

# Ο ρόλος της Μοριακής Βιολογίας στην εμφάνιση & εξέλιξη των χρόνιων νοσημάτων



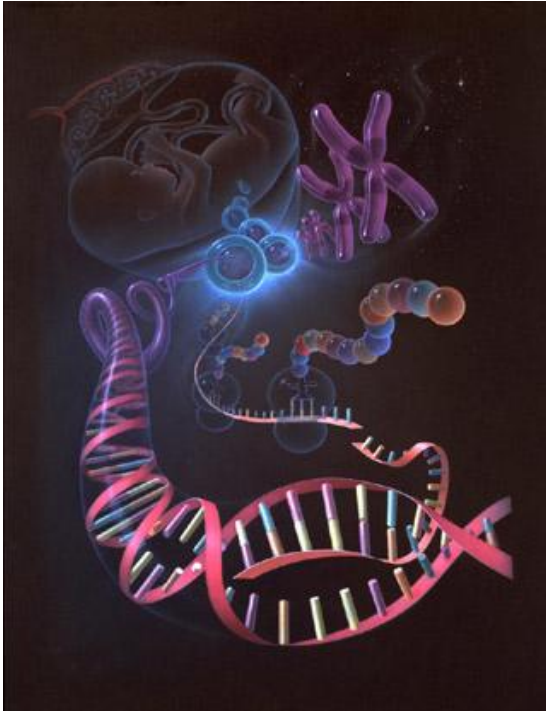
**Π.Γ.ΧΑΛΒΑΤΣΙΩΤΗΣ**

**Β' ΠΡΟΠΑΙΔΕΥΤΙΚΗ ΠΑΘΟΛΟΓΙΚΗ ΚΛΙΝΙΚΗ – ΜΟΝΑΔΑ ΕΡΕΥΝΑΣ  
& ΔΙΑΒΗΤΟΛΟΓΙΚΟ ΚΕΝΤΡΟ ΠΑΝΕΠΙΣΤΗΜΙΟΥ ΑΘΗΝΩΝ  
ΠΑΝΕΠΙΣΤΗΜΙΑΚΟ ΓΕΝ.ΝΟΣΟΚΟΜΕΙΟ "ΑΤΤΙΚΟΝ"**

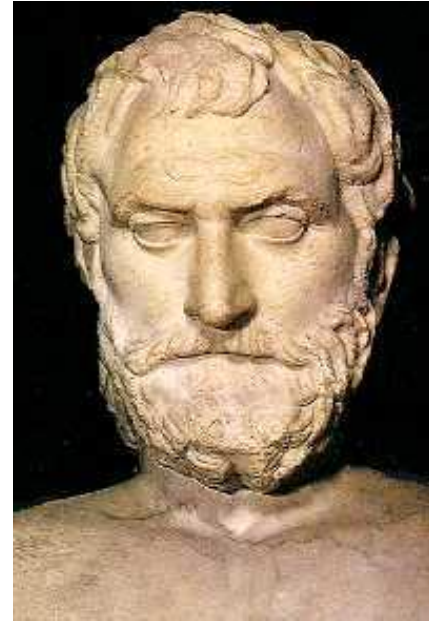


**Δεν υπάρχει σύγκρουση  
συμφερόντων**

# «THE GENE» HYPOTHESIS



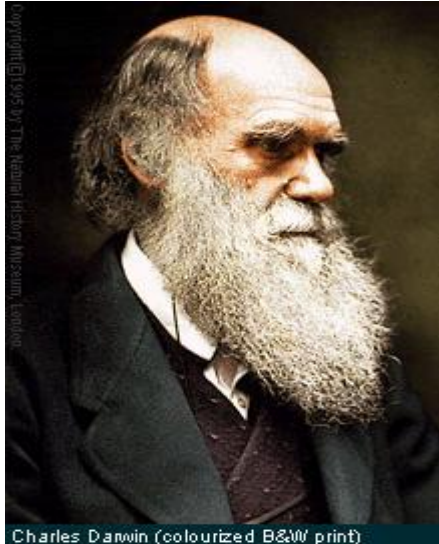
**ANAXAGORAS**  
(500 - 428 B.C.)



**ANAXIMANDROS**  
(611-546 B.C.)

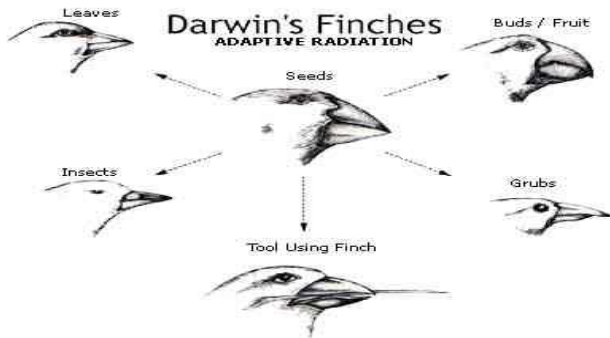


# From the 20<sup>th</sup> ..... .....to the 21<sup>st</sup> century



Charles Darwin (colourized B&W print)

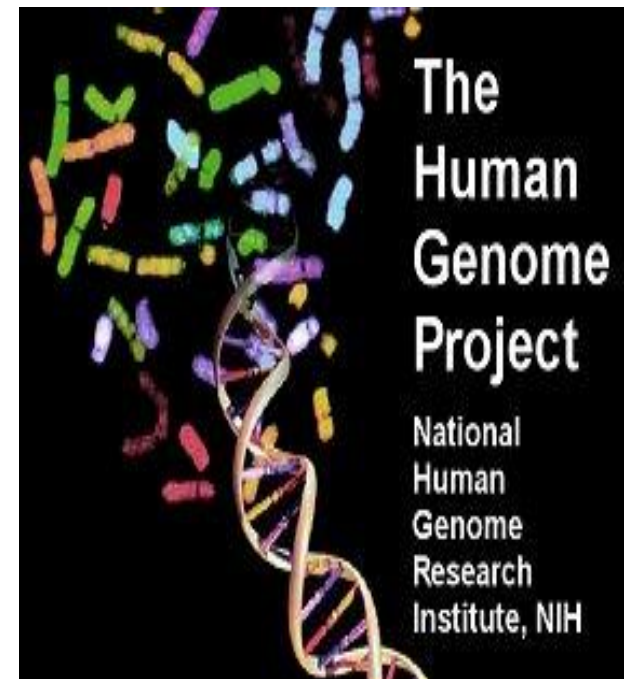
1809 - 1882



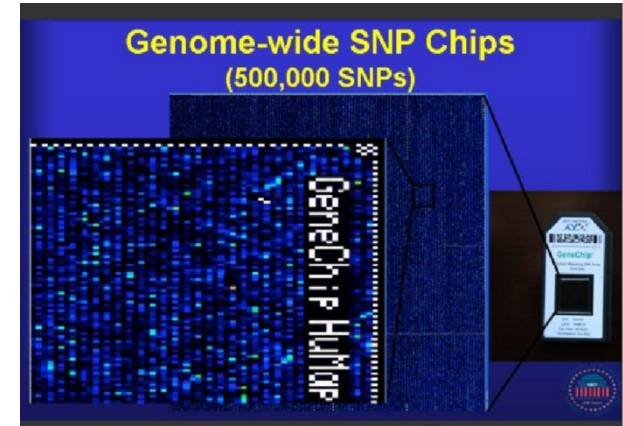
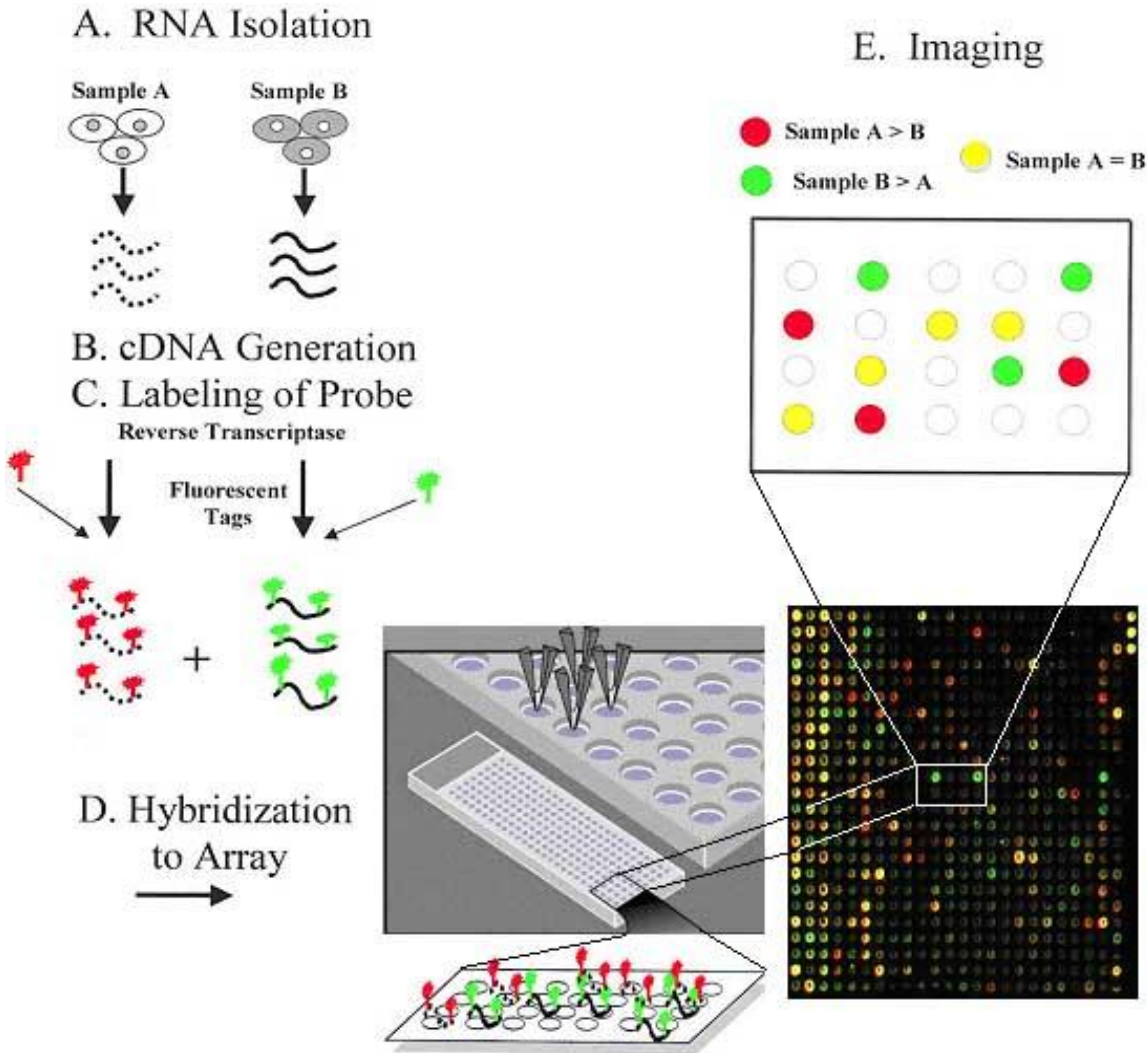
April 1953



April 2003



# MICROARRAYS GENE PROJECTS



# GENE EXPRESSION IN DIABETES MELLITUS

- Studied 6.451 genes where hyperglycemia modified the expression of 85
- Insulin treatment normalized 74
- ...while modified the expression of 29, previously normal .!!!
- **But 11 remained unchanged**

*Sreekumar R, Halvatsiotis P, Nair S.  
Diabetes 51:1913-20, 2002*

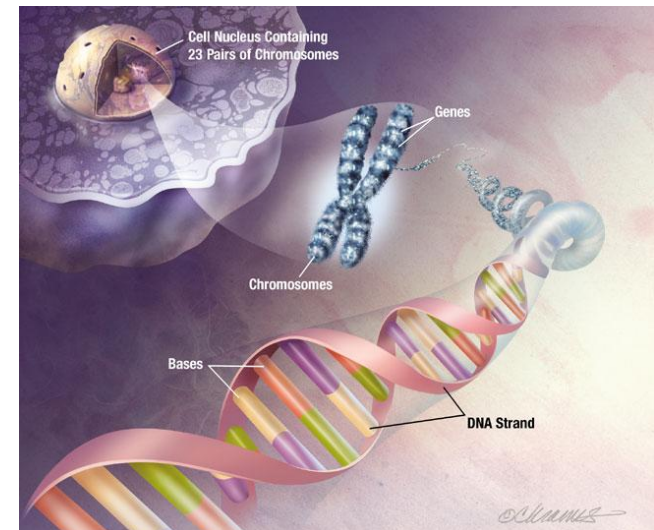
The screenshot displays a web interface for a Nature Reviews article. At the top, the title "RNA Interference" is on the left and the "nature REVIEWS" logo is on the right. Below the title, a text box explains that in eukaryotes, most protein-coding genes are transcribed by RNA polymerase II, which generates pre-mRNAs that are then processed to form mature mRNAs. These mRNAs are then transported from the nucleus to the cytoplasm, where they are translated. The main visual is a 3D model of a DNA double helix with a green, multi-lobed RNA polymerase II enzyme bound to it, actively transcribing a strand of RNA. Labels "Transcription" and "RNA polymerase II" are visible. Below the model is a control panel with navigation buttons (play, stop, back, forward, refresh) and a "Part 1: Gene expression" dropdown menu. A "Glossary" section shows "RdRp" selected. At the bottom, there is a "Download" button and a copyright notice: "Copyright © 2003 Nature Publishing Group. Created by [Artik](#) for Nature Reviews Genetics".

# GENOME & DIABETES MELLITUS

Fold	Gene name
<b>Structural/contractile genes</b>	
2.9*	Calmodulin Type I
2.1*	Troponin I fast-twitch
2.1	Troponin C fast-twitch
2.0*	Skeletal muscle C-protein
2.0	Troponin I slow-twitch
1.9	Tropomyosin
<b>Stress response/energy metabolism</b>	
3.2	Heat shock protein, 70 kDa
2.0	NADH dehydrogenase-ubiquinone
<b>Growth factor/tissue development</b>	
2.9	IGFBP-5
2.2*	MCL1
2.1*	Cadherin FIB3

Gene Expression Profile in Skeletal Muscle of Type 2 Diabetes and the Effect of Insulin Treatment

Raghavakaimal Sreekumar, Panagiotis Halvatsiotis, et al *Diabetes* 51:1913-1920, 2002



# «DIABETOGENIC» GENES

## Type 2 Diabetes (T2D):

### “The geneticist’s nightmare”

- Family history as a substantial risk factor
  - But relative risk to a sibling is only ~3.5
- Environment as a major contributor
- Family linkage studies relatively disappointing
- Validated genes prior to 2007:
  - *PPARG* (candidate gene)
  - *KCNJ11* (candidate gene)
  - *TCF7L2* (linkage study)

# cases + controls

### FUSION

S1: 1161 + 1174

S2: 1215 + 1258

### DGI

S1: 1464 + 1467

S2: 5065 + 5785

### WTCCC/UKT2D

S1: 1924 + 2938

S2: 3757 + 5346

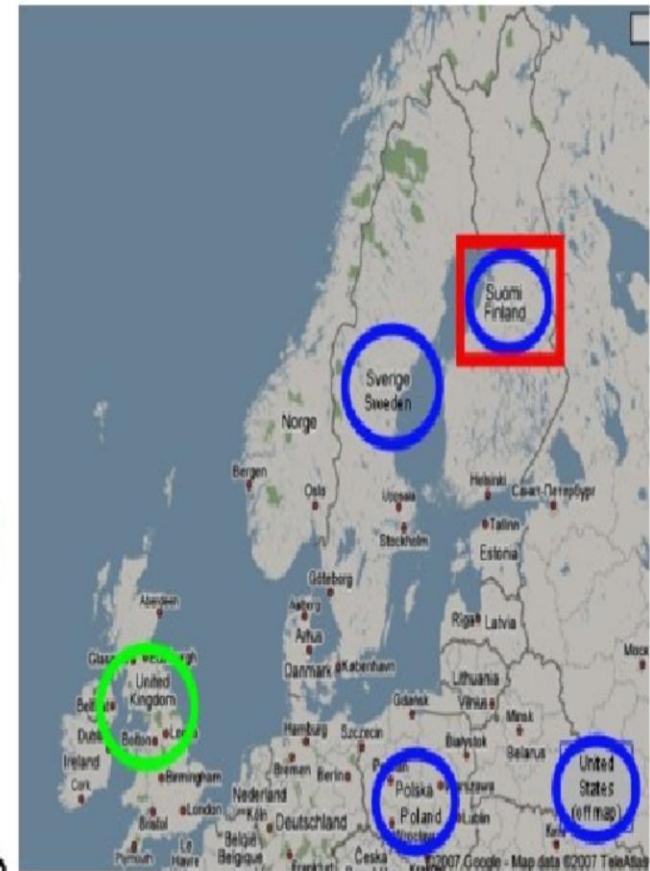
### Totals

S1 = 4549 + 5579

S2 = 10053 + 12389

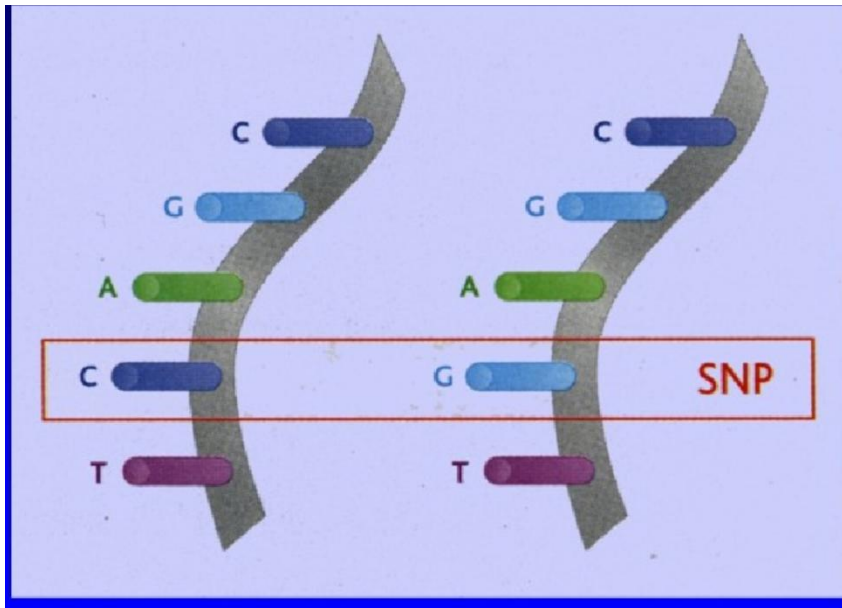
(n=32,554)

## Three Groups Working Together





# SINGLE NUCLEOTIDE POLYMORPHISM



But in practice,  
only two are observed

...C...A...A...

...C...A...G...

...C...C...A...

...C...C...G...

...T...A...A...

...T...A...G...

...T...C...A...

...T...C...G...

# HAPLOTYPES

Virtually All Diseases (Except Maybe Trauma)  
Have a Genetic Component



Cystic fibrosis




Type 2 diabetes

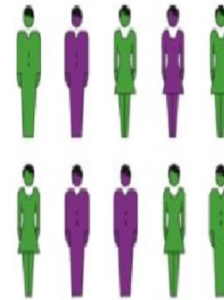


AIDS

Genetic Component 

Environmental Component 

SNP A

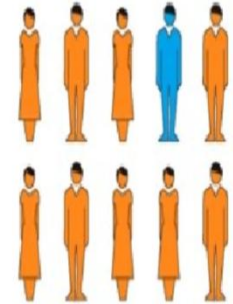


Diabetic

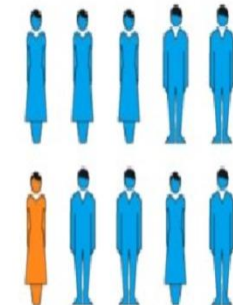


Unaffected

SNP B



Diabetic

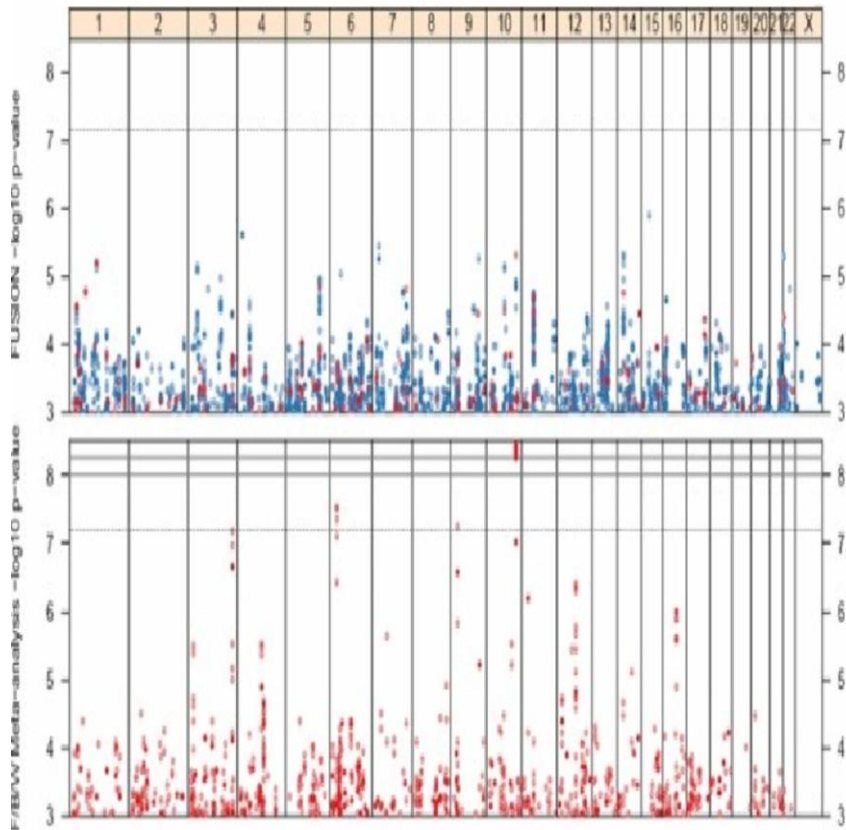


Unaffected

# «DIABETOGENIC» GENES

Results of GWA with 317,503 SNPs

Stage 1: FUSION only (1161 cases + 1174 controls)



Stage 1 – FUSION + DGI + WTCCC  
(4549 cases + 5579 controls)

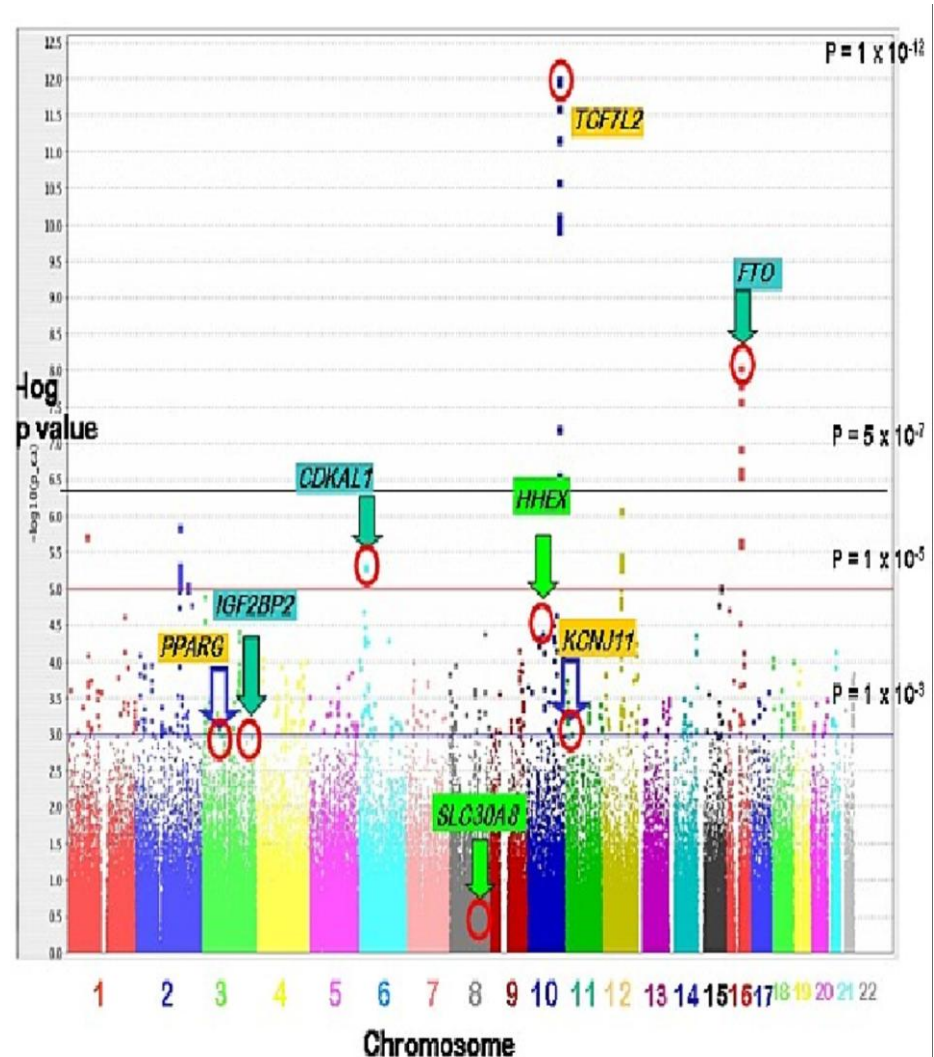
Top 10 Results From Combined Analysis

$n = 32,554$

Gene	FUSION		DGI		WTCCC/UKT2D		All Samples	
	OR	p-value	OR	p-value	OR	p-value	OR	p-value
<i>TCF7L2</i>	1.34	$1.3 \times 10^{-8}$	1.38	$2.3 \times 10^{-31}$	1.37	$6.7 \times 10^{-13}$	1.37	$1.0 \times 10^{-48}$
<i>IGF2BP2</i>	1.18	$2.1 \times 10^{-4}$	1.17	$1.7 \times 10^{-9}$	1.11	$1.6 \times 10^{-4}$	1.14	$8.9 \times 10^{-16}$
<i>CDKN2A/B</i>	1.20	.0022	1.20	$5.4 \times 10^{-8}$	1.19	$4.9 \times 10^{-7}$	1.20	$7.8 \times 10^{-15}$
<i>FTO</i>	1.11	0.016	1.03	0.25	1.23	$7.3 \times 10^{-14}$	1.17	$1.3 \times 10^{-12}$
<i>CDKAL1</i>	1.12	0.0095	1.08	0.0024	1.16	$1.3 \times 10^{-8}$	1.12	$4.1 \times 10^{-11}$
<i>KCNJ11</i>	1.11	0.013	1.15	$1.0 \times 10^{-7}$	1.15	0.0013	1.14	$6.7 \times 10^{-11}$
<i>HHEX</i>	1.10	0.026	1.14	$1.7 \times 10^{-4}$	1.13	$4.6 \times 10^{-6}$	1.13	$5.7 \times 10^{-10}$
<i>SLC30A8</i>	1.18	$7.0 \times 10^{-5}$	1.07	0.047	1.12	$7.0 \times 10^{-5}$	1.12	$5.3 \times 10^{-8}$
Chr 11	1.48	$5.7 \times 10^{-8}$	1.16	0.12	1.13	0.068	1.23	$4.3 \times 10^{-7}$
<i>PPARG</i>	1.20	0.0014	1.09	0.019	1.23	0.0013	1.14	$1.7 \times 10^{-6}$

# TCF7L2

- Type 2 susceptibility gene (linkage study in Iceland)
- Widely replicated in type 2 diabetes
- Caucasians and Africans, lower in Asian

