

Glucose and Mitochondrial Function

Wednesday, March 11, 2015

Adam R. Wende, Ph.D.

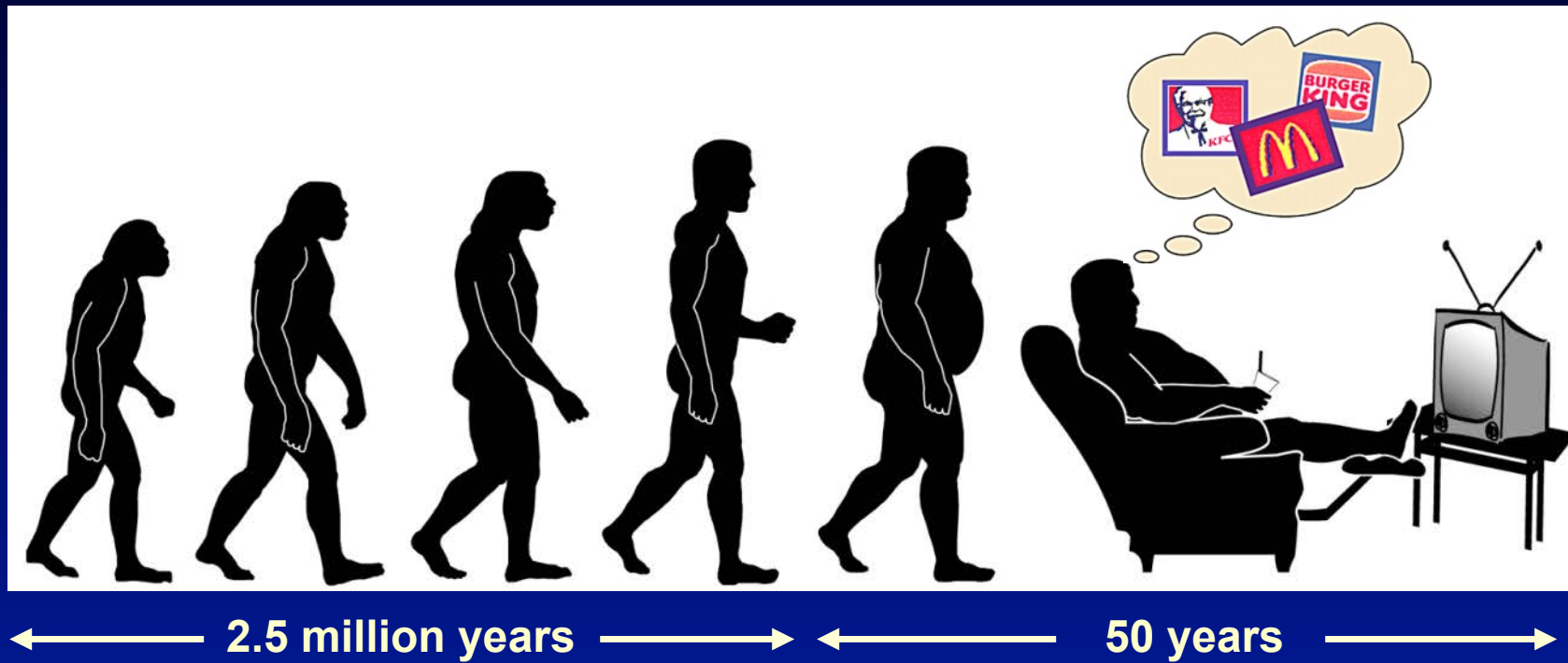
Assistant Professor
Inaugural Pittman Scholar
Division of Molecular and Cellular Pathology



