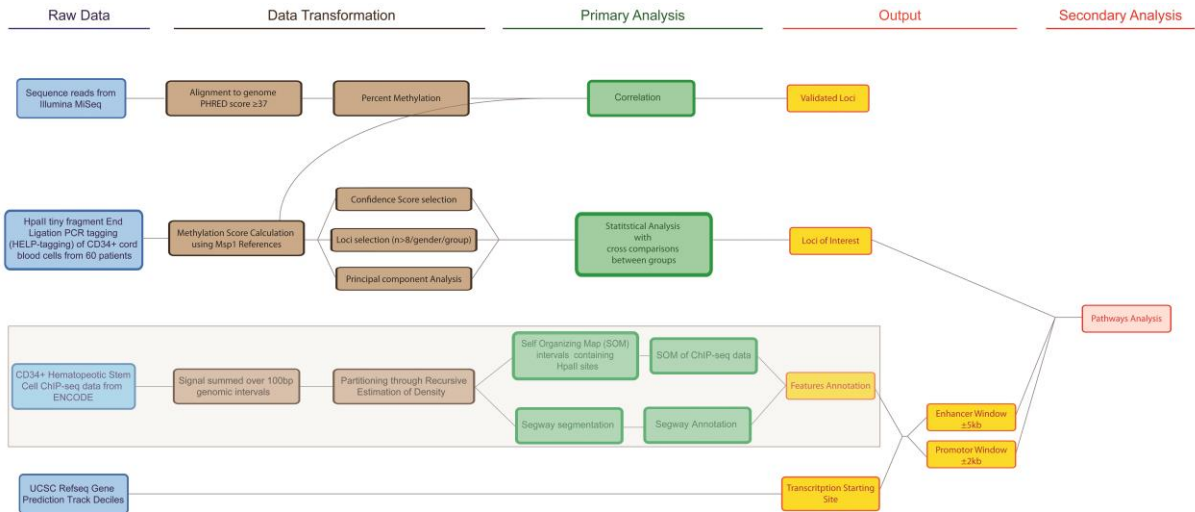
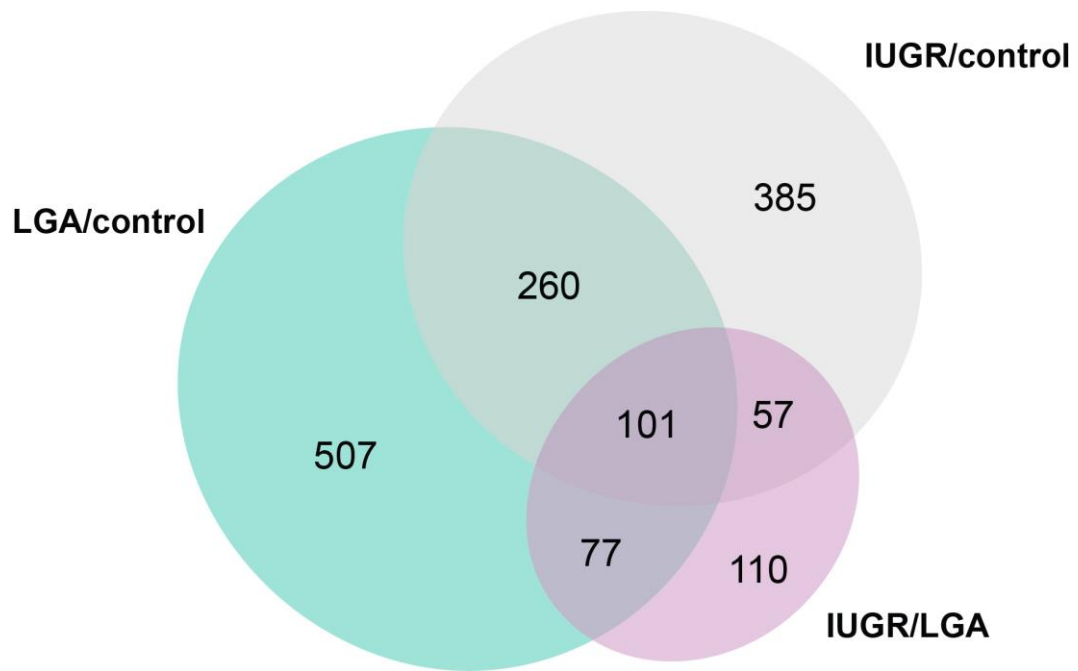