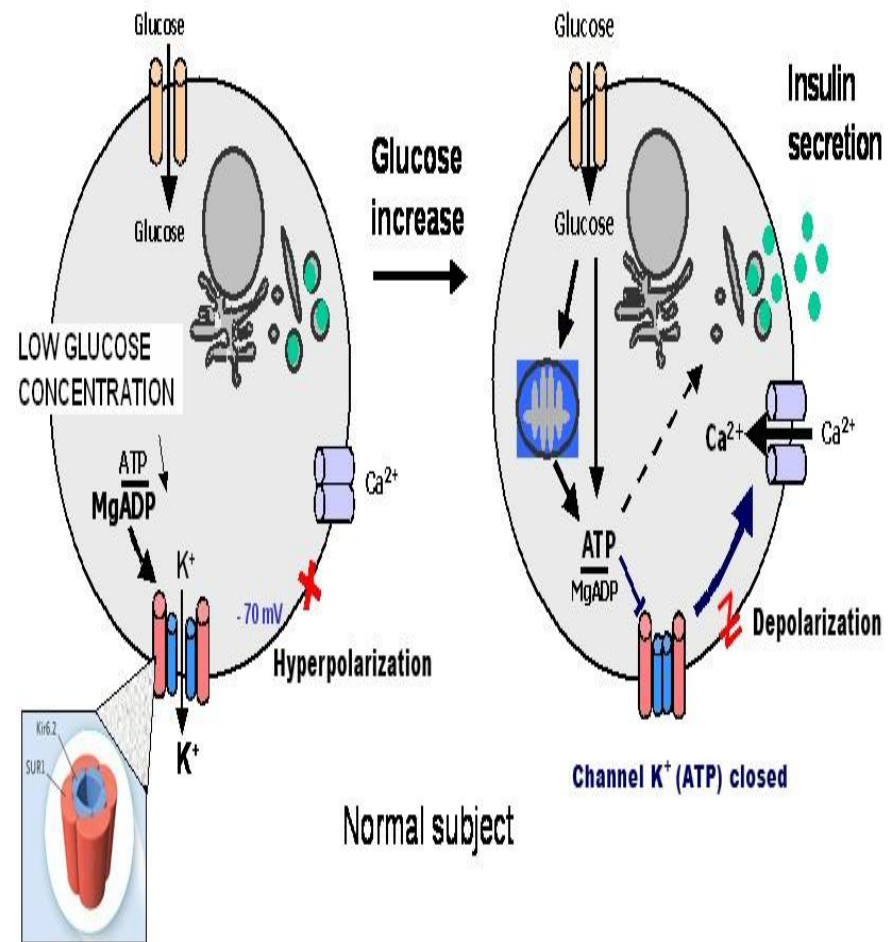


# KCNJ11

Defected insulin secretion

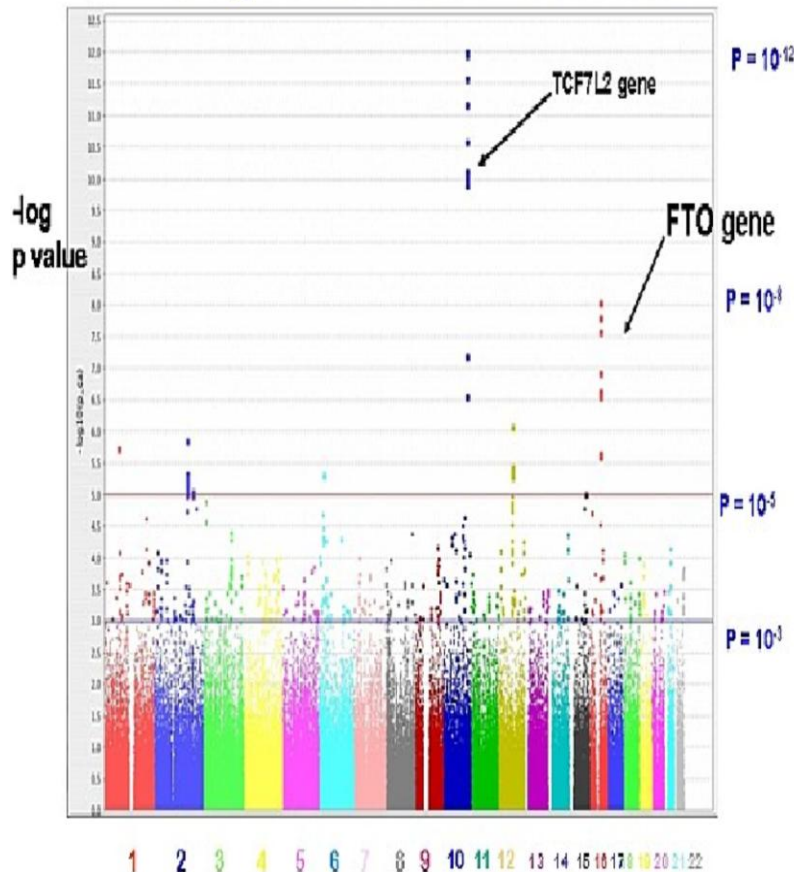
Coding of Kir6.2 subunit, in *ATP-sensitive K<sup>+</sup> channels*

(ages <6 mo)



# FTO GENE

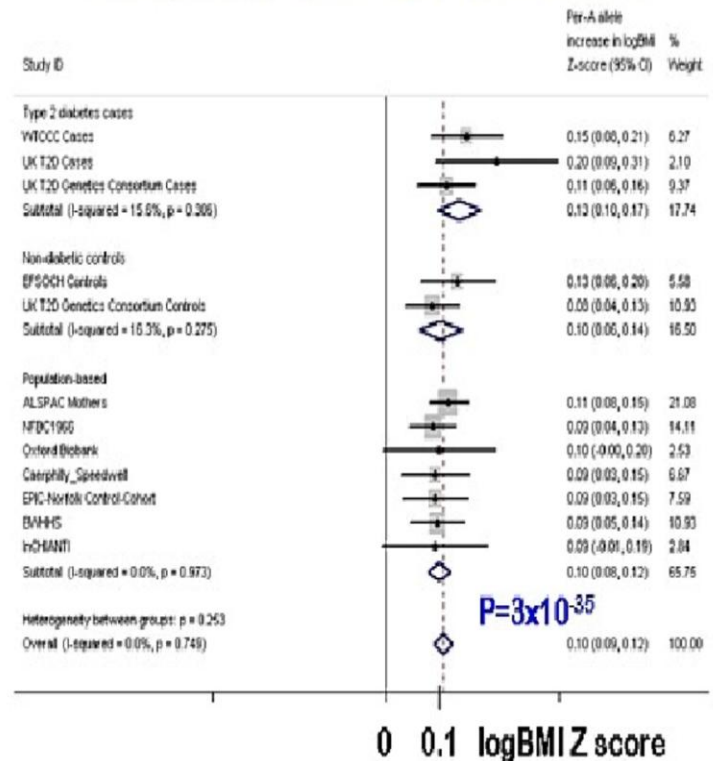
The FTO gene is the second most important gene for Type 2 diabetes risk in the UK scan



Chromosome

Frayling et al Science 2007

FTO consistently associated with BMI in 30,081 adults from 13 studies



AA (16%) v TT(37%)  $\sim 1.0 \text{ kgm}^{-2} = \sim 2\text{-}3\text{kg heavier}$

Frayling et al Science 2007

# CDKN2A/B & CARDIOVASCULAR DISEASE

Scienceexpress

Report

## A Common Allele on Chromosome 9 Associated with Coronary Heart Disease

Ruth McPherson,<sup>1,4†</sup> Alexander Pensevskiy,<sup>2,8</sup> Nihan Kavasar,<sup>1</sup> Alexandre Stewart,<sup>1</sup> Robert Roberts,<sup>1</sup> David R. Cox,<sup>1</sup> David A. Hinds,<sup>1</sup> Len A. Pennacchio,<sup>4</sup> Anne Tybjerg-Hansen,<sup>5</sup> Aaron R. Folsom,<sup>6</sup> Eric Boerwinkle,<sup>7</sup> Helen H. Hobbs,<sup>2,9</sup> Jonathan C. Cohen,<sup>2,8,†</sup>

<sup>1</sup>Division of Cardiology, University of Ottawa Heart Institute, Ottawa K1Y4W7, Canada. <sup>2</sup>Donald W. Reynolds Cardiovascular Clinical Research Center and the Eugene McDermott Center for Human Growth and Development, University of Texas Southwestern Medical Center, Dallas, TX 75390, USA. <sup>3</sup>Perlegen Sciences, Mountain View, CA 94043, USA. <sup>4</sup>Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA & U.S. Department of Energy Joint Genome Institute, Walnut Creek, CA 94598, USA. <sup>5</sup>Department of Clinical Biochemistry, Rigshospitalet, Copenhagen University Hospital, Copenhagen DK-2100, Denmark. <sup>6</sup>Division of Epidemiology and Community Health, University of Minnesota, Minneapolis, MN 55454, USA. <sup>7</sup>Human Genome Center and Institute for Molecular Medicine, University of Texas Health

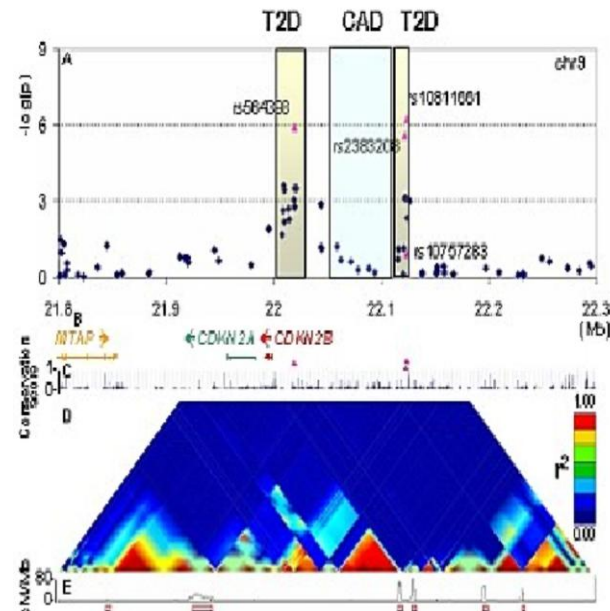
Scienceexpress

Report

## A Common Variant on Chromosome 9p21 Affects the Risk of Myocardial Infarction

Anna Helgadottir,<sup>1\*</sup> Gudmar Thorleifsson,<sup>1\*</sup> Andrei Manolescu,<sup>1\*</sup> Solveig Gretarsdottir,<sup>1</sup> Thorarinn Blondal,<sup>1</sup> Aslaug Jonasdottir,<sup>1</sup> Adalbjorg Jonasdottir,<sup>1</sup> Asgeir Sigurdsson,<sup>1</sup> Adam Baker,<sup>1</sup> Arnar Palsson,<sup>1</sup> Gisli Masson,<sup>1</sup> Daniel Gudbjartsson,<sup>1</sup> Kristinn P. Magnusson,<sup>1</sup> Karl Andersen,<sup>2</sup> Allan I. Levey,<sup>3</sup> Valgerdur M. Backman,<sup>1</sup> Sigurborg Matthiasdottir,<sup>1</sup> Thorbjorg Jonsdottir,<sup>1</sup> Stefan Palsson,<sup>1</sup> Helga Einarsdottir,<sup>1</sup> Steinunn Gunnarsdottir,<sup>1</sup> Arnaldur Gylfason,<sup>1</sup> Viola Vaccarino,<sup>3</sup> W. Craig Hooper,<sup>3</sup> Muredach P. Reilly,<sup>4</sup> Christopher B. Granger,<sup>5</sup> Harland Austin,<sup>3</sup> Daniel J Rader,<sup>4</sup> Svati H. Shah,<sup>5</sup> Arshed A. Quyyumi,<sup>3</sup> Jeffrey R. Gulcher,<sup>1</sup> Gudmundur Thorgerisson,<sup>3</sup> Unnur Thorsteinsdottir,<sup>1</sup> Augustine Kong,<sup>1,†</sup> Karl Stefansson<sup>1,†</sup>

## Type 2 diabetes and CAD map to adjacent haplotypes close to CDKN2A/2B



Chr9 signal maps near *CDKN2A/2B* genes

	OR	p
WTCCC	1.22 (1.09-1.37)	7.6x10 <sup>-4</sup>
UK rep	1.18 (1.08-1.28)	1.7x10 <sup>-4</sup>
DGI	1.20 (1.12-1.28)	5.4x10 <sup>-5</sup>
FUBION	1.20 (1.07-1.35)	2.2x10 <sup>-6</sup>
All	1.20 (1.14-1.26)	7.8x10 <sup>-55</sup>

	OR	p
WTCCC	1.16 (1.07-1.27)	3.2x10 <sup>-4</sup>
UK rep	1.12 (1.05-1.19)	8.6x10 <sup>-4</sup>
DGI	1.05 (0.94-1.17)	0.6
FUBION	1.18 (1.01-1.27)	0.04
all	1.12 (1.07-1.17)	1.2x10 <sup>-2</sup>

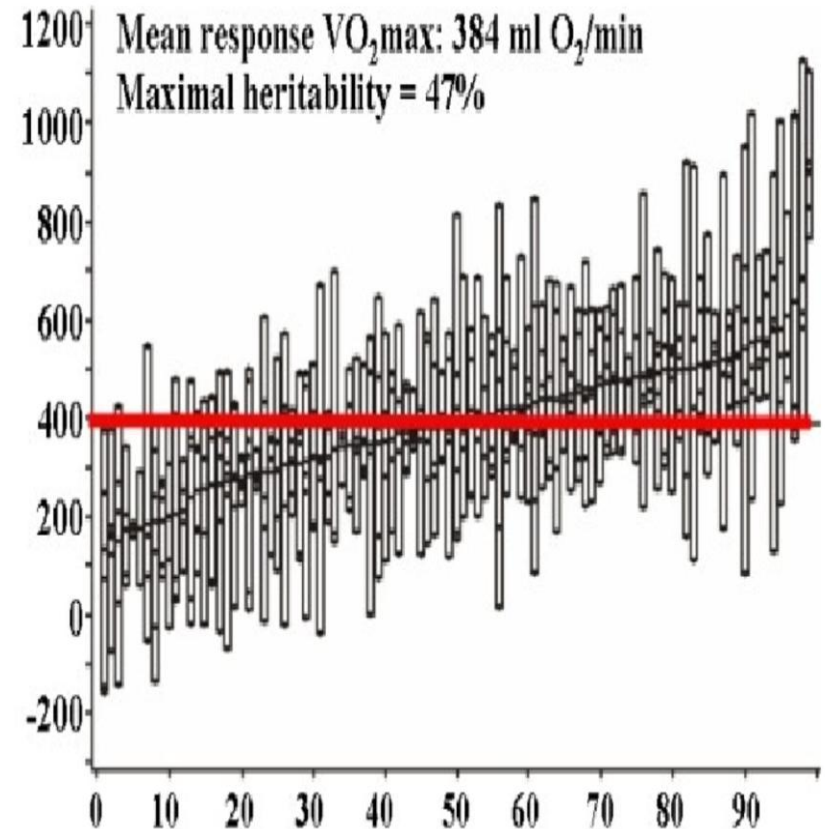
Zeggini et al Science 2007 & WTCCC Nature 2007

# HERITAGE FAMILY STUDY

## The HERITAGE Family Study Exercise Training Program

- Duration: 20 weeks
- Frequency: 3 times per week
- Intensity and duration:
  - Wks 1-2: HR at 55%  $VO_{2max}$  for 30 min
  - Wks 3-14: gradually to HR at 75% max, 50 min
  - Wks 15-20: HR at 75%  $VO_{2max}$  for 50 min
- Computer-controlled cycle ergometers
- Training supervised in the laboratory

## $VO_{2max}$ Response in Whites of HFS

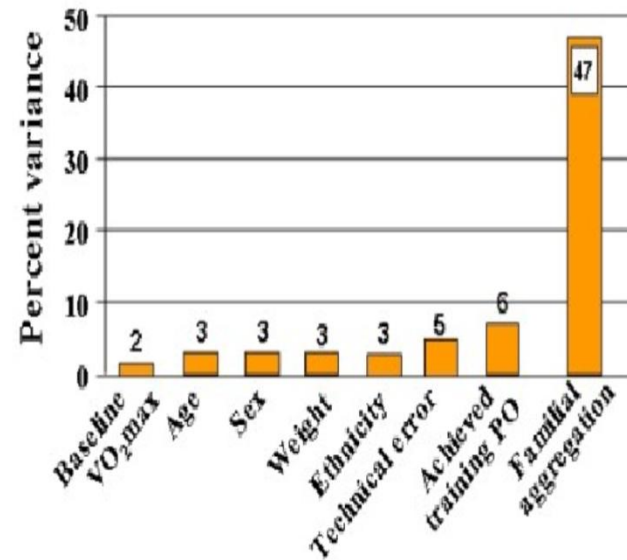




# ΑΠΟΔΟΣΗ ΣΤΗΝ ΑΣΚΗΣΗ



## VO<sub>2</sub>max Training Response in HFS

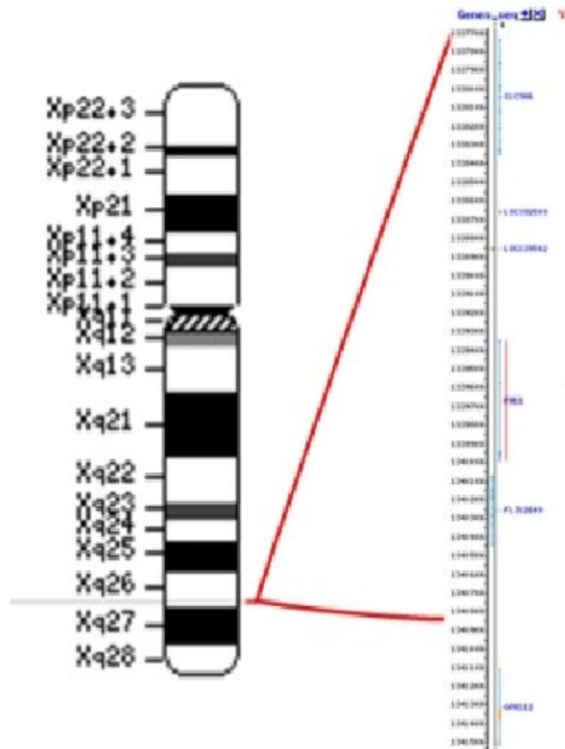


483 Whites, 259 Blacks, 17-65 years of age;  
Mean gain = 384 ml O<sub>2</sub>, SD > 202 ml

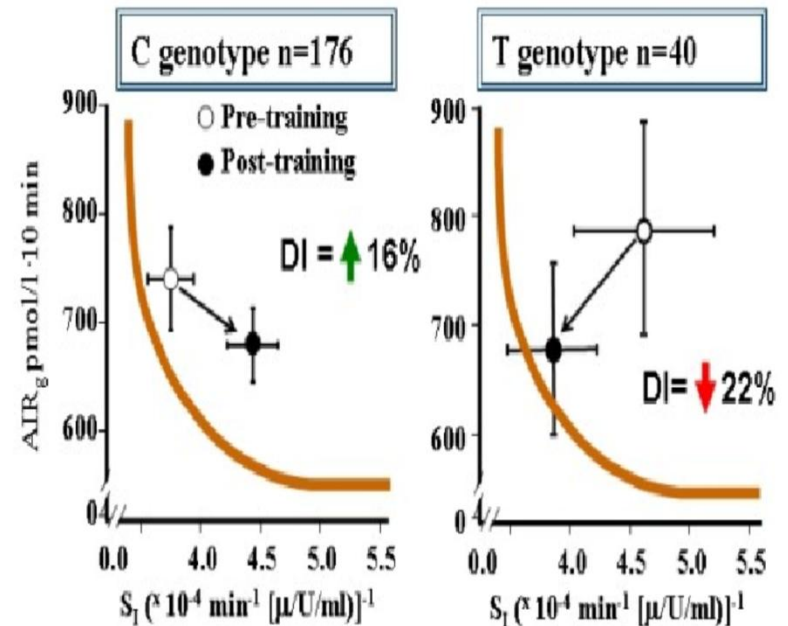
Bouchard et al, JAP, 1999

# ΑΣΚΗΣΗ - ΓΟΝΙΔΙΑΚΟ ΥΠΟΣΤΡΩΜΑ & ΙΝΣΟΥΛΙΝΙΚΗ ΕΥΑΙΣΘΗΣΙΑ

FHL1 is Encoded on Chr X p27



Pre- and Post-training Effects for White Males of HFS with FHL1 rs2180062C>T

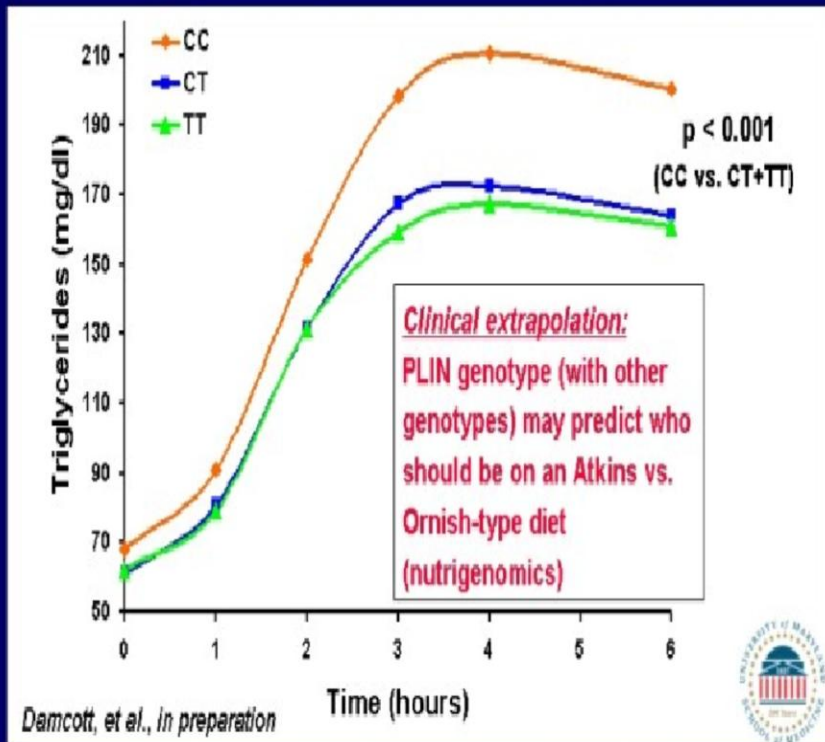


Teran-Garcia et al, Diabetologia, in press

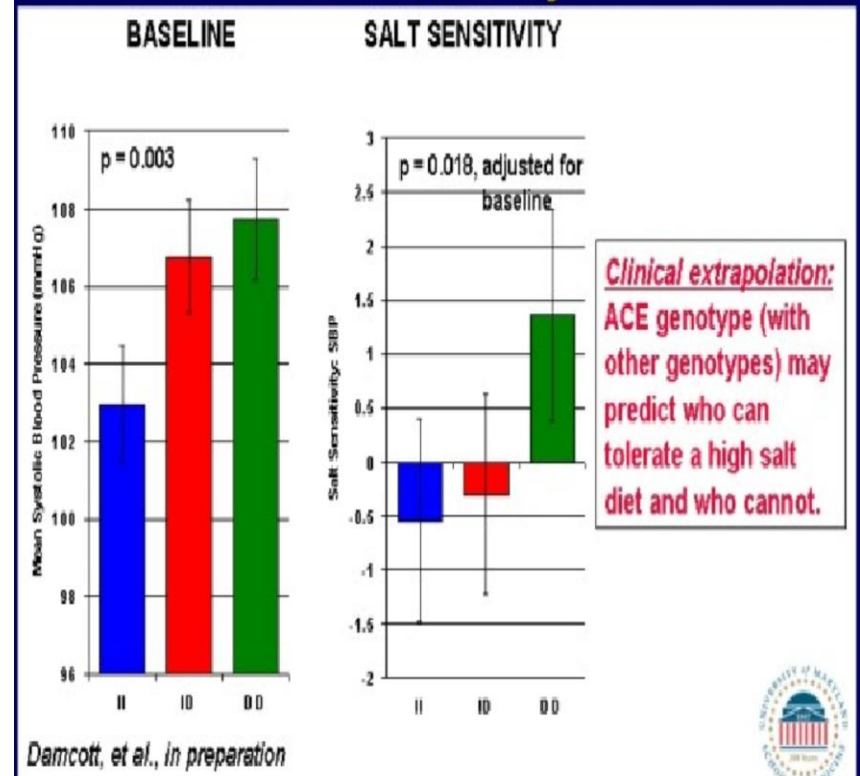


# ΜΕΤΑΒΟΛΙΚΕΣ ΠΑΡΑΜΕΤΡΟΙ & ΑΠΛΟΥΠΟΙ

Perilipin Gene Variant (rs2304795) Is Associated with Greater TG Excursions During a High Fat Meal



ACE I/D Predicts Baseline SBP and Salt Sensitivity



# COMMON GENETIC BACKGROUND

Vol 447 | 7 June 2007 | doi:10.1038/nature05911

ARTICLES

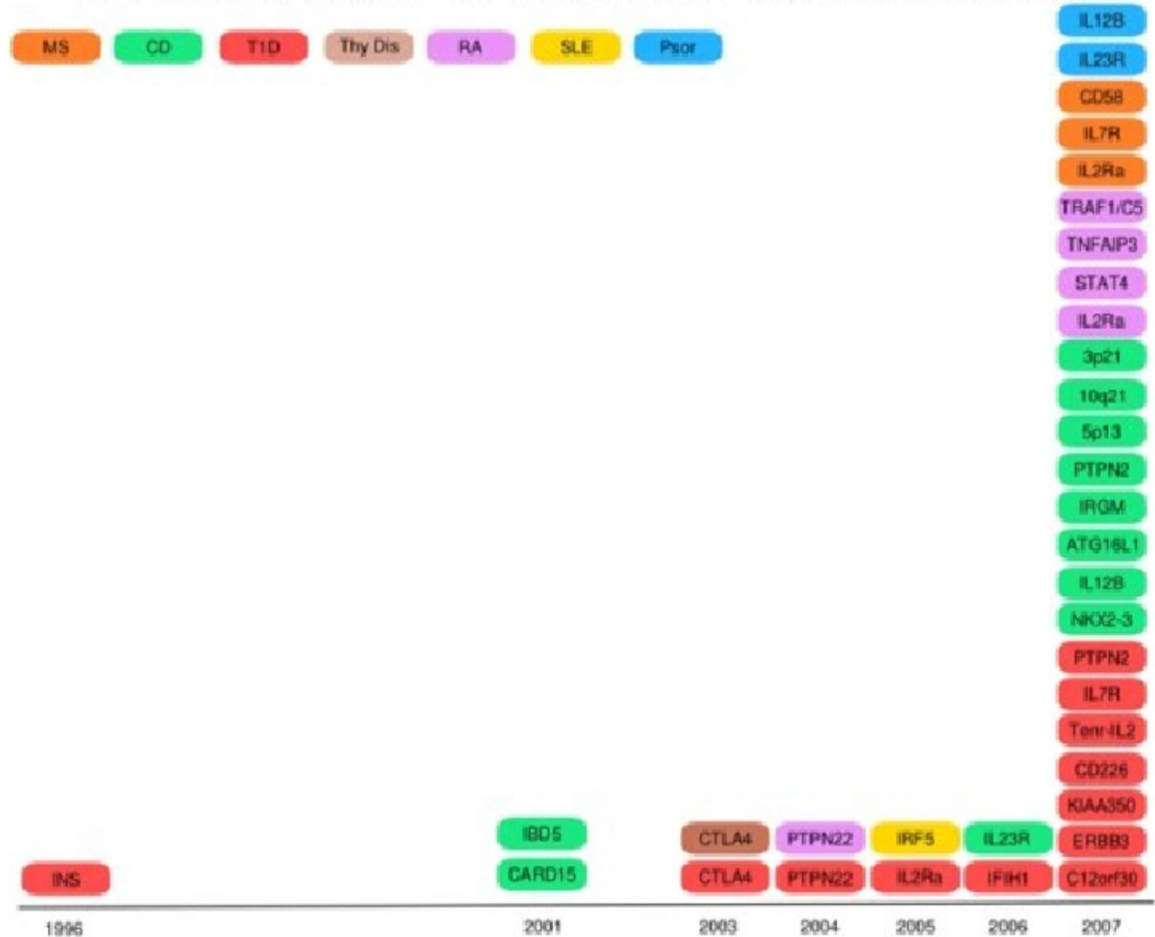
## Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls