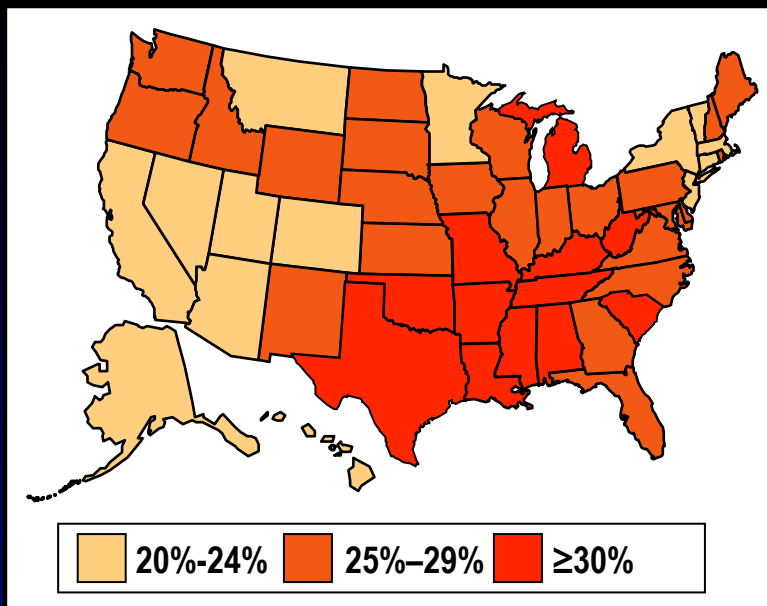
Outline

- Define the question and model to determine the connection between metabolism and diabetic heart disease.
- Identify the molecular mechanisms by which glucose directly alters molecular function using systems biology.
 - Transcriptomics
 - Proteomics
 - Metabolomics
 - Methylomics and epigenetics

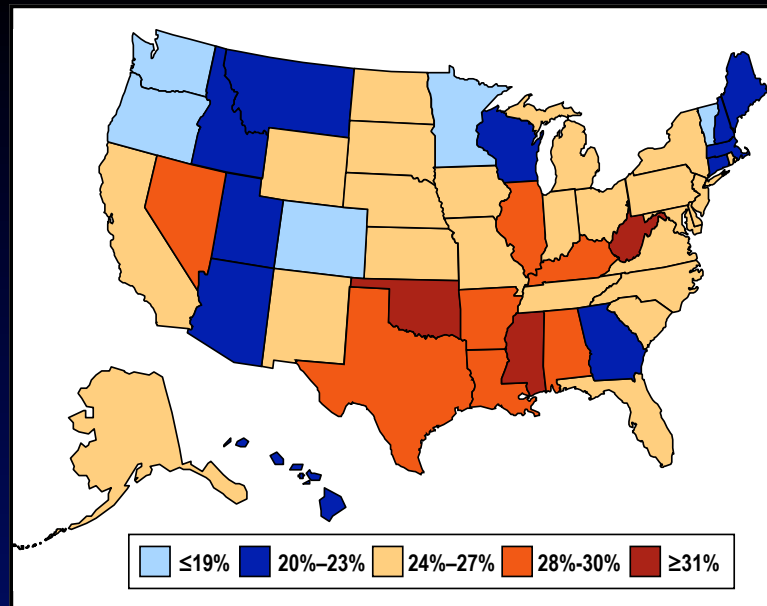
Obesity, Metabolic Syndrome, Diabetes, and Heart Failure



