

JEAN MAYER  
USDA  
HUMAN  
NUTRITION  
RESEARCH  
CENTER ON  
AGING

HNRCA



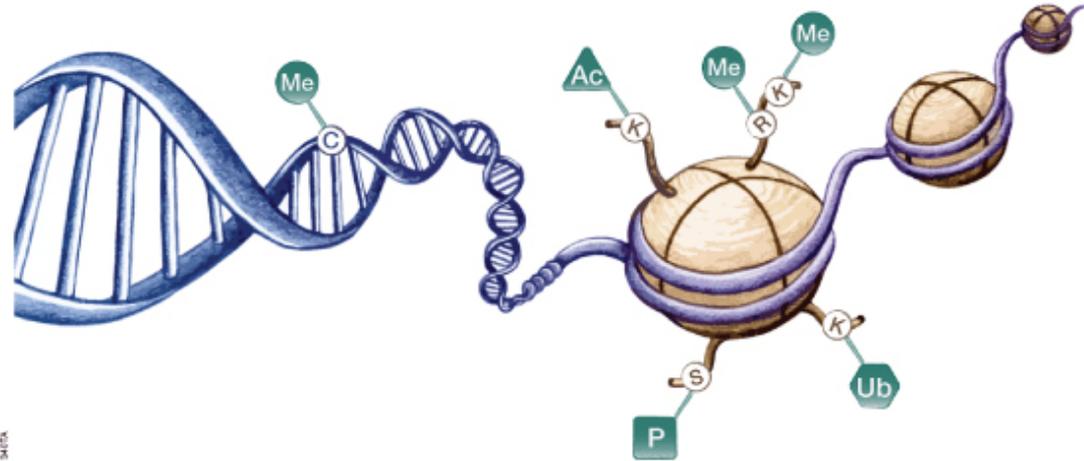
**Jose M Ordovas**  
**JM-USDA-HNRCA at Tufts**

***Genotypes and  
Disease Risk: What Do  
We Currently Know  
about Nutrition and  
Epigenetics?***

**December, 2017**

**Tufts**  
UNIVERSITY

# Genome versus Epigenome



The total length of the human genome is over **3 billion base pairs**. The genome is organized into 22 paired chromosomes, plus the X chromosome (one in males, two in females) and, in males only, one Y chromosome.

## Genetic Variation

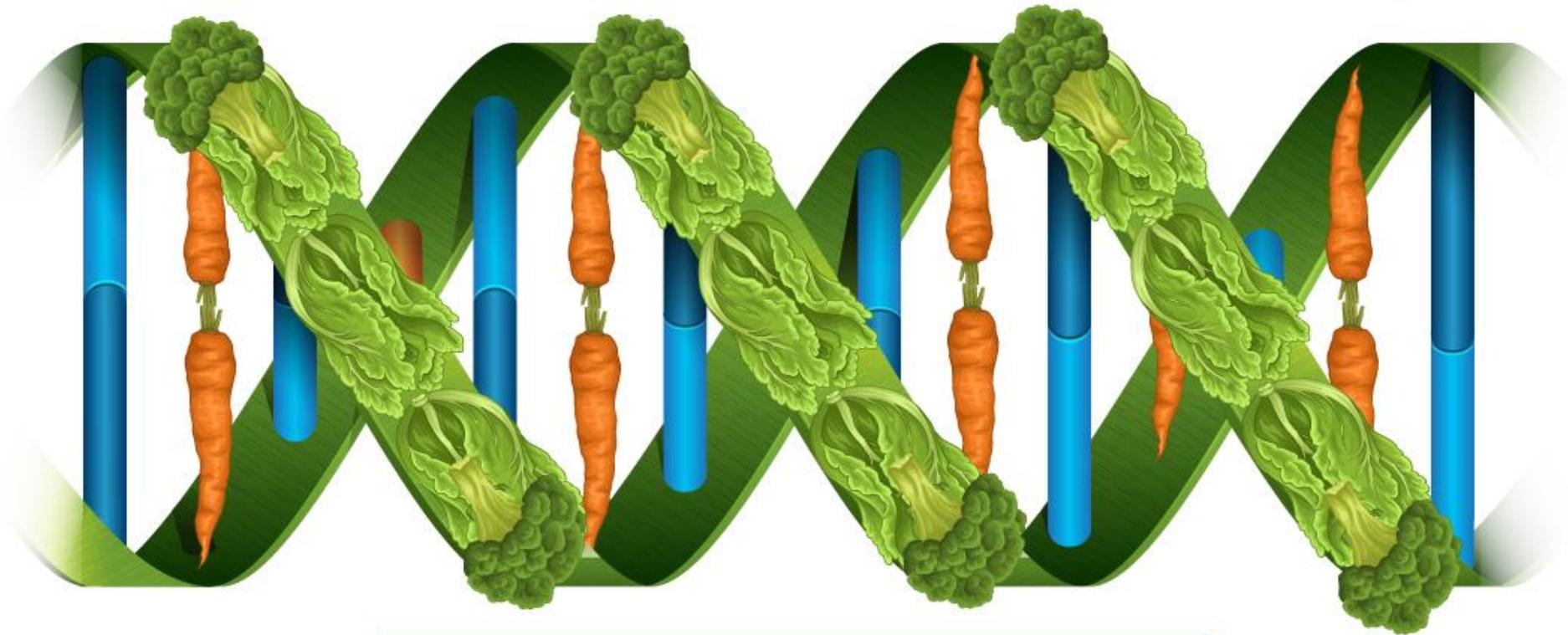
Last Updated: Build 150 (Feb 3, 2017)

RefSNP Count: **325.7 Million**

SubSNP Count: 907.2 Million

Residing within the human genome are approximately **30 million CpG dinucleotides** which are unmethylated, hemi-methylated or abundantly methylated; varying according to region on chromosome, alleles, type of cell or phase of development

# NUTRITION



# GENOME



# The CDC Recognizes Newborn Screening in the "Ten Great Public Health Achievements"



*Newborn Screening:*  
Saves or Improves  
the Lives of Over  
**12,000**  
Babies a Year!

## PARENT EDUCATION

Obstetrician explains newborn screening process to expectant parents.

## HOSPITAL SCREENING

Hospital nurse tests baby's hearing and heart, and collects blood from baby's heel.

## LAB SCREENING

State public health lab tests baby's blood for at least 29 genetic conditions.

## NORMAL RESULTS

Pediatrician reviews test results with parents at baby's first wellness visit.

## POSITIVE RESULTS

Health Department staff calls pediatrician/parents to request re-testing baby. Medical specialists perform tests and make diagnosis.

## FOLLOW-UP

Medical specialists and pediatrician develop a treatment plan and guide parents in caring for baby.

The American College of Medical Genetics estimates that about **12,000** of the **4.2 million** babies born each year in the United States will be identified with one of the conditions for which early intervention will have a significant impact on the child's life and long-term health."



# The Economic Benefits of Newborn Screening in the United States

The overall health benefits of treating infants for inherited disorders are clear. But there's a strong economic case for screening as well. Scott Grosse, PhD, a research economist with the CDC, has studied the economic benefits, using congenital hypothyroidism (CH) as a model.

CH is one of the most common conditions detected by newborn screening: about 4,000 infants each year in the United States are found to have it. Left untreated, CH can cause cognitive problems and even severe intellectual disability in many of these babies.

## BENEFITS

Each year

**1,170 INFANTS**

born with CH are saved from negative cognitive outcomes

**160** would have had

intellectual disability: **IQ < 70**

**1 IQ point = 1%-2%** rise in earnings

Each **IQ < 70 = \$1.3 MILLION COST**

in care and lost productivity

**160** people x **\$1.3 MILLION =**

**\$200+ MILLION**

in care and lost productivity

## CH screening saves

**14,900 IQ points**

each year

**14,900 IQ points =**

**\$200 MILLION GAINED**

in lifetime earnings

**\$200 MILLION + \$200 MILLION =**

**\$400 MILLION**

in costs avoided and potential realized

## COSTS

**\$35**

cost of CH screening per infant

**\$20 MILLION**

cost of an annual nationwide CH screening program

**\$400 MILLION** in gains and avoided costs - **\$20 MILLION** in cost of screening =  
**\$380 MILLION benefit**

*Benefits of CH Screening =*  
**20x the costs**

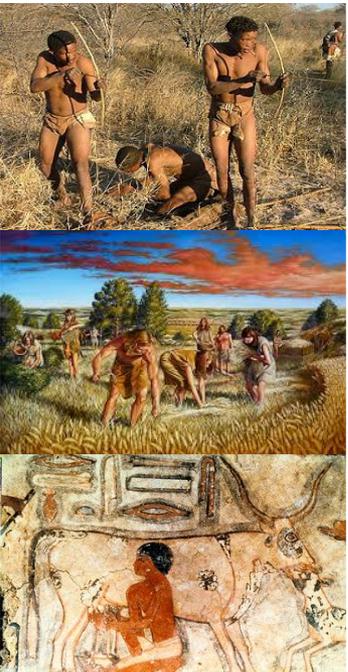
If undiagnosed and untreated, these disorders can cause irreversible mental retardation (ranging from mild to severe), physical disability, neurological damage and even fatality.



**Medical Foods:** Annual costs range from \$2,254 for an infant to almost \$25,000 for an adult male or pregnant woman.

# POSITIVE SELECTION IN THE HUMAN GENOME

Correlation coefficients of allele frequencies at specific gene variants with economic-cultural type