## Supplementary Figure 1. Data analysis overview

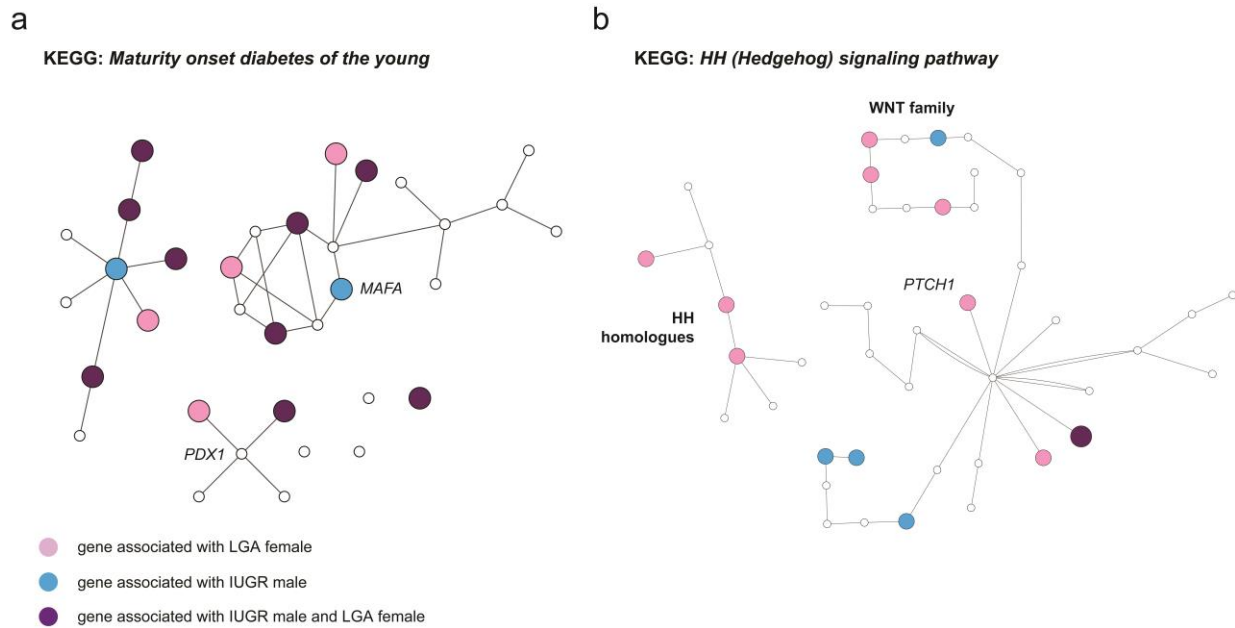


We show a flowchart of analytical procedures from raw data through the data processing steps used in generation of primary and secondary analysis. The gray box represents analysis shared between this study and that of a co-submitted manuscript (Wijetunga, Delahaye *et al.*).

**Supplementary Figure 2.** Overlap of genes dysregulated as a response to extreme fetal growth

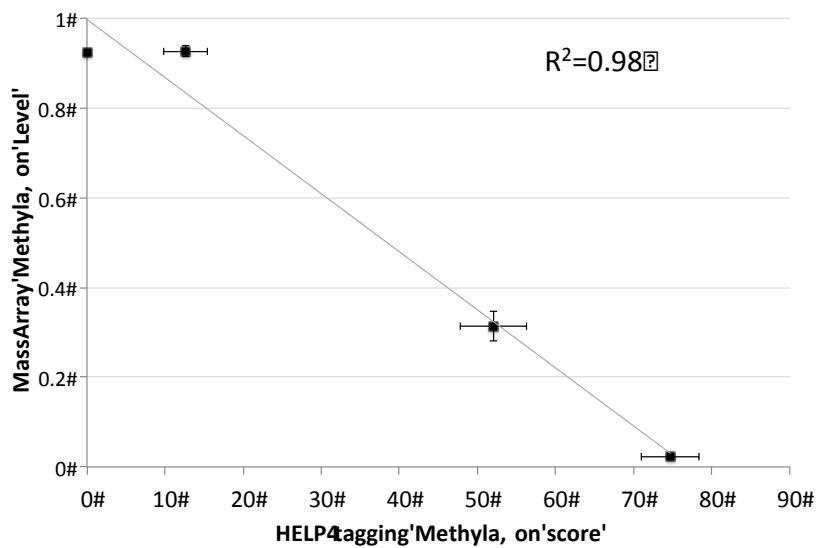


**Supplementary Figure 3** Sex-specific Gene Set Enrichment Analysis (GSEA) plot onto KEGG pathways



Network representations of KEGG pathways for the (a) *Maturity onset diabetes of the young* and (b) *Hedgehog (HH) signaling pathway*. Nodes are color- and size-coded based on the gene associated with differentially-methylated loci for LGA compared with control females (pink), IUGR compared with control males (blue) and those that are common to both LGA and IUGR groups (purple). Those not associated in either comparison are shown in white. Edges (solid lines) represent known physical interactions between protein products of genes.

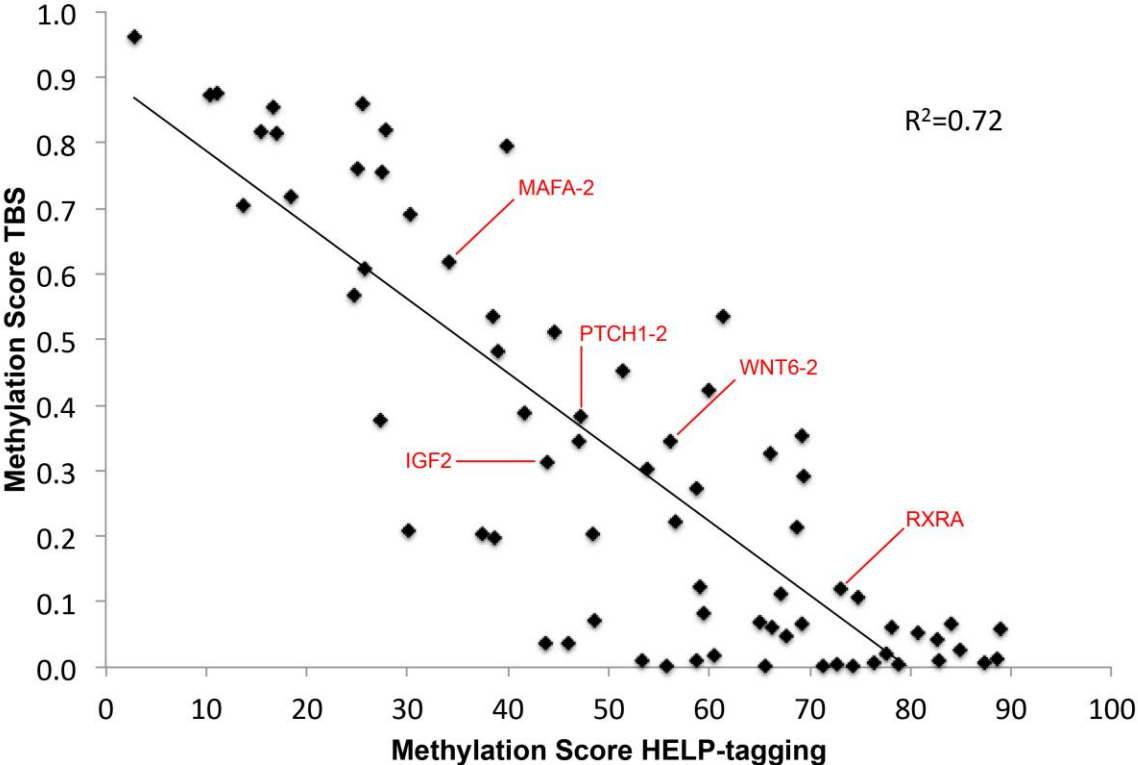
**Supplementary Figure 4** Correlations between HELP-tagging and MassArray results