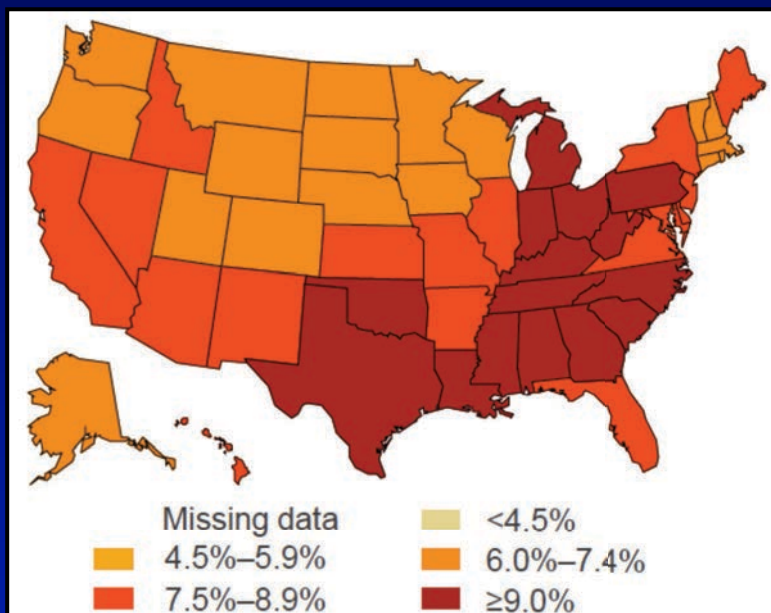
2010 – Obesity



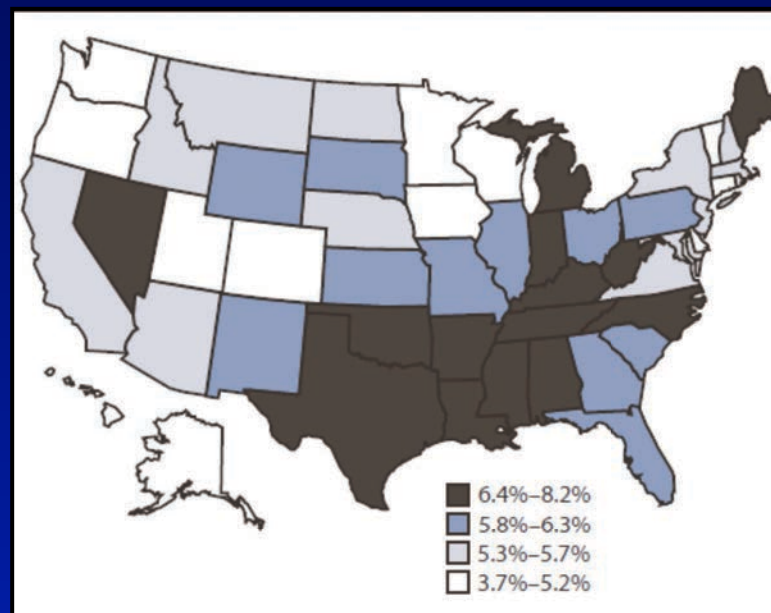
2010 – Physical Inactivity



2010 – Diabetes



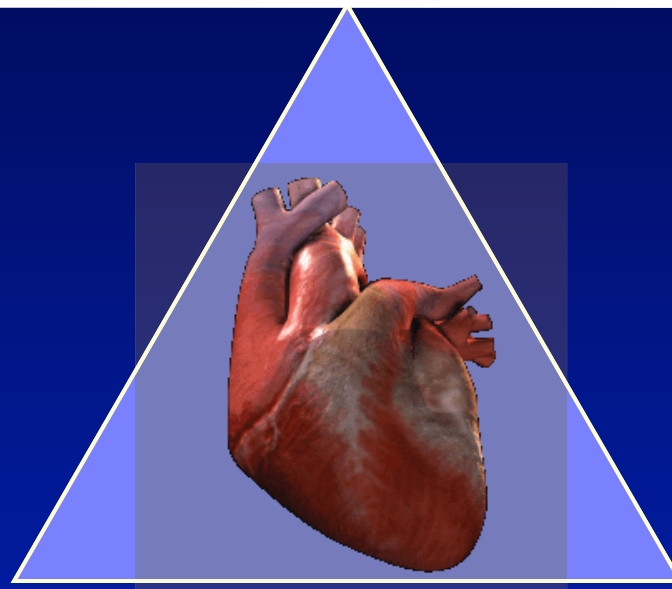
2010 – Heart Disease



Maintaining Cardiac Function Through Metabolic Substrate Balance

Glucose

Fatty Acids



Studies on Myocardial Metabolism*

IV. Myocardial Metabolism in Diabetes

I. UNGAR, M.D., M. GILBERT, M.D., A. SIEGEL, M.S., J. M. BLAIN, M.D. and R. J. BING, M.D.

lactate usage and a slight decline in that of pyruvate. There is no change in utilization of amino acids by the heart in both species. Myocardial glucose consumption is reduced in dog and man relative to the elevation in blood glucose concentration. The myocardial usage of ketones is slightly increased in diabetic hearts of patients and significantly elevated in the dog. The main difference concerns the utilization of fatty acids; this is significantly increased in the human heart but is unchanged in the dog. Whether this is due to a species difference or to differences in type and severity of diabetes is not clear. Anesthesia, which was used in the dogs, may have played some part.