The Wellcome Trust Case Control Consortium\*

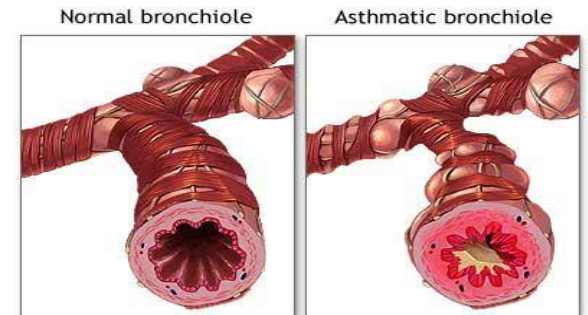
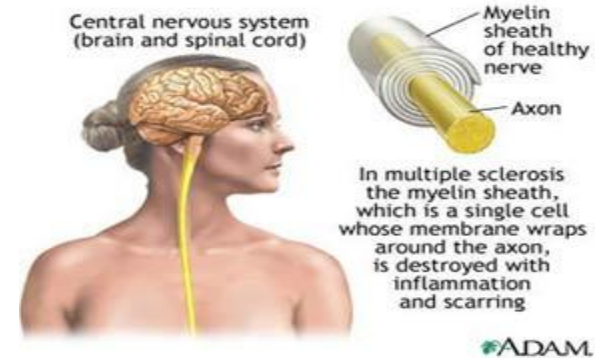
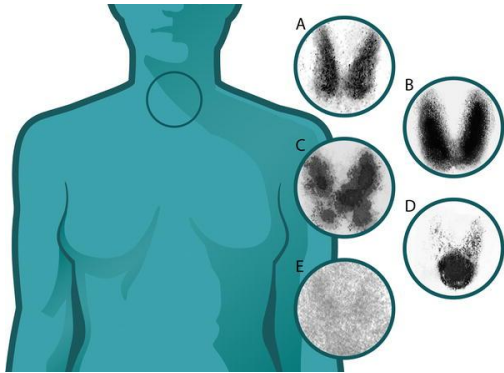
There is increasing evidence that genome-wide association (GWA) studies represent a powerful approach to the identification of genes involved in common disease. In this study, we used a GWA approach to identify common genetic variants associated with seven common diseases and 3,000 shared controls. We identified 163 loci with  $P < 5 \times 10^{-7}$ : 1 in bipolar disorder, 1 in Crohn's disease and 2 in type 2 diabetes. On the basis of these results, we provide compelling evidence that some loci confer large numbers of further signals (including additional susceptibility loci). The important signals identified in this study demonstrate that careful use of a shared multiple disease phenotypes has generated multiple disease phenotypes; has generated British population; and shown that, provide stratification in the British population is gen of these important disorders. We anticipate investigators, will provide a powerful reso

**Type 1 diabetes**  
**Bipolar illness**  
**Crohn's disease**  
**And more....**

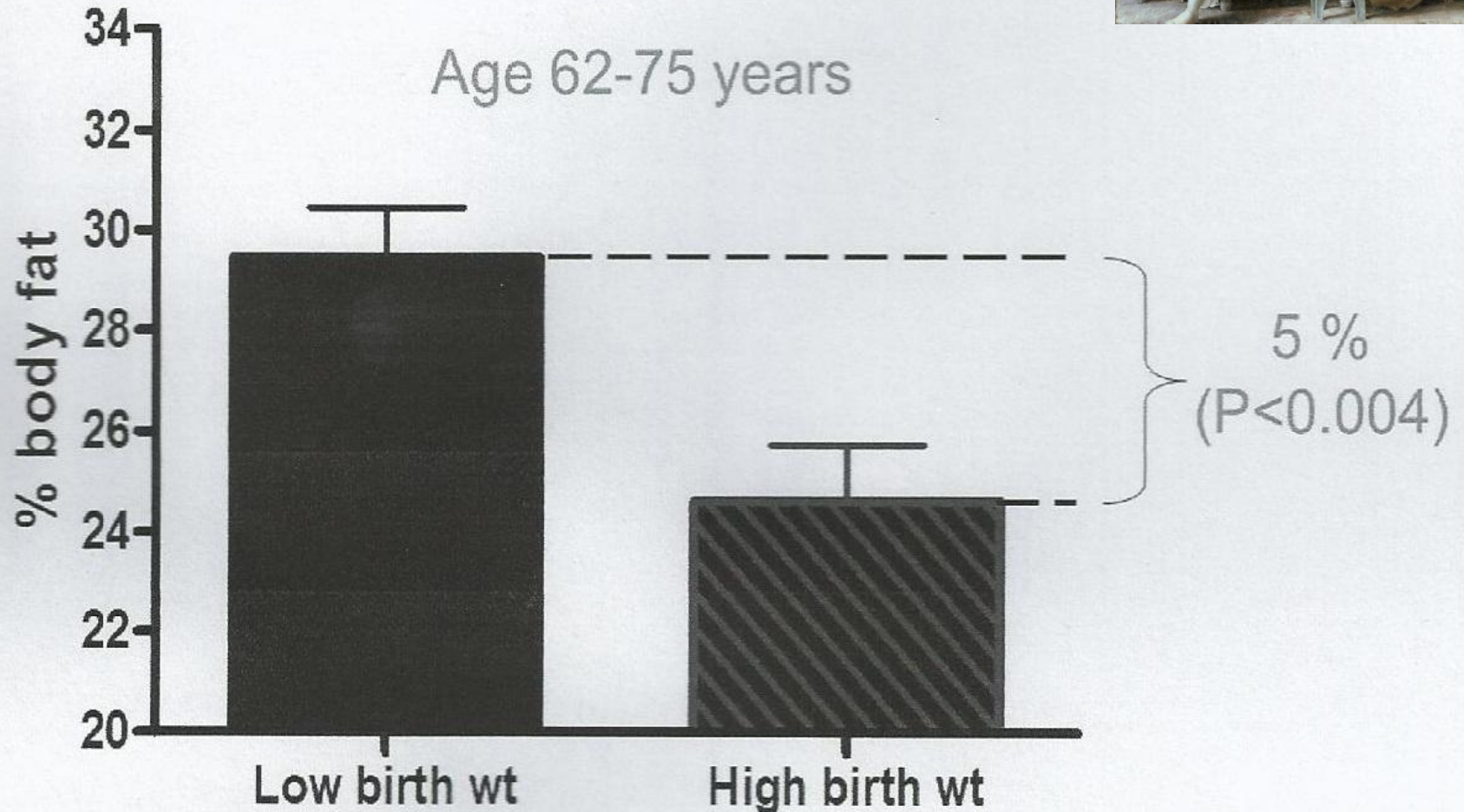
## Autoimmune disease associations



# COMMON VARIANTS - MULTIPLE DISEASE & DIABETES



# The birth weight focus

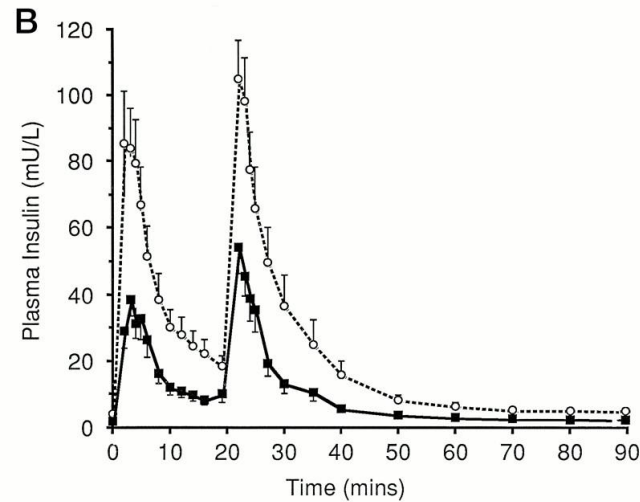
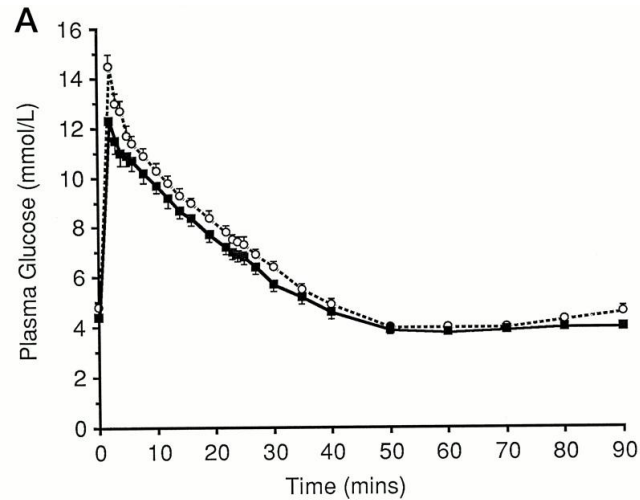


**Glucose (a)**  
**insulin (b)**  
**profiles**

**normal**  
**(closed boxes)**

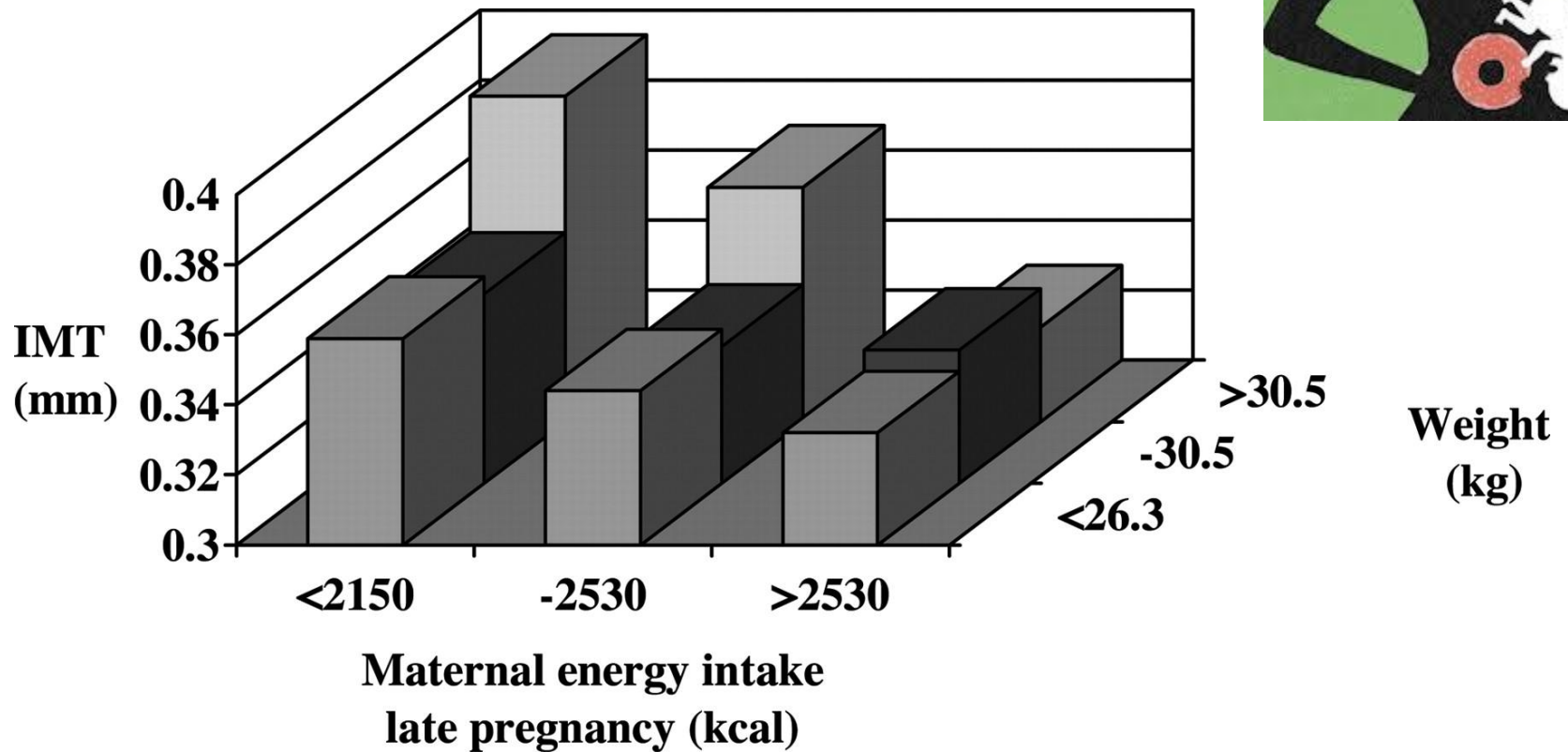
**IUGR**  
**(open circles)**

**children,**



Hofman P L et al. JCEM 1997;82:402-406

Mean carotid IMT,  
according to thirds of the distribution of current weight  
and maternal energy intake in late pregnancy.



Gale C R et al. Arterioscler Thromb Vasc Biol  
2006;26:1877-1882



# Undernutrition: Dutch Hunger



- In winter 1944-45, western region of Netherlands
  - limited food rations 400-800 cal/day for a specific time period
  - ‘natural’ experiment of restriction during pregnancy, furthermore allowing to investigate the impact of the timing of restriction and identify the ‘critical periods’

## Early gestation

- **No effect** on birth weight
- Higher risk of obesity
- Glucose intolerance
- Coronary heart diseases
- Adverse lipid profile and coagulation factors

## mid-gestation

- Impact on renal function
- Glucose intolerance
- Lower insulin secretion indices

## Late-gestation

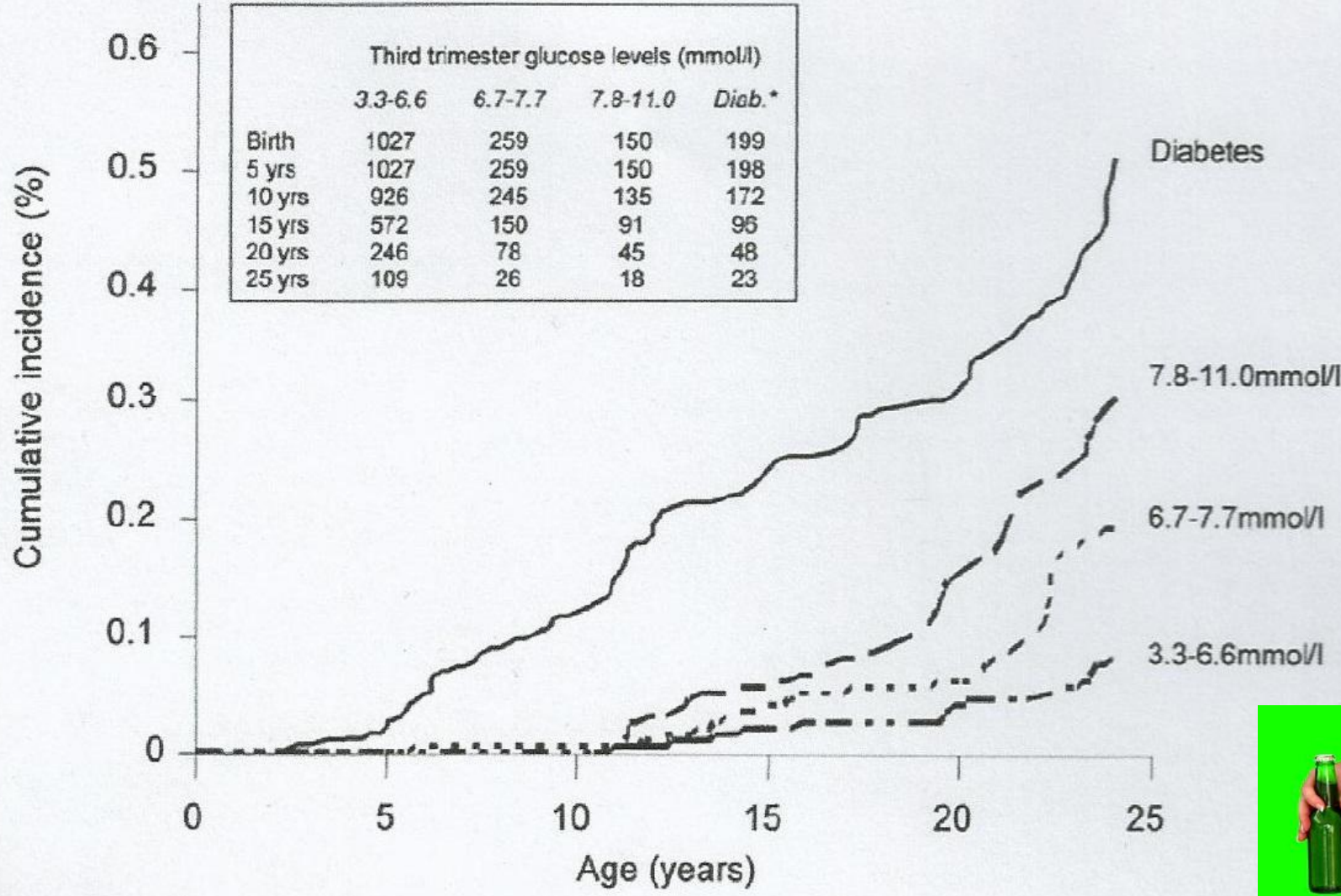
- Lower birth weight,
- **Not** higher risk of obesity
- Glucose intolerance (independent of effect of lower birth weight)

**Table 1.**

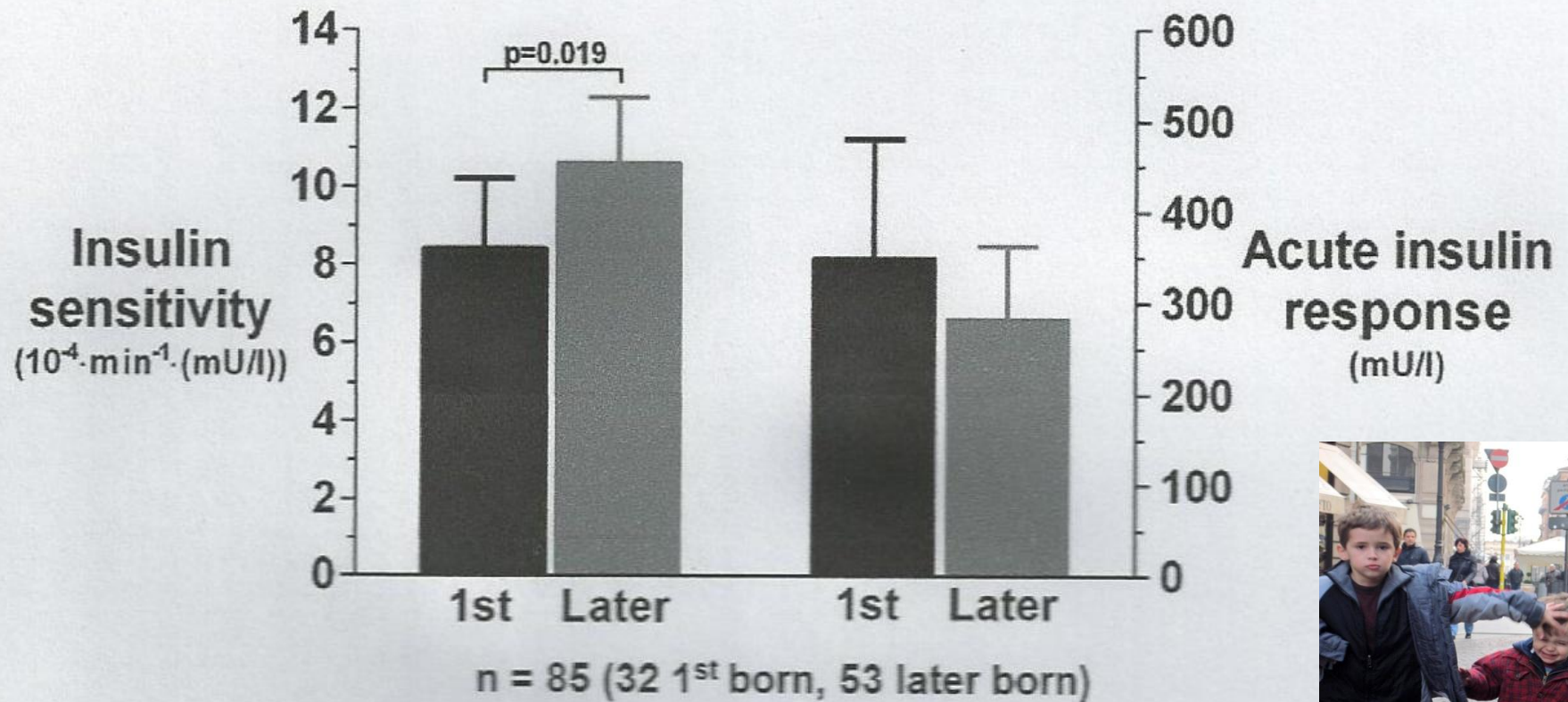
Effects of Birth Weight on Hazard Ratios for Coronary Heart Disease and the Cumulative Incidence of Hypertension in Adult Men and Women

<i>Birth weight (g)</i>	<i>Adult men</i>		<i>Adult women</i>	
	<i>Hazard ratios for coronary heart disease<sup>a</sup></i>	<i>Cumulative incidence of hypertension (%)<sup>b</sup></i>	<i>Hazard ratios for coronary heart disease<sup>c</sup></i>	<i>Cumulative incidence of hypertension (%)<sup>d</sup></i>
≤ 2500	3.63	—	1.34	—
2501–3000	1.86	19.0	1.38	21.1
3001–3500	1.99	17.0	1.24	16.3
3501–4000	2.08	14.1	1.17	13.0
> 4000	1.00	12.5	1.00	12.1

# Cumulative incidence of T2D in Pimas offspring according to maternal 2h-glucose at third trimester



# Insulin sensitivity and acute insulin response among first-born and later-born children.

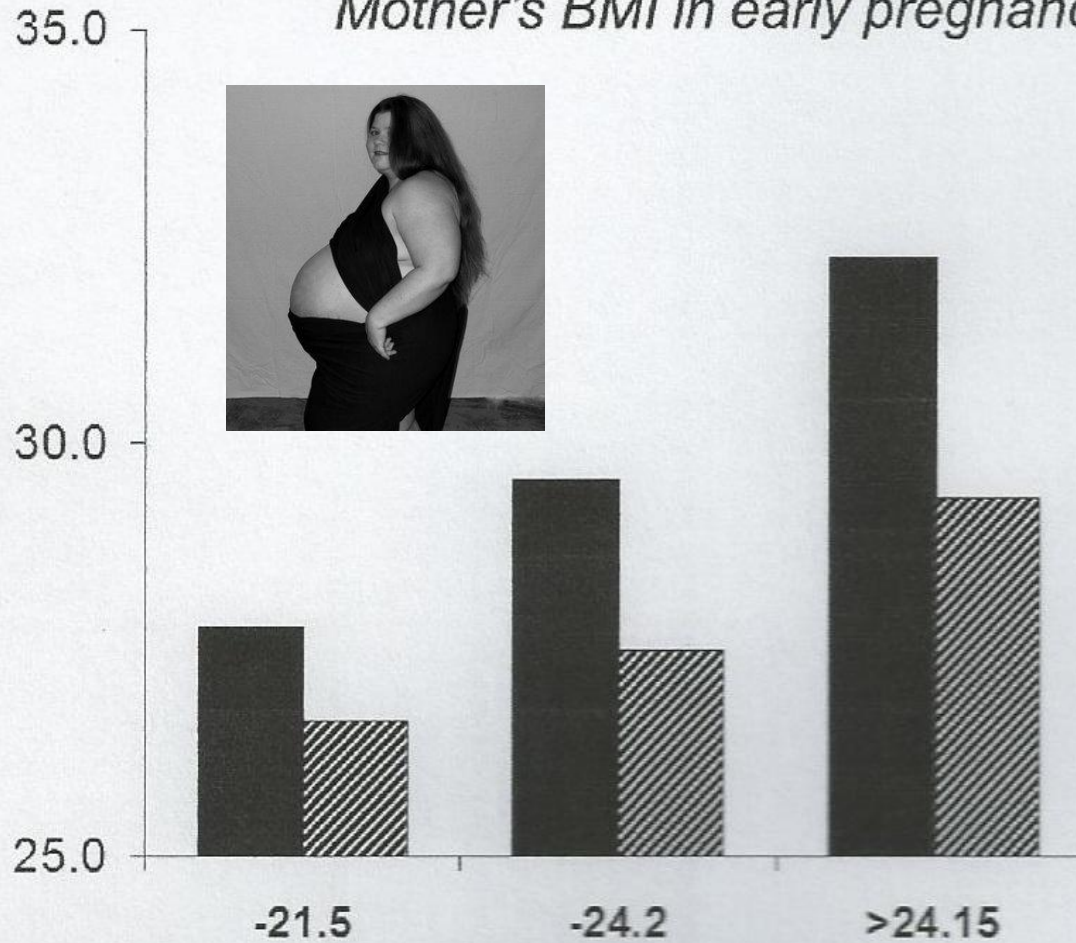


# The impact of parity

Parity  $p=0.004$

Mother's BMI in early pregnancy  $p<0.001$

% body fat at 28-31 years



■ Primiparous  
▨ Multiparous

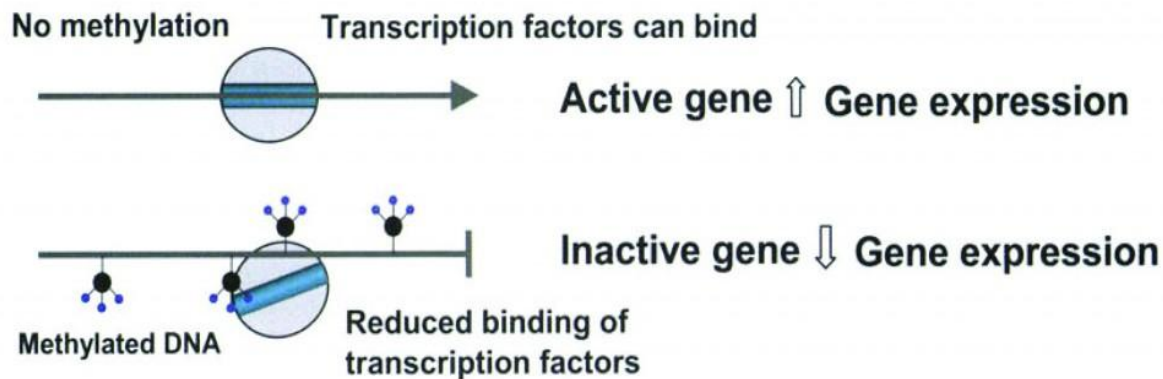


Mother's body mass index in early pregnancy (kg/m<sup>2</sup>)

Adjusted for age, sex & current smoking

# ENVIRONMENTAL EFFECTS

- **DISRUPTIVE (teratogenesis) mutations**
- **ADJUST (developmental plasticity) epigenetics**



