SUPPLEMENTARY DATA

Supplementary Table 1. Donor characteristics and sample details for adult human islets and foetal pancreas

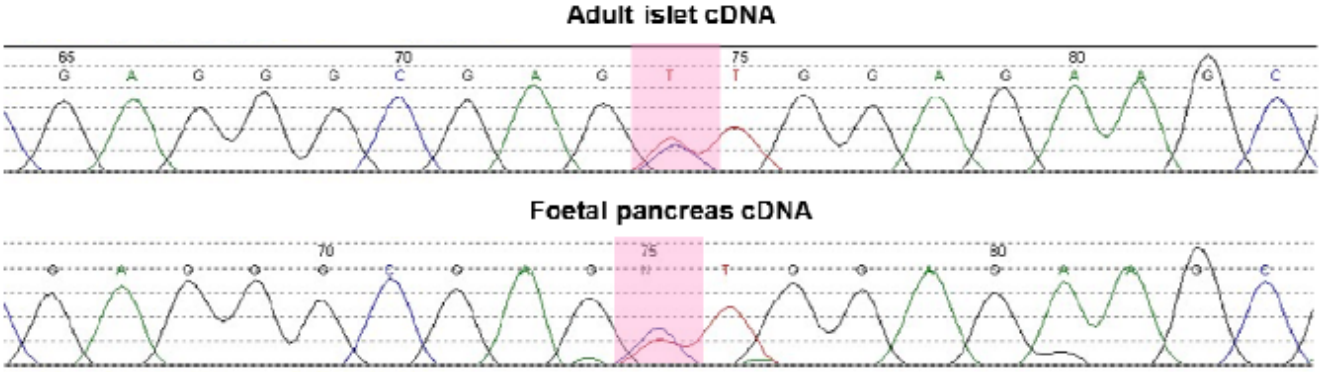
Adult Islets (n=72)	**Mean (range)**
Age (years)	53 (24-75)
BMI (kg/m2)	27.1 (17.6-36.6)
Islet Purity	91% (83%-99%)
Gender	53% male
Foetal Pancreas (n=18)	**Mean (range)**
Days post-conception	79 (42-133)

Supplementary Table 2. coding variants used to determine imprinting status of genes in the 11p15.5 cluster

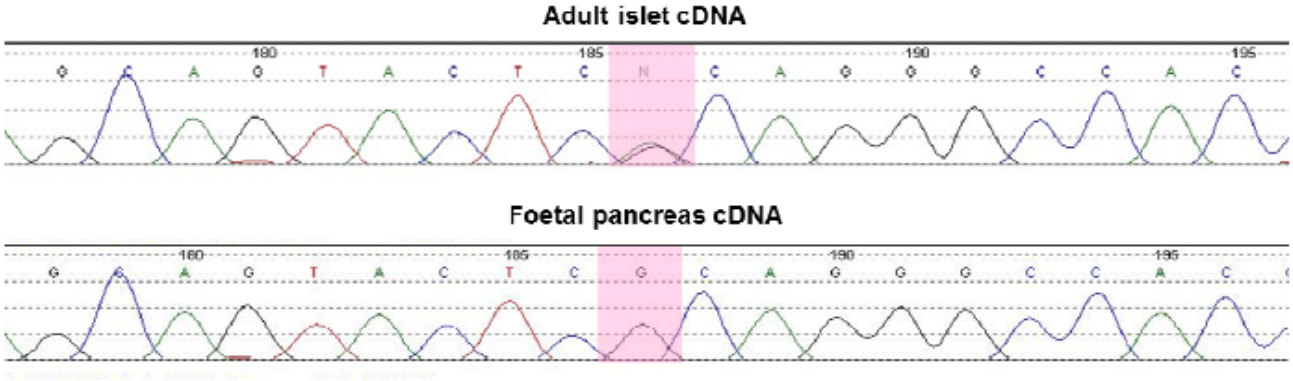
Gene	**Coding Variant** *(major/minor allele)*	**Adult islets**			**Fetal pancreas**		
		Hom *(major)*	**Het**	**Hom** *(minor)*	**Hom** *(major)*	**Het**	**Hom** *(minor)*
KCNQ1	rs1057128 *(G/A)*	51	16	3	14	3	1
KCNQ1OT1	rs231362 *(G/A)*	22	30	17	6	9	2
PHLDA2	rs13390 *(A/G)*	53	13	2	15	3	0
SLC22A18	rs1129782 *(G/C)*	50	14	7	14	4	0
SLC22A19AS	rs367035 *(A/G)*	2	1	3	3	1	3
CDKN1C	del171APVA *(ins/del)*	34	23	9	9	5	3

SUPPLEMENTARY DATA

Supplementary Figure 1. *SLC22A18AS* is biallelically expressed in both adult and foetal tissues. Electropherogram traces from capillary sequencing of cDNA across a heterozygous coding SNP within *SLC22A18AS* (highlighted in pink). Both samples retain heterozygosity, indicating transcription from both chromosomes.

