# Altered dietary ratio of folic acid and vitamin B12 during pregnancy influences the expression of imprinted H19/IGF2 locus in C57BL/6 mice

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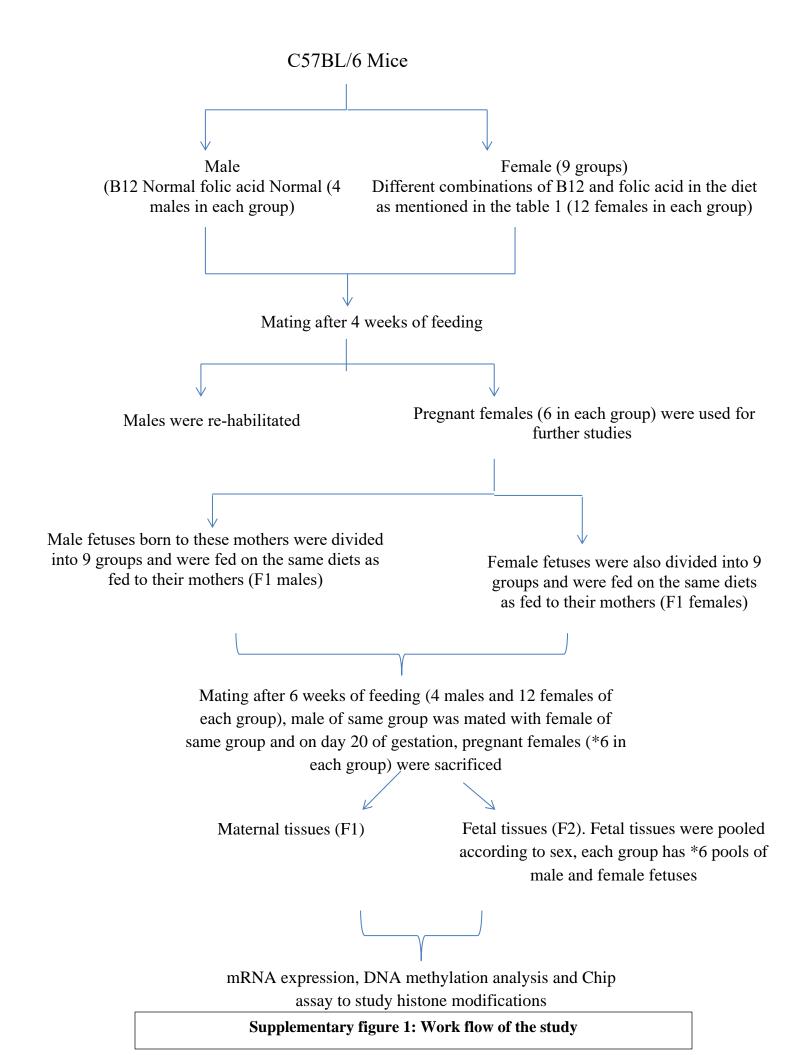
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**Key words:** Genomic imprinting; epigenetics; Folic acid; Vitamin B12, Homocysteine, DNA methylation and chromatin immunoprecipitation.



H19

(A).

			H19 Pla	acenta				
B12	В	D		BN			ВО	
Folate	FD	FN	FD	FN	FO	FD	FN	FO
mRNA	NC	NC	1	С	NC	1	NC	NC
DNA methylation	1	1	1	С	1	NC		
H3K9me3	1	1	1	С		1		
H3K27me3	NC	NC	NC	С		1		
H3K4me2	NC	1	1	С		1		

C= control

NC= No change

= up-regulated
= down-regulated
= up/downregulation of
expression associated with either

DNA methylation/histone
modification.

(B)

						H19 F	etal L	iver								
B12	В	D	В	D		BN			BN			ВО			ВО	
	(M	ale)	(Fen	(Female)		(Male	)	(F	emale	e)	(	(Male)	)	(F	emal	e)
Folate			FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO	
mRNA	1	NC	NC	NC	1	С	NC	1	С	NC	NC	NC	NC	NC	NC	NC
DNA methylation	1	1	1	1	1	С	1	1	С	1	1			1		
H3K9me3	1		NC		NC	С		1	С		1			1		
H3K27me3	1		1		1	С		1	С		1			NC		
H3K4me2	NC		1		NC	С		1			NC			1		

(C)