Metabolic Substrate Utilization in the Heart

Table 2. Brief Overview of Myocardial Metabolism in Physiological and Pathophysiological Conditions

	MV _{o2}	Glucose Metabolism	Fatty Acid Metabolism
Aging	↑	↑	↓
Female sex	↑	↓	↑
Obesity	↑	—	↑
Diabetes, types 1 and 2	— ↑	↓	↑
Hypertension: LV hypertrophy	—	↑	↓
Dilated cardiomyopathy	—	↑	↓
Ischemia	↓	↑	↓

Point/Counterpoint - The Right Balance?

Cardiac Pathology via Diet-Induced Glucolipotoxicity

High Glycemic Carbs
 ↓ ω -3 PUFA
 ↑ Saturated Fat
 Positive Energy Balance

Obesity & Metabolic Syndrome

↑ Triglycerides, FFA
 ↑ LDL, ↓ HDL
 ↓ Adiponectin
 ↑ Inflammation
 ↑ Leptin & ↑ Insulin
 ↑ Blood pressure

Atherosclerosis

↑ Myocyte size
 ↑ Apoptosis
 ↑ Fibrosis
 Mitochondria Dysfunction



Cardiac Health via Dietary Protection

Low Glycemic Carbs
 ↑ ω -3 PUFA
 ↓ Saturated Fat
 Neutral Energy Balance

No Obesity & No Metabolic Syndrome

Normal Triglycerides, FFA
 ↓ LDL, ↑ HDL
 ↑ Adiponectin
 ↓ Inflammation
 ↓ Leptin & ↓ Insulin
 Normal Blood pressure



↓ Atherosclerosis
 Normal Myocyte Size
 ↓ Apoptosis
 Optimal Mitochondria Function



Heinrich Taegtmeier,
 MD, DPhil



William C. Stanley,
 PhD
 1957 - 2013

Diabetes and Metabolomics

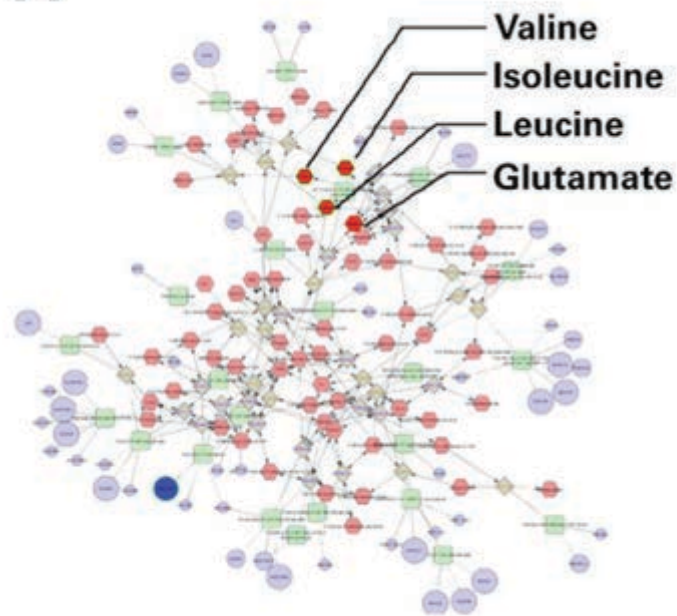
Diabetes. 2015 Mar;64(3):718-732.

Metabolomics and Diabetes: Analytical and Computational Approaches.