LCT - 13910T	APOE e4	ADH1B 48His
	R= 0.557 P= 0.000	
	R=-0.327 P= 0.007	
R= 0.463 P= 0.003		R=-0.376 P= 0.006

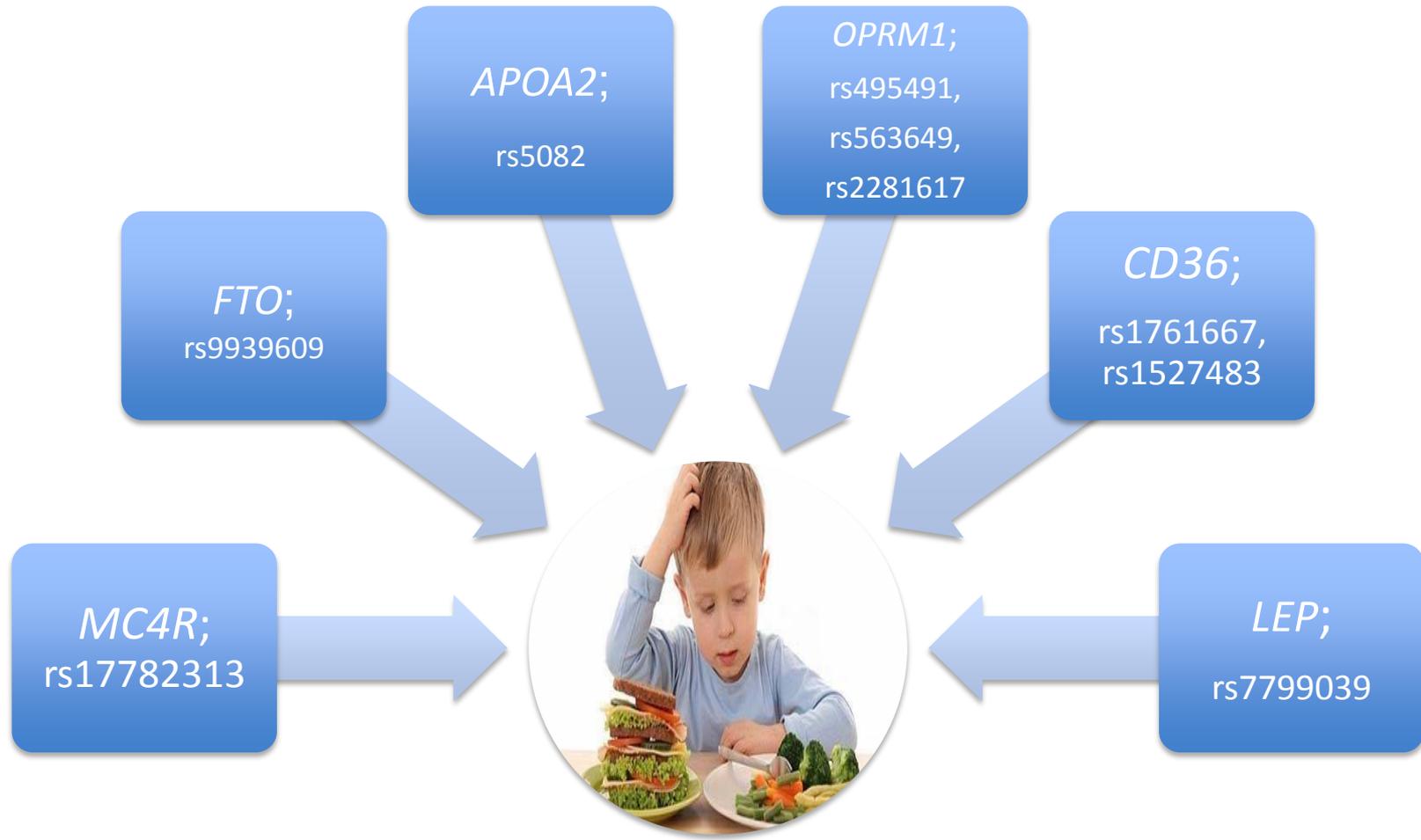
Correlation coefficients of allele frequencies at specific gene variants with pathogen load

	G6PD	ADH1B 48His
Malaria 	R= 0.520 P= 0.000	
Schistosomiasis 	R= 0.524 P= 0.000	
Filariasis 	R= 0.452 P= 0.000	R= 0.821 P= 0.001

Nutrition-related economic/cultural environment and Pathogens had a significant influence over the shaping and evolution of the human genome



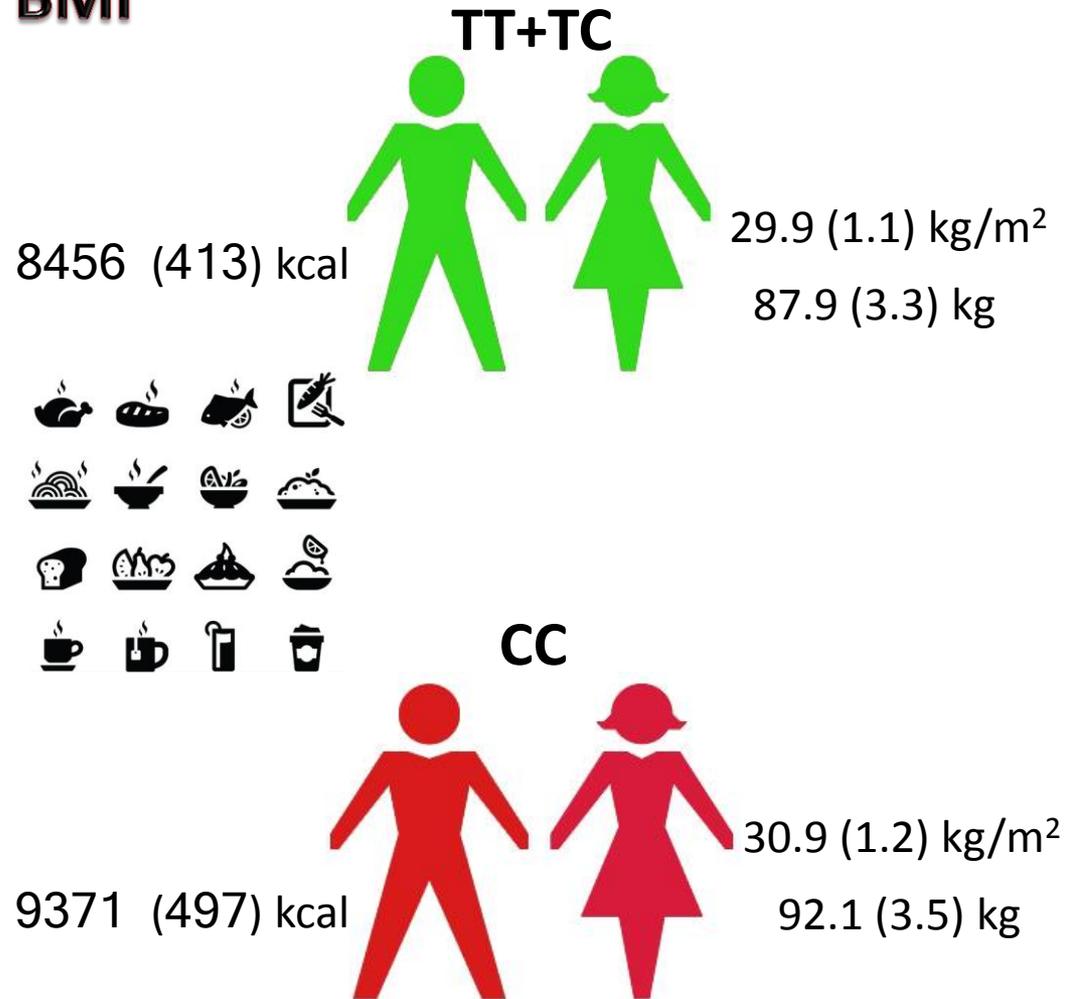
# Why some like it fatty (or not)?



**General characteristics of the study population.<sup>a</sup>**

	Men	Women
n	514	564
Age, years	49.1 (16.1)	48.1 (16.3)
Weight, kg <sup>b</sup>	90.5 (16.4)	75.9 (17.1)
Height, m <sup>b</sup>	1.78 (0.72)	1.65 (0.68)
BMI, kg/m <sup>2</sup>	28.5 (4.9)	28.0 (6.2)
Waist circumference, m <sup>b</sup>	1.00 (0.14)	0.92 (0.75)
Hip circumference, m <sup>b</sup>	1.05 (0.09)	1.08 (0.14)
Cholesterol, mmol/L	4.91 (0.97)	4.96 (1.04)
LDL cholesterol, mmol/L <sup>b</sup>	3.19 (0.79)	3.10 (0.83)
HDL cholesterol, mmol/L <sup>b</sup>	1.08 (0.25)	1.35 (0.36)
Triglycerides, mmol/L <sup>b</sup>	1.70 (1.25)	1.41 (0.93)
VLDL size, nm	51.25 (7.32)	51.17 (7.50)
LDL size, nm <sup>b</sup>	20.48 (0.78)	21.10 (0.87)
HDL size, nm <sup>b</sup>	8.65 (0.38)	9.02 (0.44)
Fasting glucose, mmol/L <sup>b</sup>	5.84 (1.10)	5.43 (0.88)
Energy intake, KJ/day <sup>b</sup>	9994 (3858)	7261 (2684)
Total fat, g/day <sup>b</sup>	97.2 (43.5)	68.1 (30.4)
SATFAT, g/day <sup>b</sup>	33.0 (15.9)	22.6 (10.8)
MUFA, g/day <sup>b</sup>	36.9 (16.8)	25.3 (11.5)
PUFA, g/day <sup>b</sup>	19.9 (9.5)	15.2 (7.3)
Proteins, g/day <sup>b</sup>	94.4 (39.9)	68.1 (26.6)
Carbohydrates, g/day <sup>b</sup>	279.8 (112.9)	218.4 (87.6)
Current smokers, n (%)	39 (7.6)	42 (7.5)
Past smokers, n (%) <sup>a</sup>	135 (26.3)	100 (17.8)
Current drinkers, n (%)	254 (49.4)	291 (51.6)
Diabetes or high blood sugar, n (%)	34 (6.6)	52 (9.2)
Heart attack, n (%) <sup>b</sup>	25 (4.7)	5 (0.9)
Stroke, n (%)	5 (1.0)	3 (0.5)
Obesity, n (%)	167 (32.5)	192 (34.0)
APOA2 -265T>C polymorphism, n (%)		
TT	188 (36.6)	213 (37.8)
TC	251 (48.8)	261 (46.3)
CC	75 (14.6)	90 (16.0)

# Genotype-Phenotype Associations: APOA2 m265T>C, caloric intake and BMI



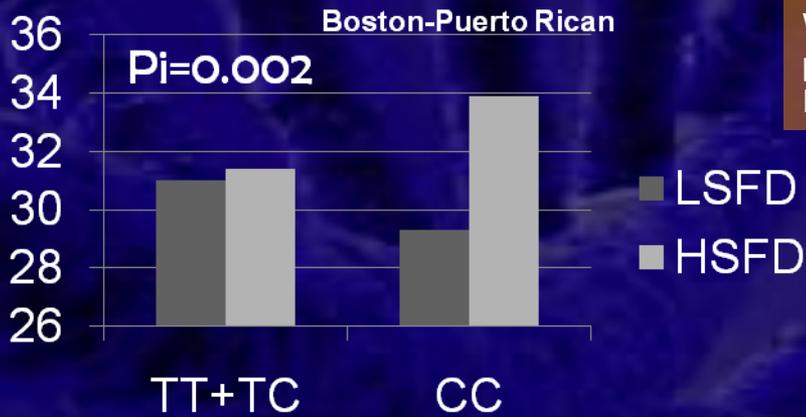
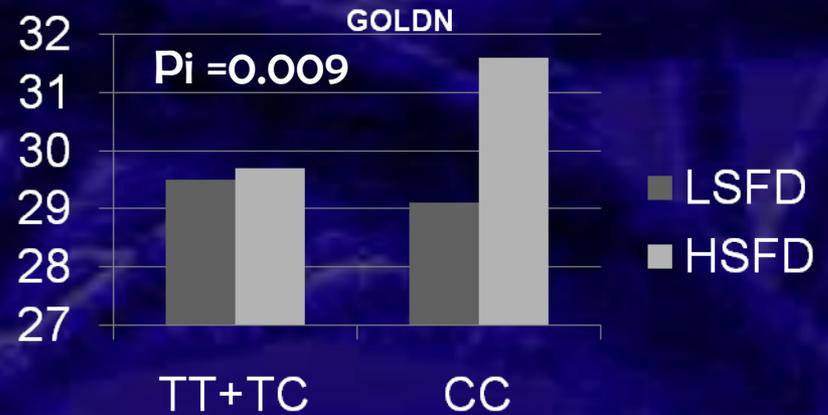
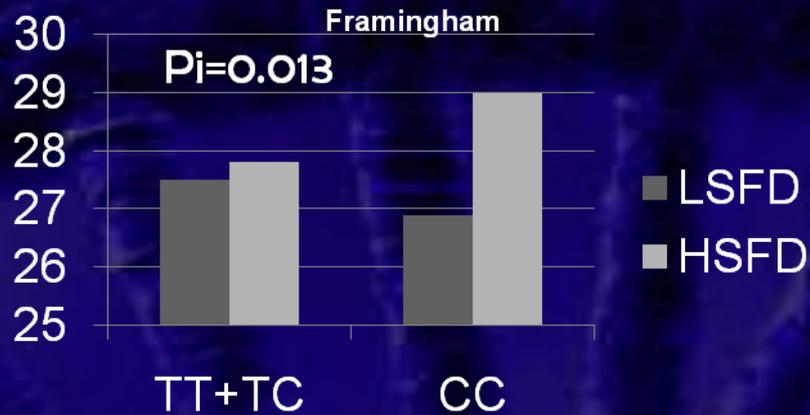
Estimated means and p values were adjusted for sex, tobacco smoking, alcohol consumption, diabetes, and CVD

