)	p-value
<i>PDE6A</i>	cg09109411	-3.0 (-6.2, 0.2)	0.06	-3.2 (-6.4, 0.1)	0.06	-1.6 (-5.0, 1.7)	0.34	-0.4 (-0.7, -0.05)	0.03
	cg11638399	-2.6 (-5.7, 0.5)	0.10	-2.7 (-6.0, 0.5)	0.09	-1.5 (-4.8, 1.8)	0.37	-0.3 (-0.6, -0.04)	0.08
<i>GTPBP5/MTG2</i>	cg21341487	-2.7 (-5.5, 0.1)	0.06	-2.9 (-5.7, 0.01)	0.05	-1.6 (-4.6, 1.3)	0.27	-0.3 (-0.6, -0.01)	0.05
<i>ESM1</i>	cg09452568	-2.8 (-5.4, 0.2)	0.04	-2.7 (-5.4, -0.03)	0.05	-1.7 (-4.4, 1.1)	0.23	-0.3 (-0.6, -0.003)	0.05
<i>TAP2</i>	cg05689267	-1.6 (-2.8, 0.4)	0.01	-1.7 (-2.9, 0.4)	0.01	-1.4 (-2.7, 0.1)	0.03	-0.1 (-0.2, 0.01)	0.23
<i>FBXL13</i>	cg05671644	-2.7 (-4.9, 0.5)	0.02	-2.8 (-5.1, 0.6)	0.01	-2.0 (-4.4, 0.3)	0.09	-0.2 (-0.4, 0.1)	0.16
<i>PRKCZ</i>	cg26930596	-2.7 (-5.3, 0.1)	0.04	-2.8 (-5.6, 0.1)	0.04	-1.8 (-4.6, 1.0)	0.21	-0.2 (-0.5, 0.04)	0.09
<i>PVT1</i>	cg07305933	-2.7 (-5.6, 0.2)	0.07	-2.8 (-5.8, 0.2)	0.07	-1.8 (-5.0, 1.3)	0.25	-0.3 (-0.6, 0.1)	0.11
<i>SYNPO2L</i>	cg19157819	-2.7 (-5.8, 0.4)	0.09	-2.7 (-5.9, 0.5)	0.09	-1.4 (-4.7, 1.9)	0.40	-0.3 (-0.6, 0.02)	0.07
<i>CSPP, COPS5</i>	cg21320567	-2.7 (-5.1, -0.3)	0.03	-2.8 (-5.3, -0.3)	0.03	-1.8 (-4.4, 0.8)	0.16	-0.2 (-0.5, 0.04)	0.10
<i>PCSK5</i>	cg13438337	-3.1 (-5.6, 0.6)	0.02	-3.2 (-5.8, 0.6)	0.02	-2.2 (-4.8, 0.5)	0.11	-0.4 (-0.4, 0.1)	0.15
<i>S100P</i>	cg26233331	-2.6 (-5.4, 0.3)	0.08	-2.7 (-5.6, 0.2)	0.07	-1.5 (-4.5, 1.5)	0.34	-0.3 (-0.6, 0.04)	0.09
<i>CAPN14</i>	cg01627252	-2.8 (-5.6, 0.02)	0.05	-3.0 (-5.9, 0.1)	0.04	-2.0 (-5.0, 1.1)	0.21	-0.2 (-0.5, 0.1)	0.18
<i>GALNT2</i>	cg1335998	-2.2 (-4.6, 0.3)	0.08	-2.2 (-4.7, 0.4)	0.09	-1.6 (-5.0, 1.7)	0.24	-0.1 (-0.4, -0.1)	0.30
<i>TSPAN14</i>	cg11411705	-1.7 (-2.8, -0.5)	0.005	-1.7 (-2.9, -0.5)	0.01	-1.5 (-2.7, -0.2)	0.02	-0.03 (-0.2, 0.1)	0.61
<i>GNAI2</i>	cg26226650	-2.4 (-5.1, 0.3)	0.09	-2.5 (-5.3, 0.3)	0.08	-1.2 (-4.0, 1.7)	0.42	-0.4 (-0.6, -0.02)	0.04