						H19 F	etal Ki	dney								
B12	В	D	В	D		BN			BN			ВО			ВО	
	(Ma	ale)	(Fen	nale)	(	(Male)		(1	Femal	e)		(Male	)	(1	Female	e)
Folate	FD	F	FD	FN	<del>                                     </del>		FD	FN	FO	FD	FN	FO	FD	FN	FO	
		N														
mRNA	NC		NC		1	С	NC	1	С	NC	NC	NC	NC	NC	NC	NC
DNAmethylation	1		1		NC	С	1	1	С	1	1			1		
H3K9me3	NC		1		NC	С		<b>1</b>	С		1			1		
H3K27me3	NC		1		NC	С		NC	С		1			NC		
H3K4me2	NC		1		NC	С		1	С		1			1		

(D)

						H19 F	etal Bı	ain								
B12	В	D	В	D		BN			BN			ВО			ВО	
	(Ma	ale)	(Fen	nale)	(Male) FD FN FO			(F	emale	e)	(	(Male	)	(1	emal	e)
Folate	FD	FN	FD	FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO
mRNA	NC	NC	1	NC	1	С	NC	1	С	1	NC	NC	NC	1	NC	NC
DNA methylation	1	<b>+</b>	NC	1	<b>+</b>	С	1	1	С	1	1			1		
H3K9me3	1		1		1	С		1	С		1			1		
H3K27me3	1		1		1	С		1	С		NC			1		
H3K4me2	1		NC		•	С		NC	С		<b>⇒</b>			1		

**Supplementary figure 2:** Summary of changes observed in expression, DNA methylation and histone modifications of **H19** with different dietary combinations of folic acid and B12.

(A)

			IGF2 Pl	acenta				
B12	В	D		BN			ВО	
Folate	FD	FN	FD	FN	FO	FD	FN	FO
mRNA	NC	1	NC	С	1	NC	NC	NC
DNA methylation	NC	NC	NC	С	1	NC		
H3K9me3	1	1	NC	С		1		
H3K27me3	1	1	NC	С		1		
H3K4me2	1	1	1	С		1		

C= control

NC= No change

= up-regulated
= down-regulated
= up/downregulation of
expression associated with either

DNA methylation/histone
modification.

(B)

					10	GF2 F	etal Liv	ver								
B12	В	D	В	D		BN			BN			ВО			ВО	
	(M	ale)	(Fen	nale)	(	(Male	)	(F	emale	e)	(	(Male	)	(F	emal	e)
Folate	FD	FN	FD	FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO
mRNA	NC	NC	1	NC	NC	С	NC	NC	С	NC	1	1	NC	NC	1	NC
DNA methylation	1	1	1	1	NC	С	1	NC	С	1	1			1		
H3K9me3	NC		NC		1	С		1	С		1			NC		
H3K27me3	1		NC		NC	С		1	С		1			1		
H3K4me2	1		1		NC	С		NC	С		1			1		

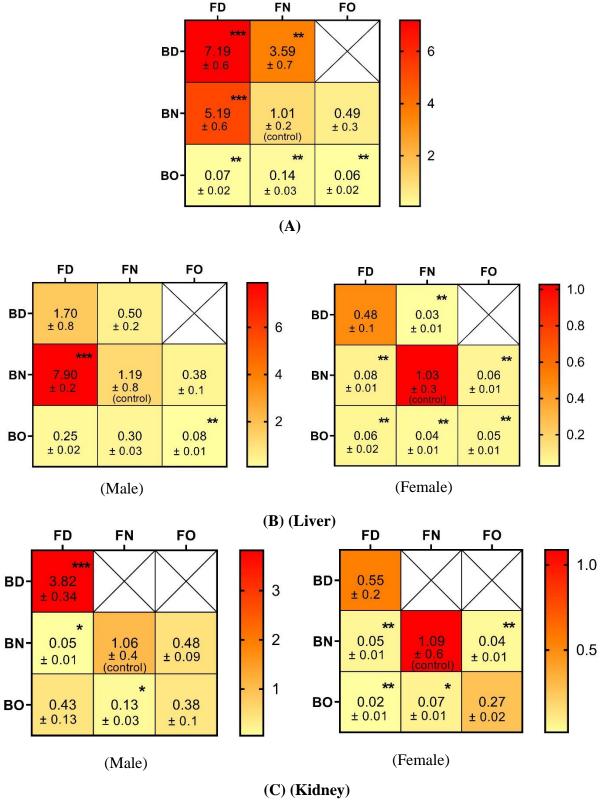
(C)