# METHYLATION

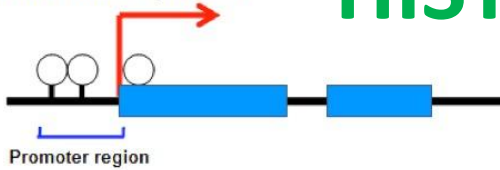
## PROMOTER ACTIVITY

### micro RNA

## HISTONE ACETYLATION

1

Genes that can be expressed



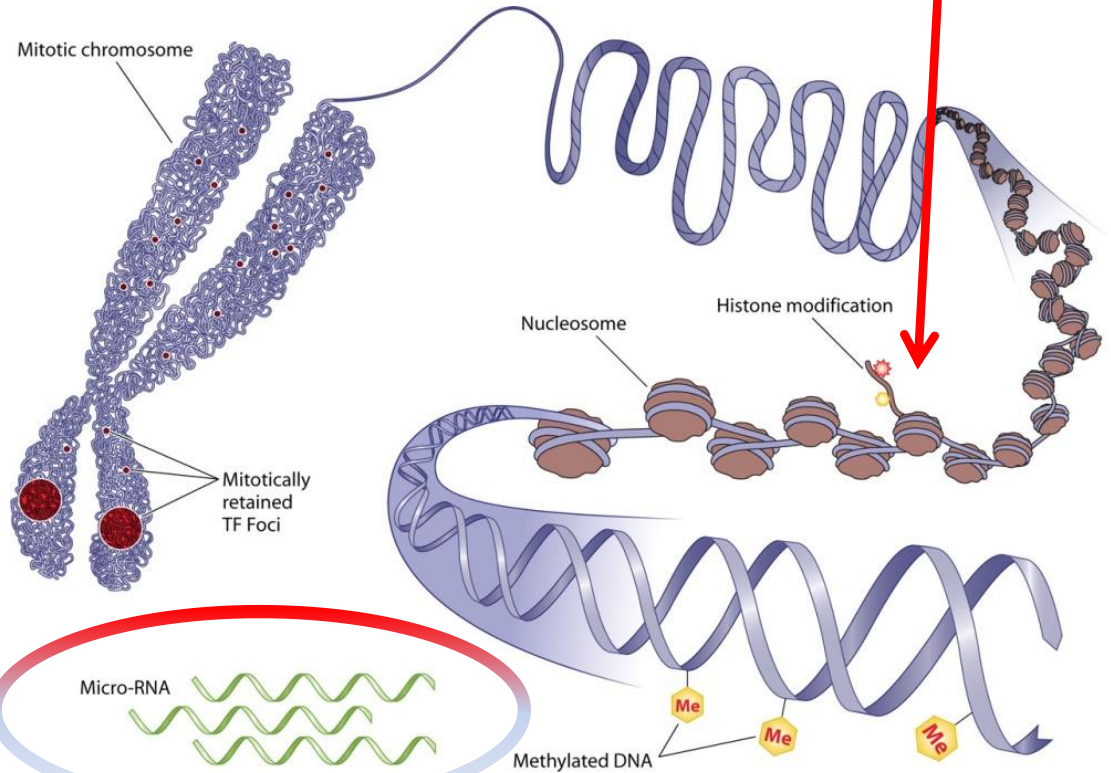
Genes inactivated by DNA methylation



**M** Methylated  
○ Unmethylated

2

DNA repair



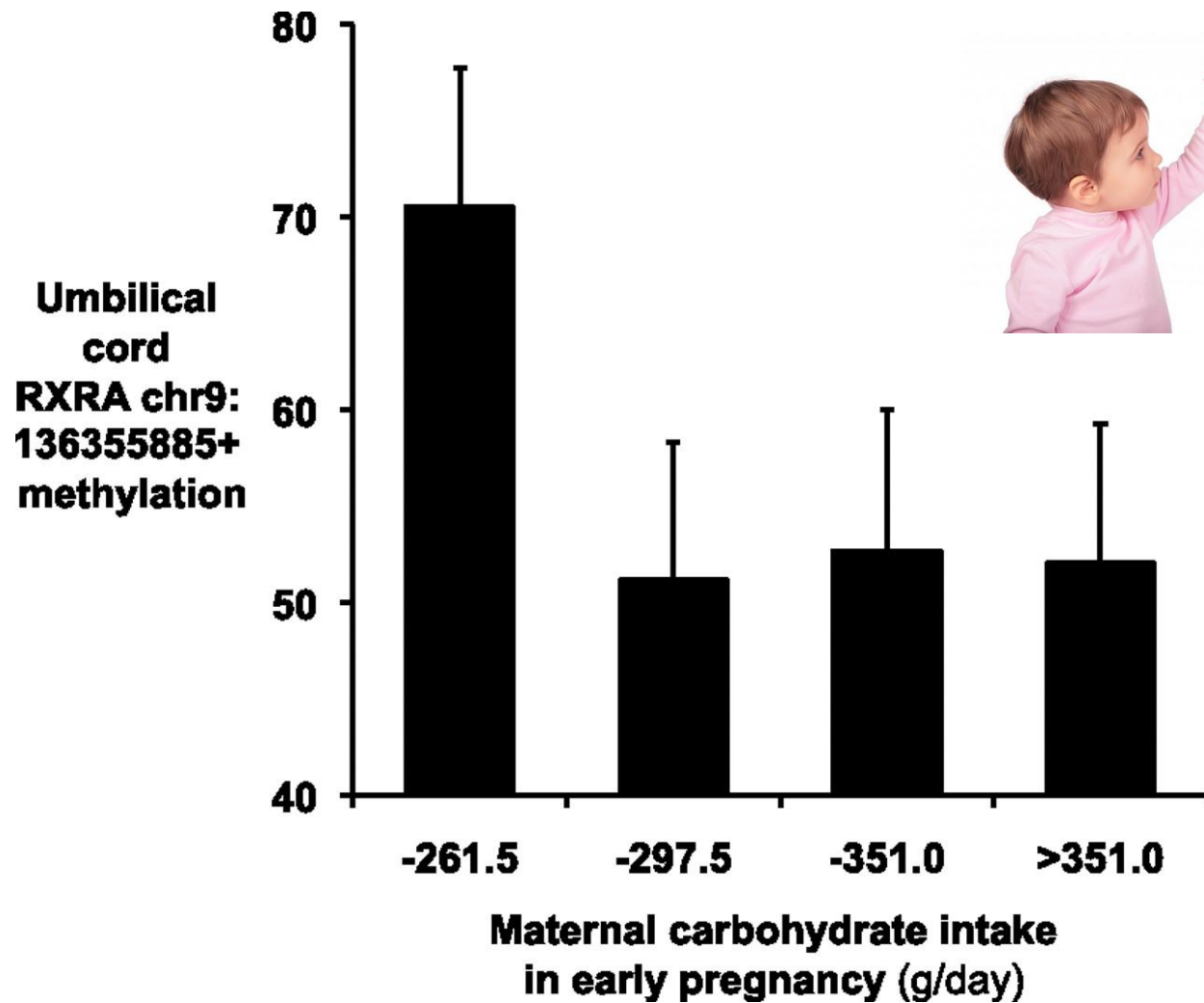
3

Micro-RNA



Methylated DNA

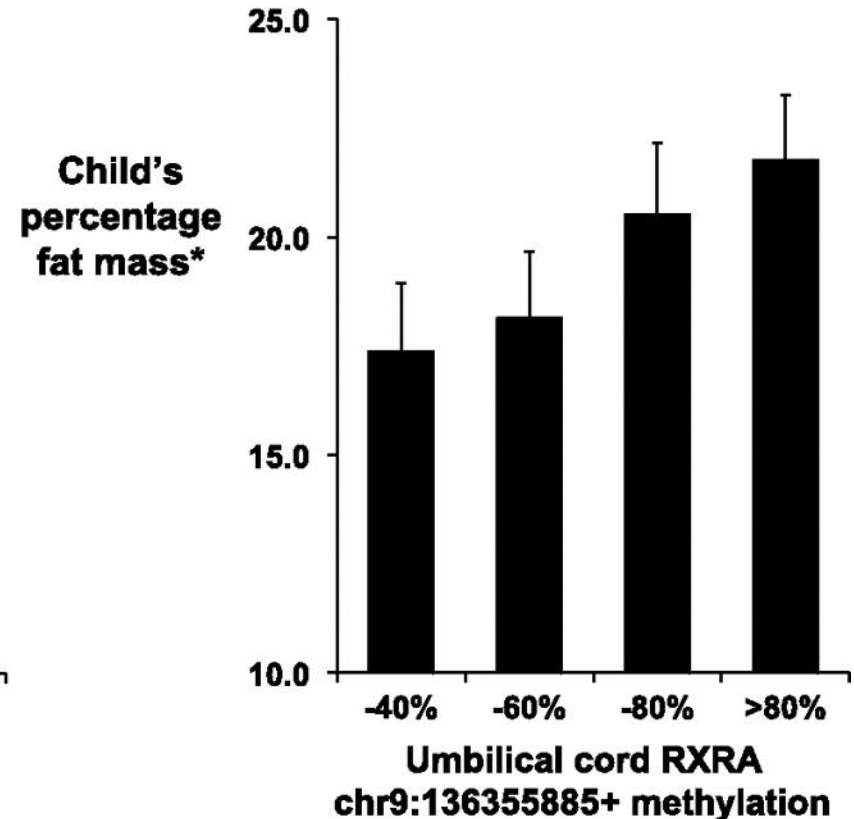
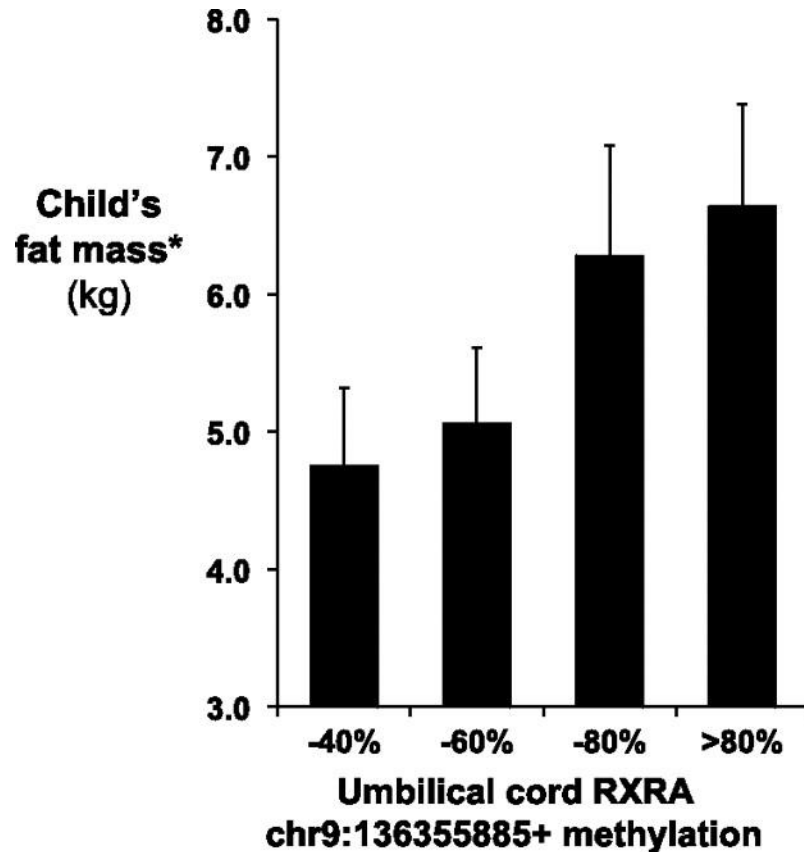
**Lower maternal carbohydrate in early pregnancy is associated with higher umbilical cord RXRA chr9:136355885+ methylation in the PAH cohort.**



Godfrey K M et al. Diabetes 2011;60:1528-1534



# Child's %fat mass & fat mass at age 9 years increase with higher umbilical cord RXRA chr9:136355885+ methylation

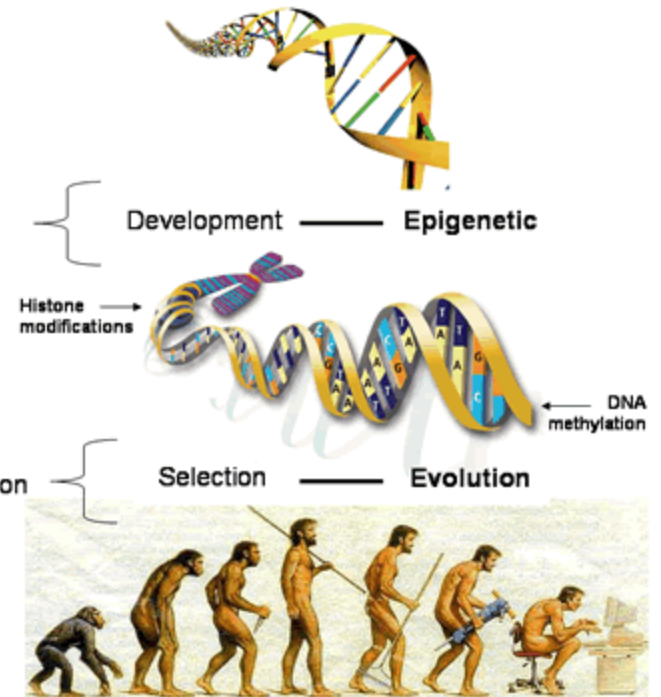
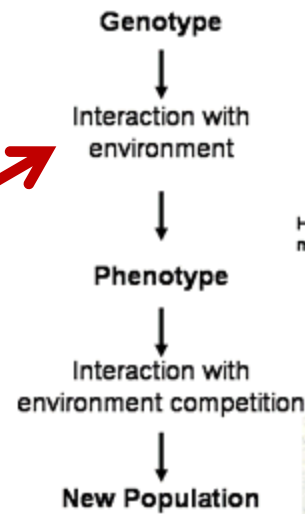
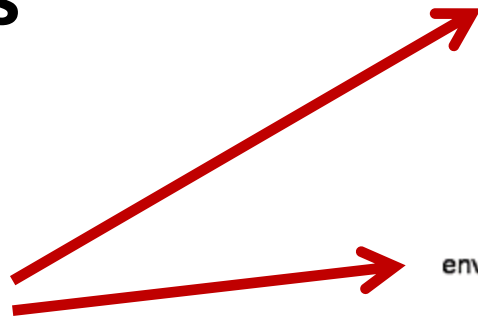


Godfrey K M et al. Diabetes 2011;60:1528-1534

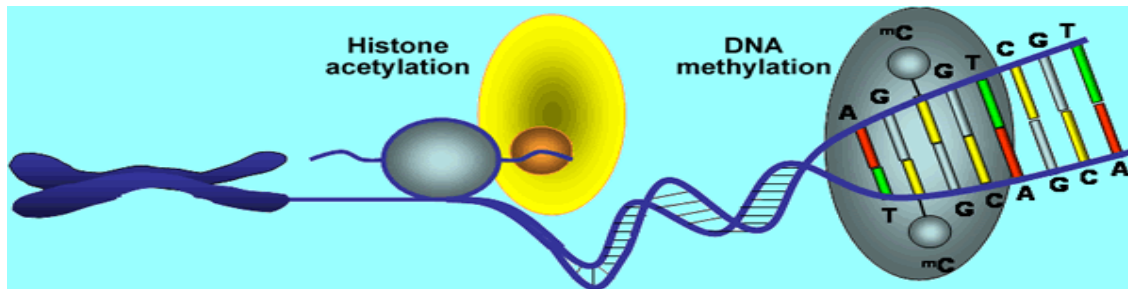
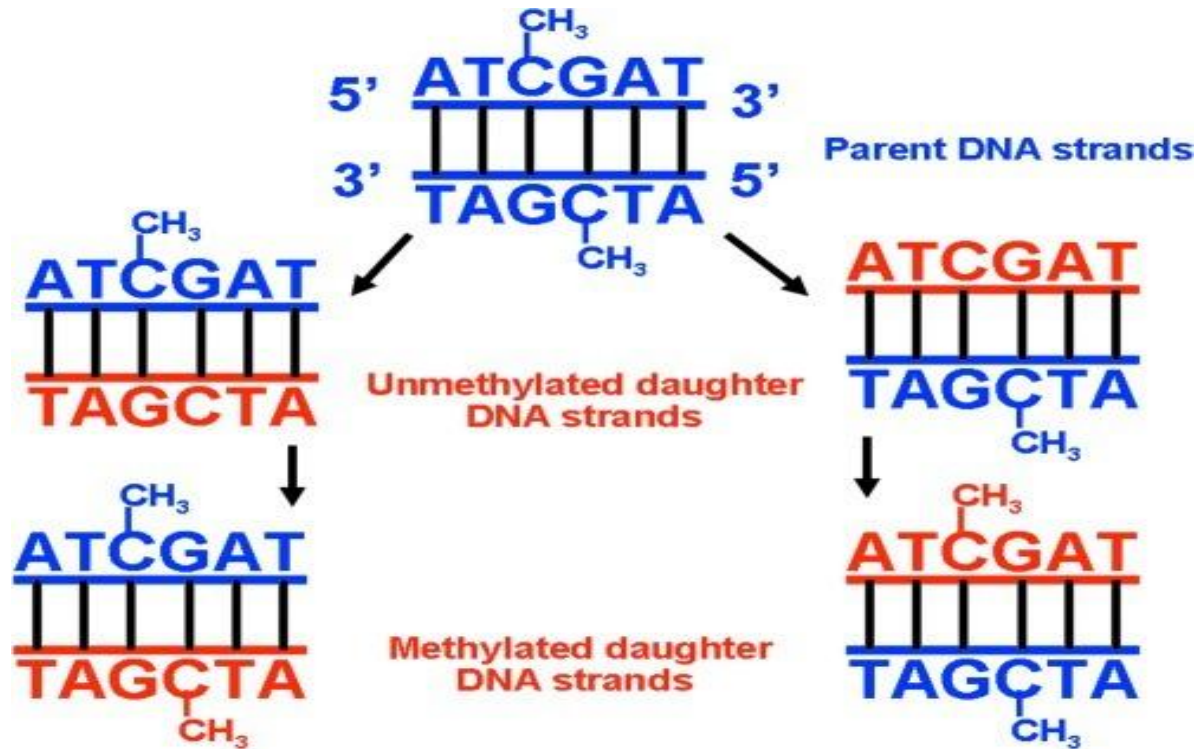
# ENVIROMENT & EVOLUTION

- Parental inheritance
- Polymorphisms (SNIPS)
- Cell types

**EPIGENOMICS**



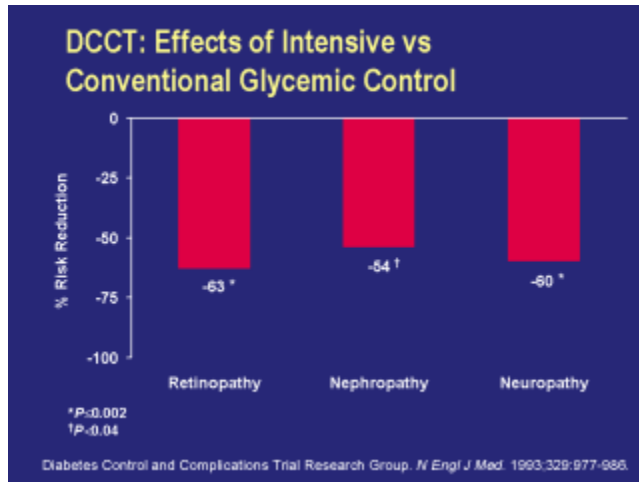
# PARENTAL EPIGENOMICS



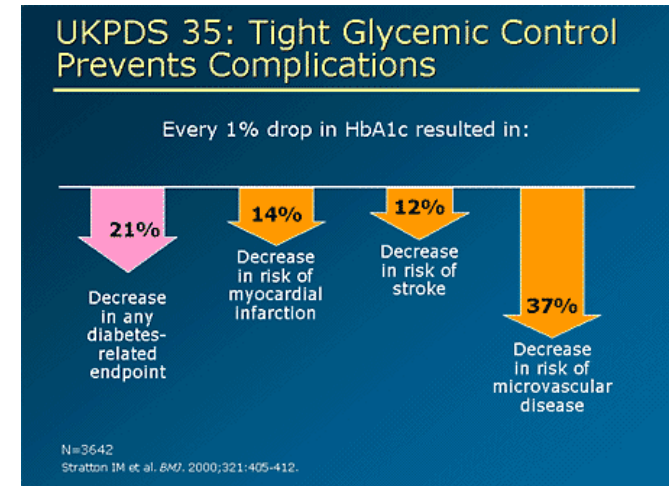
# CHRONIC DIABETES COMPLICATIONS

- Diabetic complications progress in spite of glucose control

## DCCT



## UKPDS



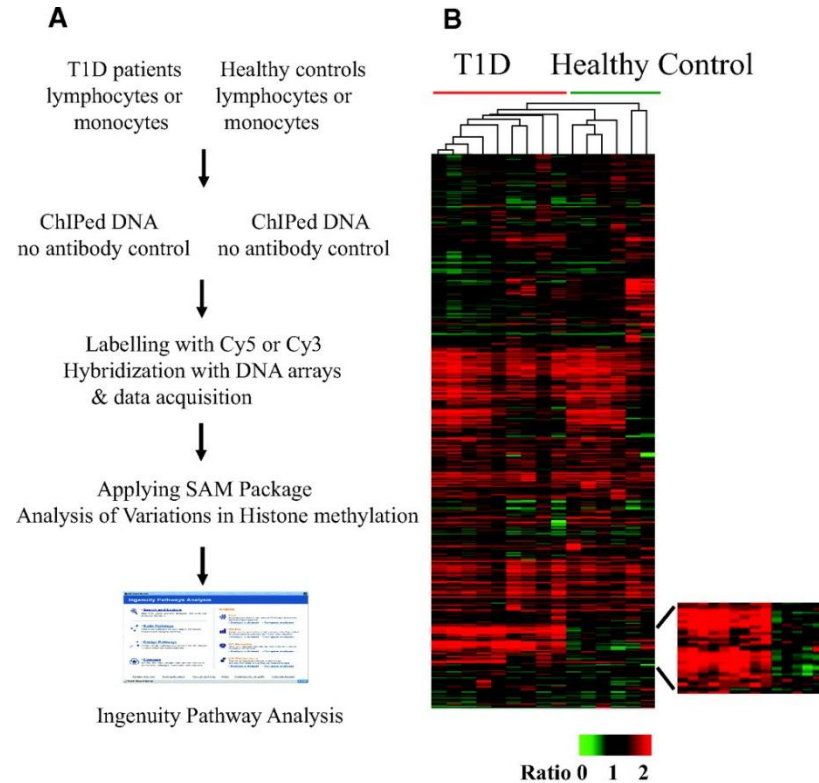
# OBJECTIVES

- Changes in covalent histone modifications in chromatin (epigenetic mechanisms) regulating the transcription of Inflammatory Genes ( $\text{TNF}\alpha$ , IL-6, MCP-1) and Fibrotic Genes (Collagen, CTGF, PAI-1) under Diabetic conditions
- Functional Relevance of chromatin changes to increased inflammation and Metabolic Memory in Diabetes
- Genome-Wide Profiling of Modified Histones with ChIP-on-chips and ChIP-Seq (Epigenomics)

Epigenetics: Heritable changes in gene expression that occur without a change in DNA sequence.

The Structural Adaptation of chromosomal regions so as to register, Signal or perpetuate altered Activity States (Bird, 2007)

# Profiling histone lysine methylation in blood cells from type 1 diabetic (T1D) patients vs healthy control subjects.

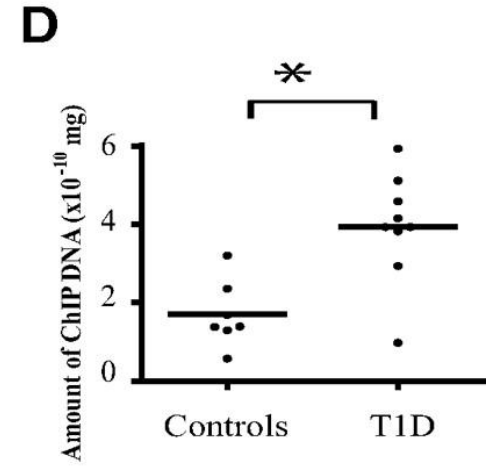
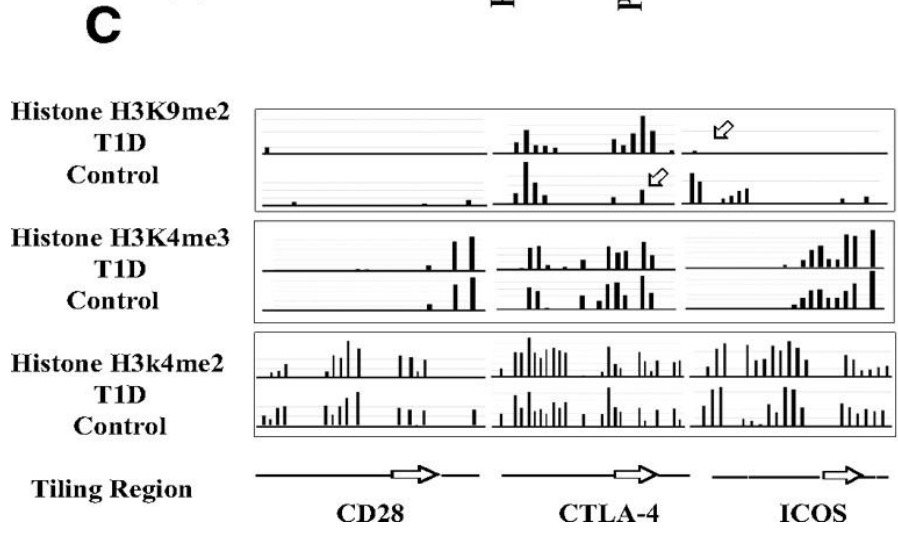
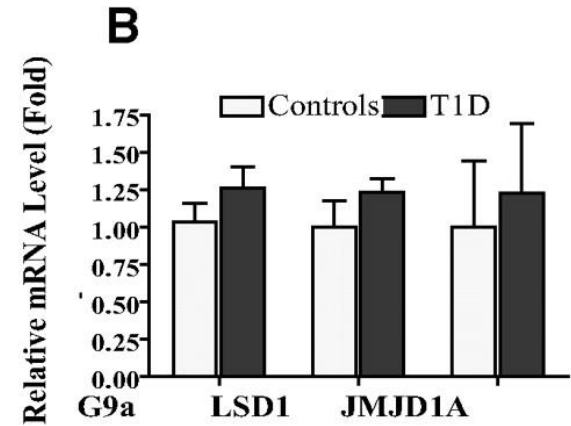
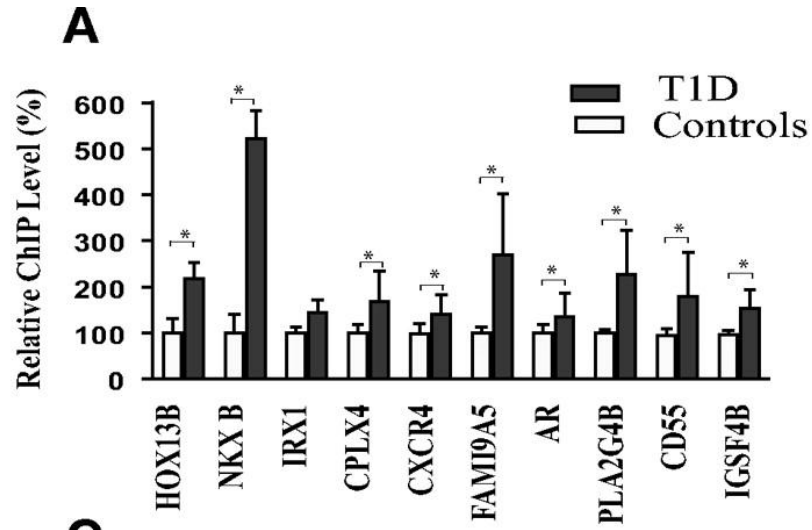


**C**

Demographics	Normal (N=7)	Diabetes (N=9)	p-value
Median Age Years (Range)	43 (35 – 60)	60 (25 – 85)	0.25
Gender Male/Female %	29% / 71%	33% / 67%	0.84
Median Hemoglobin A1c % (Range)	--	7.5% (5.4% - 10.5%)	