Corella D, et al. Clin Chem. 2007;53:1144-52;

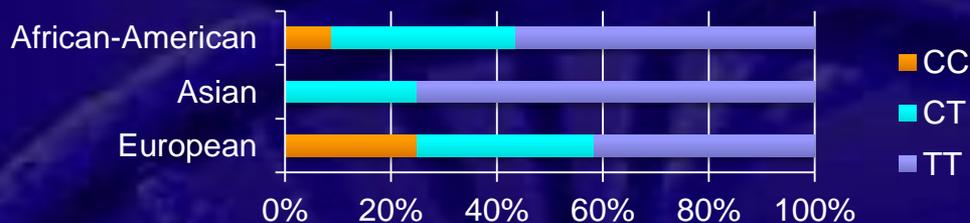
<sup>a</sup> Data are mean (SD) except where noted.

<sup>b</sup> Statistically significant differences between men and women.

# GENOTYPE-PHENOTYPE ASSOCIATIONS AND INTERACTIONS: APOA2 M265T>C, SATURATED FAT AND BMI

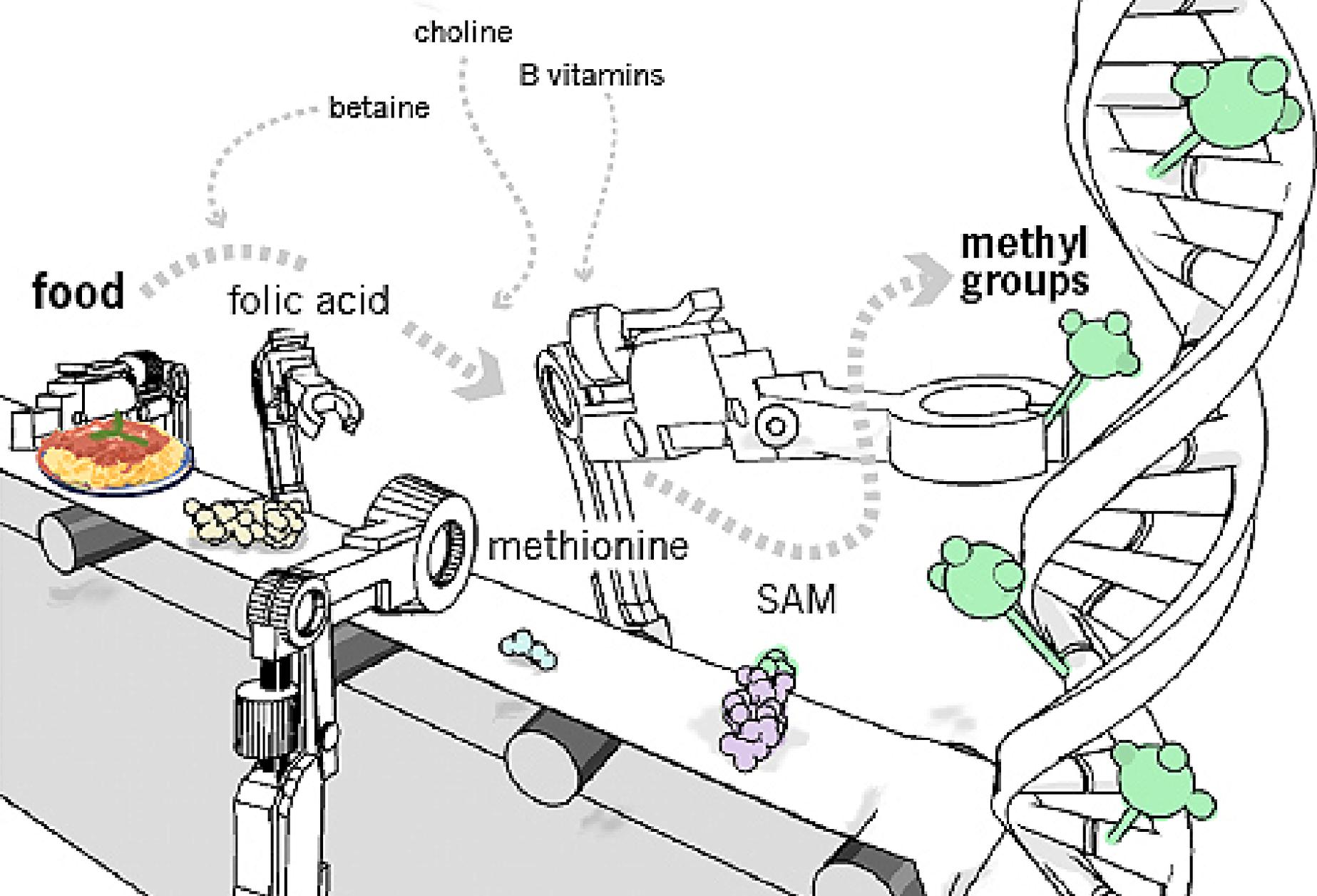


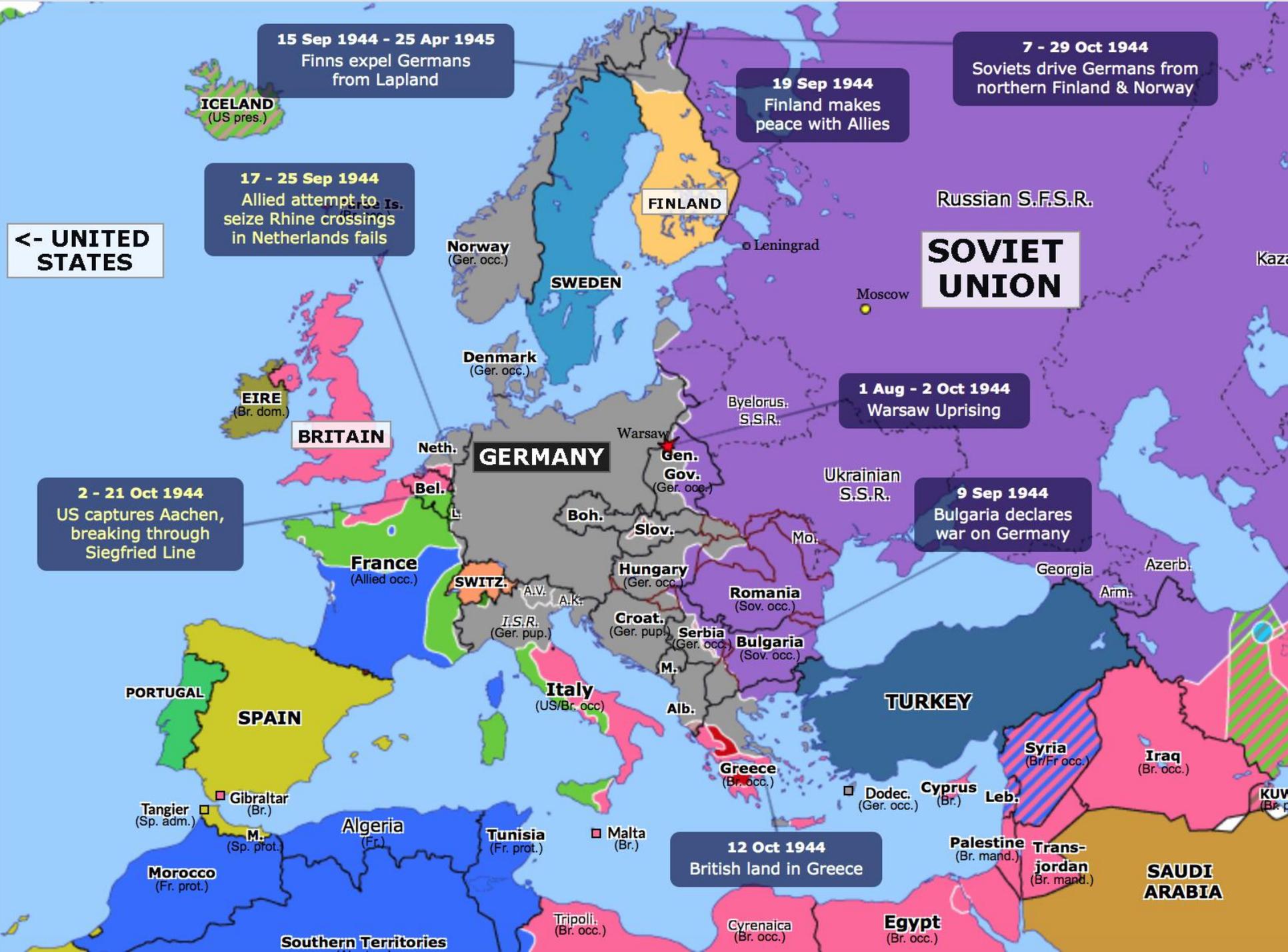
We have replicated a gene-dietary fat interaction between a functional promoter SNP at the APOA2 locus and BMI in 6 independent Populations and 5 ethnicities across the World





# Epigenetics in Nutrition Research





**15 Sep 1944 - 25 Apr 1945**  
Finns expel Germans from Lapland

**7 - 29 Oct 1944**  
Soviets drive Germans from northern Finland & Norway

**19 Sep 1944**  
Finland makes peace with Allies

**17 - 25 Sep 1944**  
Allied attempt to seize Rhine crossings in Netherlands fails

**SOVIET UNION**

**<- UNITED STATES**

**2 - 21 Oct 1944**  
US captures Aachen, breaking through Siegfried Line

**1 Aug - 2 Oct 1944**  
Warsaw Uprising

**9 Sep 1944**  
Bulgaria declares war on Germany

**GERMANY**

**BRITAIN**

**12 Oct 1944**  
British land in Greece

**ICELAND**  
(US pres.)

**EIRE**  
(Br. dom.)

**France**  
(Allied occ.)

**Norway**  
(Ger. occ.)

**SWEDEN**

**Denmark**  
(Ger. occ.)

**FINLAND**

Leningrad

Moscow

Byelor. S.S.R.

Ukrainian S.S.R.

Neth.

Bel.

Warsaw  
Gen. Gov. (Ger. occ.)

Boh.

Slov.

Mo.

Hungary (Ger. occ.)

Romania (Sov. occ.)

SWITZ.

I.S.R. (Ger. pup.)

Croat. (Ger. pup.)

Serbia (Ger. occ.)

Bulgaria (Sov. occ.)

Georgia

Azerb.

Arm.

**PORTUGAL**

**SPAIN**

**Italy**  
(US/Br. occ.)

**TURKEY**

M.

Alb.