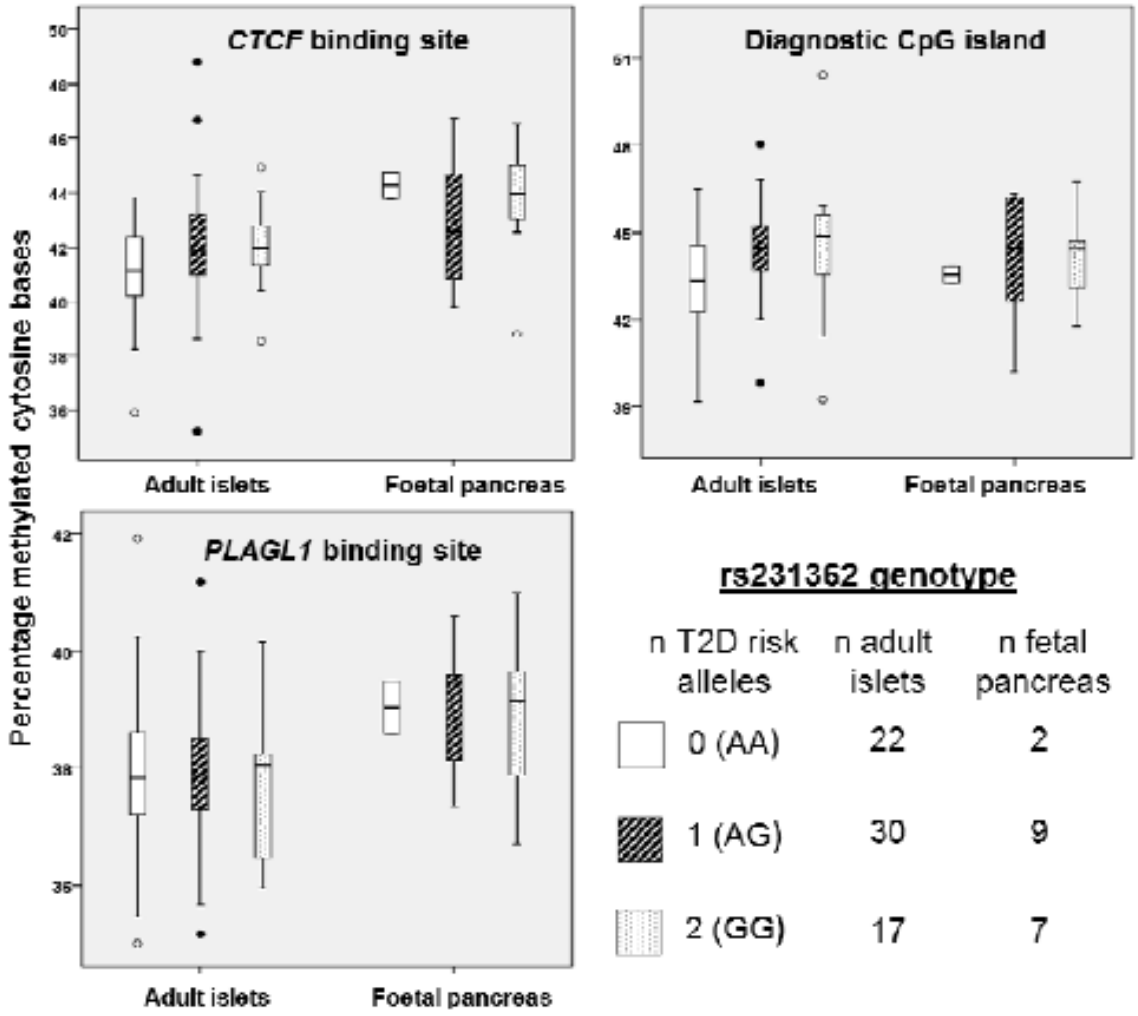


Supplementary Figure 2. *KCNQ1* and *KCNQ1OT1* are imprinted in foetal pancreas but expressed biallelically in adult islets. Electropherogram traces from capillary sequencing of cDNA across a heterozygous coding SNP within *KCNQ1* (highlighted in pink). The adult islet sample retains heterozygosity, indicating transcription from both chromosomes, whereas the foetal pancreas sample appears monoallelic – revealing imprinted expression from only one chromosome. The same pattern was seen for all samples at *KCNQ1* and *KCNQ1OT1*