						IGF2 Fe	etal Kid	lney								
B12	В	D	В	D		BN			BN			ВО			ВО	
	(Ma	ale)	(Fen	nale)		(Male)		(F	emal	e)		(Male)		(F	emale	2)
Folate	FD	FN	FD	FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO
mRNA	1		1		1	С	1	1	С	NC	NC	1	1	NC	1	NC
DNA methylation	1		1		NC	С	1	NC	С	NC	NC			NC		
H3K9me3	NC		NC		1	С		1	С		1			NC		
H3K27me3	NC		NC		NC	С		NC	С		1			NC		
H3K4me2	NC		NC		NC	С		1	С		1			NC		

(D)

						IGF2 F	etal B	rain								
B12	В	D	В	D		BN	•		BN			ВО	•		ВО	•
	(Ma	ale)	(Fen	nale)		(Male)		(F	emale	e)	(	(Male	)	(F	emal	e)
Folate	FD	FN	FD	FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO
mRNA	1	NC	1	NC	NC	С	1	NC	С	NC	1	NC	NC	1	NC	NC
DNA methylation	<b>4</b>	<b>←</b>	1	1	NC	С	NC	1	С	<b>+</b>	NC			1		
H3K9me3	1		1		1	С		NC	С		1			1		
H3K27me3	1		1		NC	С		NC	С		1			NC		
H3K4me2	NC		NC		1	С		NC	С		1			NC		

**Supplementary figure 3:** Summary of changes observed in expression, DNA methylation and histone modifications of **IGF2** with different dietary combinations of folic acid and B12.



Supplementary figure 4: Quantification of miRNA 675 in placenta and fetal tissues (A) Mother Placenta (B) Fetal Liver (C) Fetal Kidney. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001 vs BNFN. The data is presented as mean± SD.B12 normal folic acid normal (BNFN), B12 normal folic acid over-supplemented (BNFO), B12 normal folic acid deficient (BNFD), B12 deficient folic acid normal (BDFN), B12 deficient folic acid over-supplemented (BDFO), B12 over-supplemented folic acid normal (BOFN), B12 over-supplemented folic acid deficient (BOFO), B12 over-supplemented folic acid deficient (BOFO).

#### miR-675

				miR675	Placenta	1								
	B12	В	BD BN BO											
	Folate	FD	FN	FD	FN	FO	FD	FN	FO					
mRNA		1	1	1	С	NC	1	1	1					

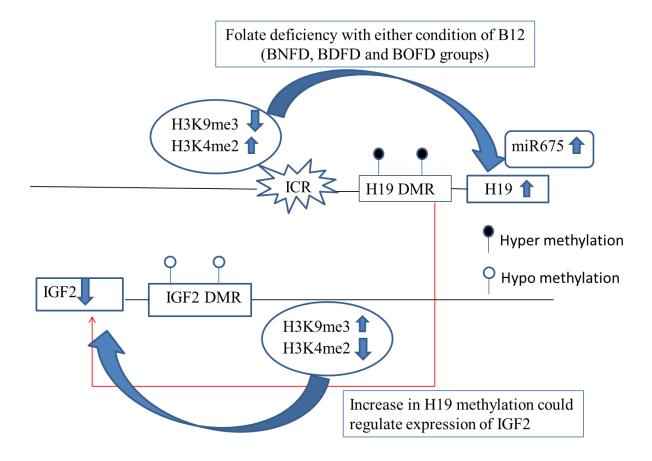
NC= No change
↑ = up-regulated
= down-regulated