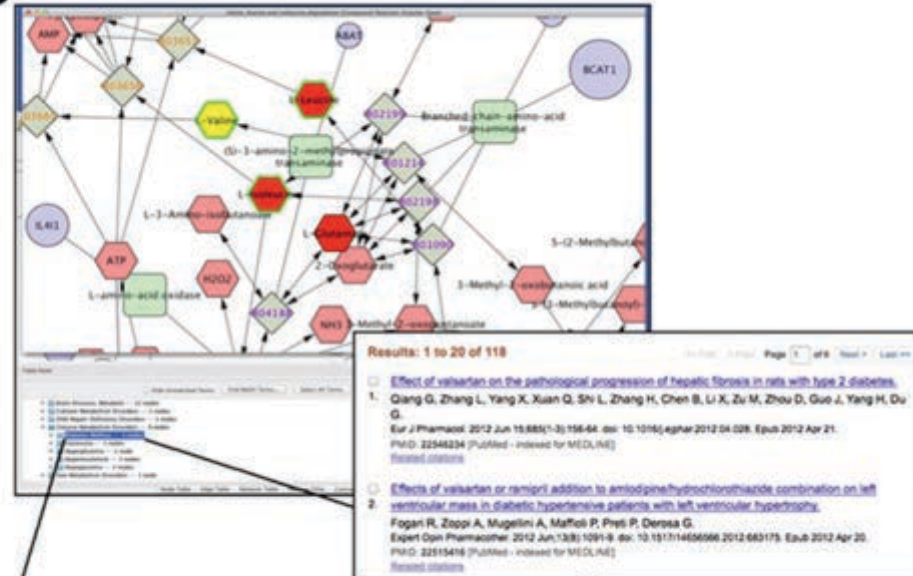
Sas KM¹, Karnovsky A², Michailidis G³, Pennathur S⁴.

Metabolomics is an integral part for understanding disease processes ... information garnered in the biomarker investigations, future research should shed more light on disease pathogenesis and explore new treatment options.

A



B



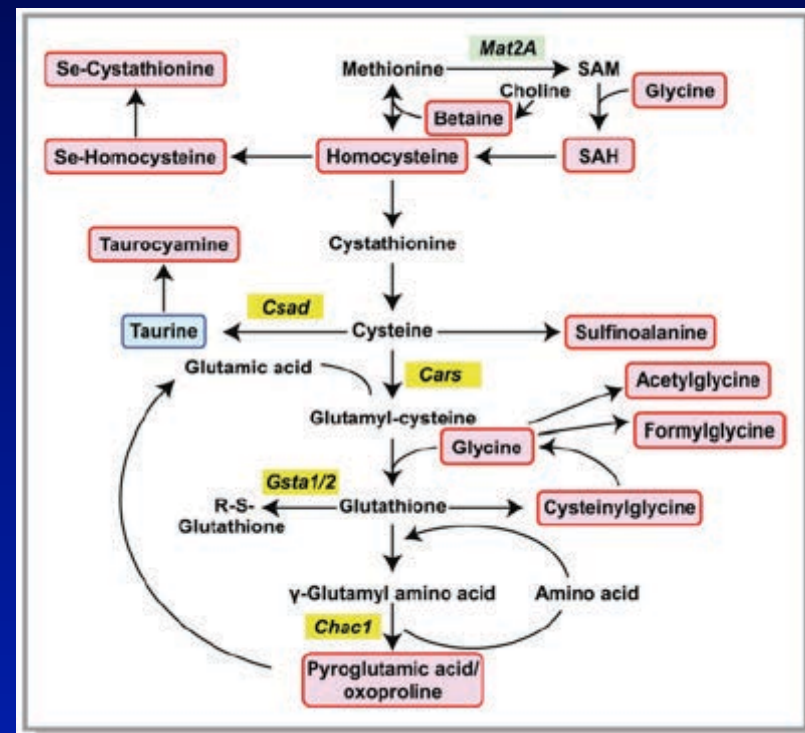
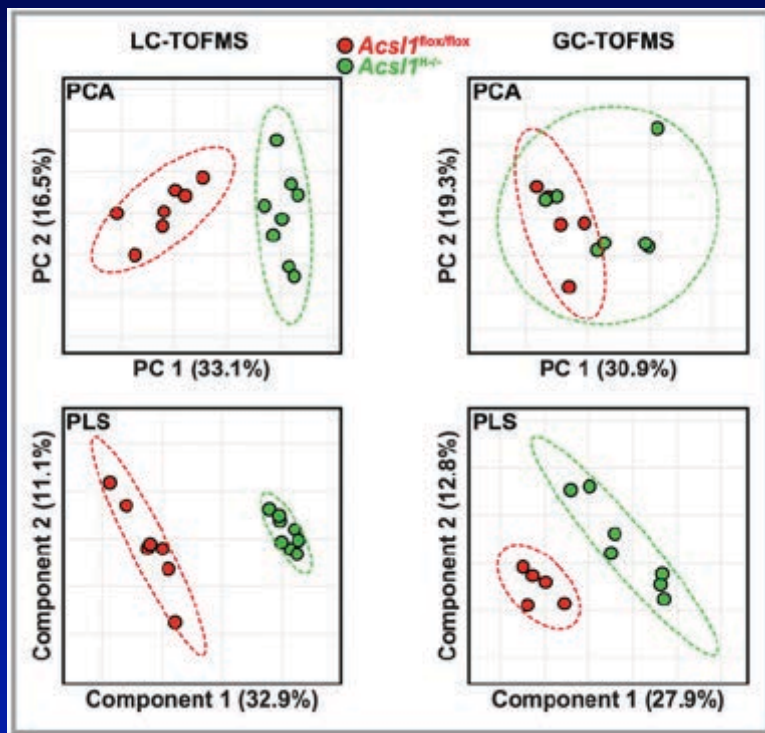
Heart failure and substrate switching