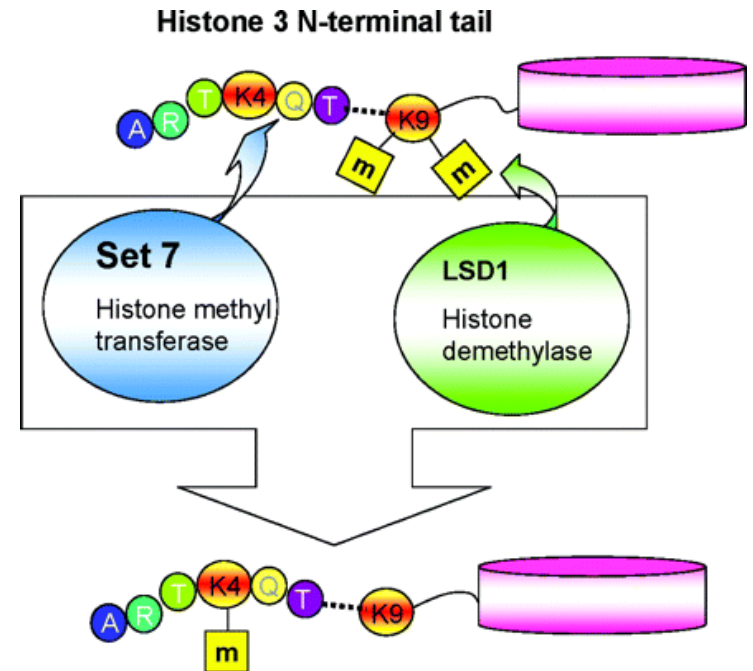
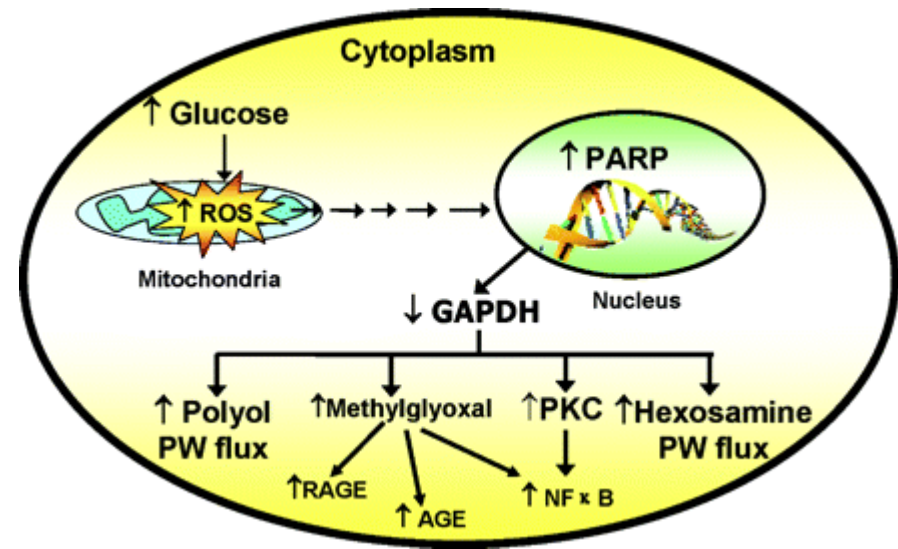
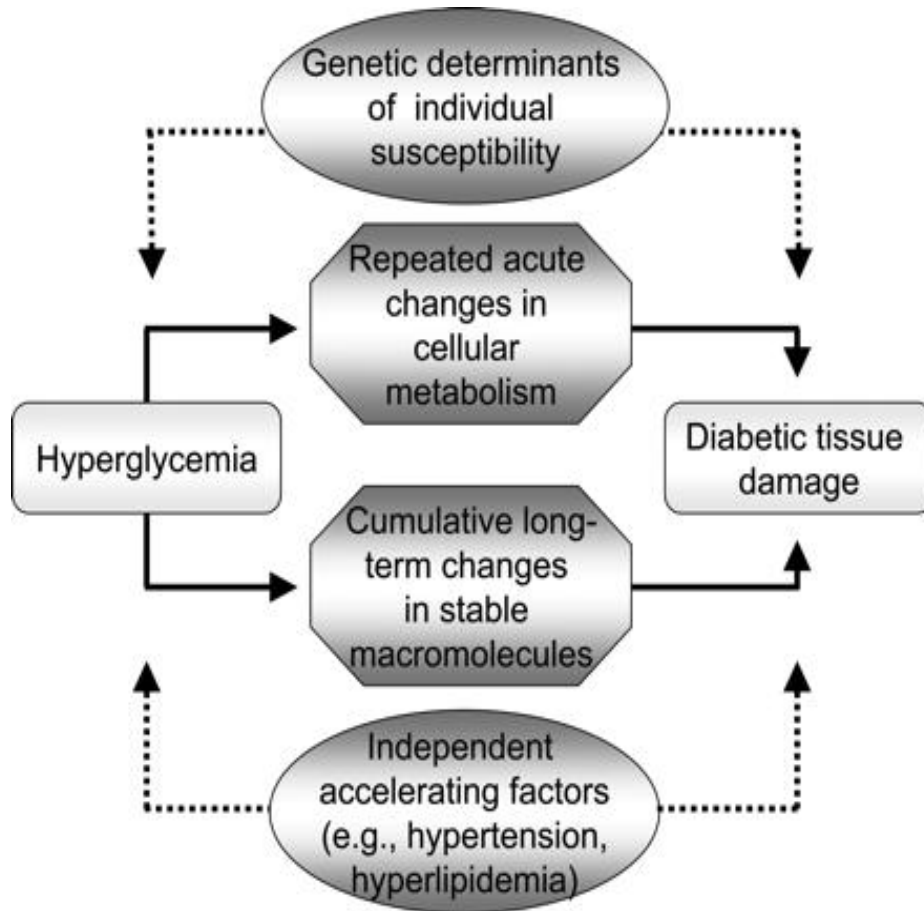
Miao F et al. Diabetes 2008;57:3189-3198

# Validation of histone methylation alterations and quantification of histone methylase/demethylase mRNA levels in type 1 diabetic patients and healthy control subjects.



Miao F et al. Diabetes 2008;57:3189-3198

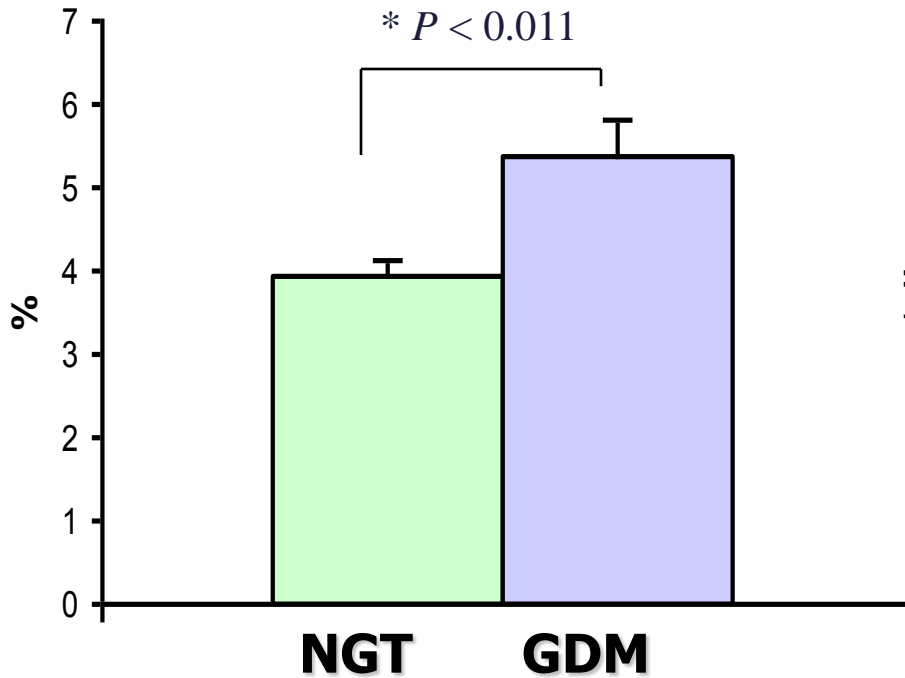
# Oxidative Stress and Diabetic Complications



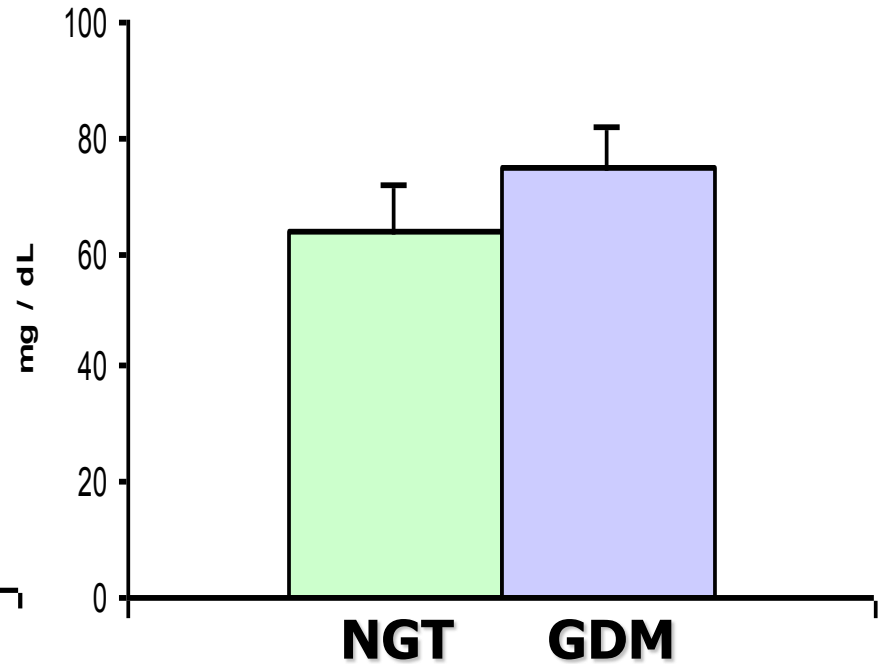


# GESTATIONAL DIABETES

## GHbA1c

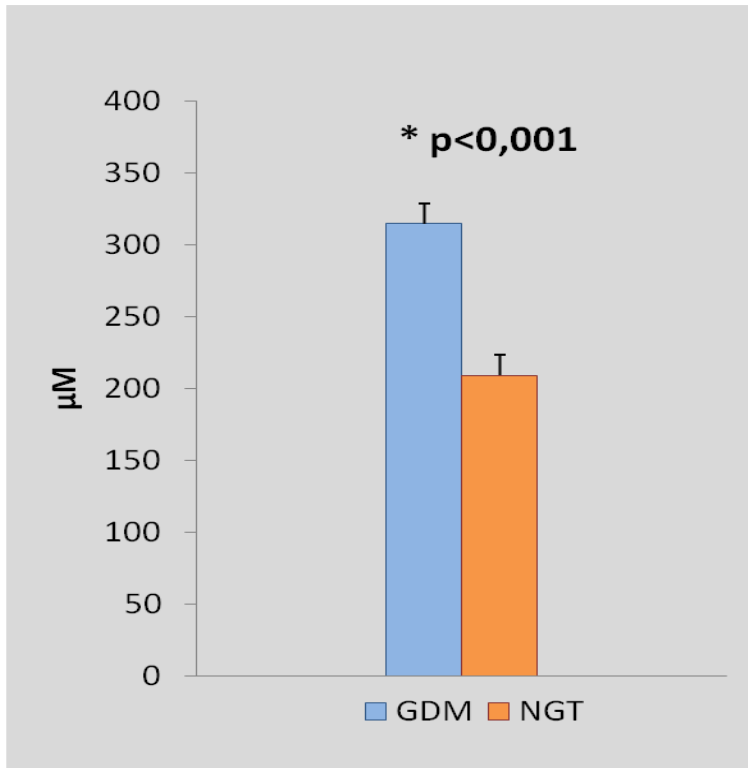


## Fasting Blood Glucose

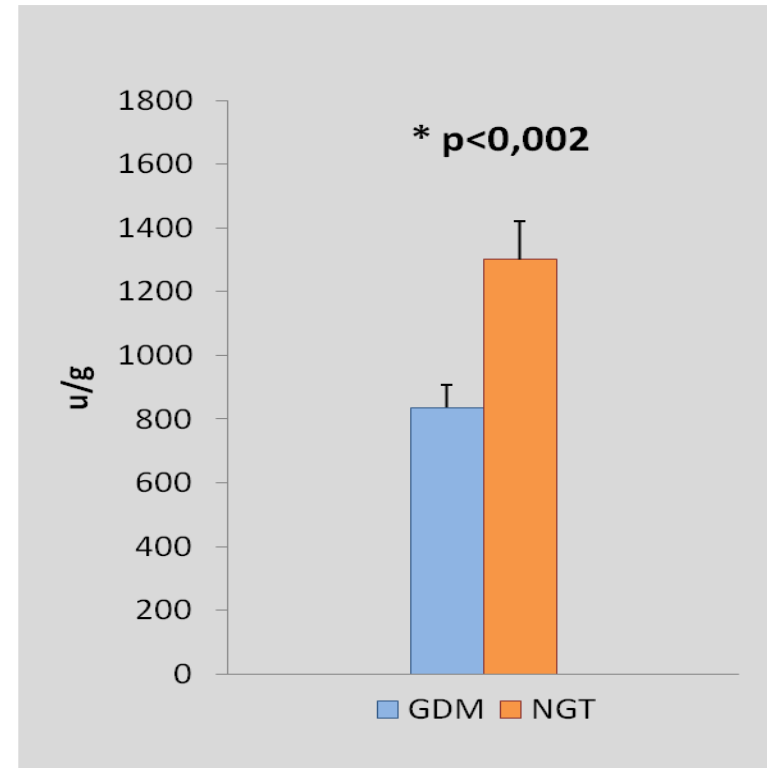


# OXIDATIVE LOAD IN GESTATIONAL DIABETES

plasma hydrogen superoxide

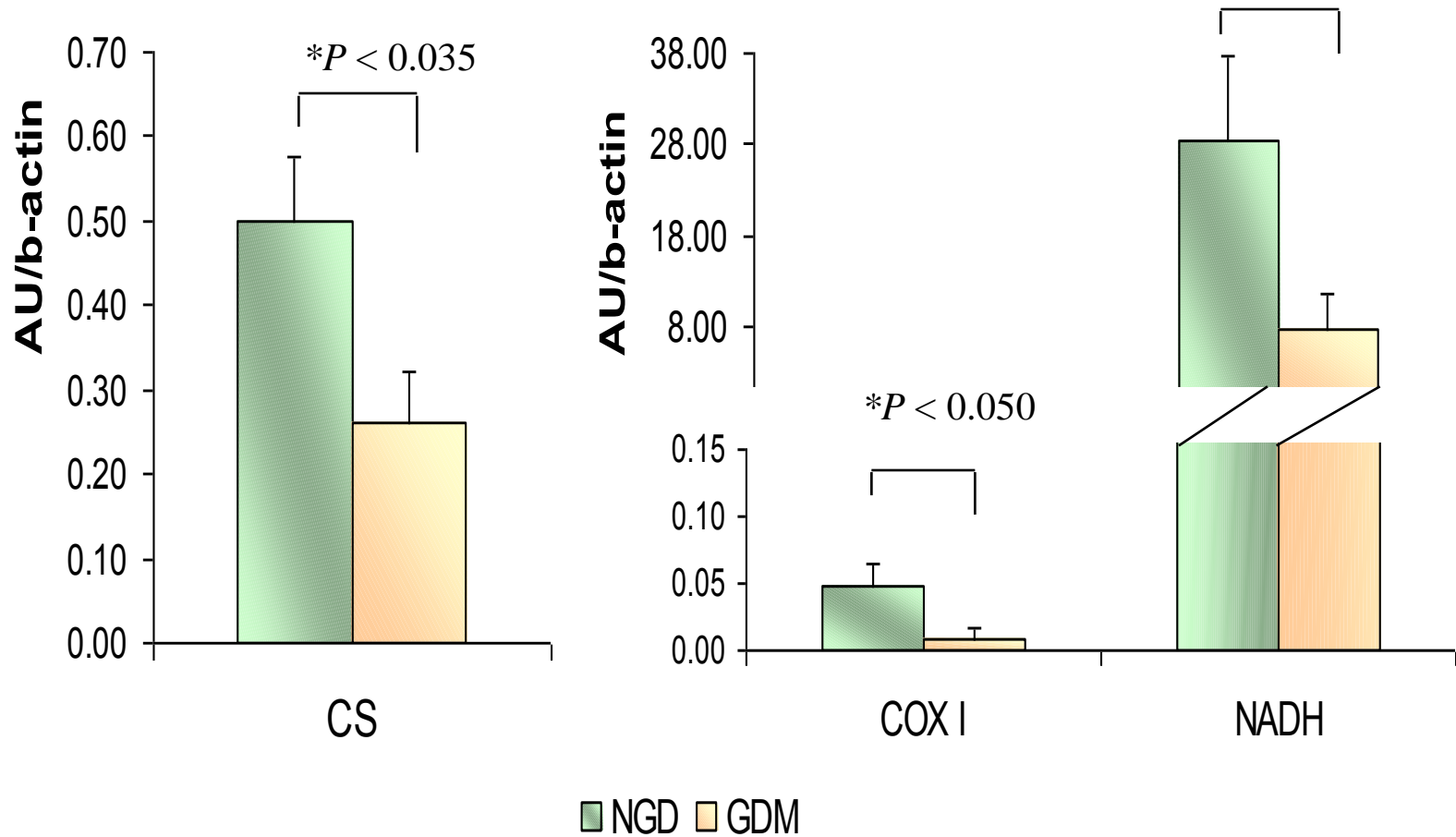


skeletal muscle SOD activity

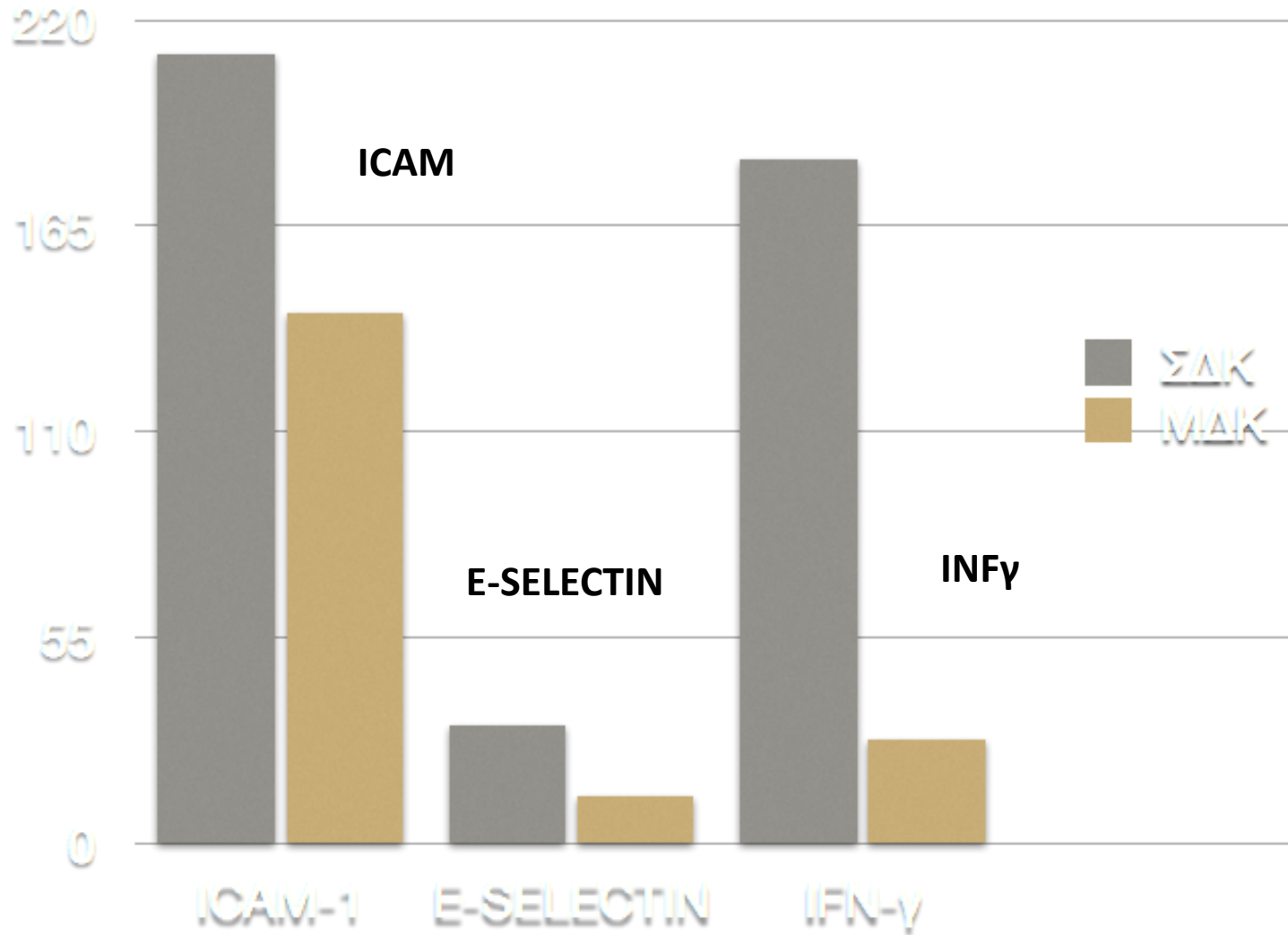


# Placental MITOCHONDRIAL ENZYME GENE EXPRESSION

\* $P < 0.050$

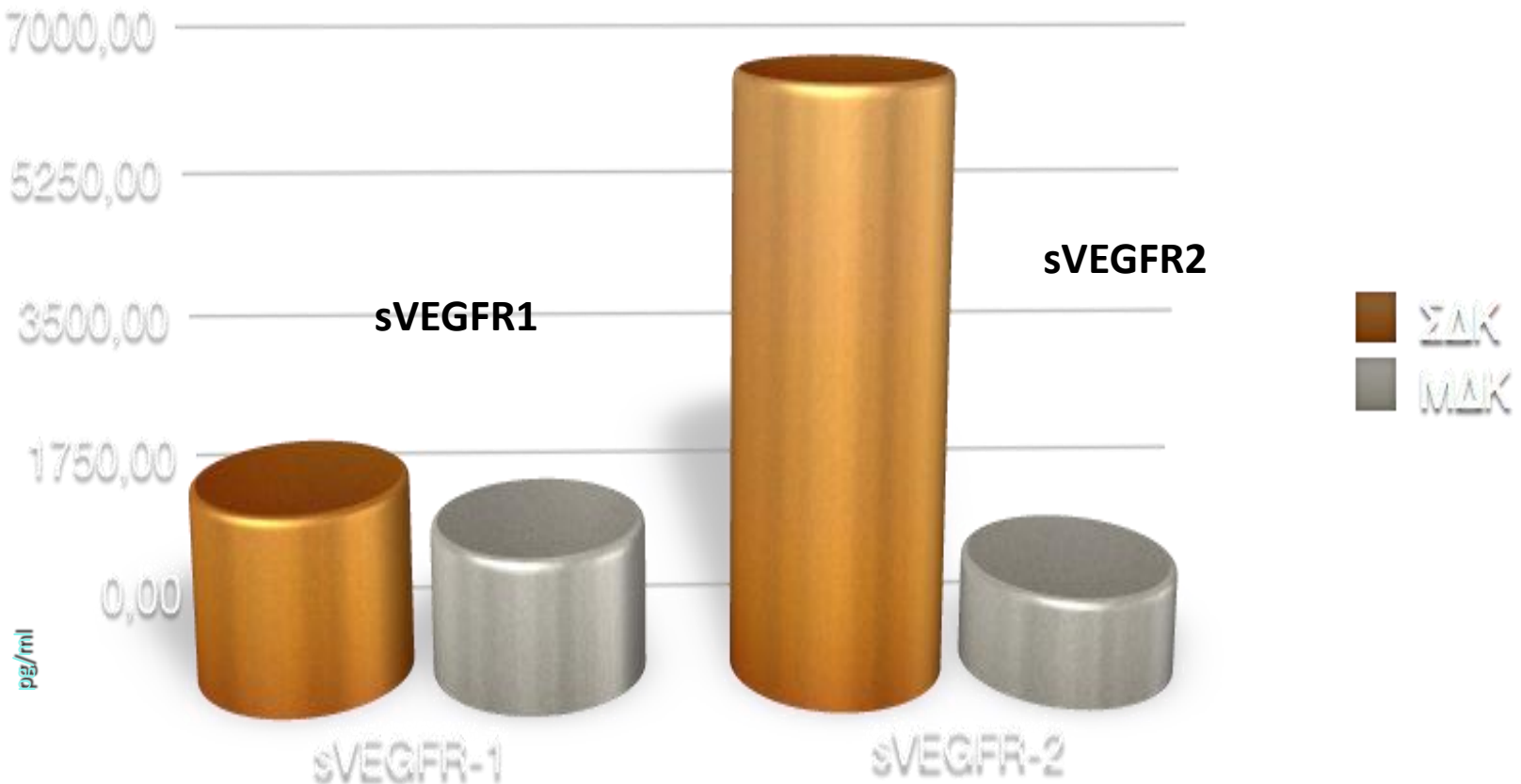


# INFLAMMATORY MARKERS



# *s*VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTORS ( pg/ml)

	NGT	GDM	P values
sVEGFR-1	1746.24 ± 36.8	2239.03 ± 170.5	0.004*
sVEGFR-2	1230.92 ± 234.2	6759.52 ± 1071.5	0.0004*

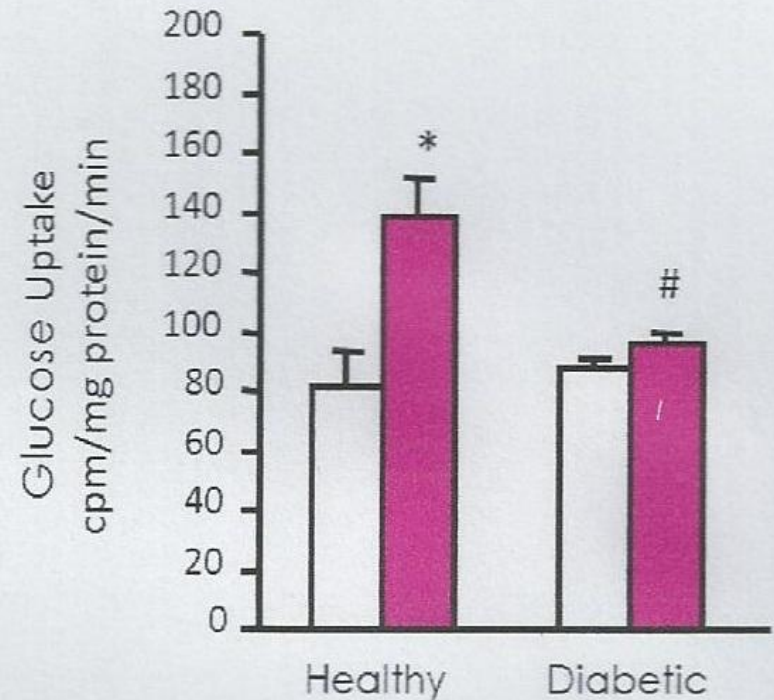
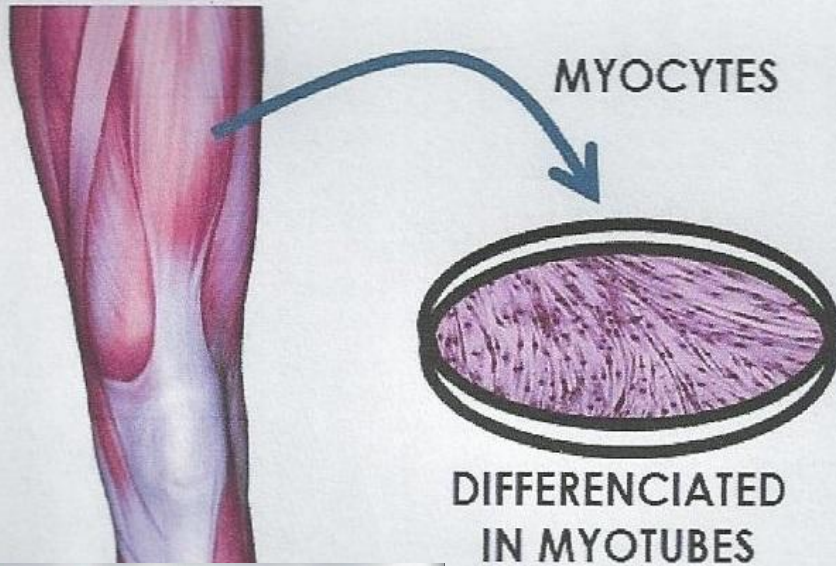


	Φ.Τ	ΣΔΚ
ATF2	7,17	52,16
GATA3	2,08	5,17
IL10RA	50	22,9
IL12A	49,01	26,49
IL12B	50	33,58
IL13	71,55	50
IL13RA1	75,8	50
IL17C	71,3	50
IL17RA	18,84	13,5
IL4R	50	14,42
IL6R	11,38	0,04
IL6ST	25,22	4,79
IL7	20,24	0,57
INHA	19,28	0,72
TYK2	40,25	18,61