Greece (Br. occ.)

Dodec. (Ger. occ.)

Cyprus (Br.)

Syria (Br/Fr occ.)

Iraq (Br. occ.)

Tangier (Sp. adm.)

M. (Sp. prot.)

Algeria (Fr.)

Tunisia (Fr. prot.)

Malta (Br.)

Palestine (Br. mand.)

Trans-jordan (Br. mand.)

**Morocco**  
(Fr. prot.)

**Southern Territories**

Tripoli. (Br. occ.)

Cyrenaica (Br. occ.)

**Egypt**  
(Br. occ.)

**SAUDI ARABIA**

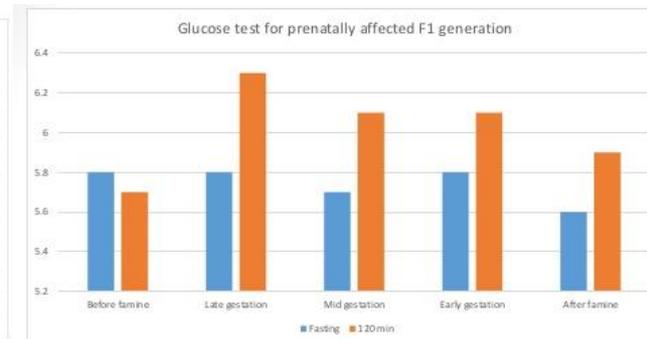
KUV (Br. p.)

# The Dutch Famine of 1944-45 (a.k.a. “Dutch Hunger Winter”)

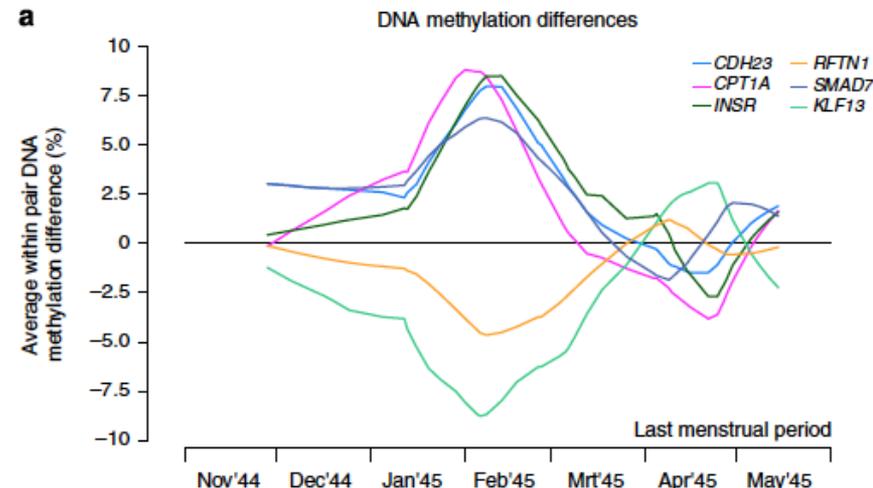
- Germany occupied parts of the Netherlands and prohibited food transport in Nov. 1944 until May 1945.
- Adult rations were as low as 400-800 calories/day
- 4.5 million people affected and the number of deaths have been estimated in 22,000.



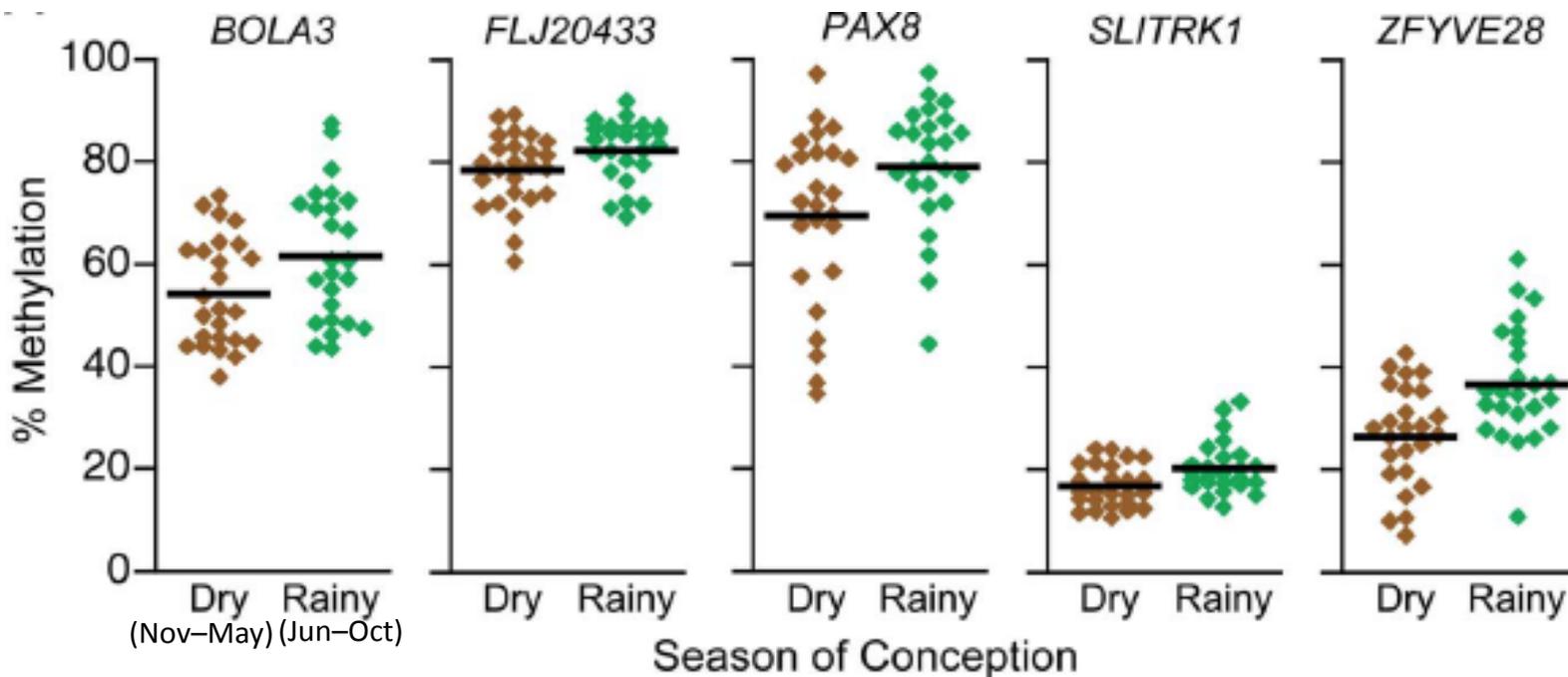
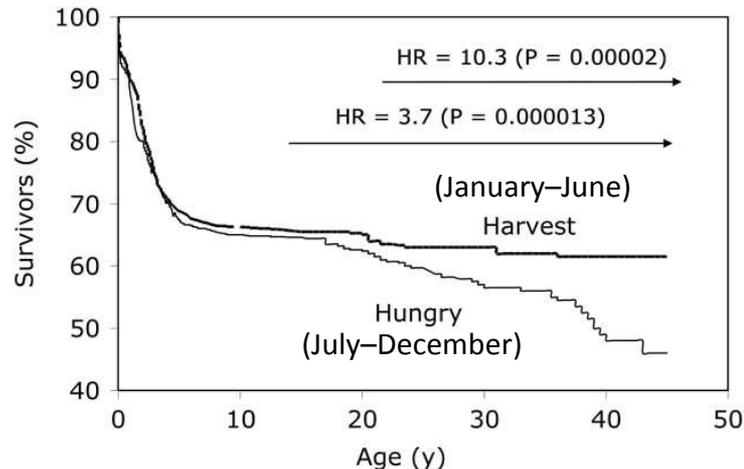
- F1 offspring affected during mid-gestation (May-Sept 1945) and late gestation (Feb-June 1945) had low birth weight. F1 offspring affected during early gestation had normal birth weight (Rooji, 2006)
- F1 adults exposed to famine had impaired glucose tolerance and developed insulin resistance. This was more prominent in F1 exposed during mid and late gestation. This increased their risk of developing type 2 diabetes. (Ravelli, 1988)



A lowess curve depicting the average within-pair difference (y axis) stratified by the estimate of the start of pregnancy (LMP; x axis). Each coloured line represents an individual prenatal malnutrition-associated differentially methylated regions (P-DMRs) (Tobi, 2014)



# Season of Conception in Rural Gambia Affects DNA Methylation at Putative Human Metastable Epialleles



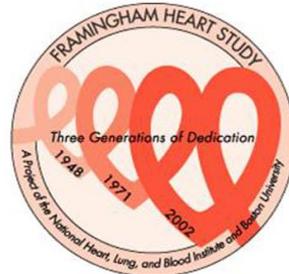
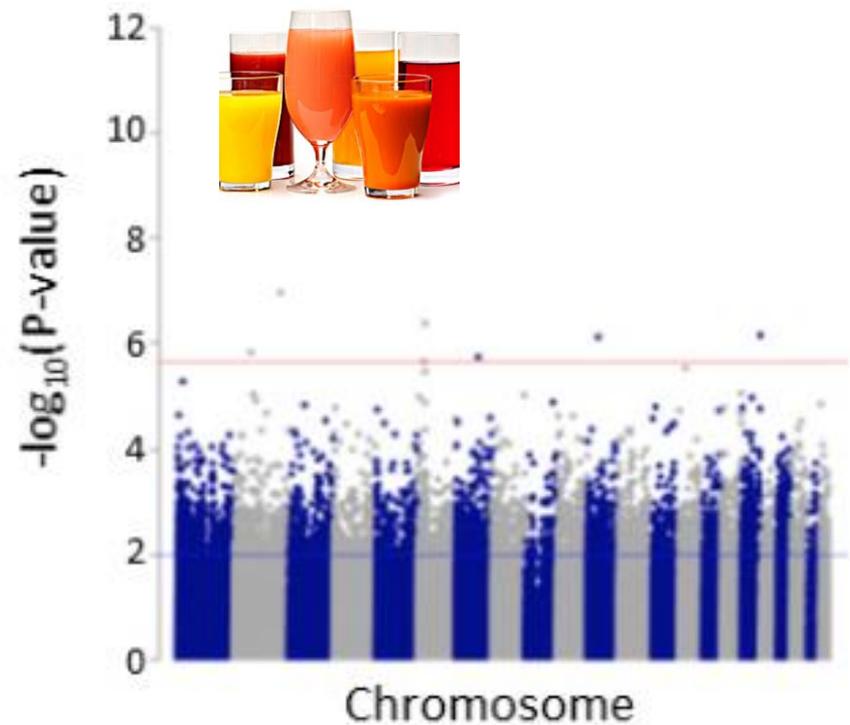
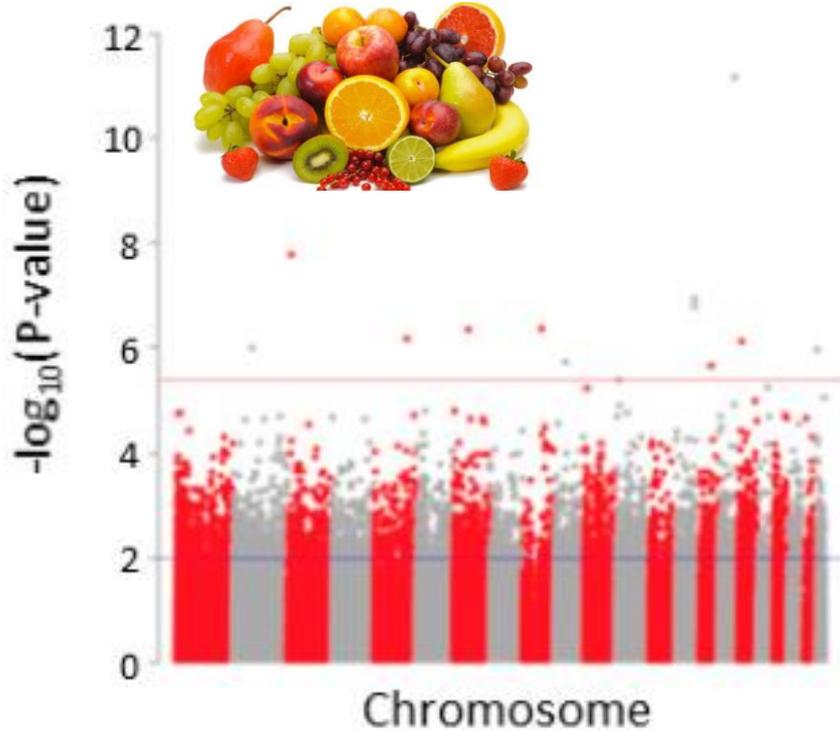


