Supplementary Material

Supplementary Table 1.
Geometric mean ratio (95% CI) of adult offspring HOMA2-IR by maternal ΣAs-associated DNA methylation (M-value).

			Unadjusted				Model 1				Model 2				Model 3			
CpG	Gene(s)	Location	GMR	*p*-value	*q*-value	Absolute Difference	GMR	*p*-value	*q*-value	Absolute Difference	GMR	*p*-value	*q*-value	Absolute Difference	GMR	*p*-value	*q*-value	Absolute Difference
cg00500428	*HCFC1R1; THOC6*	TSS1500; Body	0.99 (0.84,1.13)	0.84	0.85	-0.23 (-0.84,0.38)	1.00 (0.85,1.15)	0.97	0.99	-0.39 (-1.02,0.24)	1.01 (0.85,1.17)	0.89	0.95	-0.39 (-1.07,0.28)	0.98 (0.85,1.11)	0.76	0.93	-0.42 (-1.04,0.19)
cg06690548	*SLC7A11*	Body	0.94 (0.79,1.08)	0.38	0.51	-0.17 (-0.61,0.27)	0.94 (0.79,1.09)	0.42	0.59	-0.04 (-0.59,0.51)	0.94 (0.79,1.09)	0.43	0.61	-0.04 (-0.58,0.05)	0.99 (0.87,1.11)	0.88	0.93	0.06 (-0.49,0.60)
cg18616702	*ADAMTSL 4; MIR4257*	5'UTR; TSS1500	1.01 (0.88,1.15)	0.85	0.85	0.07 (-0.23,0.37)	1.00 (0.87,1.12)	0.94	0.99	0.09 (-0.27,0.44)	0.99 (0.86,1.12)	0.86	0.95	0.09 (-0.28,0.45)	1.00 (0.89,1.10)	0.93	0.93	0.09 (-0.24,0.42)
cg09280971	-	Intergenic	1.03 (0.87,1.18)	0.74	0.82	-0.04 (-0.34,0.26)	1.00 (0.85,1.15)	0.99	0.99	0.04 (-0.32,0.39)	0.99 (0.84,1.14)	0.90	0.95	0.03 (-0.33,0.40)	1.01 (0.09,1.12)	0.90	0.93	0.05 (-0.25,0.34)
cg22294740	*LINGO3*	5'UTR	1.03 (0.89,1.17)	0.66	0.78	0.07 (-0.33,0.48)	1.00 (0.86,1.13)	0.99	0.99	0.07 (-0.33,0.46)	1.00 (0.87,1.14)	0.95	0.95	0.07 (-0.32,0.46)	1.02 (0.89,1.14)	0.79	0.93	0.10 (-0.30,0.49)
cg04940901	*DNAH1*	Body	1.05 (0.93,1.16)	0.42	0.53	0.24 (-0.08,0.55)	1.03 (0.89,1.16)	0.69	0.90	0.29 (-0.11,0.69)	1.03 (0.90,1.16)	0.67	0.84	0.29 (-0.11,0.69)	1.05 (0.94,1.16)	0.37	0.49	0.33 (-0.06,0.72)
cg20509831	*A1BG-AS1; A1BG; ZNF497*	Body; TSS1500; 3'UTR	1.08 (0.93,1.24)	0.30	0.47	0.07 (-0.34,0.48)	1.08 (0.94,1.23)	0.28	0.49	0.05 (-0.38,0.48)	1.08 (0.94,1.23)	0.26	0.45	0.05 (-0.38,0.48)	1.05 (0.94,1.16)	0.35	0.49	0.00 (-0.40,0.40)
cg12106731	*NCDN; KIAA0319L*	TSS200; TSS1500	1.14 (1.03,1.24)	0.02	0.15	0.36 (0.00,0.71)	1.14 (1.02,1.25)	0.03	0.31	0.48 (0.05,0.91)	1.13 (1.02,1.25)	0.03	0.33	0.48 (0.04,0.92)	1.06 (0.96,1.15)	0.26	0.43	0.36 (-0.04,0.75)
cg07317306	-	Intergenic	1.08 (0.92,1.25)	0.33	0.47	0.17 (-0.17,0.51)	1.09 (0.93,1.24)	0.28	0.49	0.19 (-0.15,0.53)	1.10 (0.95,1.25)	0.21	0.45	0.19 (-0.14,0.52)	1.07 (0.95,1.18)	0.28	0.43	0.15 (-0.14,0.44)
cg27178850	-	Intergenic	1.08 (0.93,1.22)	0.31	0.47	0.31 (-0.1,0.71)	1.03 (0.86,1.21)	0.72	0.90	0.36 (-0.16,0.89)	1.06 (0.89,1.23)	0.51	0.68	0.38 (-0.16,0.93)	1.09 (0.95,1.22)	0.23	0.42	0.45 (-0.02,0.93)
cg21369801	*CSNK1D*	Body; 3'UTR	1.11 (0.95,1.26)	0.21	0.38	0.33 (-0.05,0.72)	1.09 (0.94,1.24)	0.27	0.49	0.42 (-0.03,0.86)	1.09 (0.94,1.24)	0.27	0.45	0.42 (-0.03,0.86)	1.09 (0.98,1.21)	0.13	0.26	0.42 (0.02,0.83)
cg01538969	*DHX16*	Body	1.13 (0.98,1.29)	0.11	0.28	0.30 (0.01,0.59)	1.11 (0.95,1.27)	0.21	0.49	0.35 (0.01,0.69)	1.11 (0.95,1.26)	0.20	0.45	0.35 (0.01,0.69)	1.11 (0.99,1.22)	0.08	0.20	0.35 (0.06,0.64)
cg14827056	*AGO2*	Body	1.10 (0.97,1.23)	0.15	0.32	0.34 (-0.04,0.71)	1.07 (0.93,1.21)	0.32	0.50	0.39 (-0.03,0.81)	1.07 (0.93,1.22)	0.32	0.49	0.39 (-0.03,0.81)	1.11 (0.99,1.22)	0.09	0.20	0.45 (0.05,0.84)
cg20493718	*CSNK1D*	Body; 3'UTR	1.10 (0.95,1.25)	0.21	0.38	0.31 (-0.07,0.70)	1.09 (0.93,1.24)	0.29	0.49	0.40 (-0.04,0.84)	1.09 (0.94,1.23)	0.26	0.45	0.40 (-0.03,0.84)	1.12 (1.01,1.24)	0.05	0.15	0.46 (0.05,0.87)