	Φ.Τ	ΣΔΚ
CCL25	50	44,08
CXCL14	35,64	3,14
CXCL3	22,08	0,4
CXCL5	26,66	3,4
CXCL6	27,53	0,88
FADD	12,89	0,21

# GESTASIONAL DIABETES EPIGENETICS

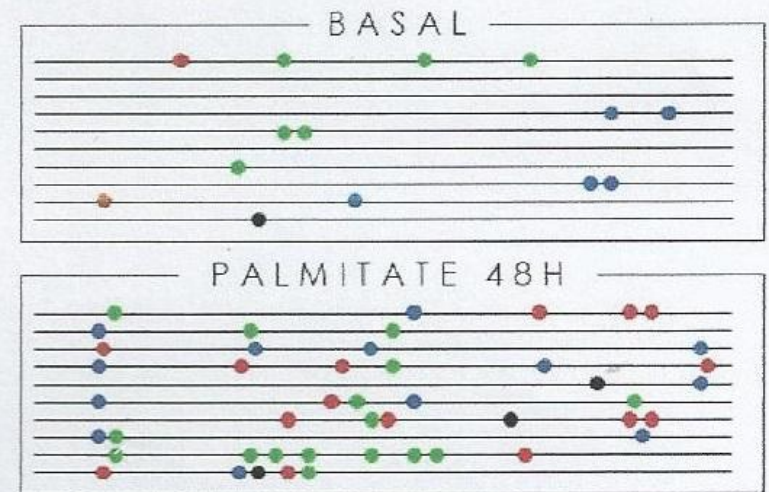
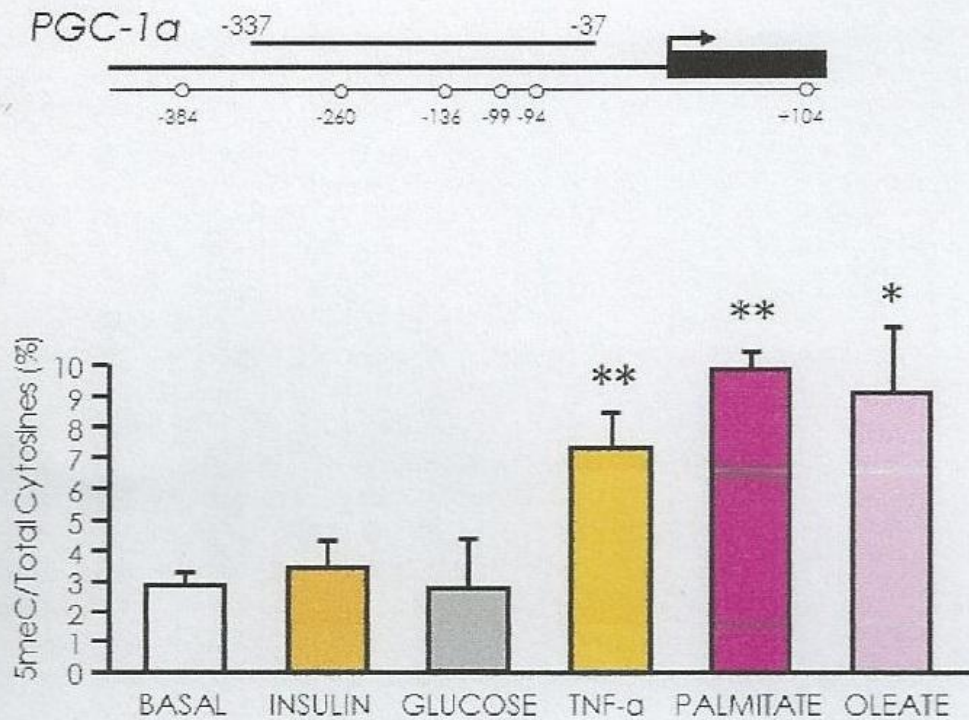
# NON-GENETIC MEMORY OF DIABETIC PHENOTYPE IN PRIMARY HUMAN MUSCLE CELL CULTURES



Bouzakri and Zierath, J. Biol. Chem, 2007

Cultured muscle cells maintain the "insulin resistant phenotype" of the donor, even after several passages

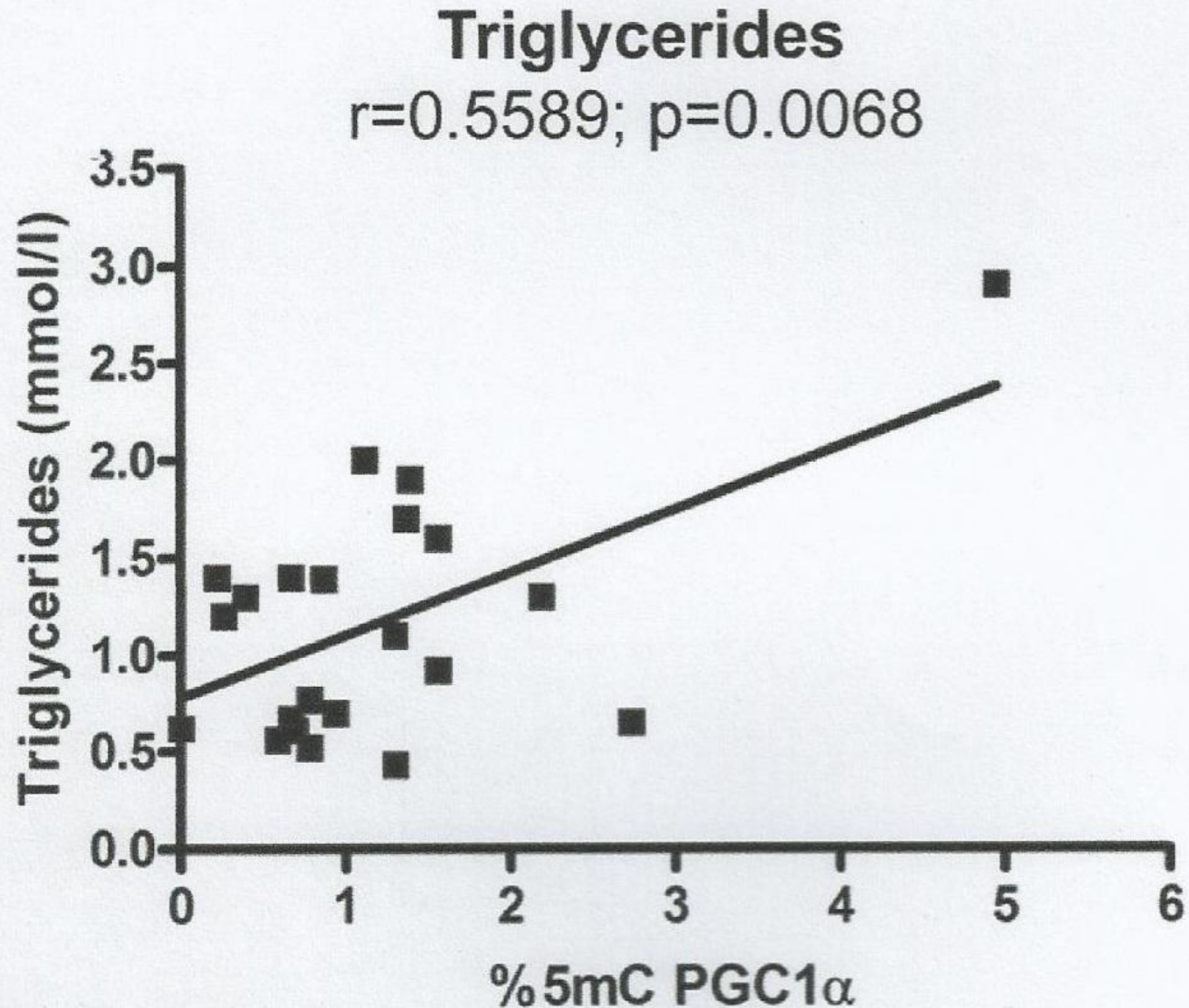
# TNF- $\alpha$ and Free Fatty Acids Exposure Induce Acute Methylation of the PGC-1 $\alpha$ Promoter



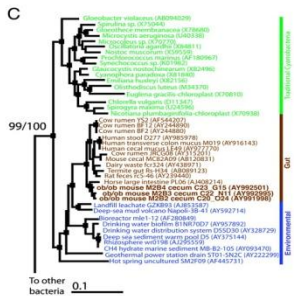
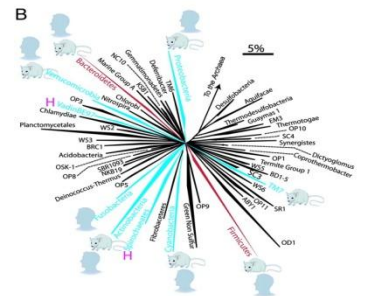
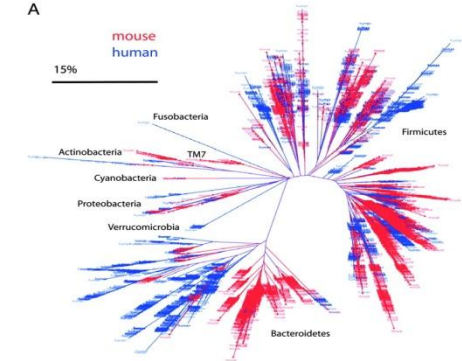
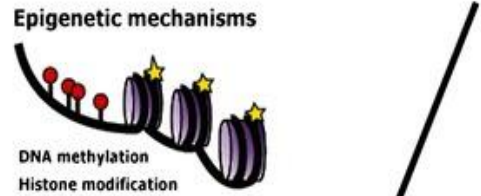
- 5meCpG
- 5meCpA
- 5meCpT
- 5meCpC



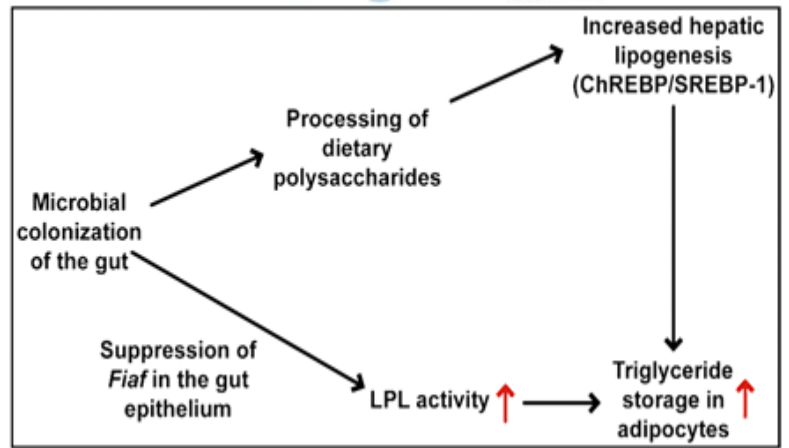
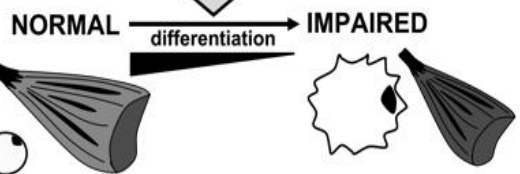
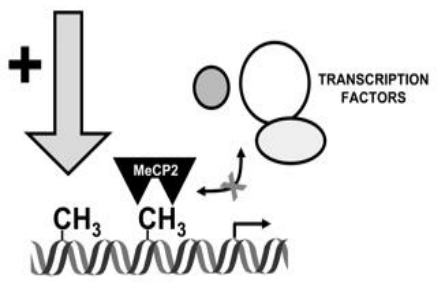
# PGC-1 $\alpha$ PROMOTER METHYLATION IS ASSOCIATED WITH TRIGLYCERIDE LEVELS



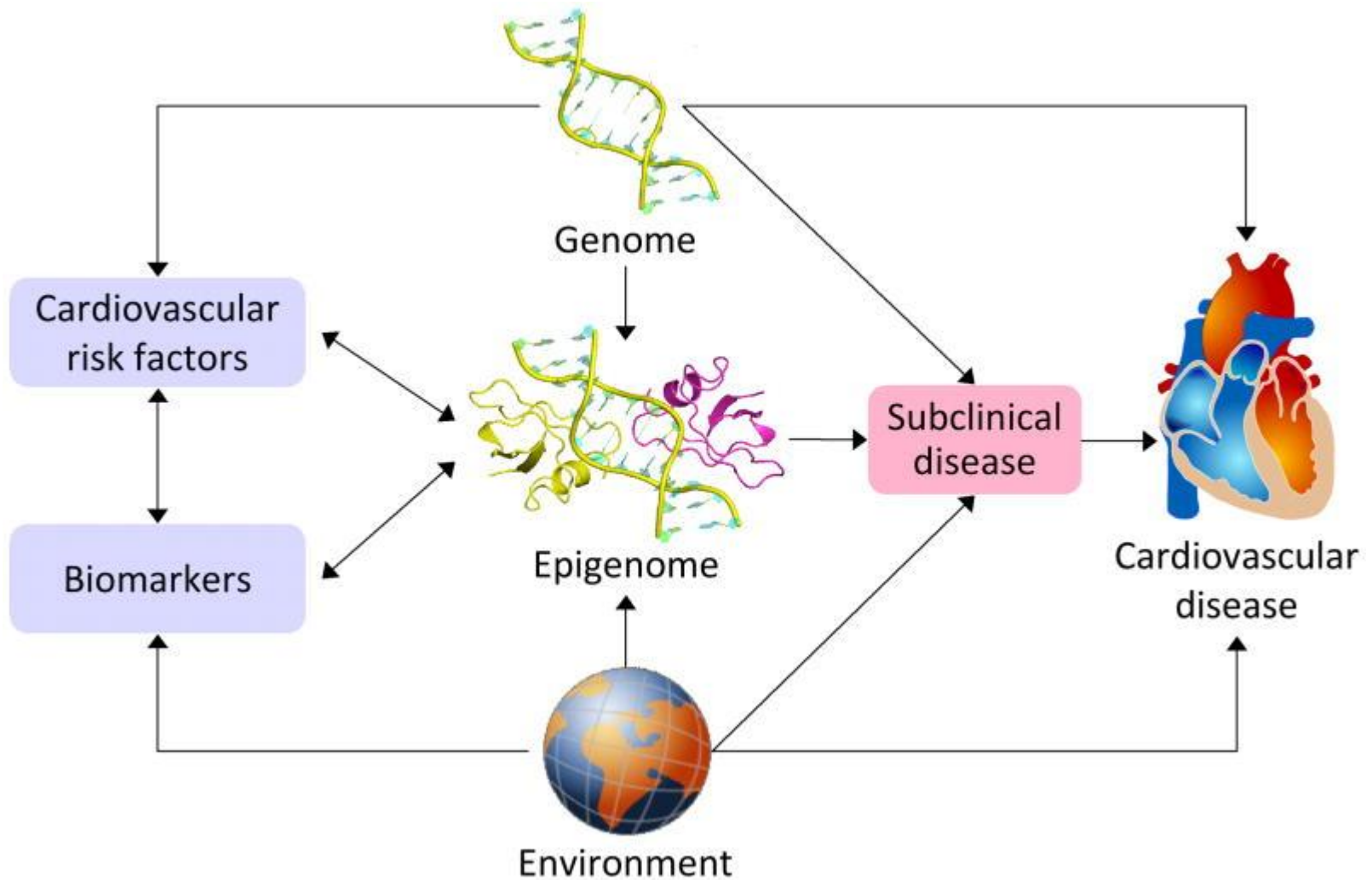
# OBESITY & EPIGENETICS



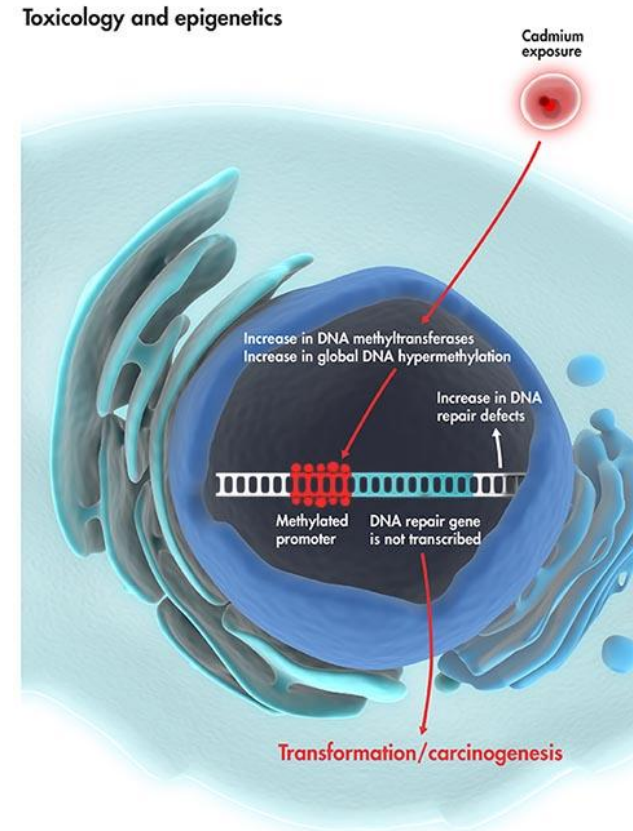
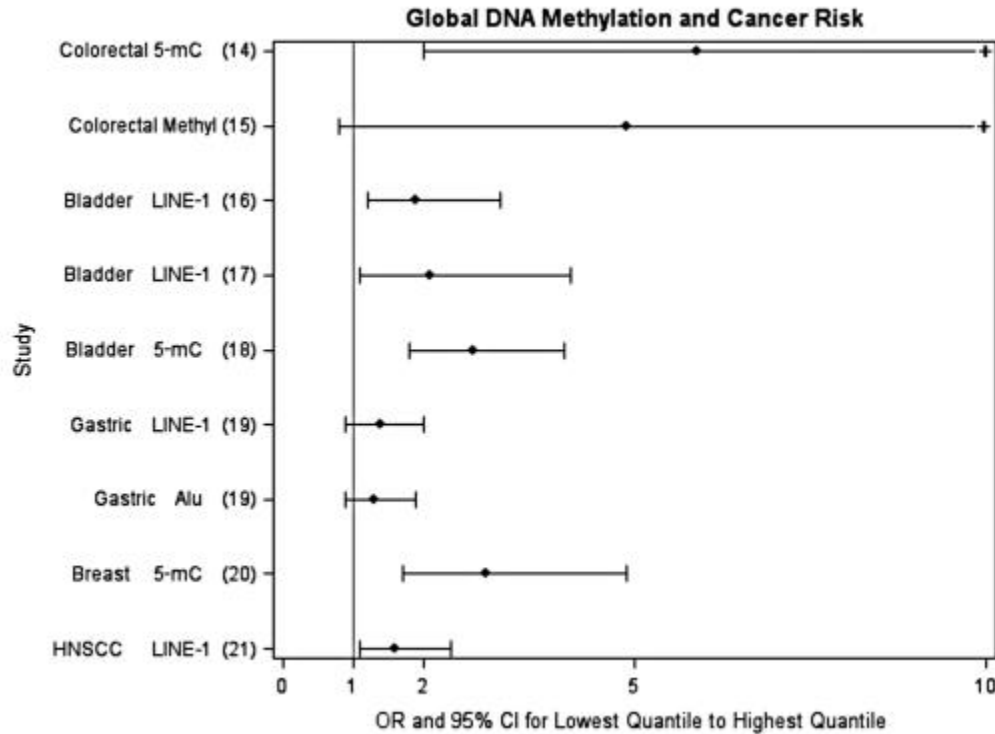
**ENVIRONMENTAL FACTORS**  
(nutrients, hormones, toxins)



# Cardiovascular epigenetics



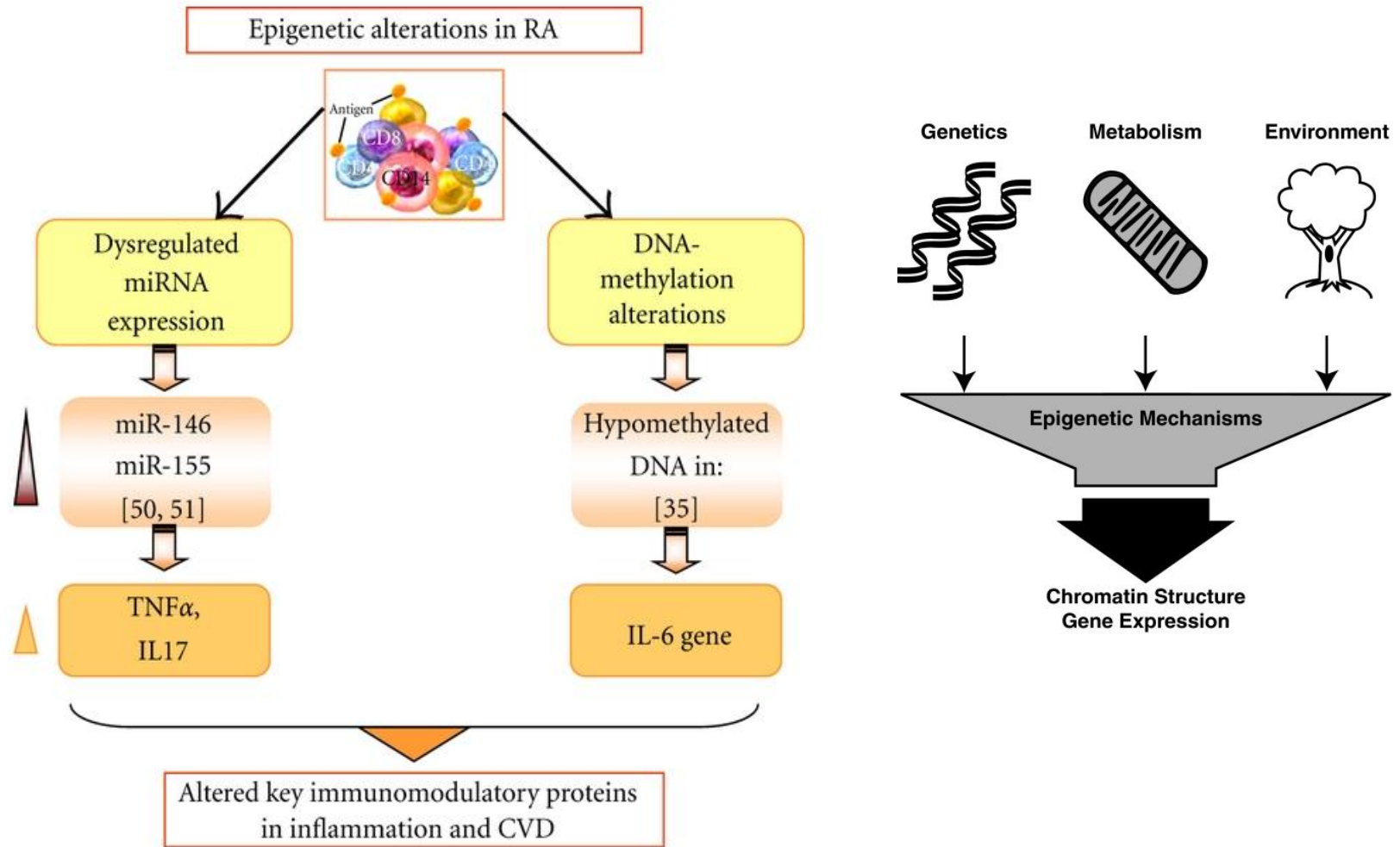
# CANCER & EPIGENETICS



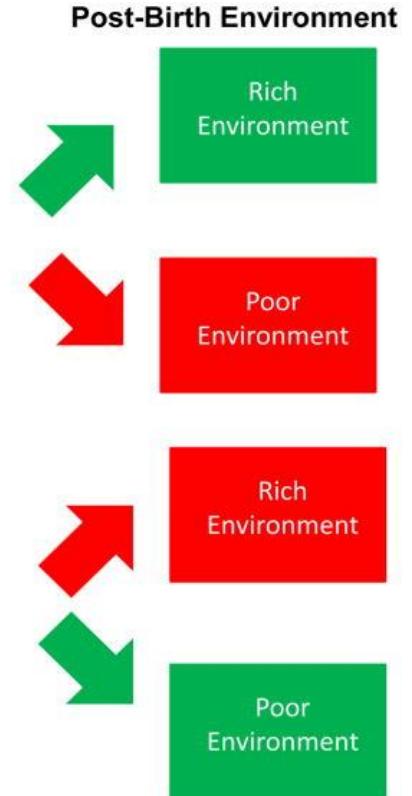
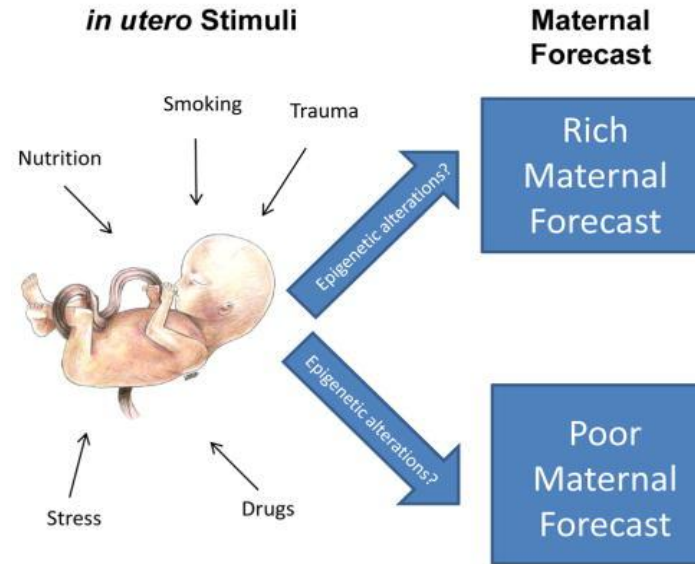
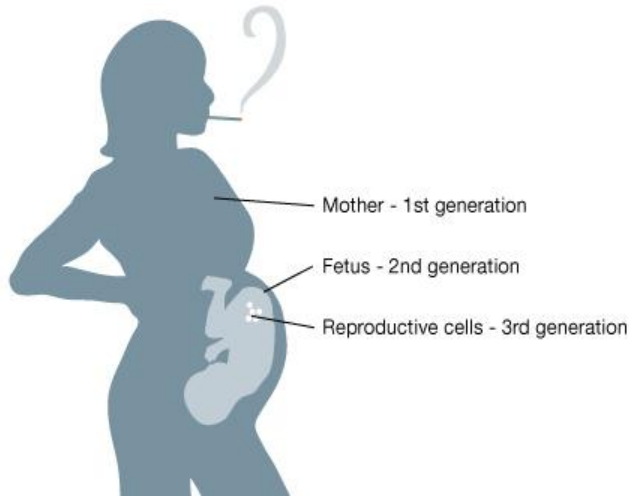
**DNA methylation in white blood cells:  
association with risk factors in epidemiologic studies.**

Epigenetics. 2011 Jul;6(7):828-37. Epub 2011 Jul 1.

