

SUPPLEMENTARY DATA

Supplementary Table 1. Taqman Gene Expression Kits (Applied Biosystems, Warrington, U.K.) used to assess placental gene expression in samples from the Cambridge Baby Growth Study.

Kit	Kit Number (RefSeq that kit codes for)	Amplicon Length
<i>IGF2</i> transcript variant 1	Hs00171254_m1 (NM_000612.4)	94
<i>IGF2</i> transcript variant 2	Hs01005962_m1 (NM_001007139.4)	64
<i>IGF2</i> transcript variant 3	Hs04188276_m1 (NM_001127598.1)	83
Antisense <i>IGF2</i>	Hs00212651_m1	107
<i>INS-IGF2</i> readthrough transcript	Hs02743135_m1	52
<i>YWHAZ</i>	Hs01122445_g1	62
<i>TOP1</i>	Hs00243257_m1	101
<i>UBC</i>	Hs00824723_m1	71

Supplementary Table 2. Parentally transmitted fetal SNP alleles inferred from the father's, mother's and fetus' genotype for a SNP that nominally could consist of different combinations of major allele "A" and minor allele "a". This table was used to infer parentally transmitted alleles for each of the 17 *IGF2* SNPs analysed in this study.

Paternal Genotype	Maternal Genotype	Fetal Genotype	Paternally-transmitted Allele	Maternally-transmitted Allele
A/A	A/A	A/A	A	A
A/A	A/a	A/A	A	A
A/A	A/a	A/a	A	a
A/A	a/a	A/a	A	a
A/a	A/A	A/A	A	A
A/a	A/A	A/a	a	A
A/a	A/a	A/A	A	A
A/a	A/a	A/a	uninformative	uninformative
A/a	A/a	a/a	a	a
A/a	a/a	A/a	A	a
A/a	a/a	a/a	a	a
a/a	A/A	A/a	a	A
a/a	A/a	A/a	a	A
a/a	A/a	a/a	a	a
a/a	a/a	a/a	a	a

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Supplementary Table 3. Associations between paternally-transmitted fetal *IGF2* variants and maternal glucose z-scores one hour after a 50 or 75 g glucose load around week 28 of pregnancy in the (a) Cambridge Baby Growth Study and (b) Cambridge Wellbeing Study. The four polymorphisms shown were all significantly associated with maternal glucose z-scores in the combined cohort. Data are arithmetic mean (95 % confidence interval), n = number of DNA trios.

(a) Cambridge Baby Growth Study

<i>IGF2</i> SNP	Allele 1	Allele 2	p
rs6578987	-0.047 (-0.141, 0.047) (n=394)	0.208 (0.042, 0.375) (n=126)	0.009
rs680	-0.049 (-0.144, 0.046) (n=395)	0.166 (-0.004, 0.337) (n=122)	0.030
rs10770125	-0.078 (-0.199, 0.043) (n=246)	0.142 (0.026, 0.258) (n=268)	0.010
rs7924316	-0.044 (-0.159, 0.070) (n=280)	0.113 (-0.015, 0.241) (n=233)	0.072

(b) Cambridge Wellbeing Study

<i>IGF2</i> SNP	Allele 1	Allele 2	p
rs6578987	-0.101 (-0.244, 0.042) (n=202)	0.060 (-0.204, 0.325) (n=59)	0.3
rs680	-0.106 (-0.247, 0.035) (n=206)	0.096 (-0.168, 0.359) (n=59)	0.2
rs10770125	-0.223 (-0.405, -0.042) (n=122)	0.133 (-0.042, 0.307) (n=132)	0.006
rs7924316	-0.177 (-0.347, -0.007) (n=137)	0.085 (-0.103, 0.274) (n=111)	0.04