<i>MS4A3</i>	cg14328641	-2.4 (-5.1, 0.3)	0.08	-2.6 (-5.4, 0.3)	0.07	-1.4 (-4.3, 1.5)	0.34	-0.2 (-0.5, 0.1)	0.14
<i>NEO1</i>	cg11357013	-2.6 (-5.6, 0.5)	0.1	-2.7 (-5.9, 0.3)	0.08	-1.5 (-4.7, 1.8)	0.37	-0.3 (-0.6, 0.03)	0.07
	cg02399831	-3.0 (-5.8, -0.2)	0.04	-3.1 (-6.0, -0.2)	0.04	-1.6 (-5.1, 0.8)	0.16	-0.2 (-0.5, 0.1)	0.18
<i>CERK</i>	cg06766034	-3.0 (-5.4, -0.5)	0.02	-3.0 (-5.5, -0.4)	0.02	-2.0 (-4.6, 0.6)	0.12	-0.3 (-0.5, -0.004)	0.05
<i>MIR1304, SNORA8</i>	cg01580228	-2.7 (-5.8, 0.4)	0.09	-2.8 (-6.0, 0.5)	0.10	-1.7 (-5.1, 1.6)	0.31	-0.3 (-0.6, 0.1)	0.14
<i>SNORD5, SNORA18</i>									
<i>IL1RN</i>	cg03989987	-2.1 (-4.6, 0.5)	0.11	-2.1 (-4.7, 0.5)	0.11	-1.1 (-3.9, 1.6)	0.41	-0.2 (-0.5, 0.04)	0.10
<i>AVIL</i>	cg26620147	-2.4 (-5.1, 0.2)	0.07	-2.5 (-5.2, 0.3)	0.08	-1.4 (-4.2, 1.4)	0.33	-0.3 (-0.6, 0.01)	0.06
<i>AP2A1</i>	cg07377519	-2.3 (-4.9, 0.4)	0.09	-2.3 (-5.1, 0.4)	0.09	-1.4 (-4.2, 1.5)	0.35	-0.2 (-0.5, 0.1)	0.12
<i>POR</i>	cg20720686	-2.4 (-5.0, 0.2)	0.07	-2.6 (-5.3, 0.1)	0.06	-1.6 (-4.3, 1.2)	0.25	-0.2 (-0.5, 0.03)	0.09
<i>AGXT</i>	cg16967583	-2.4 (-5.2, 0.5)	0.10	-2.5 (-5.4, 0.4)	0.10	-1.2 (-4.2, 1.8)	0.43	-0.3 (-0.6, 0.01)	0.06
	cg05627557	-3.0 (-6.2, 0.2)	0.07	-3.3 (-6.6, 0.1)	0.05	-2.2 (-5.6, 1.3)	0.21	-0.3 (-0.6, 0.1)	0.14
<i>UACA</i>	cg12157761	-2.4 (-5.2, 0.4)	0.09	-2.6 (-5.5, 0.3)	0.08	-1.4 (-4.4, 1.5)	0.34	-0.3 (-0.6, 0.03)	0.07
<i>PRRT2</i>	cg19769182	-4.3 (-7.2, -1.4)	0.004	-4.9 (-7.9, -1.9)	0.001	-3.4 (-6.4, -0.4)	0.03	-0.2 (-0.5, 0.1)	0.18
<i>ZNF516</i>	cg20429104	-1.5 (-3.0, -0.1)	0.04	-1.6 (-3.1, -0.1)	0.04	-1.0 (-2.5, 0.6)	0.22	-0.1 (-0.3, 0.01)	0.06
<i>ENTPD1</i>	cg13471990	-2.3 (-5.1, 0.1)	0.11	-2.5 (-5.4, 0.4)	0.09	-1.3 (-4.4, 1.7)	0.39	-0.2 (-0.6, 0.06)	0.11
<i>PHACTR1</i>	cg13246235	-5.1 (-8.2, -2.0)	0.001	-5.9 (-9.1, -2.7)	0.0003	-5.5 (-8.9, -2.1)	0.002	-0.02 (-0.4, 0.3)	0.90