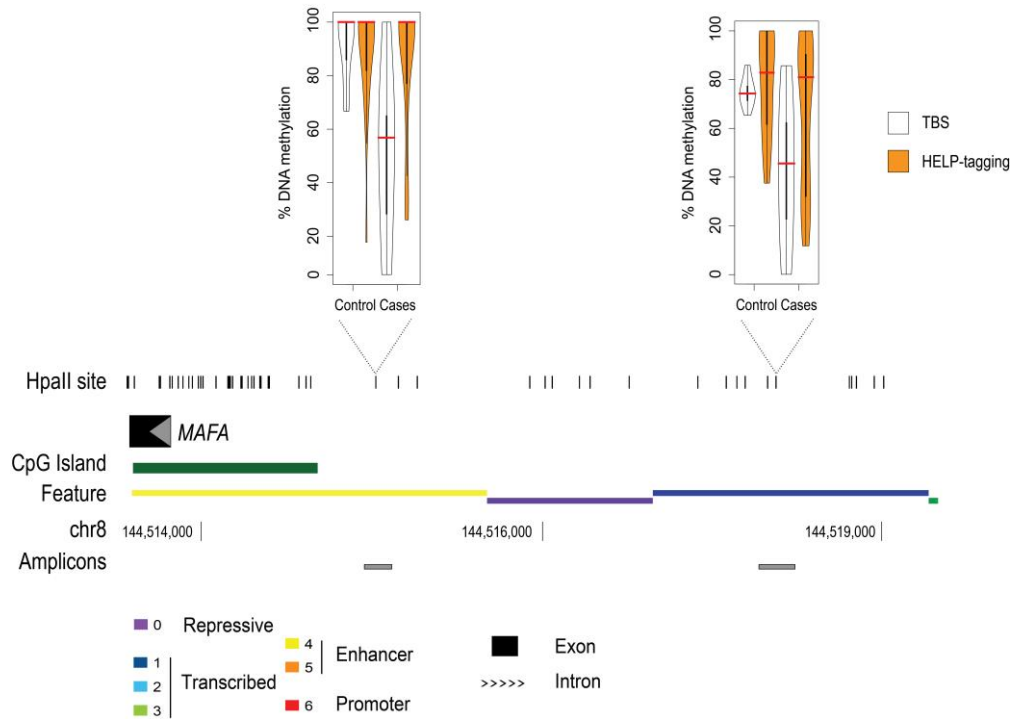
Primer	Locus		Methylation Score MassArray	Methylation Score HELP-Tagging
DL5.1	chr1	32704998 32704999	0.923±0.005	0±0.000
DL4.3	chr7	2661007 2661008	0.926±0.01	12.649±2.769
DL1.5	chr2	28830072 28830073	0.31±0.003	52.054±4.234
DL1.4	chr1	42204926 42204927	0.02±0.003	12.649±3.677

Correlation between HELP-tagging and bisulphite MassArray (Sequenom) is high for the control loci shown. Standard error values for each type of assay at each locus are shown.