# REUMATOID ARTHRITIS & CVD



# PERINATAL SMOKING EXPOSURE



**reduced birth weight**

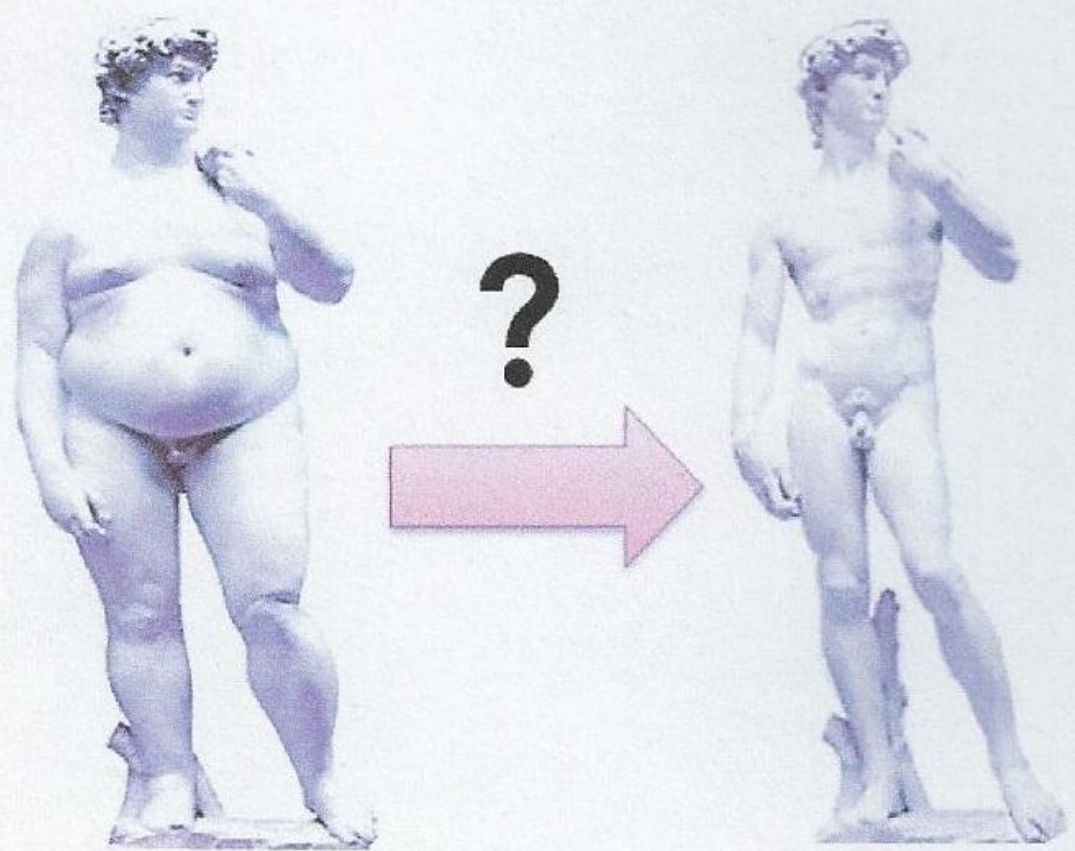
**poor developmental and psychological outcomes**

**increased risk for diseases**

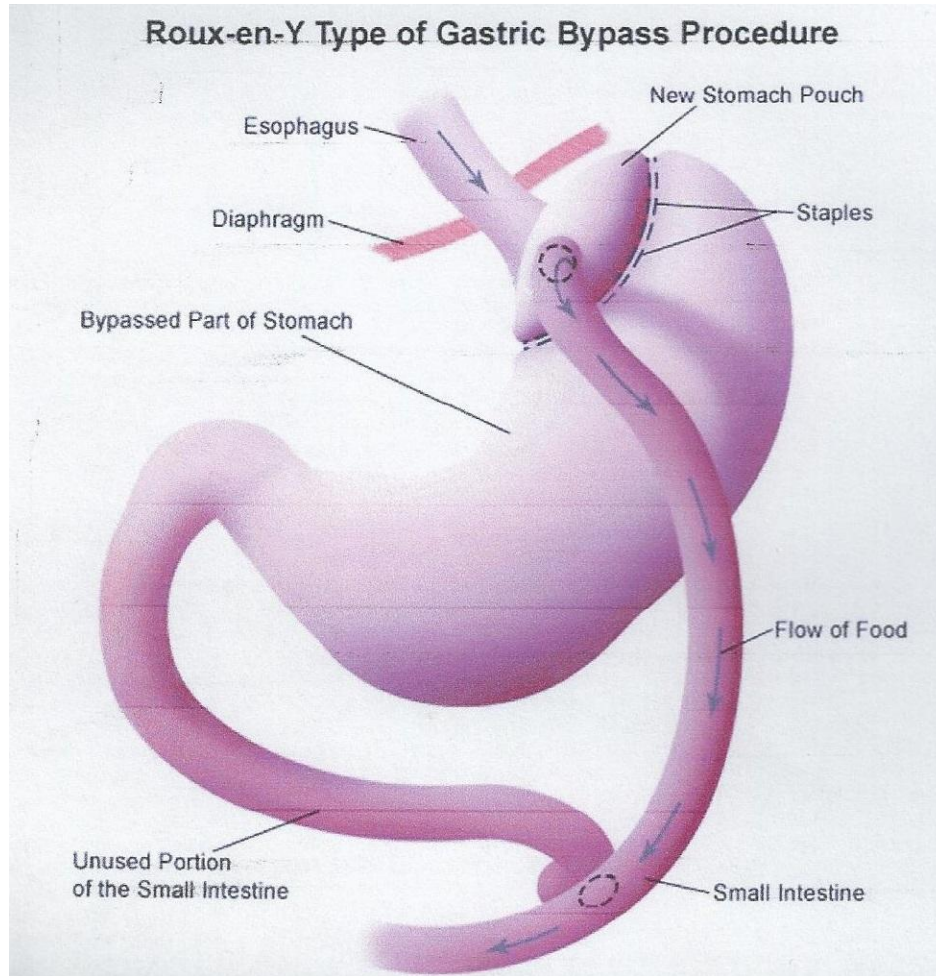
**behavioral disorders later in life**



# DOES WEIGHT LOSS REMODELS DNA METHYLATION PROFILE?



# BARIATRIC WEIGHT LOSS

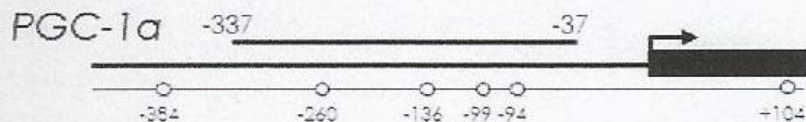


**Loss of 30 kg**

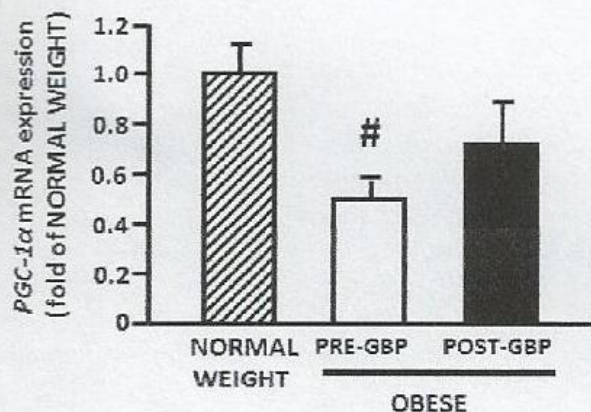
**4 mo**



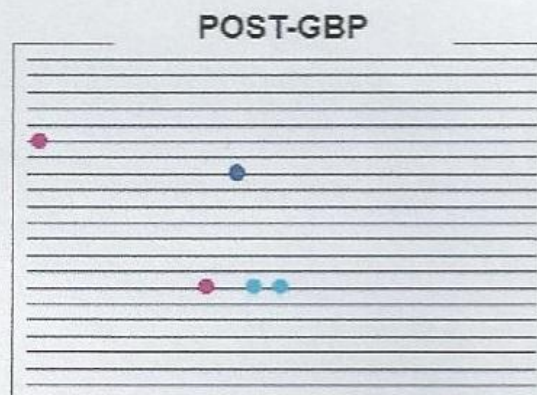
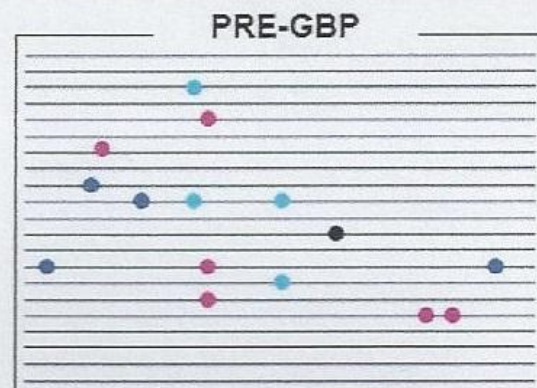
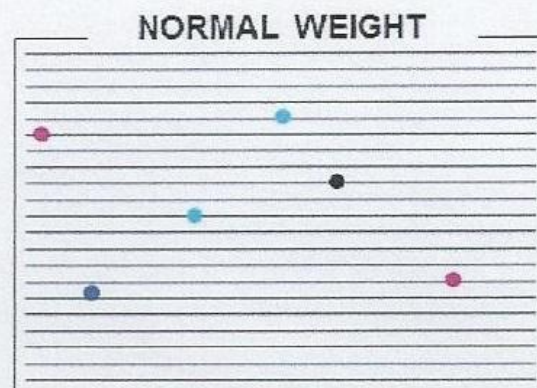
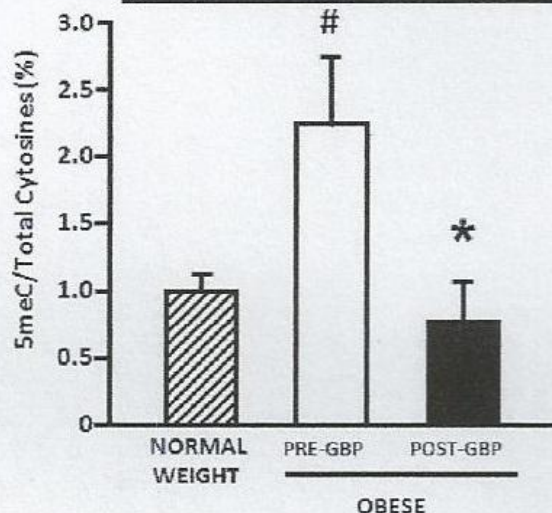
# OBESITY-ASSOCIATED ALTERED *PGC-1 $\alpha$* PROMOTER METHYLATION IS REVERSED BY WEIGHT LOSS



## GENE EXPRESSION



## METHYLATION



● 5mCpG    ● 5mCpT  
● 5mCpA    ● 5mCpC

# OBESITY-ASSOCIATED ALTERED DNA METHYLATION PROFILE IS REVERSED BY WEIGHT LOSS

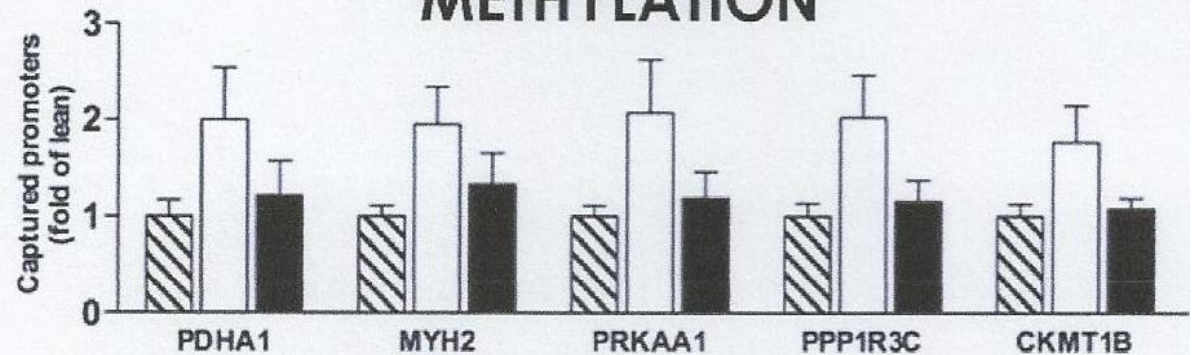
## Transcriptomics

OBESE    NORMAL  
PRE    POST WEIGHT

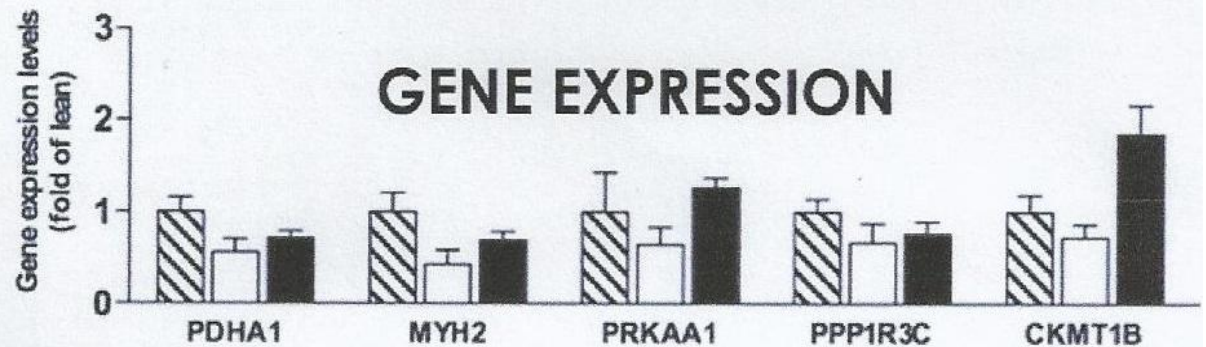


## Gene specific analysis

### METHYLATION



### GENE EXPRESSION

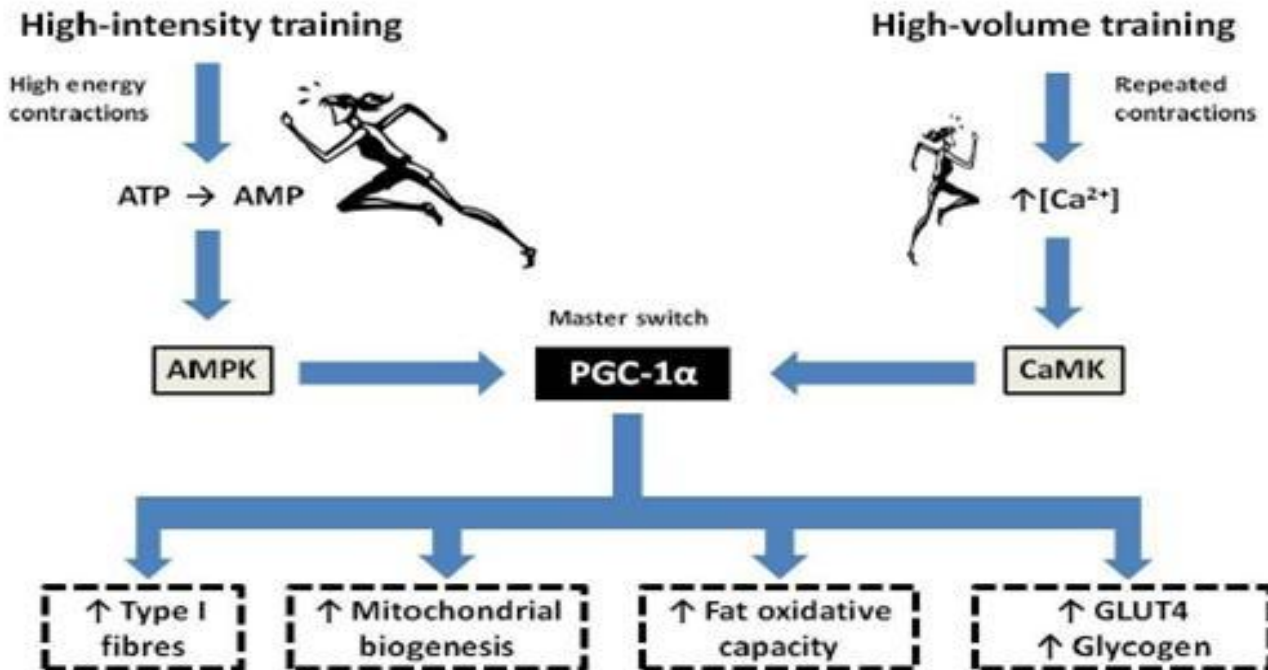


# DOES EXERCISE REMODELS DNA METHYLATION PROFILE

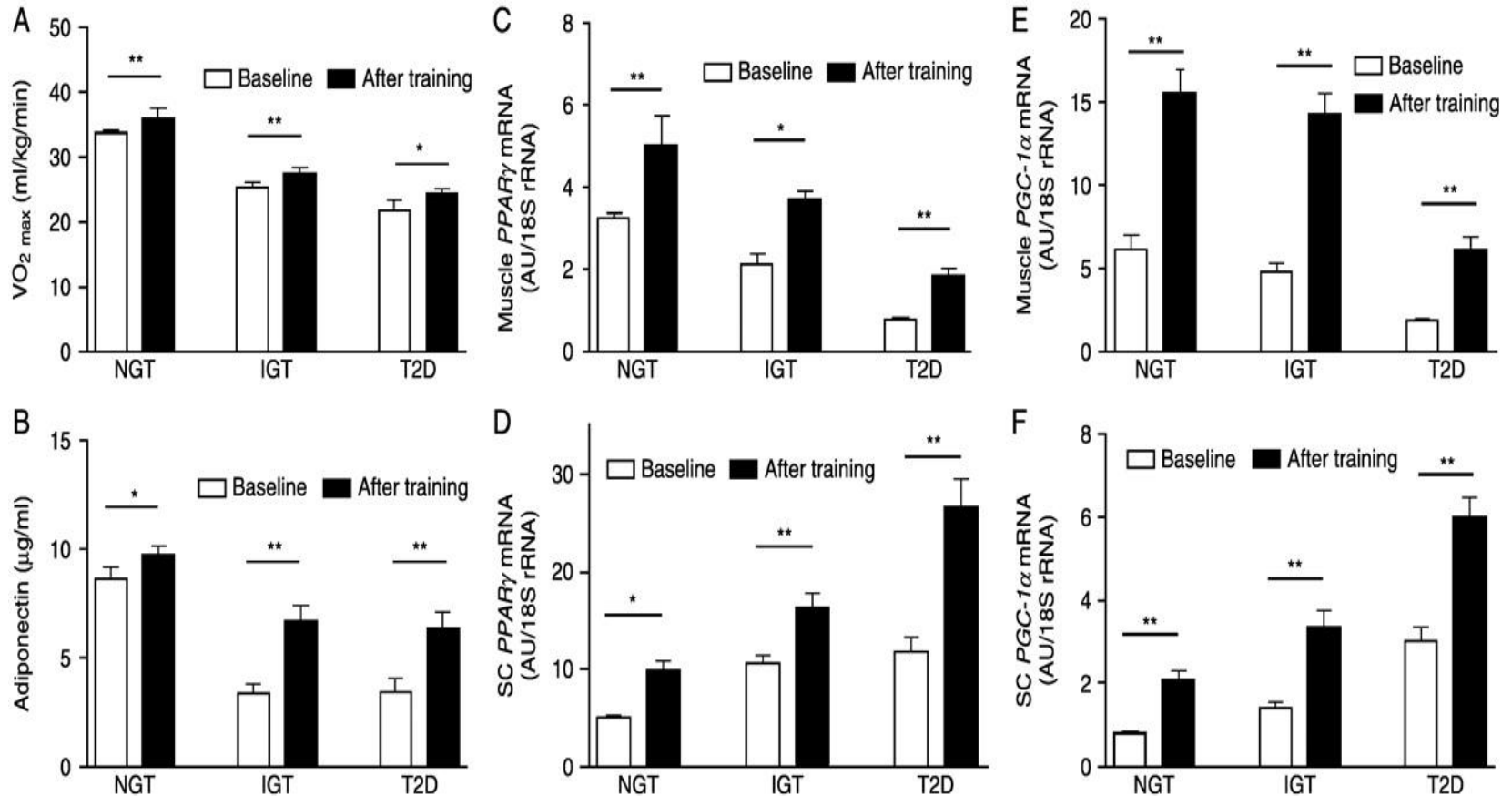


# PGC1α & ΑΣΚΗΣΗ

Figure 2.



# Effect of 4 w of exercise on skeletal muscle & adipose tissue PPAR $\gamma$ & PGC-1 $\alpha$ in normal glucose-tolerant (NGT) and in IGT or type 2 diabetes (T2D).

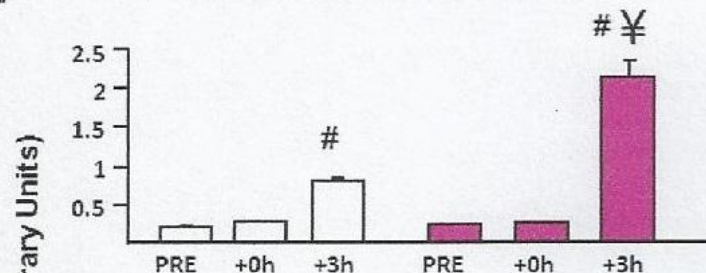


# TIME-COURSE AND EXERCISE INTENSITY ANALYSIS OF DNA METHYLATION AND GENE EXPRESSION

□ LOW  
■ HIGH

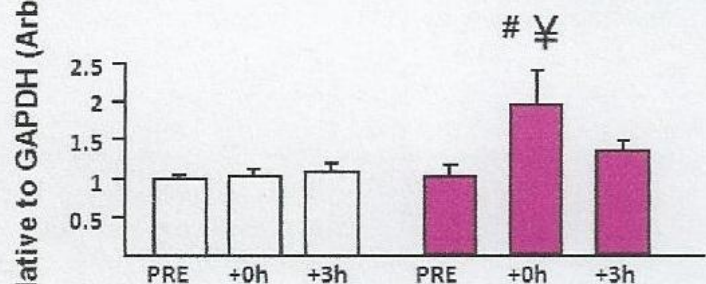
## GENE EXPRESSION

*PGC-1 $\alpha$*



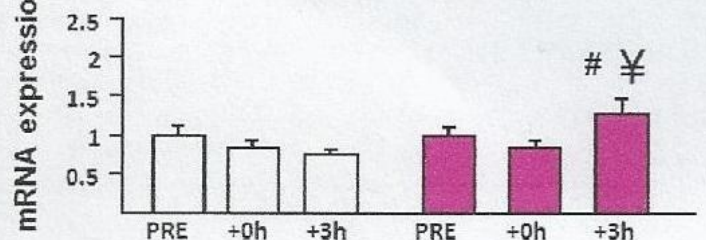
*PGC-1 $\alpha$*

*TFAM*



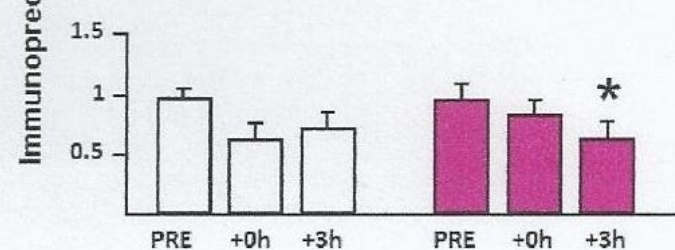
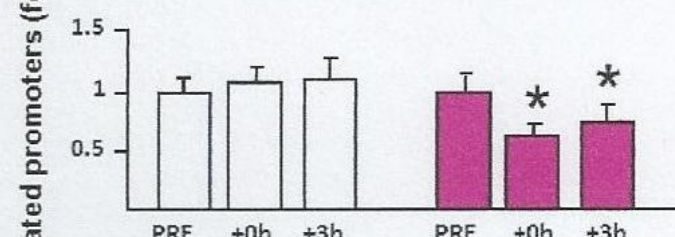
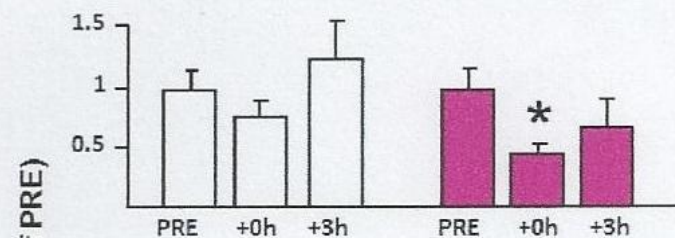
*TFAM*

*PPAR- $\delta$*



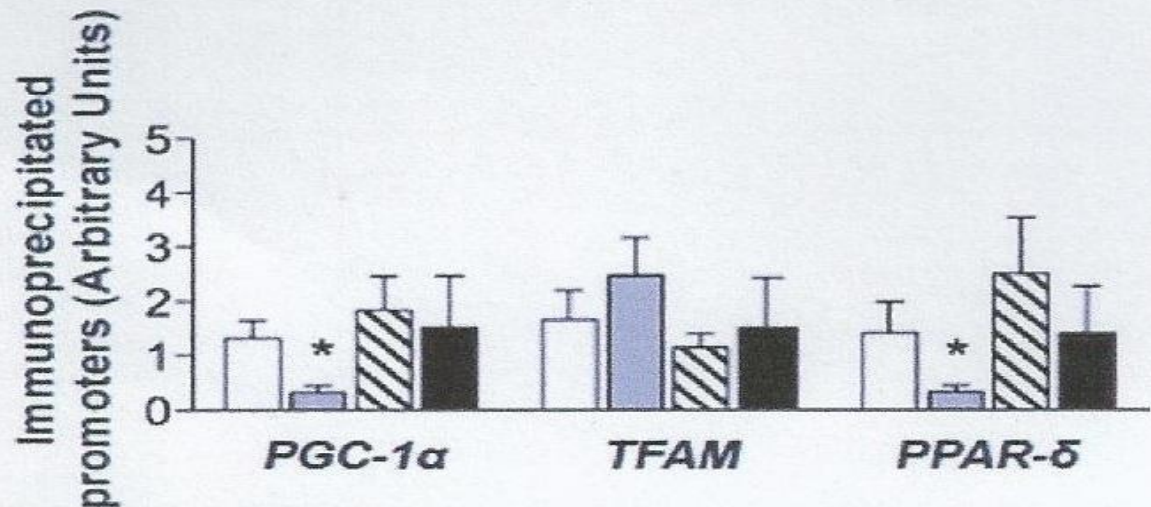
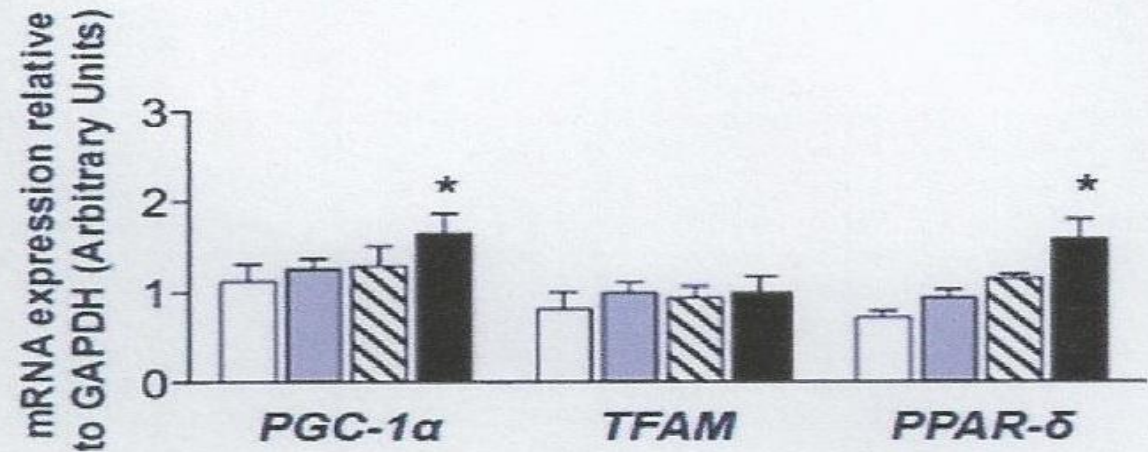
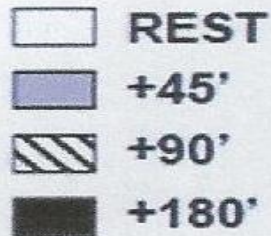
*PPAR- $\delta$*

## METHYLATION



Inverse relationship between mRNA expression and promoter methylation

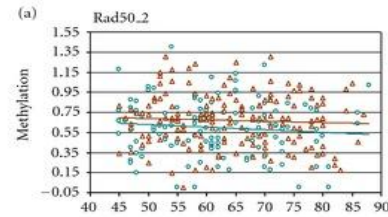
# MUSCLE CONTRACTION INDUCES PROMOTER HYPOMETHYLATION



# TAI CHI

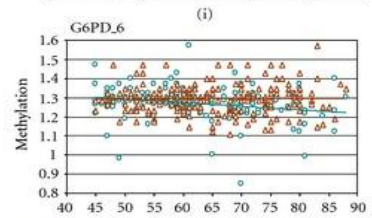


Evid Based Complement  
Alternat Med. 2012; 2012: 841810.