<i>BAHCC1</i>	cg25348105	-0.9 (-1.3, -0.4)	0.0001	-1.0 (-1.4, -0.5)	0.0001	-0.9 (-1.3, -0.4)	0.0002	-0.003 (-0.05 0.04)	0.90
	cg19987129	-2.5 (-5.2, 0.1)	0.06	-2.8 (-5.5, 0.03)	0.05	-1.4 (-4.1, 1.4)	0.33	-0.3 (-0.6, 0.006)	0.05
<i>TEX2</i>	cg17837191	-2.5 (-5.5, 0.4)	0.09	-2.7 (-5.7, 0.4)	0.08	-1.5 (-4.7, 1.6)	0.34	-0.3 (-0.6, 0.03)	0.08
<i>ZDHHC14</i>	cg23206115	-2.4 (-4.9, 0.1)	0.06	-2.5 (-5.1, 0.1)	0.06	-1.4 (-4.0, 1.3)	0.31	-0.3 (-0.5, 0.01)	0.06
<i>NDUFS6</i>	cg11442326	-1.9 (-3.6, 0.2)	0.03	-1.9 (-3.6, 0.1)	0.04	-1.2 (-3.1, 0.6)	0.19	-0.2 (-0.3, 0.02)	0.08
	cg04932082	-2.5 (-5.5, 0.5)	0.11	-2.8 (-5.9, 0.4)	0.08	-1.4 (-4.6, 1.8)	0.38	-0.3 (-0.6, 0.05)	0.09
<i>FUT3</i>	cg09001777	-1.9 (-3.7, -0.1)	0.04	-1.9 (-3.8, -0.1)	0.04	-1.2 (-3.2, 0.7)	0.20	-0.1 (-0.3, 0.1)	0.25
<i>XDH</i>	cg09842053	-1.2 (-1.9, -0.4)	0.003	-1.2 (-2.0, -0.4)	0.003	-1.0 (-1.9, -0.2)	0.01	-0.1 (-0.2, -0.01)	0.04
<i>ESM1</i>	cg00992687	-1.9 (-3.4, -0.5)	0.009	-1.9 (-3.4, -0.4)	0.01	-1.4 (-2.9, 1.1)	0.07	-0.1 (-0.3, 0.003)	0.06
<i>DCBLD1</i>	cg04344000	2.0 (-0.6, 4.5)	0.13	2.1 (-0.6, 4.7)	0.13	1.0 (-1.7, 3.8)	0.47	0.3 (0.01, 0.6)	0.04
	cg24219974	2.1 (-0.1, 4.6)	0.09	2.3 (-0.2, 4.9)	0.07	1.1 (-1.6, 3.7)	0.43	0.3 (-0.02, 0.5)	0.07
	cg06873024	-2.4 (-4.4, -0.4)	0.02	-2.6 (-4.4, -0.3)	0.02	-1.7 (-3.9, 0.5)	0.12	-0.2 (-0.4, 0.1)	0.14
<i>KLHDC4</i>	cg04043336	0.8 (-0.4, 1.2)	0.0002	0.9 (-0.4, 1.3)	0.0001	0.9 (0.5, 1.4)	0.0001	-0.01 (-0.1, 0.03)	0.56
	cg03580292	-2.4 (-5.1, 0.5)	0.10	-2.5 (-5.4, 0.4)	0.09	-1.1 (-4.1, 1.9)	0.47	-0.3 (-0.6, 0.005)	0.05
<i>LOC152225</i>	cg05429448	-2.6 (-5.1, -0.2)	0.03	-2.9 (-5.4, -0.3)	0.03	-1.8 (-4.5, 0.9)	0.19	-0.2 (-0.5, 0.1)	0.14
<i>CEACAM8</i>	cg14779825	-2.2 (-4.5, 0.004)	0.05	-2.4 (-4.7, 0.01)	0.05	-1.4 (-3.8, 1.1)	0.26	-0.2 (-0.5, 0.03)	0.08