**Supplementary Figure 5.** Correlations between HELP-tagging and targeted bisulphite sequencing (TBS) results

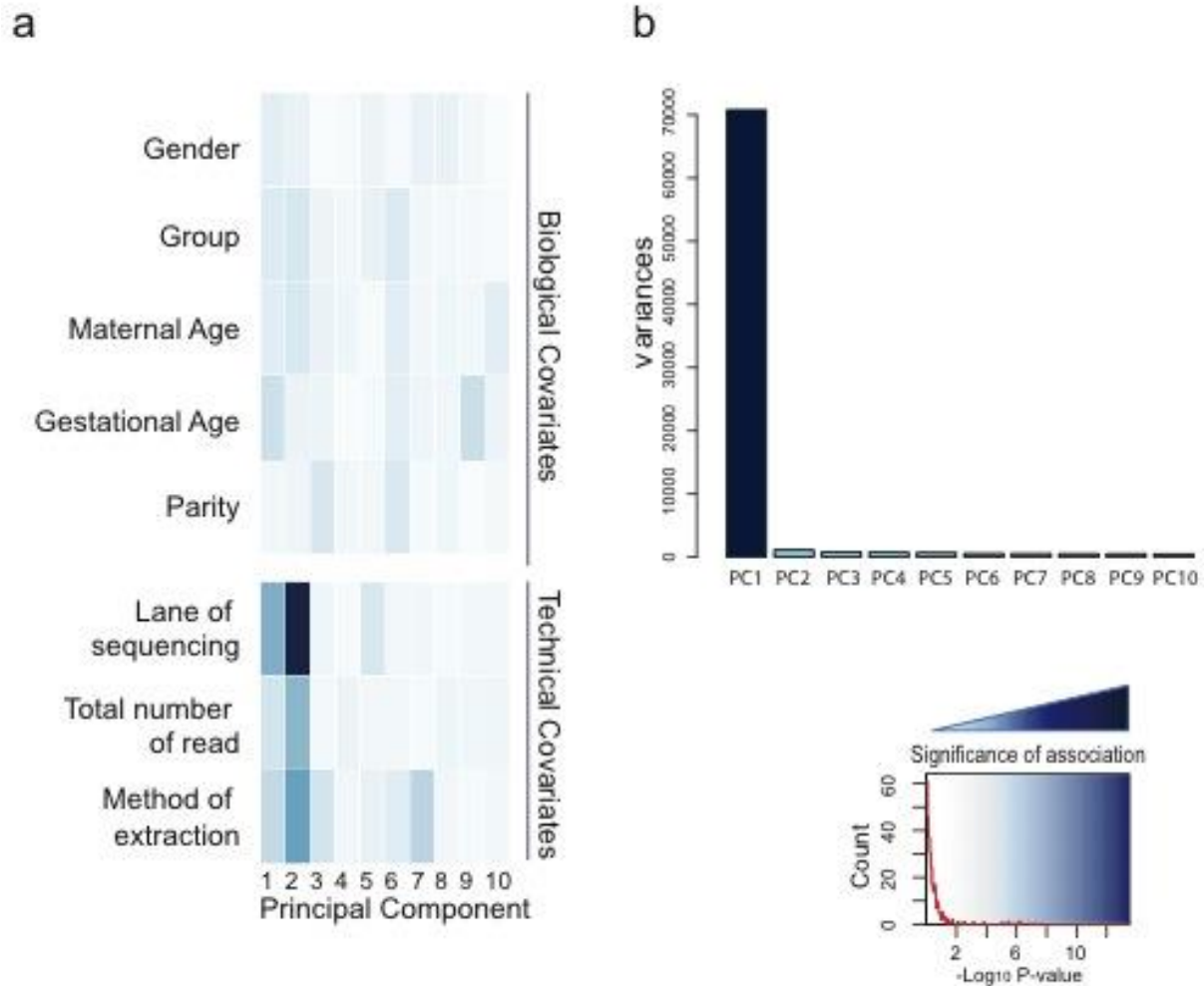


**Supplementary Figure 6.** Illustration of validation data for *MAFA*



Validation of significant loci of interest by targeted bisulphite sequencing (TBS) in Cohort 2 for loci at the *MAFA* gene. Candidate differentially-methylated loci are shown as the HpaII sites within the amplicon regions (gray boxes), with results of DNA methylation distributions for controls and cases (IUGR and LGA combined) from HELP-tagging (orange) and TBS (white) depicted as violin plots (mean shown in red). The results show concordance for similar types of changes between HELP-tagging and TBS results at these loci.

## Supplementary Figure 7 Principal Component Analysis



**a)** A heatmap is shown displaying the  $-\log_{10} p$  values of linear regression for top ranking principal components for each known covariate. The color keys correspond to numeric values for each covariate, with dark blue indicating greatest significance. The majority of variation is accounted for by experimental influences, with PC2 significantly associated with lane of sequencing, indicating samples run simultaneously, an indicator of experimental batch effects.

**b)** The relative contributions of the top 10 principal components are shown, demonstrating that the greatest variance is linked to principal component 1. The potential confounding effects of this variability were included in our statistical model.

**Supplementary Table 1** Top 10 pathways from Gene Set Enrichment Analysis

	UGR/control (males only)	LGA/control (females only)	Cases/control	LGA/control	UGR/control
KEGG MATURITY ONSET DIABETES OF THE YOUNG					
KEGG HEDGEHOG SIGNALING PATHWAY					
KEGG NEUROACTIVE LIGAND RECEPTOR INTER					
KEGG BASAL CELL CARCINOMA					
KEGG MAPK SIGNALING PATHWAY					
KEGG PATHWAYS IN CANCER					
KEGG MELANOMA					
KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION					
KEGG ECM RECEPTOR INTERACTION					
KEGG WNT SIGNALING PATHWAY					
KEGG FOCAL ADHESION					
KEGG CALCIUM SIGNALING PATHWAY					
KEGG SMALL CELL LUNG CANCER					
KEGG REGULATION OF ACTIN CYTOSKELETON					
KEGG TGF BETA SIGNALING PATHWAY					
KEGG SYSTEMIC LUPUS ERYTHEMATOSUS					
KEGG TGF BETA SIGNALING PATHWAY					



**Supplementary Table 2** Gene set enrichment scores for KEGG *Maturity onset diabetes of the young* and *Hedgehog signaling* pathways

Comparison	Pathways	KEGG code	Rank	FDR q-value	Number of candidate genes in pathway	Total number of genes in pathway	Total number of genes compared
IUGR/control	Maturity onset diabetes of the young	4950	3	1.16E-06	9	25	577
	Hedgehog signaling	4340	8	1.50E-04	8	56	577
LGA/control	Maturity onset diabetes of the young	4950	7	4.96E-05	9	25	712
	Hedgehog signaling	4340	5	7.20E-06	10	56	712
Cases/control	Maturity onset diabetes of the young	4950	4	1.25E-08	12	25	817
	Hedgehog signaling	4340	9	1.33 E-04	10	56	817
IUGR/control (males only)	Maturity onset diabetes of the young	4950	2	3.89E-05	6	25	284
	Hedgehog signaling	4340	8	9.47E-03	5	56	284
LGA/control (females only)	Maturity onset diabetes of the young	4950	6	5.41E-07	8	25	571
	Hedgehog signaling	4340	9	1.25E-04	8	56	571

“Cases” include both IUGR and LGA.