cg08059112	*LINGO3*	5'UTR	1.15 (1.00,1.31)	0.07	0.28	0.24 (-0.19,0.66)	1.15 (0.98,1.31)	0.10	0.33	0.35 (-0.14,0.84)	1.14 (0.98,1.30)	0.10	0.38	0.35 (-0.15,0.84)	1.15 (1.02,1.28)	0.03	0.11	0.35 (-0.10,0.81)
cg07021906	*SLC7A5 (LAT1)*	Body	1.15 (1.03,1.28)	0.02	0.15	0.24 (-0.04,0.52)	1.15 (1.01,1.30)	0.05	0.31	0.40 (0.02,0.78)	1.15 (1.01,1.28)	0.05	0.34	0.40 (0.01,0.79)	1.15 (1.03,1.27)	0.02	0.10	0.40 (0.04,0.76)
cg14595618	*HK1*	Body	1.15 (1.00,1.30)	0.07	0.28	0.20 (-0.15,0.54)	1.14 (0.98,1.29)	0.11	0.33	0.25 (-0.11,0.60)	1.13 (0.98,1.28)	0.12	0.38	0.25 (-0.11,0.60)	1.15 (1.04,1.25)	0.01	0.10	0.26 (-0.03,0.56)
cg12116137	*PRPF8*	Body	1.14 (0.99,1.28)	0.08	0.28	0.41 (0.05,0.77)	1.14 (0.98,1.30)	0.10	0.33	0.60 (0.11,1.09)	1.13 (0.97,1.28)	0.13	0.38	0.61 (0.09,1.12)	1.16 (1.03,1.29)	0.03	0.11	0.63 (0.16,1.09)
cg03497652	*ANKS3*	Body	1.14 (0.99,1.29)	0.10	0.28	0.39 (-0.01,0.80)	1.14 (0.98,1.30)	0.12	0.33	0.55 (-0.02,1.11)	1.13 (0.97,1.29)	0.13	0.38	0.55 (-0.03,1.12)	1.17 (1.04,1.29)	0.02	0.10	0.59 (0.06,1.13)
cg03036214	*CA12*	Body	1.19 (1.05,1.34)	0.02	0.15	0.36 (0.05,0.67)	1.17 (1.02,1.32)	0.04	0.31	0.36 (0.02,0.70)	1.17 (1.03,1.32)	0.03	0.33	0.36 (0.02,0.69)	1.17 (1.07,1.27)	0.003	0.06	0.36 (0.07,0.64)

All models used generalized estimating equations (GEE) to account for family clustering. β-coefficients were exponentiated (shown here) to geometric mean ratios (95% CI).

Absolute difference represents actual change in HOMA2-IR score.

Model 1: adjusted for offspring sex, age, smoking status, and log(Σas), and for maternal age, smoking status, log(Σas), and log(fasting glucose).

Model 2: further adjusted for maternal waist circumference.

Model 3: model 1 and further adjusted for offspring waist circumference.