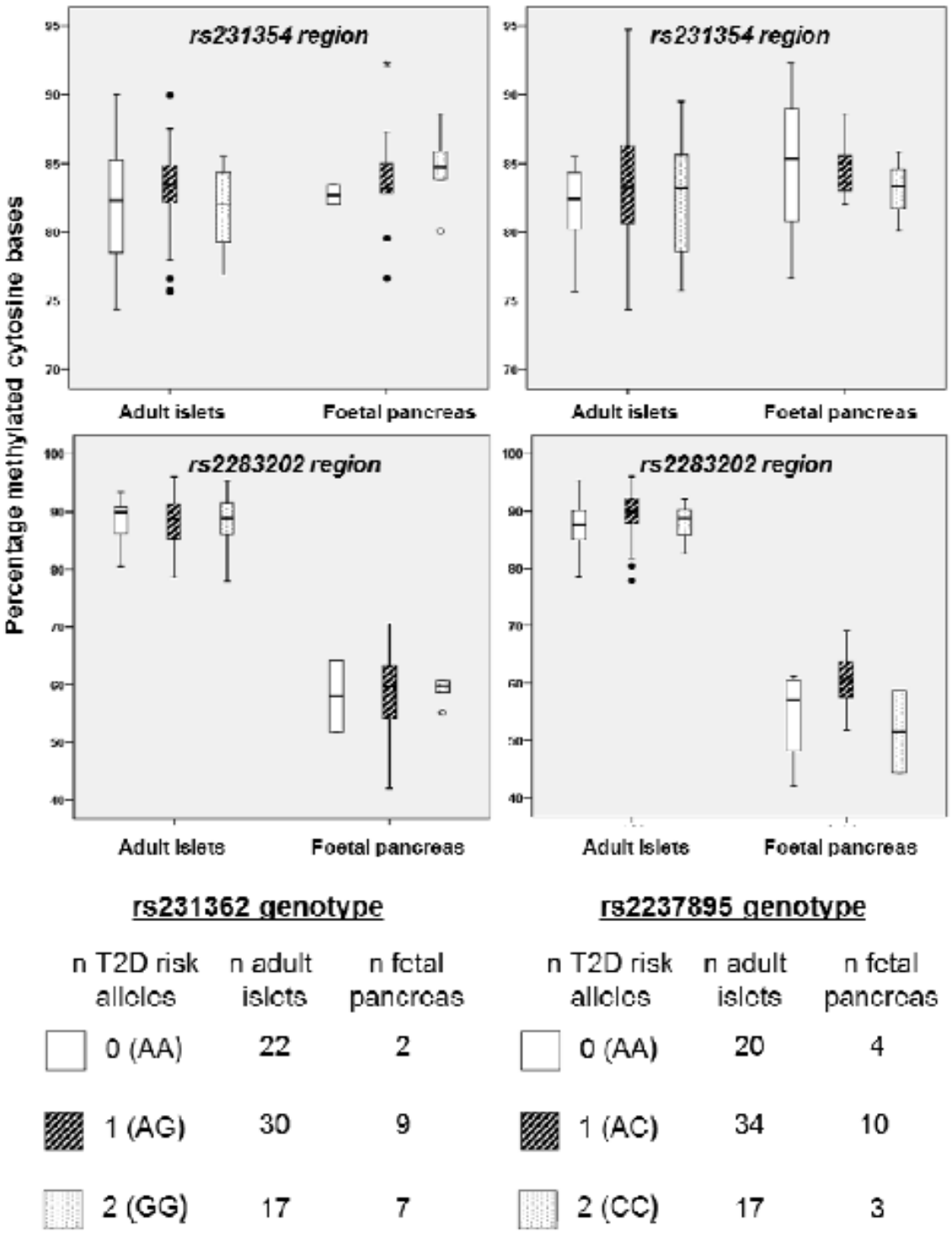
SUPPLEMENTARY DATA

Supplementary Figure 3. Methylation according to rs231262 T2D risk genotype. Boxplots show the effect of rs231362 T2D risk allele number (x-axis) upon methylation level (y-axis), separated by tissue type. Boxes represent quartiles; whiskers encompass values within 1.5x interquartile range. No significant associations were identified.



Supplementary Figure 4. Methylation at the two candidate assays (rs231354 and rs2283202 regions) according to T2D risk genotypes. Boxplots show the effect of rs231362 and rs2237895 T2D risk allele number (x-axis) upon methylation level (y-axis), separated by tissue type. Boxes represent quartiles; whiskers encompass values within 1.5x interquartile range. No significant associations were identified.

SUPPLEMENTARY DATA



Supplementary Figure 5. Total expression according to rs231362 T2D risk genotype. Boxplots show the effect of rs231362 T2D risk allele number (x-axis) upon total mRNA expression level (y-axis), separated by tissue type. Boxes represent quartiles; whiskers encompass values within 1.5x interquartile range. There was no evidence for an effect of risk allele number on expression levels of any of the tested genes in either tissue type ($p>0.05$ in all cases).

SUPPLEMENTARY DATA