C= control

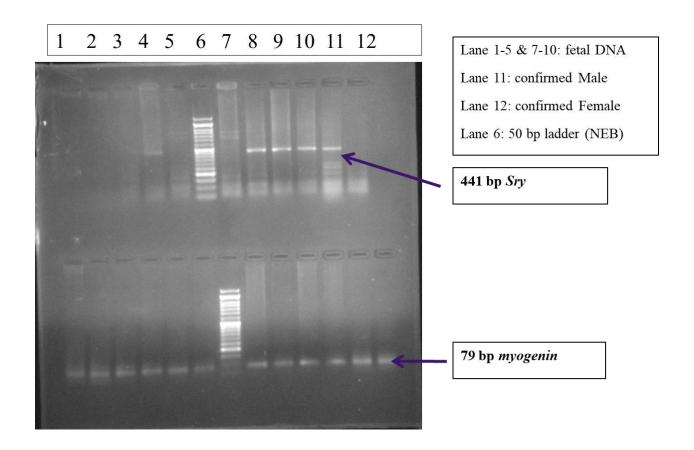
						mil	R675 I	Fetal L	iver								
	B12	В	BD BD BN BO BO														
		(M:	ale)	(Female) (Male)					(F	emale	2)	(	Male)		(F	emale	2)
	Folate	FD	FN	(Female) (Male) FD FN FD FN FO				FD	FN	FO	FD	FN	FO	FD	FN	FO	
mRNA		NC	NC	NC	1	1	С	NC	1	С	1	NC	NC	1	1	1	1

						m	niR675 I	etal K	idney								
	B12	В	D	В	D		BN			BN			ВО			ВО	
		(Ma	ale)	(Fen	nale)		(Male)	)	(F	emal	e)		(Male)		(F	emale	÷)
	Folate	FD	FN	FD	FN	FD	FN	FO	FD	FN	FO	FD	FN	FO	FD	FN	FO
mRNA		1		NC		1	С	NC	1	С	1	NC	1	NC	1	1	NC

**Supplementary figure 5:** Summary of changes observed in the expression of **miR-675** with different dietary combinations of folic acid and B12.



Supplementary figure 6: Overall diagrammatic representation of results showing that the dietary conditions of folate deficiency (BNFD, BDFD and BOFD) leads to increase in expression of maternally expressed gene (H19), which is regulated by increase in activating histone mark (H3K4me2) and decrease in repressive histone mark (H3K9me3) at its ICR. IGF2, a paternally expressed gene was found to be downregulated under dietary deficiency which was regulated by an increase in suppressive mark (H3K9me3) and decrease in activating mark (H3K4me2). Further, increased H19 DNA methylation at DMR may be responsible for decrease in the expression of IGF2.



**Supplementary Figure 7: Fetal sex determination by using SRY gene.** PCR reaction generated a male-specific SRY band of 441 bp against a control MYOGENIN band of 79 bp which was run on 1.5% agarose gel

#### Supplementary Table 1: Primer sequences for SRY and MYOGENIN

Gene	Primer sequence	Length
SRY	F: 5'-TCATGAGACTGCCAACCACAG- 3'	441bp
	R: 5'-CATGACCACCACCACCAA-3'	
MYOGENIN	F: 5'-CGTGGGCATGTAAGGTGTGTA-3'	79bp
	R: 5'-CCTGCGCTTCTCCCTCAGT-3'	

#### **Supplementary Table 2: mRNA primer sequence**

Gene	Primers sequence	Product
GAPDH	F: AGCTTGTCATCAACGGGAAG R: TTTGATGTTAGTGGGGTCTCG	61 bp
H19	F: TGTGCCTGCCAGTCACTGA R: CCATCACACCGGACCATGT	79bp
IGF2	F: CAACTCAGTCCCTCTAACATGCAT R: GTTTGCGAGCGTTAACAGGTT	79bp

#### Supplementary Table 3: miRNA primer sequence

MiRNA	Sequence
miRNA-675	F:GGACTGGTGCGGAAAGGGCCCACAGTGGACTTGGTACACTGTATG
Universal reverse	GAATCGAGCACCAGTTACGC
primer	

#### **Supplementary Table 4: MS-HRM primer sequence**

Gene	Primer sequence
H19	F:CGAACGTGCGTTGGAACGATAT
	R:CGATACTTCGAACCCTCTAACC
IGF2 DMR2	F: CGTGTTAATCGTCGTAGTCGTGGT
	R: TCGCTACCTACCGAAAATACGACC

#### **Supplementary Table 5: ChIP primer sequence**

H19 (ICR)	F:TCCCCGGACATGAAAATAG R:TTGCCTACAGTTCCCGAATCA
IGF2	F:CAGAACATGAAAACTGGAAATAGAACTT R:AGTATAATCATGTGCTTTTTAGGGTAGGT