# *Whole Fruit Vs. Fruit Juice*

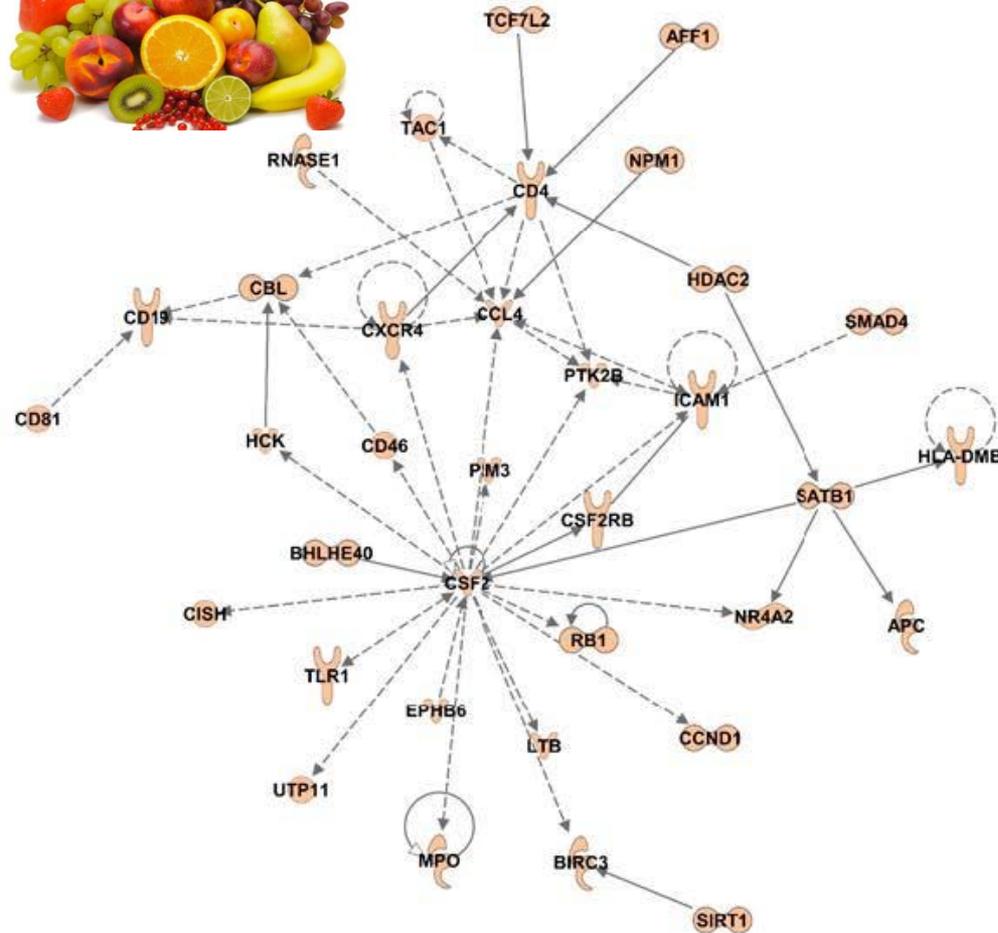
## **Whole fruits vs. Fruit Juices**

- Rich in fiber
- Low energy
- Vitamins and minerals are intact
- Deficient in fiber
- High energy (added sugar)
- Most of the vitamins and minerals are lost

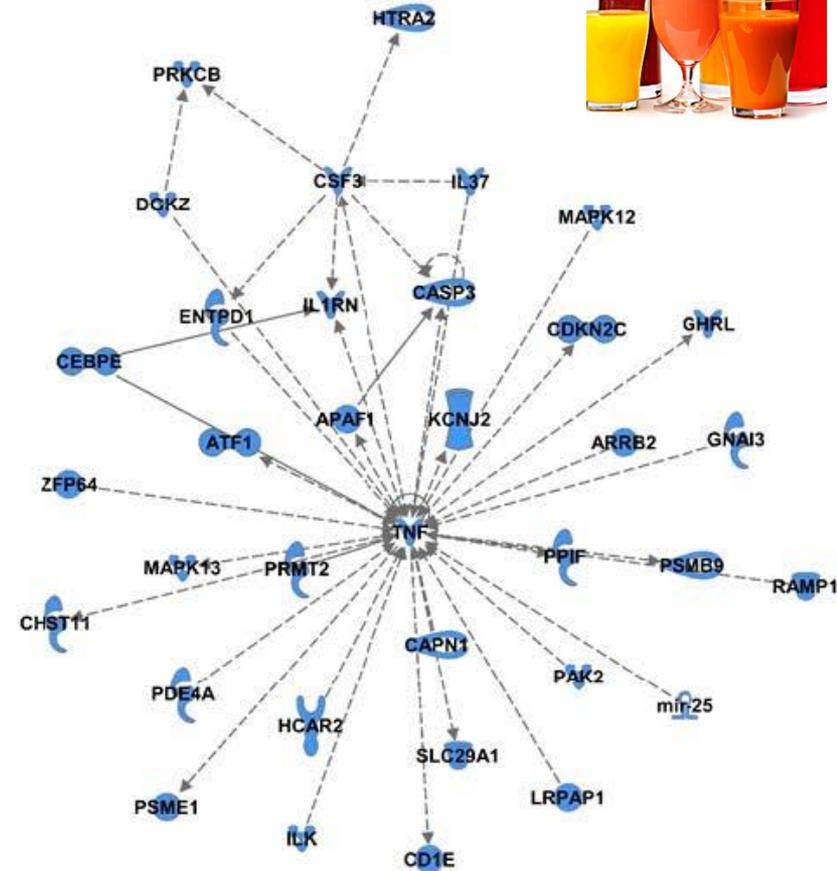
# Fruit and Juice Epigenetic Signatures Are Associated with Independent Immunoregulatory Pathways



# Fruit and Juice Epigenetic Signatures Are Associated with Independent Immunoregulatory Pathways



B



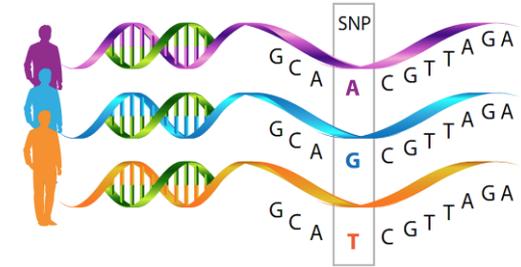
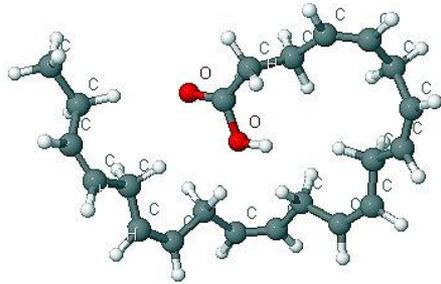
The fruit-specific epigenetic signature was enriched for only adaptive immune system genes, as well as those involved in cell cycle regulation and chromosome or telomere maintenance.

The juice-specific epigenetic signature was enriched for innate and adaptive immune system genes,

# The integration of Genetics and Epigenetics in Nutrition Research



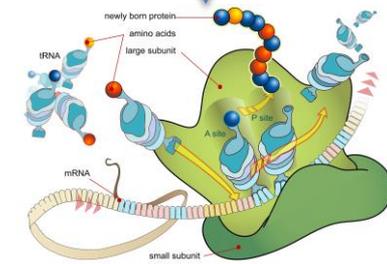
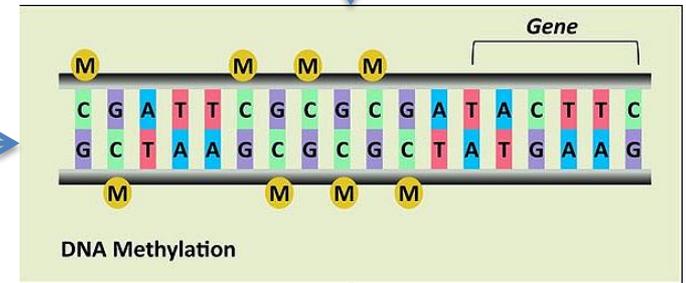
# Epigenetics Meets Genetics (and Nutrition)



- We found that over 80% of genetic variants at CpG sites (meSNPs) are meQTL loci ( $P$  value  $< 10^{-9}$ ), and meSNPs account for over two thirds of the strongest meQTL signals ( $P$  value  $< 10^{-200}$ ).

- Beyond direct effects on the methylation of the meSNP site, the CpG-disrupting allele of meSNPs were associated with lowered methylation of CpG sites located within 45 bp. The effect of meSNPs extends to as far as 10 kb and can contribute to the observed meQTL signals in the surrounding region, likely through correlated methylation patterns and linkage disequilibrium.

- Therefore, meSNPs are behind a large portion of observed meQTL signals and play a crucial role in the biological process linking genetic variation to epigenetic changes.