— △ Tai chi:  $y = -0.0016x + 0.7731, R^2 = 0.0041$   
 — ○ Controls:  $y = -0.0018x + 0.7005, R^2 = 0.0044$

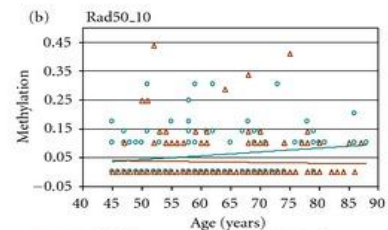
Age (years)	45-54	55-64	65-74	75-88
Tai chi (162)	0.69	0.68	0.66	0.64
Control (205)	0.61	0.59	0.58	0.55
Difference	0.08	0.08	0.09	0.09
Difference (%)	13.53	14.22	15.01	16.03



— △ Tai chi:  $y = 7E - 05x + 1.2877, R^2 = 1E - 04$   
 — ○ Controls:  $y = -0.0018x + 1.3769, R^2 = 0.0278$

Age (years)	45-54	55-64	65-74	75-88
Tai chi (203)	1.29	1.29	1.29	1.29
Control (223)	1.29	1.27	1.25	1.23
Difference	0	0.02	0.04	0.06
Difference (%)	0.34	1.7	3.21	5.09

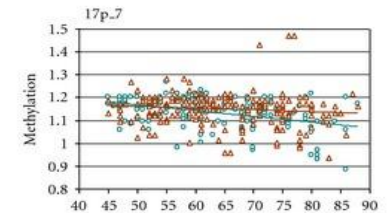
(iii)



— △ Tai chi:  $y = -0.0004x + 0.0583, R^2 = 0.0026$   
 — ○ Controls:  $y = 0.0017x - 0.0484, R^2 = 0.0233$

Age (years)	45-54	55-64	65-74	75-88
Tai chi (159)	0.04	0.03	0.03	0.03
Control (206)	0.04	0.05	0.07	0.09
Difference	0	-0.02	-0.04	-0.06
Difference (%)	7.89	-32.67	-55.33	-70.68

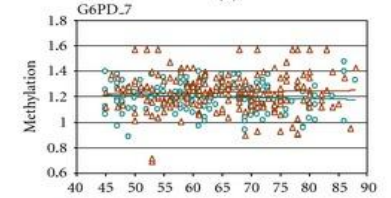
(i)



— △ Tai chi:  $y = -0.0008x + 1.2025, R^2 = 0.0134$   
 — ○ Controls:  $y = -0.0025x + 1.2903, R^2 = 0.1011$

Age (years)	45-54	55-64	65-74	75-88
Tai chi (203)	1.16	1.16	1.14	1.14
Control (218)	1.17	1.14	1.12	1.09
Difference	0	0.01	0.03	0.05
Difference (%)	-0.24	1.13	2.67	4.63

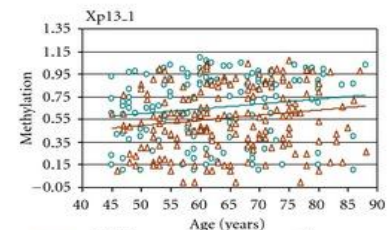
(ii)



— △ Tai chi:  $y = 0.0006x + 1.1926, R^2 = 0.0017$   
 — ○ Controls:  $y = -0.0009x + 1.2527, R^2 = 0.0071$

Age (years)	45-54	55-64	65-74	75-88
Tai chi (203)	1.23	1.23	1.23	1.24
Control (223)	1.21	1.2	1.19	1.18
Difference	0.01	0.03	0.04	0.06
Difference (%)	1.23	2.39	3.67	5.23

(iv)



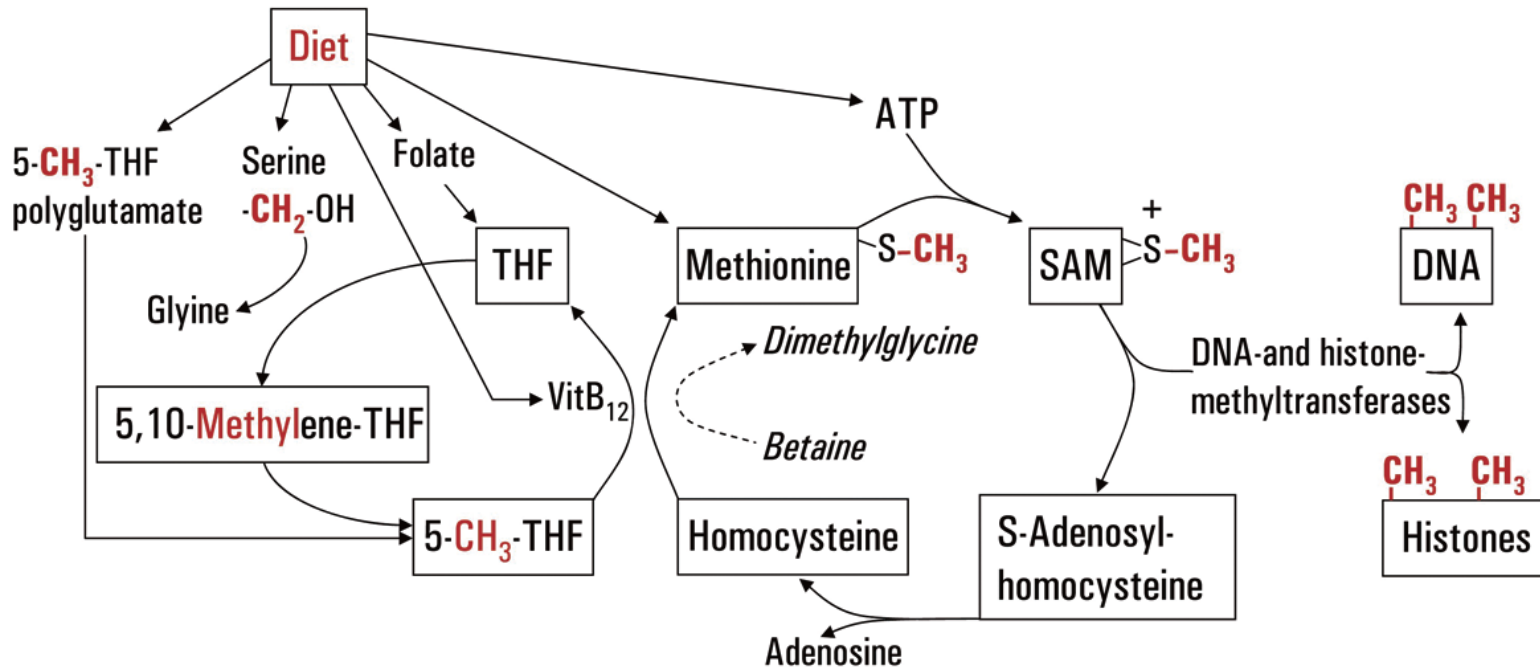
— △ Tai chi:  $y = 0.0047x + 0.2566, R^2 = 0.0288$   
 — ○ Controls:  $y = 0.004x + 0.4028, R^2 = 0.0211$

Age (years)	45-54	55-64	65-74	75-88
Tai chi (184)	0.49	0.53	0.58	0.64
Control (220)	0.6	0.64	0.68	0.73
Difference	-0.11	-0.1	-0.1	-0.09
Difference (%)	-18.46	-16.4	-14.4	-12.31

(ii)



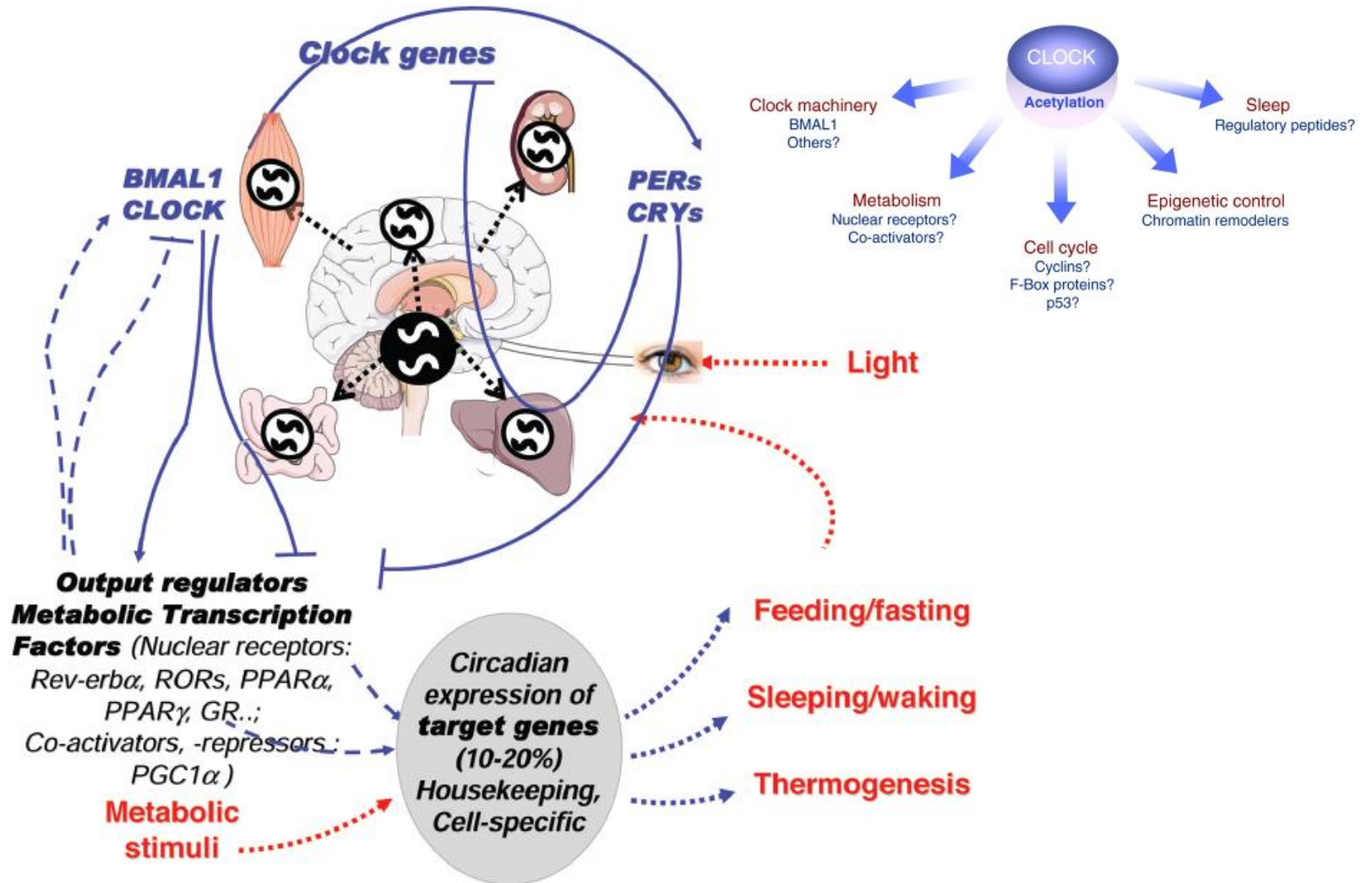
# Epigenetic aspects of post-traumatic stress disorder



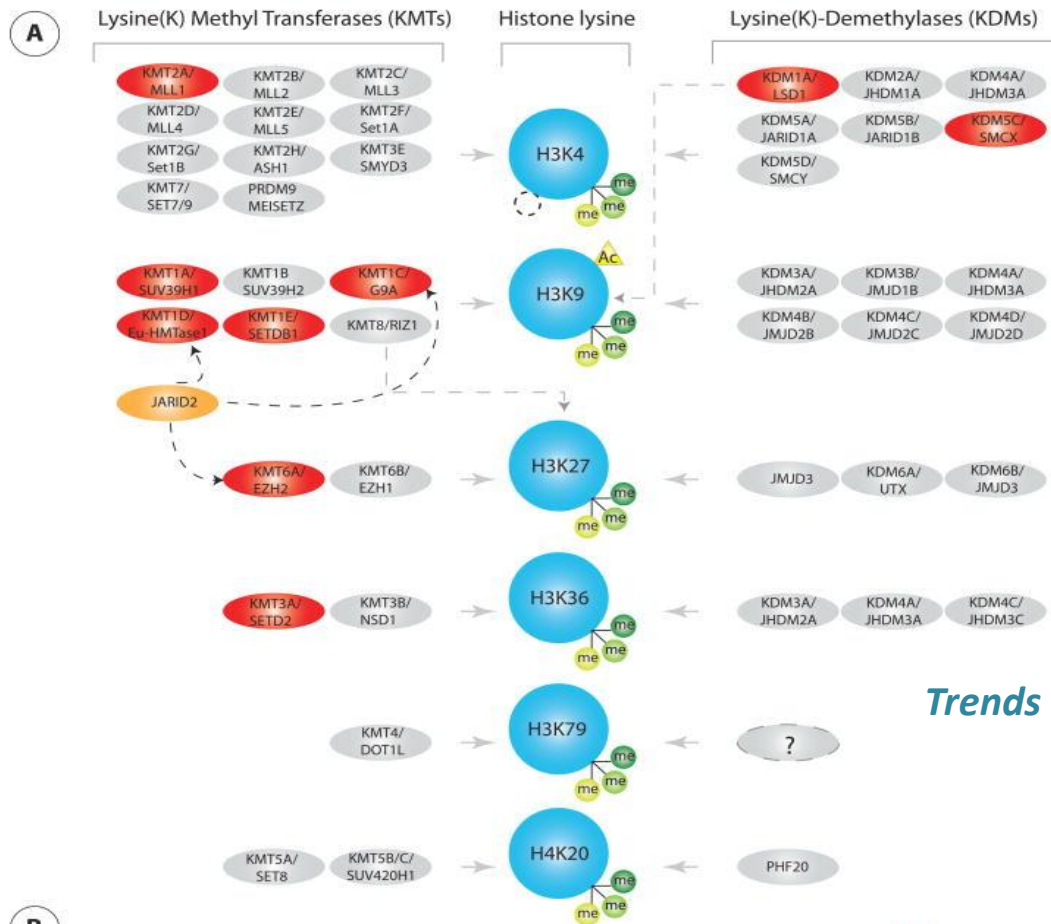
*Disease Markers 30 (2011) 77–87 77*

# DIURNAL METHYLATION

## CIRCARDIAN RHYTHM & CHRONOTHERAPEUTICS

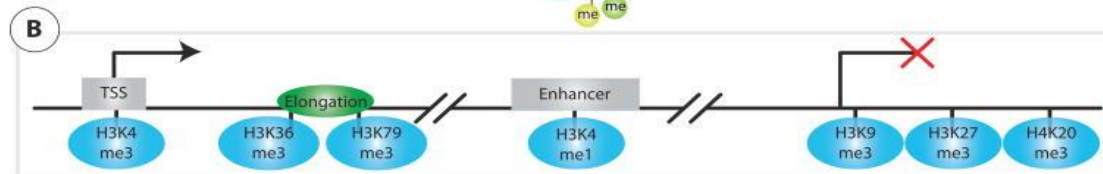


# Balancing histone methylation activities in psychiatric disorders



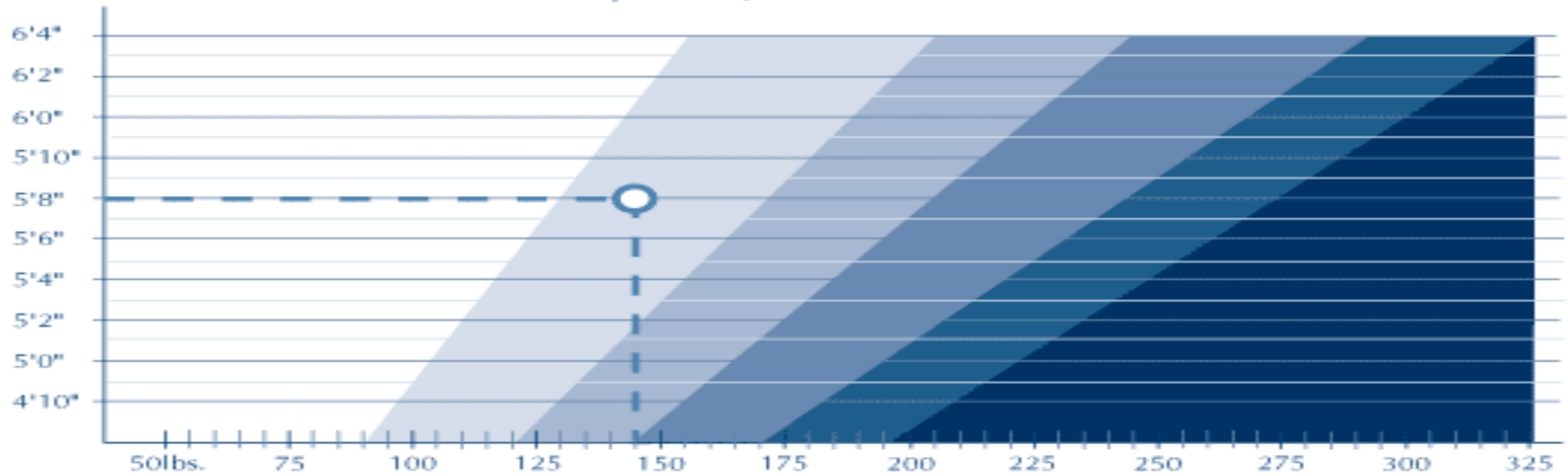
Red marked KMT/KDM are implicated in neurodevelopment or psychiatric disease

*Trends Mol Med. 2011 17(7): 372–379.*

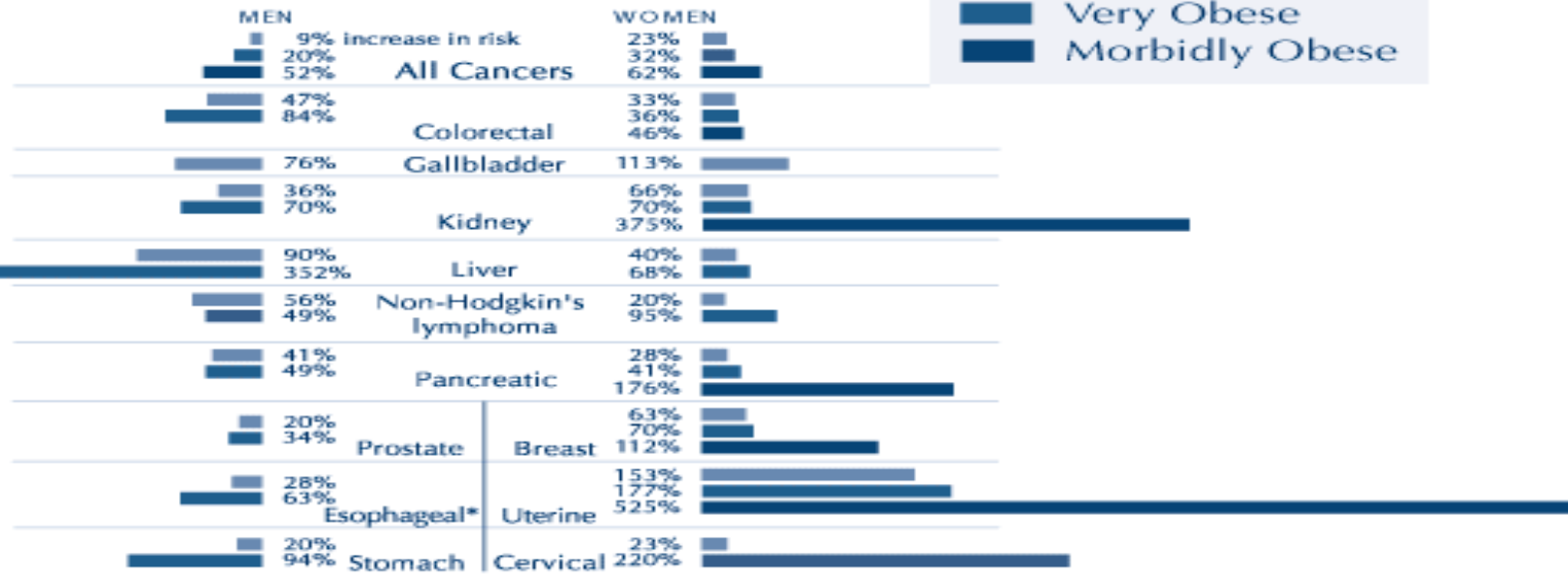


Simplified scheme for selected mono- and trimethylated histone lysine

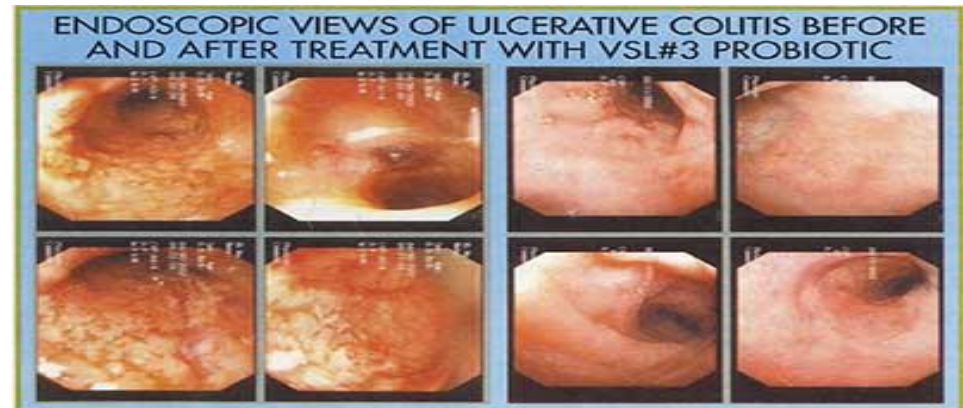
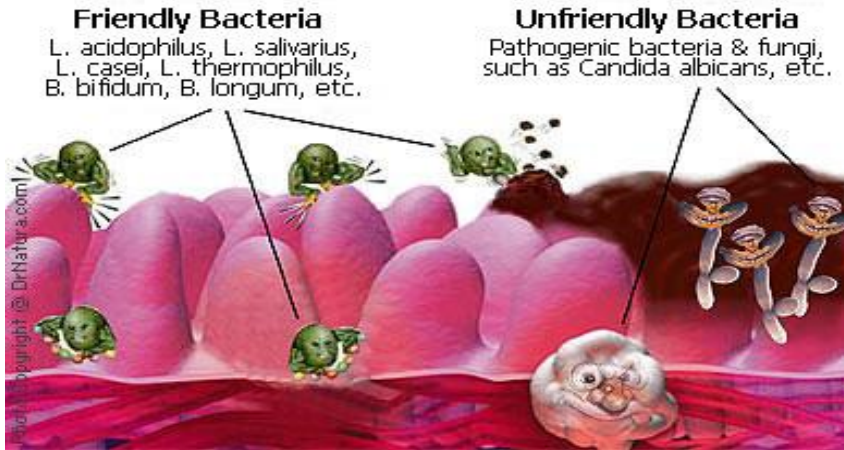
# More Pounds, More Cancers



## Risk for Cancer

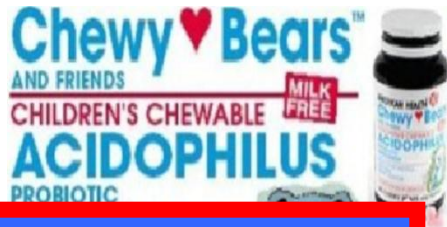


# BACTERIA & HEALTH



THE FOUR IMAGES TO THE LEFT ARE BASELINE ENDOSCOPIC VIEWS FROM A PATIENT WITH ULCERATIVE COLITIS WHO DID NOT RESPOND TO CONVENTIONAL DRUG THERAPY. THE IMAGES TO THE RIGHT ARE FROM THE SAME PATIENT AFTER SIX WEEKS OF TREATMENT WITH THE VSL#3 PROBIOTIC COMBINATION. IMAGES REPRINTED WITH PERMISSION OF RICHARD FEDORAK, MD, UNIVERSITY OF ALBERTA.

# MICROBIAL ENVIRONMENT & METABOLIC SYNDROM



- 100 trillion bacteria
- 10% of our cell population
- 17 certain polymorphisms responsible for high LDL & low glutathione

Recent changes in lifestyles have altered the human gut microbiome and linked disease patterns forever!

## Special Biological Bandits:

Weird dietary fads  
Antibiotic abuse  
General drug popping  
Western Post WW2 Diet  
Dietary supplements  
  
Exotic travel at an early age...exposures?  
Immunological  
'overprotection' of children?

... Is this really a good idea?

Some major 'non-infectious' human diseases and conditions with associated gut microbial disorders: All "modern" diseases.

**Gastric ulcers** (*Helicobacter pylori*) - Barry J Marshall & J Robin Warren (2005 Nobel Prize for Medicine)

**Colonic cancer**

**Inflammatory bowel conditions**

Ulcerative Colitis & Crohn's disease

**Allergies & related immune disorders**

asthma, eczema, psoriasis...

**Insulin resistance related diseases- type 2 diabetes and obesity...**

**Many neuropsychiatric disorders....**

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# HOW HUMANS WE ARE?

Vol 444 | 21/28 December 2006 | doi:10.1038/nature05414

nature

ARTICLES

## An obesity-associated gut microbiome with increased capacity for energy harvest

Peter J. Turnbaugh<sup>1</sup>, Ruth E. Ley<sup>1</sup>, Michael A. Mahowald<sup>1</sup>, Vincent Magrini<sup>2</sup>, Elaine R. Mardis<sup>1,2</sup> & Jeffrey I. Gordon<sup>1</sup>

**BRIEF COMMUNICATIONS**

**MICROBIAL ECOLOGY**

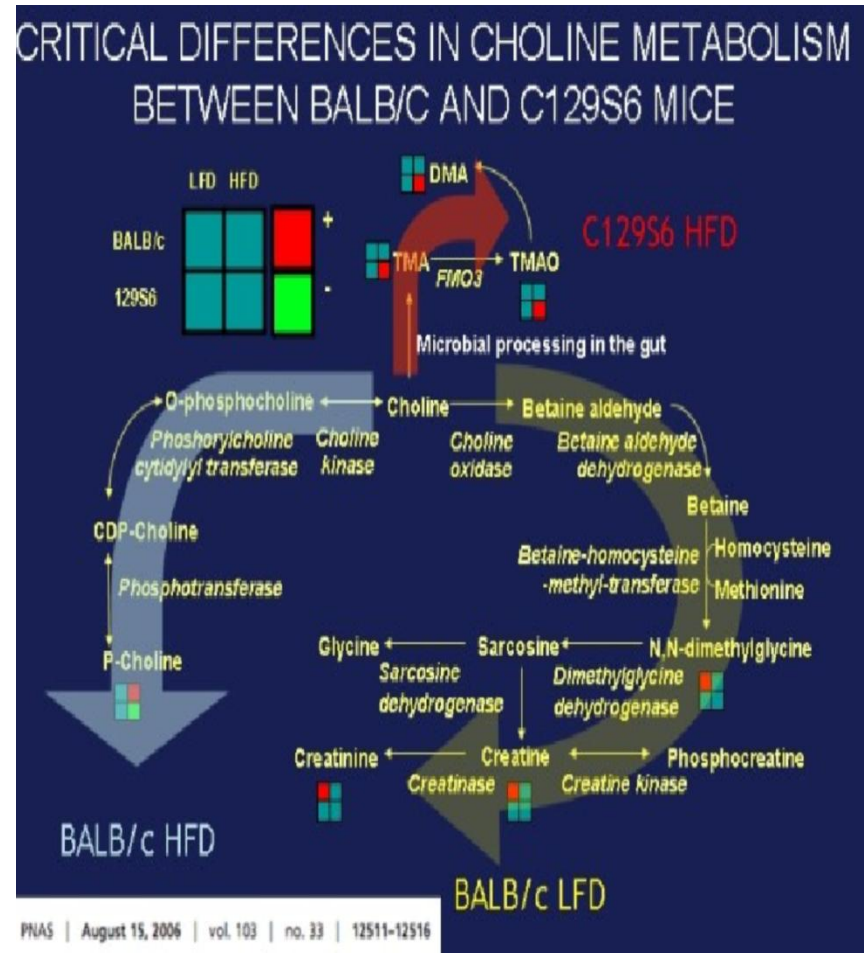
### Human gut microbes associated with obesity

Ruth E. Ley, Peter J. Turnbaugh, Samuel Klein, Jeffrey I. Gordon  
Washington University School of Medicine, St Louis, Missouri 63108, USA

Obese/Type 2 Diabetics have > Firmicutes: Bacteroidetes ratio than normal

Weeks on diet	Firmicutes (%)	Bacteroidetes (%)
0	~85	~15
12	~85	~15
26	~80	~20
52	~85	~15
Lean	~85	~15

Change in body weight (%)	Change in bacteroidetes abundance (%)
-10	~10
-15	~15
-20	~20
-25	~25



# EPIGENETICS

INFILTRATING

EVOLUTIONARY

REVERSAL

PROCCES





Messages

Dad

Edit

Dad... I got my girlfriend pregnant...

WHAT?!?!?!?!?!?

Nah I'm just kidding. I just failed my Bio exam

OH THANK GOD!!!



Send