J Am Heart Assoc. 2015 Feb 24;4(2). pii: e001136. doi: 10.1161/JAHA.114.001136.

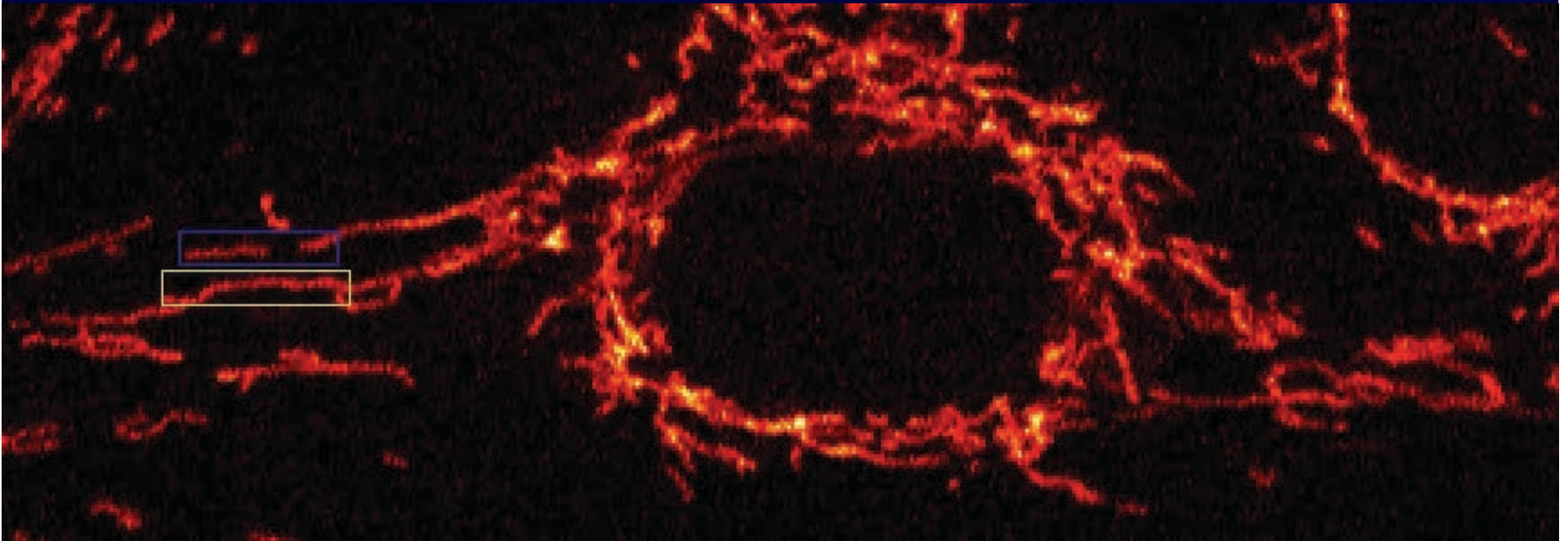
Cardiac energy dependence on glucose increases metabolites related to glutathione and activates metabolic genes controlled by mechanistic target of rapamycin.

Schisler JC¹, Grevengoed TJ², Pascual F², Cooper DE², Ellis JM², Paul DS², Willis MS³, Patterson C¹, Jia W⁴, Coleman RA².

