

ESM Table 2. Degree of DNA methylation for each genotype of the T2D associated CpG-SNPs and surrounding CpG sites in human pancreatic islets.

SNP ID	Gene symbol	Genotype	n	CpG 1		CpG 2		CpG 3		CpG 4		CpG 5	
				Mean ± SD	P-value	Mean ± SD	P-value	Mean ± SD	P-value	Mean ± SD	P-value	Mean ± SD	P-value
rs7754840	<i>CDKAL1</i>	GG	29	0.12 ± 0.32									
		CG	38	36.1 ± 3.2	1.3 x 10⁻¹³								
		CC	10	65.7 ± 7.8									
rs13292136	<i>CHCHD9</i>	TT	0	-									
		CT	11	53.9 ± 4.6	4.2 x 10⁻⁶								
		CC	49	88.5 ± 3.9									
rs2334499	<i>DUSP8</i>	AA	17	0.3 ± 0.9									
		AG	44	35.7 ± 4.5	1.6 x 10⁻¹³								
		GG	19	67.9 ± 2.8									
rs7578326	<i>IRS1</i>	AA	26	0.0 ± 0.0									
		AG	30	25.9 ± 4.4	7.2 x 10⁻¹⁵								
		GG	22	53.0 ± 5.9									
rs391300	<i>SRR</i>	AA	12	14.6 ± 2.7									
		AG	45	51.9 ± 3.5	1.2 x 10⁻¹³								
		GG	25	88.0 ± 2.7									
rs7961581	<i>TSPAN8</i>	TT	32	0.1 ± 0.5									
		TC	18	37.4 ± 2.2	1.8 x 10⁻¹⁰								
		CC	5	72.2 ± 3.4									
rs564398	<i>CDKN2A</i>	AA	28	6.9 ± 2.8		65.89 ± 2.0							
		AG	39	55.0 ± 3.4	6.3 x 10⁻¹⁵	70.7 ± 2.6	6.1 x 10 ⁻¹²						
		GG	17	91.4 ± 1.6		76.0 ± 2.7							
rs5015480	<i>HHEX</i>	AA	11	66.3 ± 3.3		1.6 ± 0.2							
		AG	40	70.1 ± 4.5	0.22	36.1 ± 2.9	4.2 x 10⁻¹²						
		GG	22	70.9 ± 4.7		70.2 ± 4.9							
rs1801282	<i>PPARG</i>	CC	43	1.8 ± 0.4		82.9 ± 7.5							
		CG	15	24.6 ± 1.9	1.6 x 10⁻⁷	83.5 ± 6.2	> 0.99						
		GG	0	-		-							

rs7901695	<i>TCF7L2</i>	AA	43	3.9 ± 1.1	5.6 × 10 ⁻¹²	5.6 × 10 ⁻¹²	5.3 ± 1.4							
		AG	32	48.2 ± 3.0			49.6 ± 2.9							
		GG	2	93.8 ± 2.3			89.9 ± 0.1							
rs5945326	<i>DUSP9</i>	AA	52	3.2 ± 1.1	7.7 × 10 ⁻¹³	0.23	77.0 ± 6.8	73.5 ± 7.4						
		AG	8	39.3 ± 2.7			77.7 ± 2.3	68.9 ± 4.1	> 0.99					
		GG	24	77.7 ± 5.1			80.6 ± 3.3	73.4 ± 6.5						
rs13266634	<i>SLC30A8</i>	AA	5	0.66 ± 0.6	2.3 × 10 ⁻⁵	> 0.99	8.4 ± 1.6	14.4 ± 4.3						
		AG	31	2.3 ± 1.1			9.8 ± 2.4	17.5 ± 4.5	> 0.99					
		GG	40	3.8 ± 1.5			9.6 ± 2.5	17.4 ± 4.2						
rs1531343	<i>HMGA2</i>	GG	43	71.4 ± 3.0	6.7 × 10 ⁻⁶	1.8 × 10 ⁻⁵	85.7 ± 3.0	n.a.	74.2 ± 4.4					
		CG	12	58.8 ± 1.7			77.4 ± 3.1	32.5 ± 3.1	3.0 × 10⁻¹¹	52.8 ± 12.1	0.0010			
		CC	1	47.2 ± 0.0			73.6 ± 0.0	72.3 ± 0.0		51.4 ± 0.0				
rs2237895	<i>KCNQ1</i>	AA	16	98.9 ± 1.5	0.047	0.96	98.9 ± 1.8	9.8 ± 4.0	85.9 ± 2.3					
		AC	29	97.1 ± 3.0			98.9 ± 1.7	49.2 ± 4.9	3.6 × 10⁻⁹	79.7 ± 7.7	6.2 × 10 ⁻⁷			
		CC	10	94.6 ± 3.9			96.5 ± 2.8	80.0 ± 4.7		75.1 ± 3.4				
rs11708067	<i>ADCY5</i>	AA	45	8.6 ± 2.3	0.00020	8.6 × 10 ⁻¹¹	3.9 ± 1.5	14.2 ± 5.4	8.1 ± 1.8	12.3 ± 4.6				
		AG	26	12.5 ± 4.0			15.9 ± 4.0	16.3 ± 3.7	0.11	12.2 ± 3.5	0.00011	18.4 ± 5.6	0.0015	
		GG	2	15.0 ± 0.1			31.0 ± 4.8	17.6 ± 0.0		12.9 ± 0.0	21.1 ± 0.0			
rs1801214	<i>WFS1</i>	TT	21	95.3 ± 3.2	> 0.99	> 0.99	99.0 ± 3.4	87.5 ± 3.9	10.6 ± 1.8	87.9 ± 6.7				
		CT	26	96.4 ± 3.0			99.8 ± 0.5	90.1 ± 3.3	0.0096	38.2 ± 5.3	7.4 × 10⁻¹⁰	93.5 ± 2.6	7.2 × 10 ⁻⁵	
		CC	10	97.8 ± 2.0			99.9 ± 0.3	93.3 ± 4.2		71.2 ± 4.2		94.6 ± 1.4		

CpG-SNP data is in bold. n.a., not analyzable due to lack of CpG site (i.e., 0% DNA methylation). *P*-values are corrected for multiple testing using Bonferroni correction (n=16).