### Supplementary table 6: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in maternal placenta

	-		-	-	H19	Placenta		=			
	pendent	mRNA (fold change)		DNA methylation		H3K9me3			27me3	H3K4me2	
	riable:	ì	<u> </u>	(% Meth		(fold enric			richment)	(fold enri	,
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.15	0.62	42.18	1.20	12.65	1.65	3.88	1.15	0.32	0.24
BN	FD	15.89	2.24	62.73	2.33	18.01	0.14	4.72	0.07	18.12	0.70
	FO	1.92	0.47	77.10	0.92						
	FN	0.78	0.07	10.41	0.40	2.76	0.75	5.94	0.75	5.64	0.65
BD	FD	3.95	1.08	80.91	2.93	2.49	0.30	2.32	1.40	1.17	0.06
	FN	0.84	0.25								
во	FD	6.77	3.61	45.19	3.27	24.28	0.36	37.29	1.11	24.42	1.04
	FO	0.42	0.38								

#### Supplementary table 7: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal brain (Male)

				ŀ	H19 Fetal	Brain (Male	)				
	pendent	mRNA		DNA methylation		H3K9me3			7me3	H3K4me2	
va	riable:	(fold ch	nange)	(% Methy	lation)	(fold enric	nment)	(told enr	ichment)	(tola enr	ichment)
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.02	0.25	90.81	2.38	20.89	0.77	3.55	0.89	8.31	0.70
BN	FD	46.24	8.02	23.70	0.45	1.85	0.70	45.38	1.41	2.10	0.37
	FO	6.03	2.25	41.84	2.32						
	FN	7.04	2.17	79.76	1.04						
BD	FD	3.55	0.88	69.44	1.81	0.41	0.09	0.42	0.23	0.71	0.14
	FN	2.86	1.74								
во	FD	8.44	2.23	84.26	3.54	24.66	1.41	2.52	0.61	0.46	0.17
	FO	1.91	0.45								

### Supplementary table 8: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal brain (female)

	H19 Fetal Brain (female)														
•	pendent	mRNA			DNA methylation		ne3		ne3 (fold	H3K4me2					
va	riable:	(fold ch	nange)	(% Methy	rlation)	(fold enric	nment)	enrich	ment)	(fold er	richment)				
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD				
	FN	1.13	0.13	59.26	2.00	4.82	0.95	5.32	0.42	0.74	0.08				
BN	FD	25.58	1.81	84.30	2.28	7.88	0.63	1.94	0.25	0.81	0.14				
	FO	16.52	3.49	36.44	1.42										
	FN	4.18	1.32	49.52	4.17										
BD	FD	40.55	19.25	56.27	.26	2.52	0.47	22.38	2.12	1.17	0.19				
	FN	1.98	1.16												
во	FD	18.86	4.97	83.91	3.47	11.40	0.98	2.52	0.61	28.28	0.70				
	FO	5.79	2.50												

### Supplementary table 9: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal kidney (Male)

				Н	119 Fetal k	idney (Male	e)				
	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)			7me3	H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.04	0.30	82.37	1.26	1.63	0.73	1.03	0.14	2.63	0.77
BN	FD	7.94	2.39	81.10	2.76	0.42	0.11	0.63	0.28	0.76	0.13
	FO	0.57	0.09	39.86	1.97						
	FN										
BD	FD	2.28	0.63	57.51	.96	2.33	0.36	0.54	0.24	0.26	0.17
	FN	0.18	0.05								
во	FD	2.02	0.86	55.91	0.008	55.43	2.82	25.13	0.70	8.28	0.70
	FO	0.54	0.29								

### Supplementary table 10: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal kidney (female)

	H19 Fetal Kidney (female)													
•	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)				
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD			
	FN	1.45	0.03	83.23	1.89	11.21	0.37	2.23	0.53	20.66	1.41			
BN	FD	3.92	1.17	93.00	0.64	2.92	0.81	0.78	0.21	5.26	0.56			
	FO	1.42	0.12	43.50	1.651									
	FN													
BD	FD	3.00	1.71	65.03	3.35	0.60	0.20	0.42	0.28	1.86	0.10			
	FN	1.13	0.07											
во	FD	1.45	0.45	75.73	3.03	14.15	0.70	1.95	0.46	3.58	0.34			
	FO	2.69	0.58											