**Supplementary Table 3** Correlations between HELP-tagging and targeted bisulphite sequencing (TBS) results

Rank	Primer	Locus		Methylation Score TBS	Methylation Score HELP-Tagging	Significance in HELP-Tagging	
10	FGF19-1	chr11	69520932	69520933	0.424	59.883	Cases/control
<b>14</b>	<b>PTCH1-2</b>	<b>chr9</b>	<b>98275047</b>	<b>98275048</b>	<b>0.619</b>	<b>34.110</b>	<b>Cases/control</b>
19	TNF	chr6	31540201	31540202	0.346	56.093	Cases/control
23	CACNA1H-1	chr16	1201802	1201803	0.821	27.804	Cases/control
24	FGF17	chr8	21899104	21899105	0.568	24.645	Cases/control
26	PIK3CD	chr1	9704167	9704168	0.047	67.702	Cases/control
27	ZIC2	chr13	100632469	100632470	0.010	58.752	Cases/control
28	ADAM17	chr2	9696571	9696572	0.002	55.812	Cases/control
29	WNT9A	chr1	228136504	228136505	0.071	48.614	Cases/control
<b>1</b>	<b>MAFA-2</b>	<b>chr8</b>	<b>144518163</b>	<b>144518164</b>	<b>0.691</b>	<b>30.332</b>	<b>IUGR/control</b>
6	PIK3CG	chr7	106499616	106499617	0.291	69.436	IUGR/control
7	MAFA-1	chr8	144514749	144514750	0.813	17.054	IUGR/control
25	PRDM8	chr4	81111178	81111179	0.860	25.505	IUGR/control
26	NOTCH1-2	chr9	139446647	139446648	0.272	58.732	IUGR/control
27	PDE2A	chr11	72353085	72353086	0.203	48.457	IUGR/control
15	HDAC5	chr17	42201632	42201633	0.510	44.525	LGA/control
28	KIF21B	chr1	200990764	200990765	0.483	38.941	LGA/control
30	CACNA1H-2	chr16	1195201	1195202	0.609	25.671	LGA/control
<b>31</b>	<b>WNT6-2</b>	<b>chr2</b>	<b>219718849</b>	<b>219718850</b>	<b>0.382</b>	<b>47.212</b>	<b>LGA/control</b>
32	FGF19-3	chr11	69521455	69521456	0.303	53.908	LGA/control
33	MAP3K6	chr1	27693783	27693784	0.346	47.064	LGA/control
34	PDGFB-1	chr22	39648277	39648278	0.387	41.652	LGA/control
35	AKT3-1	chr1	244012361	244012362	0.112	67.121	LGA/control
36	WNT1	chr12	49364443	49364444	0.122	59.077	LGA/control
37	TGFB3	chr14	76448169	76448170	0.019	60.550	LGA/control
28	DVL1-2	chr1	1289556	1289557	0.060	66.172	IUGR/control (male only)
11	FAS	chr10	90743066	90743067	0.818	15.468	IUGR/control (male only)
12	CREBBP	chr16	3931839	3931840	0.754	27.549	IUGR/control (male only)
13	SOCS3-3	chr17	76357669	76357670	0.704	13.688	IUGR/control (male only)
14	PDGFB-2	chr22	39649169	39649170	0.020	77.537	IUGR/control (male only)
15	SOCS3-1	chr17	76356948	76356949	0.005	78.834	IUGR/control (male only)
16	FGF19-2	chr11	69521089	69521090	0.222	56.657	IUGR/control (male only)
17	IRS1	chr2	227665923	227665924	0.004	72.704	IUGR/control (male only)
18	DUSP4	chr8	29211512	29211513	0.378	27.241	IUGR/control (male only)
19	PRR5	chr22	45125757	45125758	0.197	38.727	IUGR/control (male only)
20	PTCH1-1	chr9	98275305	98275306	0.209	30.055	IUGR/control (male only)
5	IL11	chr19	55889042	55889043	0.327	65.980	LGA/control (female only)
8	CACNA1B-1	chr9	140768206	140768207	0.853	16.610	LGA/control (female only)
13	ASPSR1	chr17	79973811	79973812	0.452	51.463	LGA/control (female only)
17	IHH	chr2	219926005	219926006	0.059	88.891	LGA/control (female only)
18	NOTCH1-1	chr9	139446428	139446429	0.536	38.446	LGA/control (female only)
22	CACNA1A	chr19	13618496	13618497	0.215	68.695	LGA/control (female only)
23	HDAC9	chr7	18535586	18535587	0.106	74.834	LGA/control (female only)
24	FGF19-4	chr11	69524084	69524085	0.537	61.399	LGA/control (female only)
25	WNT6-1	chr2	219723712	219723713	0.060	78.045	LGA/control (female only)
26	AKT3-2	chr1	244012457	244012458	0.010	82.822	LGA/control (female only)
27	SOCS3-4	chr17	76357130	76357131	0.066	69.250	LGA/control (female only)
28	MTOR	chr1	11322845	11322846	0.001	74.241	LGA/control (female only)
29	SOCS3-2	chr17	76361238	76361239	0.068	64.956	LGA/control (female only)
30	PKLR	chr1	155278154	155278155	0.009	53.269	LGA/control (female only)
31	EN2	chr7	155252927	155252928	0.036	45.914	LGA/control (female only)
9	DVL1-1	chr1	1287677	1287678	0.875	10.372	LGA/control (male only)
16	CACNA1B-2	chr9	140771750	140771751	0.353	69.176	LGA/control (male only)
17	DNMT3A	chr2	25517428	25517429	0.084	59.364	LGA/control (male only)
<b>31</b>	<b>RXRA</b>	<b>chr9</b>	<b>137216751</b>	<b>137216752</b>	<b>0.119</b>	<b>73.037</b>	<b>Published</b>
<b>33</b>	<b>IGF2</b>	<b>chr11</b>	<b>2169273</b>	<b>2169274</b>	<b>0.312</b>	<b>43.906</b>	<b>Published</b>
2	IDO2	chr8	39828379	39828380	0.962	2.790	Technical
3	MAD1L1	chr7	1882979	1882980	0.762	25.045	Technical
4	ATG5	chr6	106641124	106641125	0.876	11.086	Technical
20	TUBBP5	chr9	141044663	141044664	0.066	84.119	Technical
21	FCER2	chr19	7767120	7767121	0.718	18.454	Technical
24	CMTM4	chr16	66730037	66730038	0.013	88.609	Technical
25	CACNA1H-3	chr16	1201802	1201803	0.796	39.815	Technical
26	LRP10	chr14	23341680	23341681	0.008	87.309	Technical
27	BMI	chr10	22614934	22614935	0.025	84.910	Technical
29	WWP2	chr16	69895519	69895520	0.042	82.621	Technical
30	CDNK2	chr9	21996333	21996334	0.053	80.694	Technical
32	KCNA2	chr1	111150385	111150386	0.007	76.340	Technical
34	TMEM	chr16	431296	431297	0.002	71.380	Technical
35	MLL5	chr7	104654143	104654144	0.002	65.534	Technical
36	ETV5	chr3	185824820	185824821	0.204	37.425	Technical
37	SSH1	chr12	109220314	109220315	0.036	43.659	Technical

The table summarizes mean DNA methylation scores for TBS (Cohort 2, n=24 subjects) and HELP-tagging (Cohort 1, n=60 subjects) with each primer. Primers are grouped by the comparison showing the locus to be a candidate differentially-methylated site, or whether they were loci of interest in the literature or part of our standard panel used to test a range of DNA methylation values. Within each group, loci are ranked in order of descending correlation score. The figure depicting these correlations is shown as **Supplementary Figure 3**.