	LIPID PROFILE		
	DESIRABLE	BORDERLINE	HIGH RISK
Cholesterol	<200 mg/dl	200-239 mg/dl	240 mg/dl
Triglycerides	<150 mg/dl	150-199 mg/dl	200-499 mg/dl
HDL cholesterol	60 mg/dl	35-45 mg/dl	<35 mg/dl
LDL cholesterol	60-130 mg/dl	130-159 mg/dl	160-189 mg/dl
Cholesterol/HDL ratio	4.0	5.0	6.0

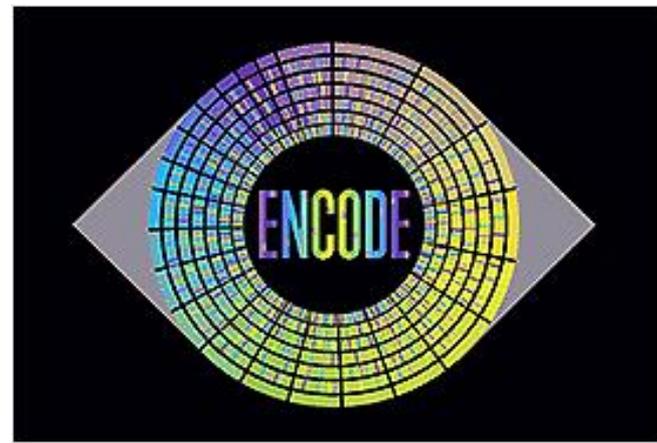
Welfare, Children, & Families  
A THREE CITY STUDY



**InCHIANTI**  
INVECCHIARE NEL CHIANTI



n=10,472

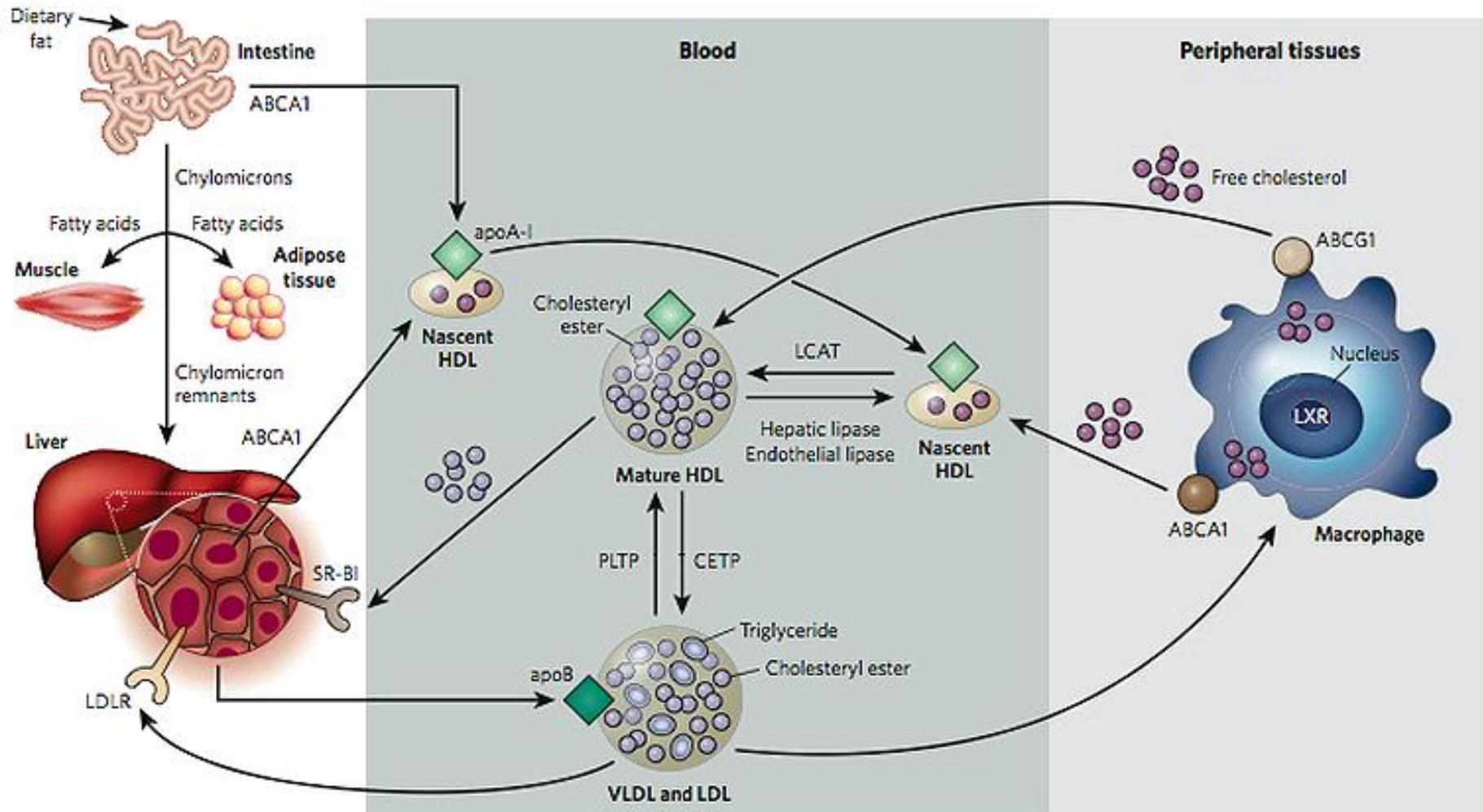
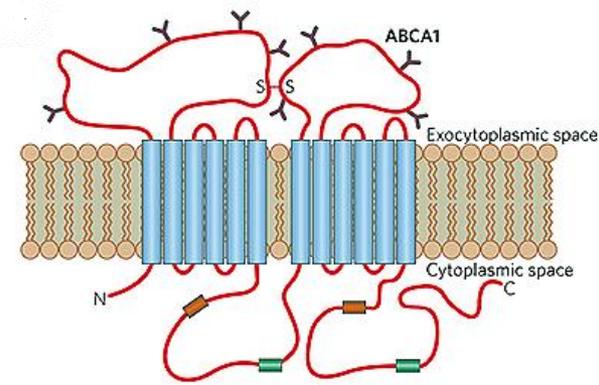


Harvard Medical School  
Brigham and Women's Hospital

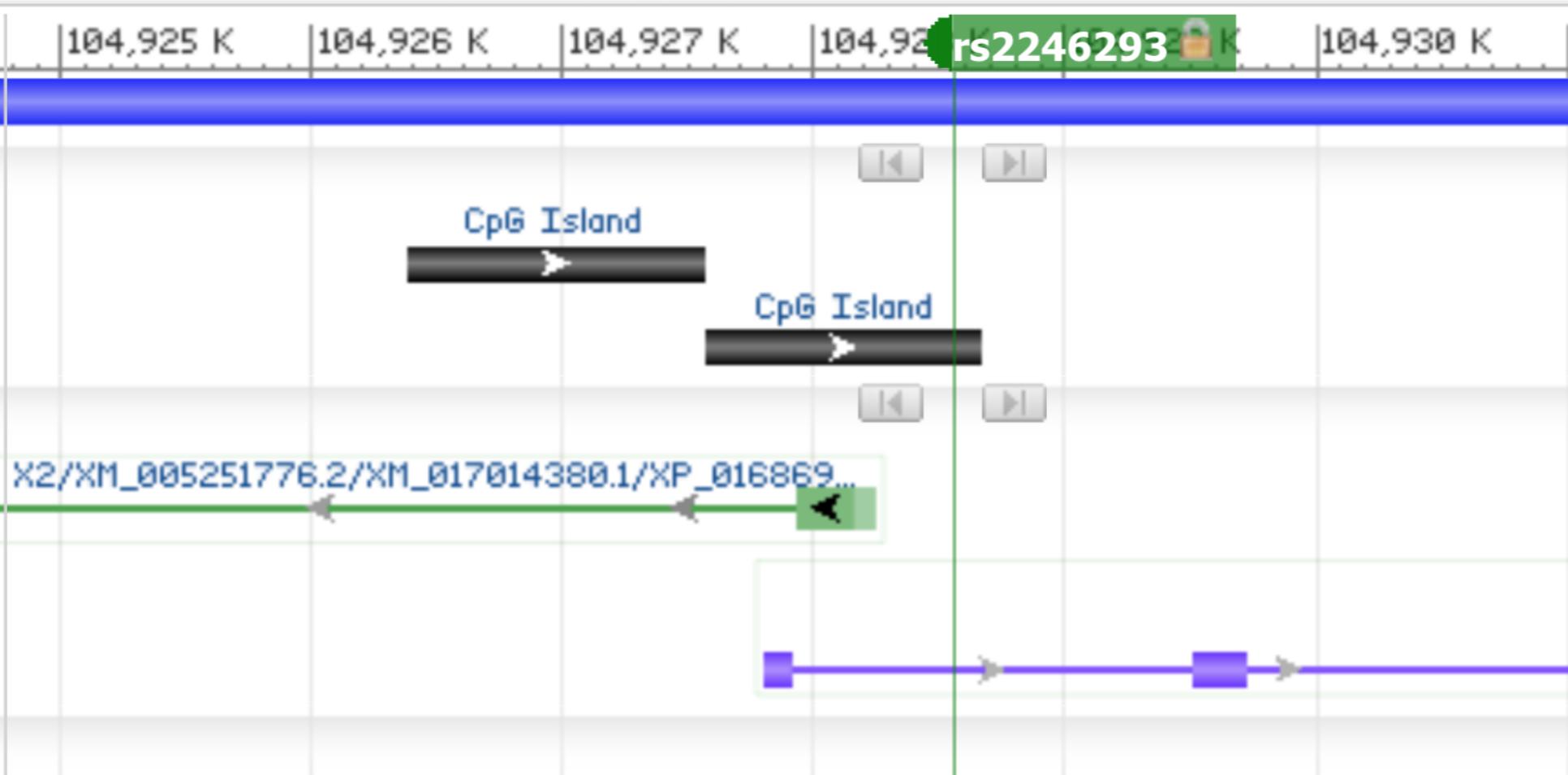
**Women's Health Study**

# ABCA1 and HDL

## Metabolism/Cholesterol Efflux

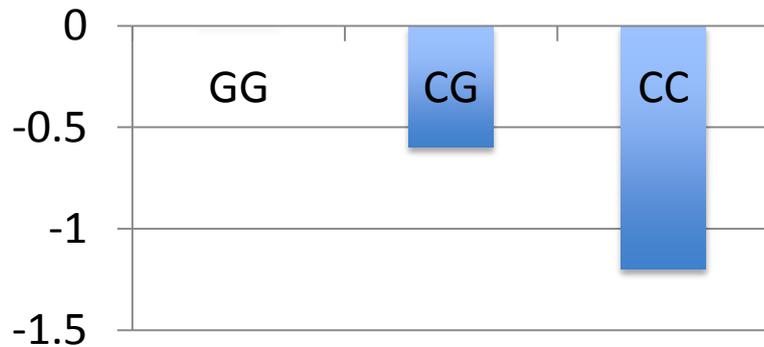


# ATP binding cassette subfamily A member 1 (*ABCA1*) rs2246293 SNP, cg14019050 CpG, circulating EPA and plasma HDLC levels

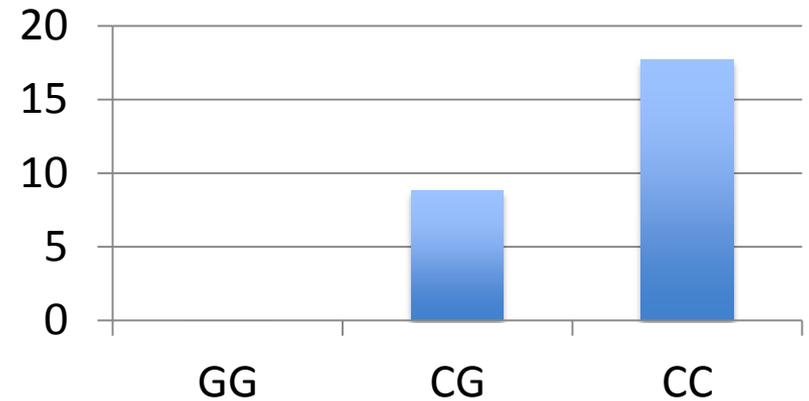


# ATP binding cassette subfamily A member 1 (ABCA1) rs2246293 SNP, cg14019050 CpG, circulating EPA and plasma HDLC levels