#### Supplementary table 11: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal liver (Male)

	-	_	_	-	H19 Fetal	Liver (Male)	)	-			
	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K2 (fold enr	7me3	H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.15	0.11	82.36	1.05	3.21	0.89	1.81	0.81	0.95	0.05
BN	FD	11.25	2.51	39.30	0.81	1.98	0.11	6.69	0.70	1.45	0.28
	FO	1.51	1.03	32.28	3.67						
	FN	2.35	1.29	37.21	2.53						
BD	FD	3.59	2.22	45.93	1.51	0.25	0.07	0.26	0.07	0.47	0.29
	FN	0.67	0.18								
во	FD	2.47	0.78	73.84	0.09	88.55	3.18	93.98	2.03	0.71	0.30
	FO	0.34	0.37								

### Supplementary table 12: Interaction between folic acid and B12 for H19 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal liver (female)

	H19 Fetal Liver (female)														
	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)					
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD				
	FN	1.24	0.22	63.64	2.36	6.95	1.03	1.66	0.76	2.61	0.32				
BN	FD	4.40	2.18	89.18	2.60	3.23	0.40	19.48	1.60	11.41	0.99				
	FO	1.59	0.21	31.88	1.26										
	FN	1.65	0.55	16.10	2.03										
BD	FD	1.93	0.72	54.62	2.80	5.38	0.82	5.29	0.73	27.63	1.63				
	FN	1.35	0.08												
во	FD	2.07	0.89	90.06	5.88	0.31	0.14	1.62	0.43	0.11	0.13				
	FO	2.64	1.20												

### Supplementary table 13: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in maternal placenta

	IGF2 Placenta										
	pendent ariable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.00	0.10	42.37	3.09	1.08	0.30	0.88	0.17	9.38	0.20
BN	FD	0.97	0.22	40.39	2.87	0.43	0.10	0.85	0.13	2.09	0.13
	FO	5.81	0.46	55.71	4.32						
	FN	0.04	0.01	41.83	1.70	3.75	0.34	3.26	0.21	1.80	0.21
BD	FD	0.84	0.06	37.80	2.53	5.51	0.42	2.79	0.13	0.14	0.06
	FN	1.15	0.60								
во	FD	1.19	0.35	40.57	3.84	4.18	0.45	8.42	0.12	4.01	0.64
	FO	0.86	0.37								

### Supplementary table 14: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal brain (Male)

	IGF2 Fetal Brain (Male)										
	endent	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.09	0.34	67.26	2.64	1.72	0.58	0.60	0.15	0.67	0.21
BN	FD	0.95	0.41	63.42	8.87	23.68	1.60	2.39	0.24	7.93	0.85
	FO	2.08	0.96	72.05	2.51						
	FN	0.67	0.35	55.42	1.12						
BD	FD	0.59	0.19	22.23	1.88	5.65	0.97	21.64	1.85	0.78	0.27
	FN	1.25	0.26								
во	FD	0.55	0.23	70.97	4.16	26.92	2.42	9.91	0.42	5.43	1.27
	FO	1.15	0.26								

#### Supplementary table 15: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal brain (female)

-	IGF2 Fetal Brain (female)										
	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.12	0.56	56.70	2.09	8.41	1.57	1.94	0.80	4.08	0.61
BN	FD	0.89	0.17	66.72	1.46	10.18	0.79	1.55	0.73	2.17	1.08
	FO	1.91	0.49	11.10	0.07						
	FN	0.93	0.35	41.88	0.44						
BD	FD	0.66	0.14	36.90	3.11	1.92	1.47	20.27	1.51	6.29	0.95
	FN	1.27	0.18								
во	FD	0.73	0.32	74.14	4.29	5.12	0.36	0.46	0.38	1.83	0.23
	FO	1.18	0.33								

### Supplementary table 16: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal kidney (Male)

	IGF2 Fetal Kidney (Male)										
	endent	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	0.82	0.26	71.24	5.07	4.97	0.28	1.41	0.30	0.53	0.10
BN	FD	0.17	0.01	77.21	4.60	10.07	0.77	2.36	0.24	1.03	0.08
	FO	2.98	0.47	78.18	1.40						
	FN										
BD	FD	0.27	0.03	42.77	3.49	3.50	0.18	1.15	0.10	0.96	0.12
	FN	4.00	0.93								
во	FD	0.42	0.09	76.98	4.86	46.51	3.41	73.44	2.54	9.21	1.54
	FO	2.77	0.49								