**Supplementary Table 4.** Correlation and significance between HELP-tagging and TBS (targeted bisulphite sequencing) for *WNT6*, *PTCH1*, *MAFA*, *IGF2*, and *RXRA*

Name	chromosome	postion start	position end	HELP-tagging			Targeted Bisulphite Sequencing			DNA methylation changes Cases/Control	HELP-tagging (cases/control) p value	TBS (cases/control) p value
				control (mean $\pm$ s.d.)	IUGR (mean $\pm$ s.d.)	LGA (mean $\pm$ s.d.)	control (mean $\pm$ s.d.)	IUGR (mean $\pm$ s.d.)	LGA (mean $\pm$ s.d.)			
<i>WNT6</i>	chr2	219718849	219718850	59.3 $\pm$ 6.04	48.8 $\pm$ 8.39	33.5 $\pm$ 7.03	0.30 $\pm$ 0.05	0.42 $\pm$ 0.03	0.42 $\pm$ 0.04	↑	0.045	0.023
<i>PTCH1</i>	chr9	98275047	98275048	54.2 $\pm$ 6.81	34.6 $\pm$ 7.84	13.5 $\pm$ 5.63	0.56 $\pm$ 0.02	0.68 $\pm$ 0.05	0.62 $\pm$ 0.03	↑	0.001	0.014
<i>MAFA</i>	chr8	144518163	144518164	21.8 $\pm$ 4.75	39.8 $\pm$ 6.35	29.4 $\pm$ 7.26	0.75 $\pm$ 0.02	0.67 $\pm$ 0.05	0.65 $\pm$ 0.04	↓		
<i>IGF2</i>	chr11	2169273	2169274	61.3 $\pm$ 5.40	41.0 $\pm$ 7.17	29.5 $\pm$ 6.29	0.28 $\pm$ 0.02	0.35 $\pm$ 0.07	0.31 $\pm$ 0.03	↑		
<i>RXRA</i>	chr9	137216751	137216752	83.8 $\pm$ 3.54	71.8 $\pm$ 7.16	63.5 $\pm$ 6.93	0.09 $\pm$ 0.03	0.16 $\pm$ 0.04	0.10 $\pm$ 0.02	↑		

↑ increased in cases compared with controls  
 ↓ decreased in cases compared with controls

(mean  $\pm$  s.d.)

“Cases” include both IUGR and LGA.

**Supplementary Table 5** Bisulphite PCR primers

	Forward Primer	Reverse Primer	Locus		
			chr	Start	End
FAS	TGATTTTAGAGGAGTGAATATAAATAGT	CCCTAAATAAATACAAAACCTTCTTATTT	chr10	90742953	90743166
MTOR	TTGAAAAATAGGTTAATAGTAATGAAGAA	AAAAATATCACAAAATCCATAAAAAAC	chr1	11322666	11323061
IGF2	GGTATTTTGTAGGATTGGGTAG	TTTACTAAAACCCCTCCTTATCTC	chr11	2169149	2169471
DVL1-1	TTTGAATTTGTGTTGAGATTTGTATT	TTCAAATTCCTTAAAACTAACCTAA	chr1	1287562	1287863
DVL1-2	TTTTTGTAAAGTATTTGGTTTTTGTAGT	ACTACCCCAATATAAATCTCCTTC	chr1	1289426	1289641
PKLR	TTTTTTTGTAGTGGTGGGATTATAG	AAACTTACTTAAAATAACTTTCTCATC	chr1	155277970	155278260
FGF19-1	TTGGAATTTGAATTTAAATAGTGGG	CCTCAAAACAAACCTAAAAACAAC	chr11	69520825	69521003
FGF19-2	TTAGGTTTGTGTTGAGGGTATAAG	ATAACAAAATCCATCCCTAAACT	chr11	69520986	69521144
FGF19-3	GGATTTTGAAGTATTTGTGTGTT	TAAACCTACTACTACCCATTACC	chr11	69521371	69521521
FGF19-4	TTGGAATTTGAATTTAAATAGTGGG	ATAAACTCACACACAACAAACC	chr11	69523935	69524148
PDE2A	GGTTTGGGTATAGTTTTAGTGTGT	AAAAAAAACCCCTCCTAATTCTA	chr11	72353010	72353210
KIF21B	GGTAATTTGATTGGGAATTAGAGAT	AAAAAATAAACAAAAACCCCTAC	chr1	200990599	200990843
SSH1	TTTAGGGGTTTGGTTGGTAGTAG	ACCAAAAAAATAAATCTCTTACTAT	chr7	155612063	155612219
WNT9A	TTTTTATTTTAAATTGTGGGAGTG	CACCATTCTACTTCAAAAACAACCT	chr1	228136336	228136559
AKT3-1	TTGATTTGTGGTAAGTATTTTTTTT	ATCACCATCCCTTATTTAAATTTT	chr1	244012247	244012387
AKT3-2	GAAATTTTAAATAAGGGATGGTGATT	TACAAATAAACAAACCAACCTCTC	chr1	244012362	244012527
WNT1	GGGAGATAAGGGGAATTGTTTAT	CCAAACCTCAAAAATACTAAAAATC	chr12	49364215	49364527
MAP3K6	TTGTAGGTATTTGTTGAATGAATGGT	ATCCCACTCAAAAATAAATACTTT	chr1	27693704	27693874
ZIC2	TTGTGGTTTTAATGTTATAGAGTAAGTTT	AATCAAAAATAAAAAACAACCCAAC	chr13	100632361	100632672
TGFB3	TATTGGAAGGTAGGGAGGTAGGT	AAAACAAAAATCAAAATCAAAAAA	chr14	76447980	76448253
CACNA1H-1	TTGGAATTTAATTGGATTTTTGAA	AAAAAAAACCCCTACCCAATAAAC	chr16	1201589	1201828
CACNA1H-2	GGTTGATTGTTGGTTGGTAGTAT	AAAAAACCCCTCCTAATAACA	chr16	1195101	1195420
CREBBP	GAGGTGTTTTTATTTAGTTAGTTATTTG	AAATTTTTTAAACAAATTTCTCCCTCT	chr16	3931650	3931954
HDAC5	GGGGTTAATTTTTGGATTGTAAA	AACACAAAATCAAAAAATCTTTC	chr17	42201290	42201657
SOCS3-1	TTGTTAGGTTTTTTGTTAATTTGA	CCTAAAATAAATAACCCCTTCTC	chr17	76356847	76357172
SOCS3-2	TTTTTAAATTTTATGGATGGGAAG	ACTAAAATAAATAACCCCAACTAC	chr17	76361080	76361344
SOCS3-3	TTAGATATTAGGATAATGAGGTGTGAAA	ATCTCACTAAATCCCAACACATAC	chr17	76357570	76357763
SOCS3-4	GTTTTTATAGGGAGGGTAGTTTG	AACCATCTAACATAACCTAAACCC	chr17	76357045	76357258
ASPCR1	GGAGTATGTTTTTATTTGGGAGAG	AAAAAAACTTCAAAAACCAAAACC	chr17	79973587	79973863
CACNA1A	TGATGAGTTAATAGTAGAAGGATTTATT	CCTTCTCTTACAAAATACTAAAAAAC	chr19	13618266	13618526
IL11	TTTTAGGTTGTGAGGGTGATATATG	AACAAAAAAACAAAATTAACCCC	chr19	55888954	55889166
PIK3CD	GTAAGTGGGTTTTTTGTTAGGATG	CCCCAAAATACTAAAATCCAAC	chr1	9703989	9704333
FCER2	GGAGTTTGGAGTTTGTGTTGTT	CACCAATTCTTACTTAAAAAATAA	chr19	7766909	7767172
WNT6-1	AGGGGGTATAGGGTATTAAGATAT	AAAAAAATAAAAAACAATAAACC	chr2	219723566	219723838
WNT6-2	AATTTGGTAGTTTTTTTGTATTGTTT	AAATACTAATAAATTATCCCACAACA	chr2	219718756	219718886
IHH	TTTTATTTATGTTTTGTTTTTTGTTG	CCTCCTACCTTTTAAATTTACTTCC	chr2	219925691	219926089
PDGFB-1	GGGGGTTATAGGTTAAAGTAGGTAG	CCCATAACCAAAACACATCTATAC	chr22	39648162	39648366
PDGFB-2	GGAGGATGAAAATATTTTTGGTAGT	CCTCCCCACTAATAATCTTAAAAA	chr22	39649072	39649205
PRR5	GGGGTTTGGATTTGTTTTATAATATT	TAAATCCATCTTAACTCCAAC	chr22	45125631	45125954