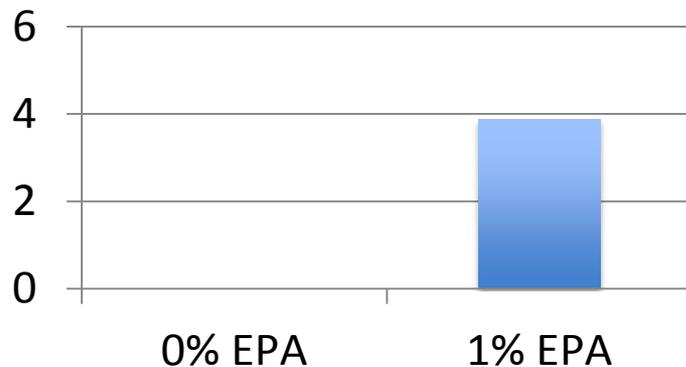
### Change HDLC (mg/dl)



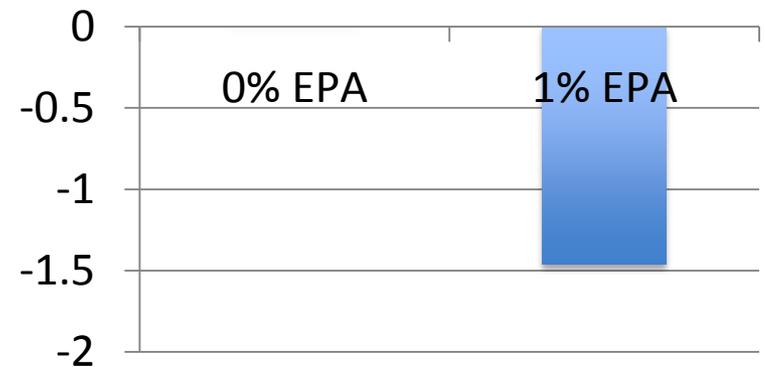
### Change % Methylation



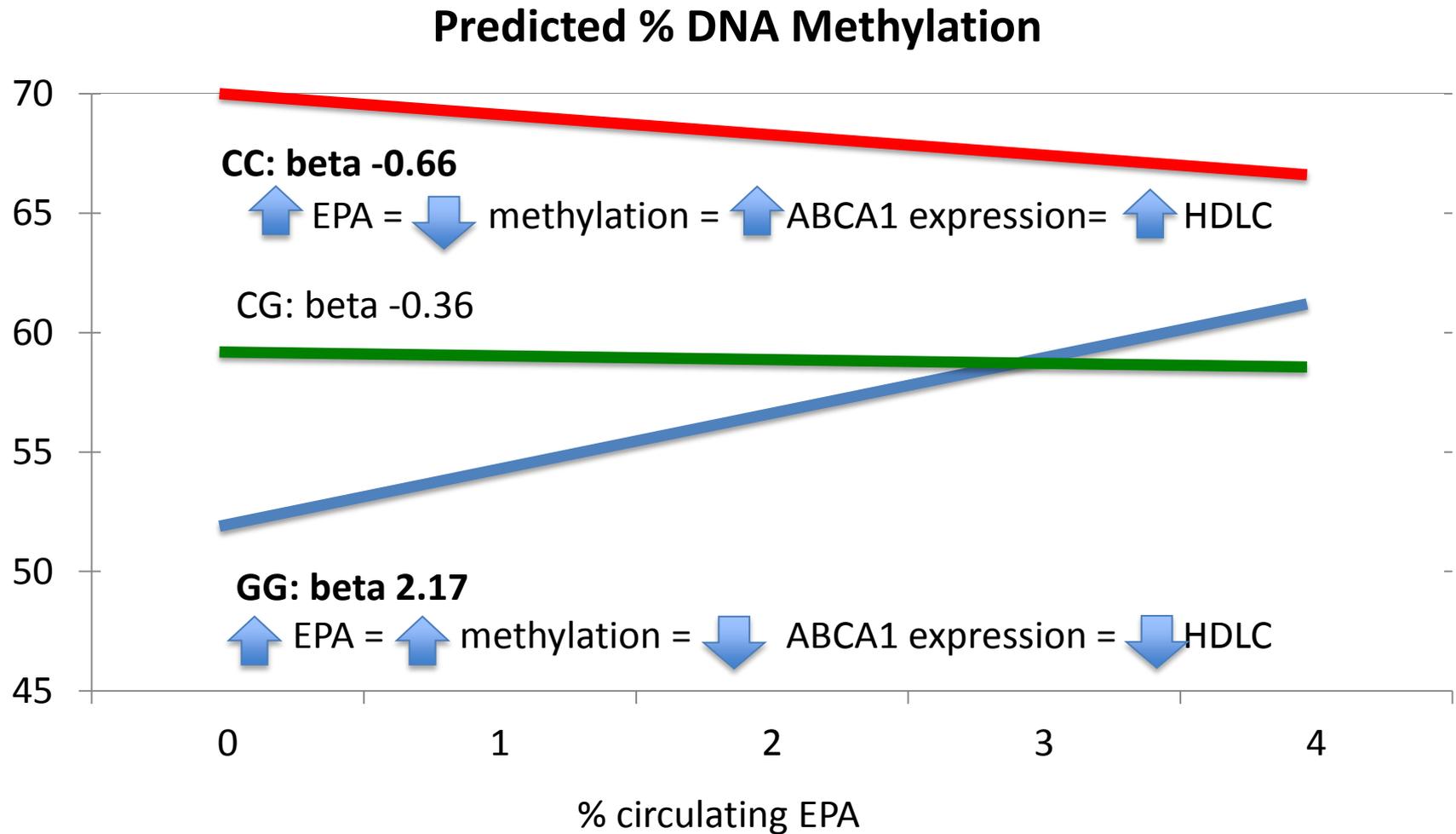
### Change HDLC (mg/dl)



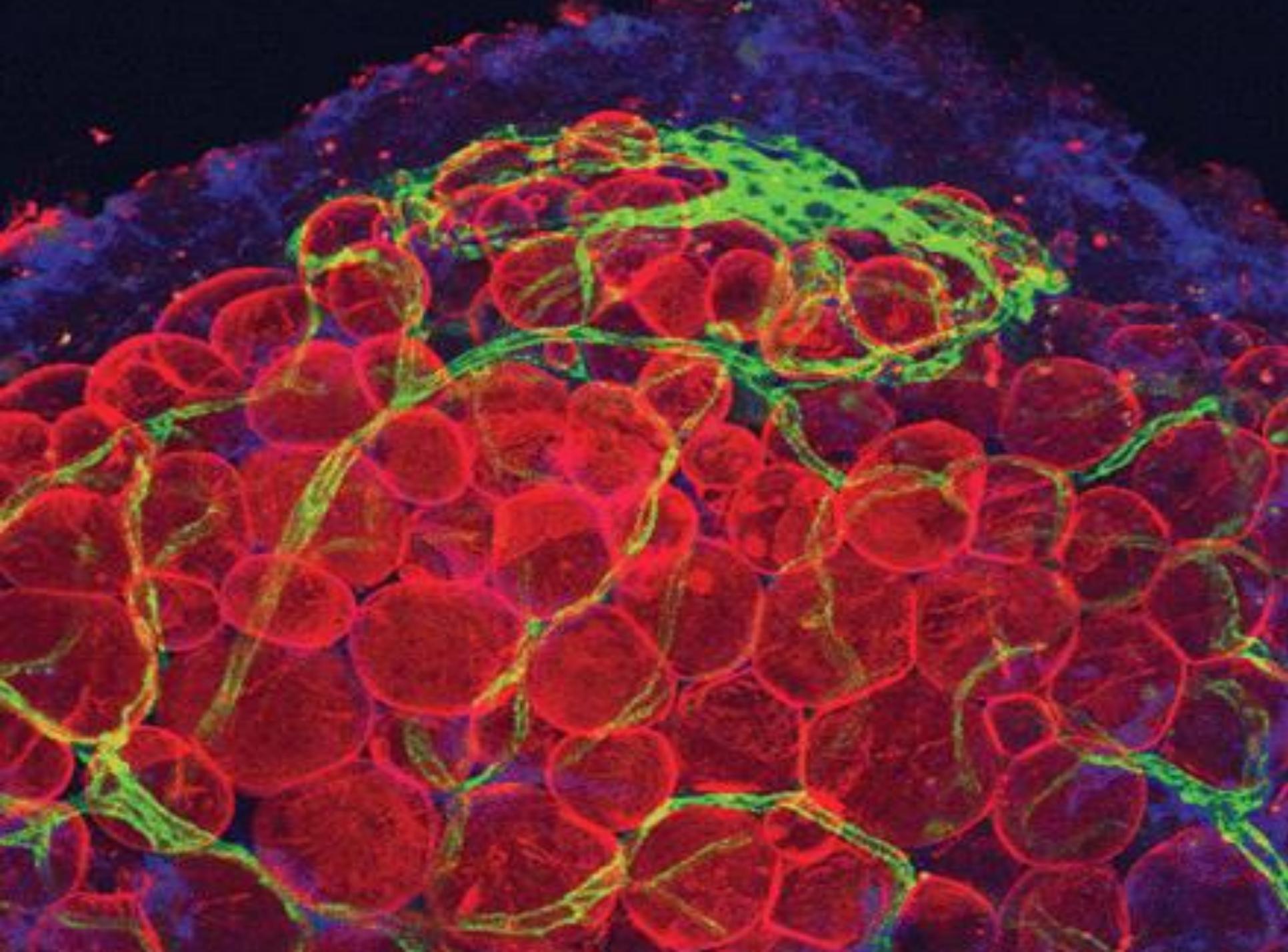
### Change % Methylation



# ATP binding cassette subfamily A member 1 (*ABCA1*) rs2246293 SNP, cg14019050 CpG, circulating EPA and plasma HDLC levels