	cg24743290	-2.8 (-4.3, -1.3)	0.0003	-2.7 (-4.3, -1.2)	0.001	-2.3 (-3.9, -0.6)	0.01	-0.4 (-0.7, -0.05)	0.09
<i>BTD</i>	cg21634628	1.5 (0.3, 2.7)	0.01	1.7 (0.5, 2.9)	0.01	1.2 (0.04, 2.5)	0.06	0.1 (-0.03, 0.2)	0.13
<i>SIK3</i>	cg06928797	-1.6 (-3.2, -0.02)	0.05	-1.7 (-3.4, -0.04)	0.05	-1.5 (-3.2, 0.3)	0.10	-0.04 (-0.2, 0.1)	0.68
<i>GJB6</i>	cg03568673	-2.3 (-5.1, 0.5)	0.10	-2.5 (-5.3, 0.4)	0.10	-1.2 (-4.2, 1.7)	0.41	-0.3 (-0.6, -0.01)	0.05
<i>CLRN1</i>	cg24721964	-2.2 (-4.8, 0.5)	0.11	-2.2 (-4.9, 0.5)	0.11	-1.2 (-4.0, 1.6)	0.39	-0.2 (-0.5, 0.04)	0.09
<i>TBC1D1</i>	cg00812557	-2.2 (-4.9, 0.5)	0.12	-2.3 (-5.1, 0.5)	0.11	-1.1 (-4.1, 1.8)	0.44	-0.3 (-0.6, 0.02)	0.07
<i>SORCS2</i>	cg19848118	1.3 (0.7, 1.8)	0.0001	1.3 (0.7, 1.9)	0.0001	1.2 (0.6, 1.8)	0.0002	0.03 (-0.04, 0.1)	0.42
<i>ZAK</i>	cg11119767	-2.9 (-5.9, 0.1)	0.06	-3.0 (-6.0, 0.2)	0.06	-2.0 (-5.2, 1.2)	0.22	-0.2 (-0.6, 0.1)	0.13
<i>MFSD6</i>	cg04144521	-2.5 (-4.7, -0.2)	0.03	-2.7 (-4.6, -0.5)	0.02	-2.0 (-4.4, 0.4)	0.10	-0.1 (-0.4, 0.1)	0.36
<i>APBA1</i>	cg14397918	-2.3 (-5.3, 0.7)	0.12	-2.5 (-5.8, 0.6)	0.11	-1.2 (-4.4, 2.0)	0.45	-0.3 (-0.7, -0.01)	0.04
<i>TTN, MIR548N</i>	cg19906284	-2.8 (-5.3, -0.3)	0.03	-3.1 (-5.7, -0.6)	0.02	-2.1 (-4.8, 0.5)	0.11	-0.2 (-0.5, 0.1)	0.14
<i>PPT1</i>	cg07033722	-2.5 (-5.4, 0.4)	0.10	-2.6 (-5.6, 0.4)	0.09	-1.1 (-4.2, 1.9)	0.46	-0.3 (-0.6, 0.01)	0.06
<i>MS4A3</i>	cg19739596	-2.2 (-5.0, 0.5)	0.11	-2.4 (-5.3, 0.5)	0.10	-1.1 (-4.1, 1.8)	0.45	-0.3 (-0.6, 0.02)	0.07
<i>NOTCH4</i>	cg20241876	-2.2 (-4.8, 0.4)	0.09	-2.3 (-4.9, 0.4)	0.10	-1.4 (-4.2, 1.4)	0.32	-0.2 (-0.5, 0.1)	0.11
	cg02551745	-2.3 (-5.1, 0.6)	0.12	-2.5 (-5.4, 0.4)	0.09	-1.0 (-4.1, 2.0)	0.49	-0.3 (-0.6, 0.01)	0.06
<i>NADK</i>	cg00992048	-2.1 (-4.4, 0.2)	0.07	-2.2 (-4.5, 0.2)	0.07	-1.3 (-3.7, 1.2)	0.30	-0.2 (-0.5, 0.02)	0.07