DNMT3A	GGTTGTAGTTTAGGAGTGGGAGATA	CCAAATTAACAAAACTCAACAAC	chr2	25517343	25517495
ADAM17	TTTTTTGTTTAGTGTGTTTAGGTGG	AAAATATCTACAACCCCTCCCTAC	chr2	9696365	9696694
PRDM8	TTGGTTTTTGAAGTGATTTTTTAT	CCTAACTCAACCTTAATTTCTCC	chr4	81111084	81111234
TNF	GAAATAGTAGTATTTTTAAGTTTTGGGG	AACTAACAAATAAAAAATCAAAACAAAA	chr6	31539936	31540275
PIK3CG	GGTTATTGGAATAAAGTTGATTTTTGT	AAAAAACCAAAAAATACCCAC	chr7	106499501	106499709
EN2	TTAGATTTGAAATTTGTTTATTGTTTT	CATTATCTTACAAAAATTTTTAAACCC	chr7	155252849	155253093
MAFA-1	TGTGGGGTTTTTTTTATGGTATTT	ACCCTCTCCTAATCTCCTTAACCTA	chr8	144514505	144514825
MAFA-2	GGGTGTATTATTGTTTGGGATT	TCCCTACCCCTATATTAACCATAAC	chr8	144518069	144518326
FGF17	AGTTGAGGTTTGAGTTTGTGTT	CAACCCCAACCTACTTCATTATAA	chr8	21898974	21899188
DUSP4	ATGGGATTGTTAAGGAGAGGTT	AAATCAAAAATTAACATCAAACTAAAAT	chr8	29211287	29211573
RXRA	GGTATGTTATGTGTAGTGGGAAGT	TTCCTAACCCCTAAACCCCTAC	chr9	137216663	137216837
NOTCH1-1	TTTTAGAGGGATAATGTTGGTGTTT	ATTTCCAAACCATATTCATTTACA	chr9	139446216	139446545
NOTCH1-2	GGAGTTGGGTTATTTTTGATTTTAT	TTATTAACCTTTTACCTTCCCCC	chr9	139446349	139446671
CACNA1B-1	TTTAATTTGTGATTTTTTTAGTGG	AAAATTTAAAATACTCATCAAAACTATA	chr9	140768015	140768385
CACNA1B-2	AGGGTAGAGTTGGGAGTTTAGGATA	CCCTAAAACCTACAACCCAAAACCTAA	chr9	140771569	140771895
TUBBP5	TTGATTTTTAGAGATTTTTTAGAGTTGT	AAAAACCTTTTCTCACCTTTAC	chr9	141044480	141044778
PTCH1-1	TTGGGGTTTTATTAGTTAGTAGGAGTT	ATCCCAACACAAAAACAAATATTT	chr9	98275124	98275440
PTCH1-2	ATGTATGTTTGTGTAGGGGATTGT	ACCAAAAAACAAAAACCATTTAAA	chr9	98274926	98275085
KCNA2	TAGGAGAGTTTAGTTGGGTGTTGT	AACCAATCTTTACTAAATAACAAAAAAA	chr1	111150231	111150519
ETV5	GTTTAAAGGTTAATTTTTTTGTTTGATA	CCTCAACTCACTACTAAAATTTCTC	chr3	185824757	185825135
ATG5	TGATTATAAATAGAAAGGAGAGTGTGT	ACAAAAATTATAAACAAAAATCAATAAAA	chr6	106641046	106641328
MAD1L1	TTTTTTTGTTTTTTGGGTTTTATAG	CCCCAAATCAACCTTCATTAC	chr7	1882879	1883041
HDAC9	GAAATGGATTGTTGAGAATAGAGTTG	ACTTCTAAACCACATCTCAAAAAAAA	chr7	18592088	18592402
MLL5	TGGAGTTTTTTAGTTTTAGTGGG	TAAAACTAATTCTTTCCCCCTTTC	chr7	104654097	104654380
IDO2	TAAAATATTTTTATTGGAAGAAGATTT	CCATCTTAACCAACATAATAAAACC	chr8	39828244	39828501
CDNK2	TTAGATTTTATAGGGGAGGAAAGTGA	AAATAACATATAACCCCAACACAA	chr9	21996087	21996397
TMEM	AGGGAATAGAAATGTAAGGGGAGTT	ATAAAAAACCCAAAAACTCTACC	chr16	431080	431394
CACNA1H-3	GAGGTGTTGTTGAAAGGATTTGTAT	CCTCCAACAAAAAACCTACT	chr16	1201709	1201971
WWP2	GTGAGGTTGGTAGTTTAGAGGTAGG	TCCTCCCACTCAAATATAAATTAA	chr16	69895419	69895588
BMI	GTAGGGAGGGTAGAATTGTTTTT	ACTTCTAATCTCTCAAAATCATTCTATAA	chr10	22614844	22615158
LRP10	TAGGATGTTGTTGTTATTTTTTT	AAATTTCTTCTTCCCTAAACAACCTC	chr14	23341508	23341901
IRS1	TTTGGTATTAAGGATTTATAGAGATGTTA	ACAAAACCTAAAAACAACCATCC	chr2	227665734	227666028
CMTM4	GGAAAATTTGTTATAGGTTGTTAAGATTA	TCTACAACCTTCTTAAAAACCC	chr16	66729872	66730091