### Supplementary table 17: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal kidney (female)

-	IGF2 Fetal Kidney (female)										
	endent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.64	0.07	71.81	3.73	0.69	0.16	1.31	0.20	1.47	0.43
BN	FD	0.38	0.10	73.60	1.92	1.95	0.35	2.16	0.35	2.78	0.70
	FO	1.37	0.34	76.70	1.67						
	FN										
BD	FD	0.24	0.04	43.41	1.42	0.68	0.30	0.20	0.08	0.63	0.12
	FN	3.10	0.86								
во	FD	0.78	.004	75.96	2.50	0.74	0.14	1.09	0.28	0.60	0.24
	FO	1.13	0.35								

### Supplementary table 18: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal liver (Male)

	IGF2 Fetal Liver (Male)										
1	endent	mRNA		DNA methylation		H3K9me3			27me3	H3K4me2	
va	riable:	(fold ch	nange)	(% Methy	(lation)	(fold enric	hment)	(fold en	richment)	(fold e	nrichment)
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	0.99	0.38	74.96	0.69	1.54	0.58	1.04	0.24	0.19	0.02
BN	FD	0.67	0.26	67.31	3.50	4.84	0.38	1.06	0.10	0.60	0.05
	FO	1.41	0.21	12.03	0.90						
	FN	0.60	0.37	44.03	1.41						
BD	FD	0.71	0.25	27.45	0.99	2.95	0.12	2.67	0.93	4.68	0.34
	FN	5.17	0.01								
во	FD	3.25	0.78	65.35	4.49	10.36	0.18	4.86	0.38	4.51	1.19
	FO	1.40	0.21								

#### Supplementary table 19: Interaction between folic acid and B12 for IGF2 imprinted gene (mRNA, DNA methylation and histone modifications) in fetal liver (female)

	IGF2 Fetal Liver (female)										
	pendent riable:	mRNA (fold change)		DNA methylation (% Methylation)		H3K9me3 (fold enrichment)		H3K27me3 (fold enrichment)		H3K4me2 (fold enrichment)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.11	0.15	58.32	10.42	0.85	0.12	0.97	0.29	2.9	0.20
BN	FD	1.61	0.79	67.06	2.76	7.45	0.92	8.96	2.31	4.31	1.20
	FO	1.22	0.07	20.27	1.06						
	FN	0.50	0.16	46.84	4.15						
BD	FD	2.33	0.80	42.86	4.48	1.39	0.30	0.68	0.06	0.31	0.09
	FN	2.93	0.50								
во	FD	1.20	0.33	77.98	3.87	2.24	0.13	14.71	0.69	0.54	0.09
	FO	1.35	0.39								

#### Supplementary table 20: Interaction between folic acid and B12 for $miR-675\ (mRNA)$ in maternal and fetal tissues

	MiRNA-675 (mRNA) (fold change)										
Dependent variable:		Placenta		Fetal Kidney (Male)		Fetal Kidney (Female)		Fetal liver (Male)		Fetal liver (Female)	
B12	Folate	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
	FN	1.01	0.20	1.05	0.48	0.66	0.02	1.19	1.04	0.79	0.001
BN	FD	5.18	0.63	0.05	0.04	0.04	0.01	7.89	0.21	0.07	0.006
	FO	0.48	0.39	0.48	0.09	0.03	0.008	0.38	0.34	0.06	0.008
	FN	3.59	0.76					0.49	0.25	0.02	0.01
BD	FD	7.18	0.63	3.81	0.33	0.55	0.25	1.70	1.88	0.47	0.29
	FN	0.14	0.03	0.12	0.03	0.07	0.01	0.30	0.02	0.04	0.03
во	FD	0.06	0.02	0.42	0.13	0.01	0.0007	0.24	0.20	0.06	0.04
	FO	0.05	0.01	0.38	0.16	0.26	0.002	0.08	0.01	0.05	0.01

# Supplementary table 21: Pearson correlation and multiple regression analysis for H19 gene in maternal and fetal tissues