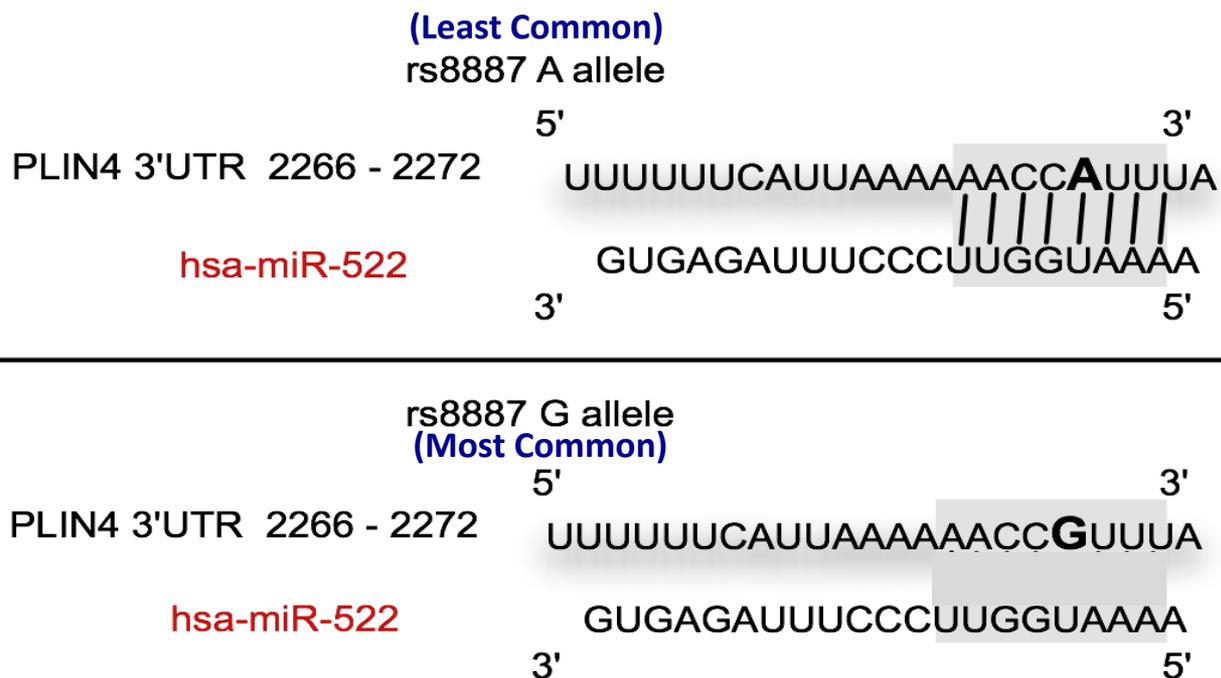
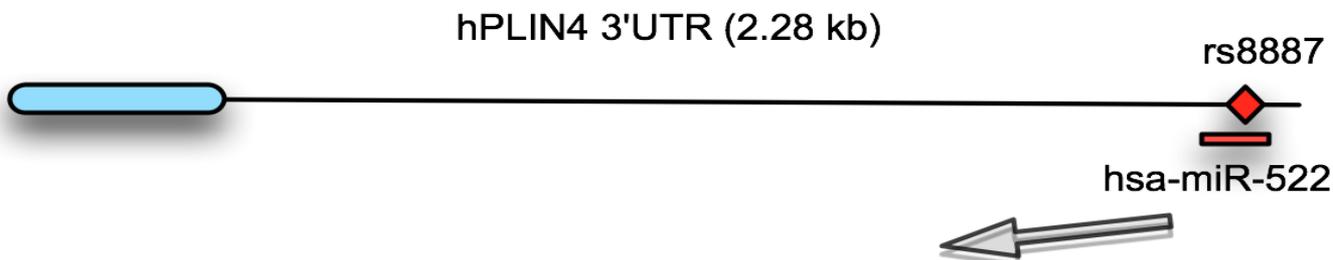
# Associations of PLIN4 rs8887 SNP in the FOS and GOLDN populations with Anthropometric traits - Main Effects

SNP	Phenotype	Gender	FOS				GOLDN				Meta-Analysis	
			Beta	Se	P	%Var	Beta	Se	P	%Var	z-score	P
rs8887	BMI	Both	0.614	0.221	0.005	0.396	.581	0.378	0.125	0.334	3.164	0.002
		Males	0.624	0.269	0.021		0.326	0.461	0.480		2.319	0.020
		Females	0.631	0.335	.060		0.704	0.586	0.230		2.231	0.026
	Weight	Both	3.106	1.431	0.030	0.200	2.374	2.271	0.296	0.081	2.387	0.017
		Males	2.917	1.980	0.141		0.584	3.146	0.853		1.332	0.183
		Females	3.524	2.010	0.080		3.465	3.242	0.286		2.050	0.040
	Waist	Both	0.423	0.221	0.056	0.157	0.252	0.440	0.567	0.023	1.911	0.056
		Males	0.483	0.269	0.073		-0.085	0.565	0.880		1.413	0.158
		Females	0.381	0.334	0.253		0.397	0.656	0.556		1.278	0.201
	VAT	Both	199.5	67.55	0.003							
		Males	345.4	100.5	0.001							
		Females	68.7	83.97	0.413							
SAT	Both	229.1	90.66	0.011								
	Males	180.4	106.2	0.090								
	Females	248.9	147.2	0.054								

**Men**  
**FOS (N = 1259) GOLDN (N = 481)**  
**Women**  
**FOS (N = 1352) GOLDN (N = 513)**

We can only speculate how lower expression of PLIN4 contributes to obesity-related phenotypes. For the related PLIN1, one study demonstrated that obesity and high lipolysis rates are independently associated with lower PLIN1 protein levels in women, whereas another demonstrated reduced levels of both PLIN1 mRNA and protein in obese compared to non-obese subjects. Conversely, the Plin1<sup>-/-</sup> mouse is characterized by a lean phenotype. These data suggest the role and regulation of the PAT gene family in human obesity may be different than in model organisms.

# PERILIPIN4 (PLIN4) rs8887 SNP creates a seed site for miR-522 and it is associated with BMI



# PLIN4 rs8887 SNP by diet interactions

SNP	Phenotype	PUFA	Gender	FOS				GOLDN				Meta-Analysis	
				Beta	Se	P	%Var	Beta	Se	P	%Var	z-score	P
rs8887	BMI	n3	Both	-0.469	0.391	0.230	0.48	-1.208	0.459	0.009	0.77	-2.447	0.014
			Males	-0.624	0.466	0.181		-1.158	0.542	0.033		-2.288	0.022
			Females	-0.438	0.625	0.484		-0.964	0.838	0.251		-1.216	0.224
	Weight	n3	Both	-3.867	2.522	0.125	0.30	-7.189		0.009	0.44	-2.707	0.007
			Males	-3.778	3.430	0.271		-7.080		0.057		-1.964	0.049
			Females	-4.553	3.750	0.225		-6.046		0.194		-1.728	0.084
	Waist	n3	Both	-0.461	0.391	0.238	0.23	-1.444	0.544	0.008	0.55	-2.445	0.015
			Males	-0.500	0.466	0.283		-1.230	0.672	0.068		-1.900	0.057
			Females	-0.421	0.621	0.498		-1.584	0.952	0.097		-1.483	0.138

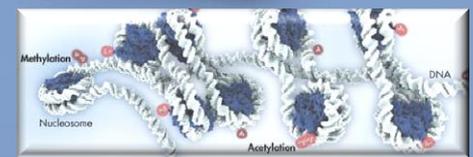
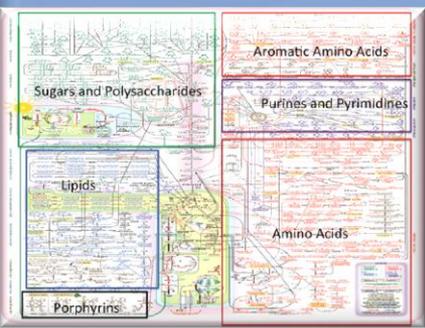
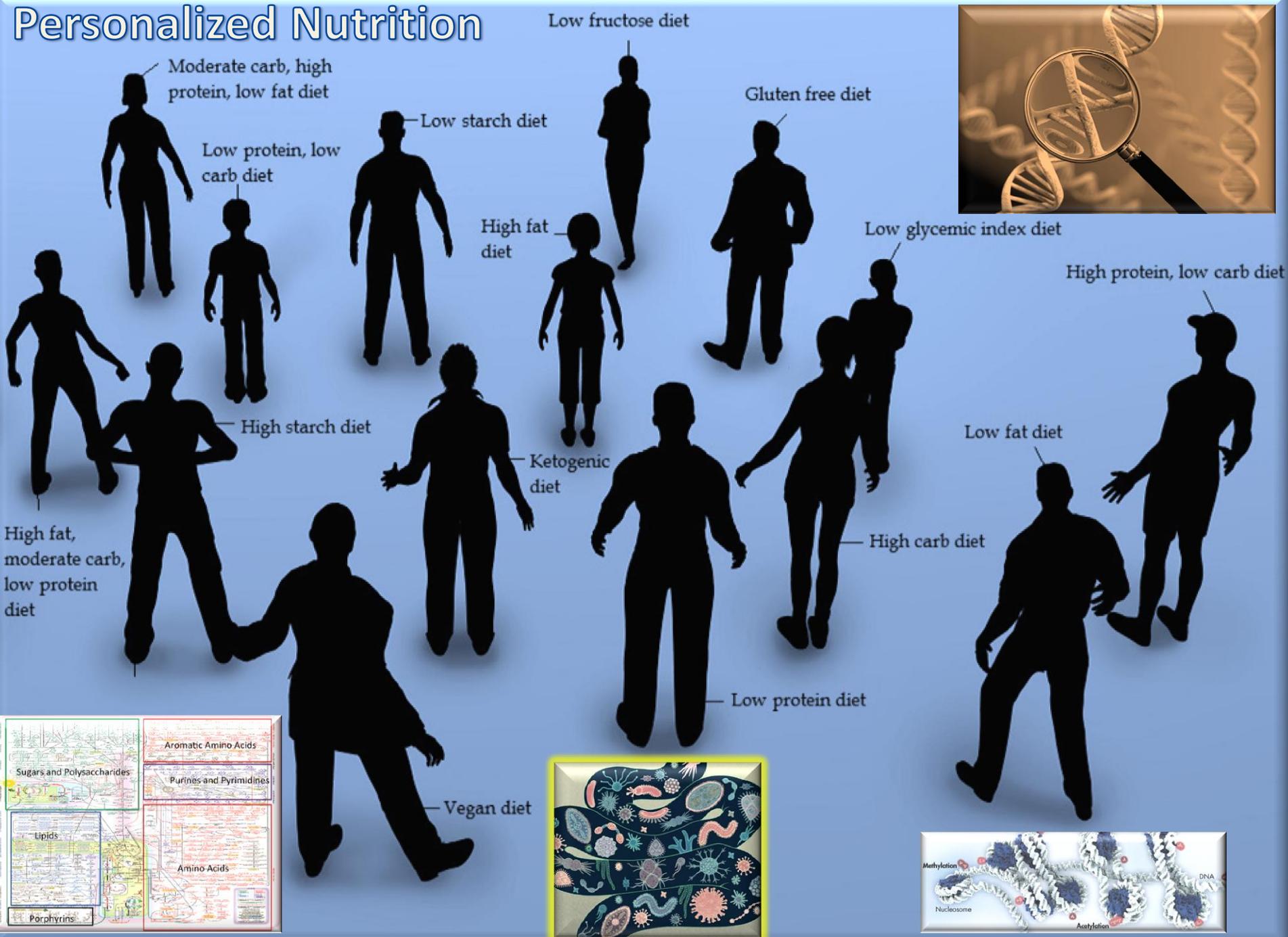
**A**



**G-like**

Our data indicate for rs8887 minor allele carriers that elevated intake of PUFA n3 results in decreasing anthropometrics compared to non-carriers. Due to what little is known of PLIN4 regulation, it is difficult to propose a mechanism by which the miR-522 rs8887 interaction together with PUFA n3 could modulate anthropometrics. It is likely that PUFA n3 alters PLIN4 expression through PPAR mediated pathways

# Personalized Nutrition



JEAN MAYER  
USDA  
HUMAN  
NUTRITION  
RESEARCH  
CENTER ON  
AGING

HNRC A



**Jose M Ordovas**

*Genotypes and Disease  
Risk: What Do We  
Currently Know about  
Nutrition and  
Epigenetics?*

Thank you

**Tufts**  
UNIVERSITY