These loci were chosen based on the criteria shown in **Supplementary Table 3**.

**Supplementary Table 6** Bisulphite conversion efficiencies (C→T in CH context)

	Conversion Efficiency (%)
CBP184	99.662
CBP196	99.669
CBP262	99.670
CBP267	99.695
CBP269	99.684
CBP270	99.727
CBP274	99.613
CBP280	99.654
CBP285	99.691
CBP295	99.634
CBP302	99.696
CBP343	99.643
CBP345	99.698
CBP349	99.651
CBP351	99.653
CBP352	99.666
CBP353	99.666
CBP354	99.677
CBP358	99.617
CBP362	99.618
CBP364	99.646
CBP368	99.651
CBP373	99.624
CBP381	99.626
Mean	99.660

**Supplementary Table 7** Genes associated with candidate differentially-methylated loci corresponding to KEGG *Maturity onset diabetes of the young* and *Hedgehog signaling* pathways

	Maturity onset diabetes of the young	Hedgehog signaling
IUGR/control	<p><i>FOXA2</i>  <i>MAFA</i>  <i>MNX1</i>  <i>NKX2-2</i>  <i>NKX6-1</i>  <i>NR5A2</i>  <i>ONECUT1</i>  <i>PAX6</i>  <i>PKLR</i></p>	<p><i>BMP7</i>  <i>GLI3</i>  <i>PTCH1</i>  <i>WNT10A</i>  <i>WNT5A</i>  <i>WNT6</i>  <i>WNT9A</i>  <i>ZIC2</i></p>
LGA/control	<p><i>FOXA2</i>  <i>MAFA</i>  <i>MNX1</i>  <i>NKX2-2</i>  <i>NKX6-1</i>  <i>NR5A2</i>  <i>ONECUT1</i>  <i>PAX6</i>  <i>PKLR</i></p>	<p><i>BMP7</i>  <i>GLI3</i>  <i>LRP2</i>  <i>PTCH1</i>  <i>WNT1</i>  <i>WNT10B</i>  <i>WNT2B</i>  <i>WNT3A</i>  <i>WNT6</i>  <i>ZIC2</i></p>
Case/control	<p><i>FOXA2</i>  <i>MAFA</i>  <i>MNX1</i>  <i>NEUROD1</i>  <i>NEUROG3</i>  <i>NKX2-2</i>  <i>NKX6-1</i>  <i>ONECUT1</i>  <i>PAX4</i>  <i>PAX6</i>  <i>PDX1</i>  <i>PKLR</i></p>	<p><i>BMP7</i>  <i>GLI1</i>  <i>GLI3</i>  <i>PTCH1</i>  <i>SHH</i>  <i>WNT10B</i>  <i>WNT2B</i>  <i>WNT6</i>  <i>WNT9A</i>  <i>ZIC2</i></p>
IUGR/control (males only)	<p><i>MAFA</i>  <i>NEUROG3</i>  <i>NKX2-2</i>  <i>NKX6-1</i>  <i>ONECUT1</i>  <i>PAX6</i></p>	<p><i>BMP4</i>  <i>BMP8A</i>  <i>PTCH1</i>  <i>WNT9A</i>  <i>ZIC2</i></p>
LGA/control (females only)	<p><i>FOXA2</i>  <i>MNX1</i>  <i>NEUROD1</i>  <i>NKX2-2</i>  <i>NKX6-1</i>  <i>ONECUT1</i>  <i>PAX6</i>  <i>PKLR</i></p>	<p><i>IHH</i>  <i>LRP2</i>  <i>PTCH1</i>  <i>SHH</i>  <i>WNT3A</i>  <i>WNT6</i>  <i>WNT7B</i>  <i>ZIC2</i></p>