	Tissue			Pearson c	orrelation anal	ysis: r	Regression analysis with
			H3K9me3	H3K27me3	H3K4me2	mRNA vs DNA methylation	mRNA as dependent variable: r <sup>2</sup> (SEM)#
F1	Placenta	mRNA	0.542 *	0.098	0.642**		
generation mother		DNA methylation	0.088	-0.136	0.014	0.438	0.895***(2.173)
F2	Liver	mRNA	-0.283	-0.231	0.651**		
generation fetus	(male)	DNA methylation	0.446	0.404	-0.304	-0.740**	0.767**(2.426)
	Liver	mRNA	-0.081	0.896***	0.220		
	(female)	DNA	0.155	0.527*	0.057	0.421	0.856***(0.713)
		methylation					
	Kidney	mRNA	-0.276	-0.259	-0.347		
	(male)	DNA methylation	-0.627**	-0.600*	-0.451	0.334	0.639*(2.108)
	Kidney	mRNA	-0.828***	-0.738**	-0.480		
	(female)	DNA	0.101	0.227	0.374	0.081	0.806**(0.816)
		methylation					
	Brain	mRNA	-0.482	0.941***	-0.243		
	(male)	DNA	0.738**	-0.932***	0.352	-0.907***	0.907**(0.799)
		methylation					
	Brain	mRNA	0.140	0.629**	0.107		
	(female)	DNA methylation	0.910***	-0.369	0.562**	0.325	0.780**(0.702)

R = Pearson coefficient,  $r^2$  = regression determination coefficient, SEM = standard error of measurement. #Equation for Prediction for each gene was "mRNA expression =  $\beta 1$  H3K9me3 +  $\beta 2$  H3K27me3 +  $\beta 3$  H3K4me2 +  $\beta 4$  DNA methylation +  $\alpha$  ", where  $\beta 1$ ,  $\beta 2$ ,  $\beta 3$ ,  $\beta 4$  are regression coefficients and  $\alpha$  is intercept of test. \*p < 0.05 and \*\*p < 0.01, \*\*p< 0.001

# Supplementary table 22: Pearson correlation and multiple regression analysis for IGF2 gene in maternal and fetal tissues

	Tr's second			Pearson corn	relation analys	sis: r	Regression analysis with
	Tissue		H3K9me3	H3K27me3	H3K4me2	mRNA vs DNA methylation	mRNA as dependent variable: r <sup>2</sup> (SEM)#
F1 generation	Placenta	mRNA	-0.135	0.168	0.333	-0.184	0.285 (0.434)
mother		DNA methylation	-0.305	-0.065	0.305		
F2 generation	Liver (male)	mRNA	0.821***	0.787**	0.428	0.315	0.931***(0.321)
fetus		DNA methylation	0.173	-0.229	-0.702**		
	Liver	mRNA	0.581**	0.131	0.034	-0.033	0.739***(0.522)
	(female)	DNA methylation	0.450*	0.863***	0.157	-0.033	0.739***(0.322)
	Kidney	mRNA	-0.061	-0.011	-0.057	0.215	0.804**(0.148)
	(male)	DNA methylation	0.464	0.376	0.374	0.213	0.804**(0.148)
	Kidney	mRNA	-0.380	0.092	0.061	0.485	0.885***(0.218)
	(female)	DNA methylation	0.372	0.783**	0.435	0.463	0.865***(0.218)
	Brain	mRNA	-0.425	-0.715**	-0.250	0.470	0.817***(0.176)
	(male)	DNA methylation	0.453	-0.840***	0.472	0.470	0.817 (0.170)
	Brain	mRNA	0.358	-0.476*	-0.144	0.207	0.561*(0.264)
	(female)	DNA methylation	0.615**	-0.635**	-0.405	0.207	0.501 (0.204)

R = Pearson coefficient,  $r^2$  = regression determination coefficient, SEM = standard error of measurement. #Equation for Prediction for each gene was "mRNA expression =  $\beta 1$  H3K9me3 +  $\beta 2$  H3K27me3 +  $\beta 3$  H3K4me2 +  $\beta 4$  DNA methylation +  $\alpha$  ", where  $\beta 1$ ,  $\beta 2$ ,  $\beta 3$ ,  $\beta 4$  are regression coefficients and  $\alpha$  is intercept of test. \*p < 0.05 and \*\*p < 0.01, \*\*p< 0.001

### Supplementary table 23: Pearson correlation for miRNA-675 with H19 in maternal and fetal tissues

	Comparison of expression of H19 with miRNA-675								
	Tissue	Pearson correlation analysis: r (H19 mRNA vs miRNA-675)							
F1 generation mother	Placenta	0.43*							
F2 generation	Liver (Male)	0.86***							
fetus	Liver (Female)	-0.30							
	Kidney (Male)	-0.07							
	Kidney (Female)	-0.02							

R = Pearson coefficient \*p < 0.05 and \*\*p < 0.01, \*\*\*p< 0.001.