<i>C20orf3</i>	cg20661985	-2.8 (-5.6, -0.04)	0.05	-3.0 (-5.9, -0.1)	0.04	-1.9 (-4.9, 1.1)	0.21	-0.2 (-0.5, 0.1)	0.16
	cg11557901	-2.9 (-5.8, 0.1)	0.06	-3.0 (-6.0, 0.1)	0.06	-1.9 (-5.0, 1.2)	0.24	-0.3 (-0.6, 0.1)	0.11
<i>MARCH3</i>	cg08975164	-2.2 (-4.2, -0.3)	0.03	-2.2 (-4.2, -0.2)	0.03	-1.7 (-3.8, 0.4)	0.11	-0.2 (-0.4, 0.04)	0.11
<i>GNRHR2</i>	cg22713444	-2.5 (-5.7, 0.7)	0.12	-2.6 (-5.9, 0.7)	0.13	-1.2 (-4.6, 2.2)	0.49	-0.3 (-0.7, 0.01)	0.05
	cg20689978	-0.8 (-1.1, -0.4)	0.0001	-0.8 (-1.2, -0.4)	0.0001	-0.9 (-1.3, -0.4)	0.0001	0.02 (-0.02, 0.1)	0.39
<i>TNFRSF17</i>	cg02368508	2.1 (0.5, 3.7)	0.01	2.3 (0.7, 3.9)	0.01	1.7 (-0.03, 3.4)	0.05	0.1 (-0.1, 0.3)	0.18
<i>HAPLN4</i>	cg03719032	-1.1 (-1.9, -0.4)	0.003	-1.3 (-2.0, -0.5)	0.001	-1.6 (-2.4, -0.8)	0.0002	0.1 (0.02, 0.2)	0.02
<i>NLK</i>	cg05475440	-2.3 (-5.2, 0.6)	0.11	-2.4 (-5.4, 0.6)	0.11	-1.1 (-4.2, 2.0)	0.48	-0.3 (-0.6, 0.01)	0.06
<i>SHF</i>	cg00042683	-0.6 (-0.9, -0.3)	0.0001	-0.6 (-0.9, -0.3)	0.0001	-0.7 (-1.0, -0.4)	0.0001	0.02 (-0.01, 0.1)	0.12
	cg02262553	-2.9 (-5.8, 0.04)	0.05	-3.0 (-6.0, 0.04)	0.05	-1.9 (-5.0, 1.2)	0.23	-0.2 (-0.5, 0.1)	0.14
<i>C1orf106</i>	cg06834507	-1.8 (-4.1, 0.6)	0.14	-1.8 (-4.2, 0.6)	0.14	-0.9 (-3.4, 1.6)	0.48	-0.2 (-0.5, 0.04)	0.09
<i>CCNH</i>	cg02021919	-3.0 (-5.8, -0.3)	0.03	-3.1 (-5.9, -0.3)	0.03	-2.1 (-5.0, 0.8)	0.16	-0.3 (-0.6, 0.03)	0.08

Estimated change in DNA methylation percentage is presented as β (95% CI). *p*-values represent association to GDM status and pre-pregnancy maternal BMI.
Model 1: n=186, Adjusted for GDM status, offspring age and sex. *p*-value represents association to GDM status.
Model 2: n=186, Adjusted for GDM status, offspring age, sex and BMI. *p*-value represents association to GDM status.
Model 3: n=175, Adjusted for GDM status, offspring age, sex and pre-pregnancy maternal BMI.