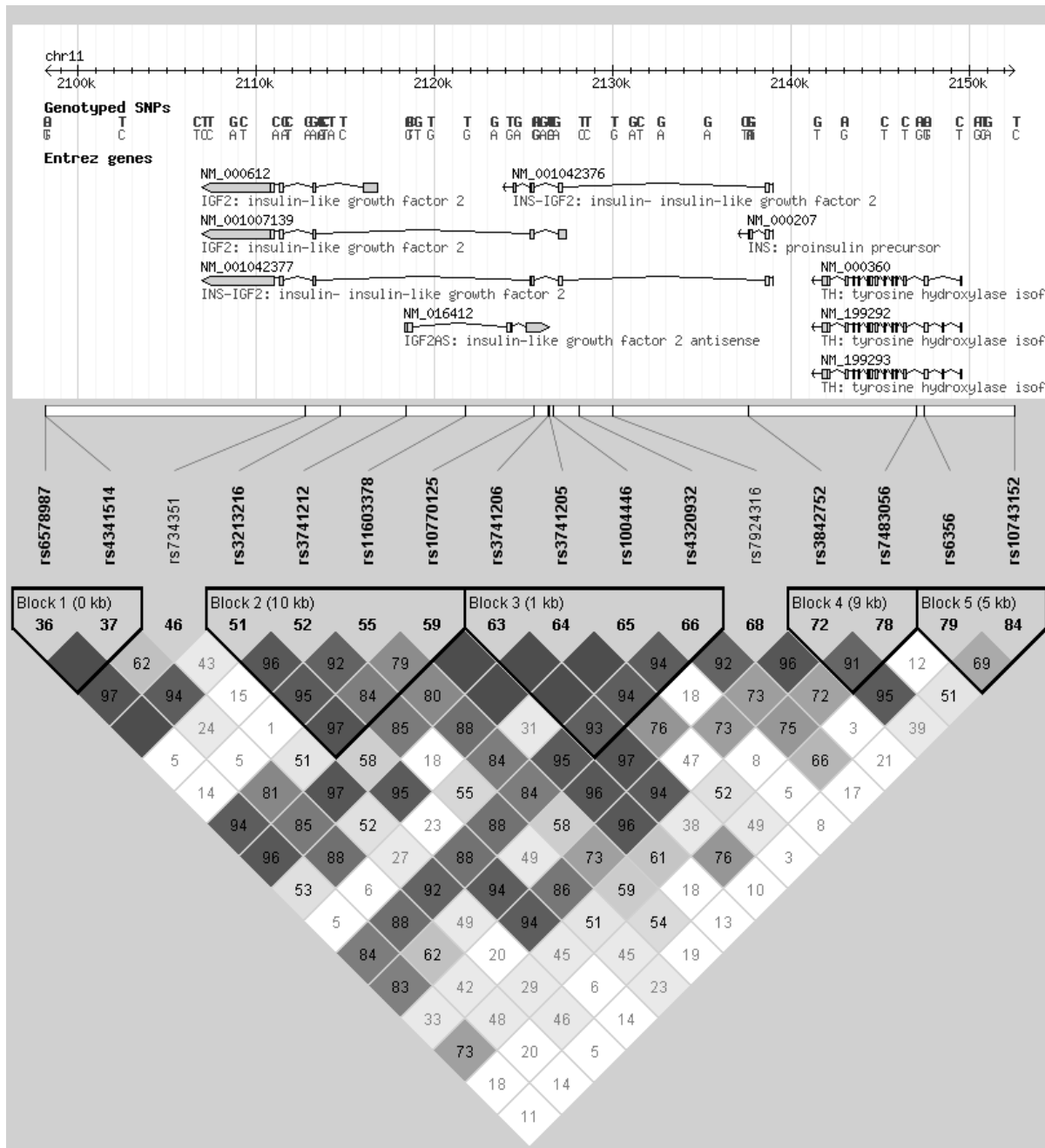
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Supplementary Table 4. Associations between paternally transmitted fetal *IGF2* SNPs and fasting plasma glucose concentrations and areas under the capillary glucose curves in the Cambridge Baby Growth Study. Data are mean (95 % confidence interval).

Paternally-Transmitted Fetal <i>IGF2</i> SNP	Fasting Venous Plasma Glucose (mmol/l)			Area under the Capillary Glucose Curve in the 75 g OGTT (mmol/min/l)		
	Allele 1	Allele 2	p	Allele 1	Allele 2	p
rs6578987	4.3 (4.2, 4.3) (n=399)	4.4 (4.4, 4.5) (n=127)	0.002	847 (833, 860) (n=327)	886 (862, 911) (n=97)	0.005
rs680	4.3 (4.2, 4.3) (n=400)	4.4 (4.3, 4.5) (n=123)	0.008	846 (833, 859) (n=327)	878 (853, 904) (n=91)	0.026
rs10770125	4.3 (4.2, 4.3) (n=250)	4.4 (4.3, 4.4) (n=270)	0.046	843 (826, 861) (n=204)	871 (854, 888) (n=210)	0.020
rs7924316	4.3 (4.2, 4.3) (n=284)	4.4 (4.3, 4.4) (n=225)	0.007	846 (829, 862) (n=229)	869 (851, 888) (n=176)	0.059

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Supplementary Figure 1. *IGF2* gene region haplotype blocks using the SNPs selected for analysis in the current study, as defined by Haploview (16). One further *IGF2* SNP (rs680) analysed by Rodríguez et al. (15) was also genotyped in the current study.



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Supplementary Figure 2. A linkage disequilibrium plot (D' top left and r^2 bottom right) across the 17 fetal *IGF2* SNPs that were genotyped. The plot was drawn using JLIN (Carter KW, McCaskie PA, Palmer LJ: JLIN: a java based linkage disequilibrium plotter. *BMC Bioinformatics* 7:60, 2006).