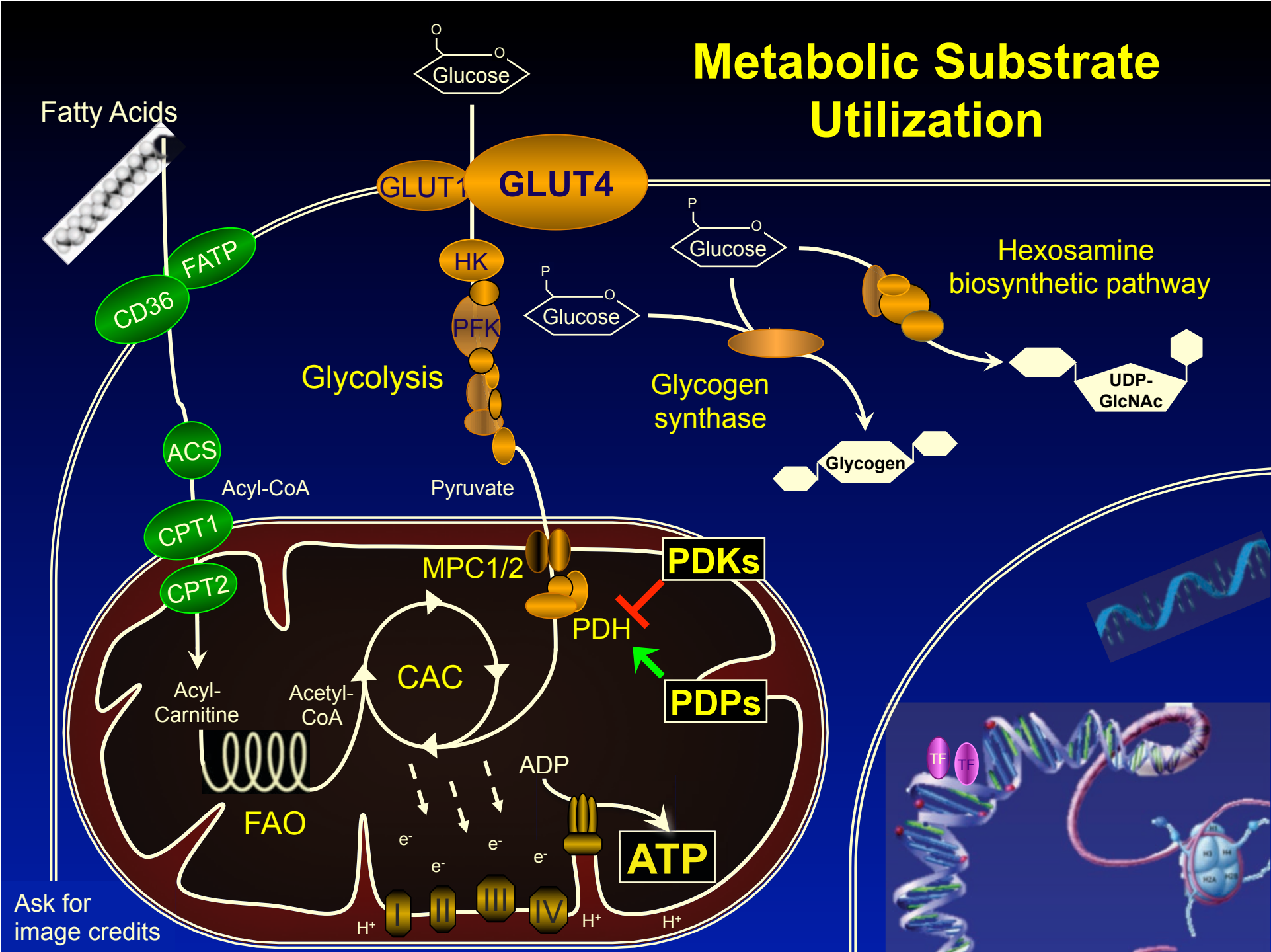
The hypertrophy, oxidative stress, and metabolic changes that occur within the heart when glucose supplants FA as a major energy source suggest that substrate switching to glucose is not entirely benign.



Mitochondria – a Dynamic Network



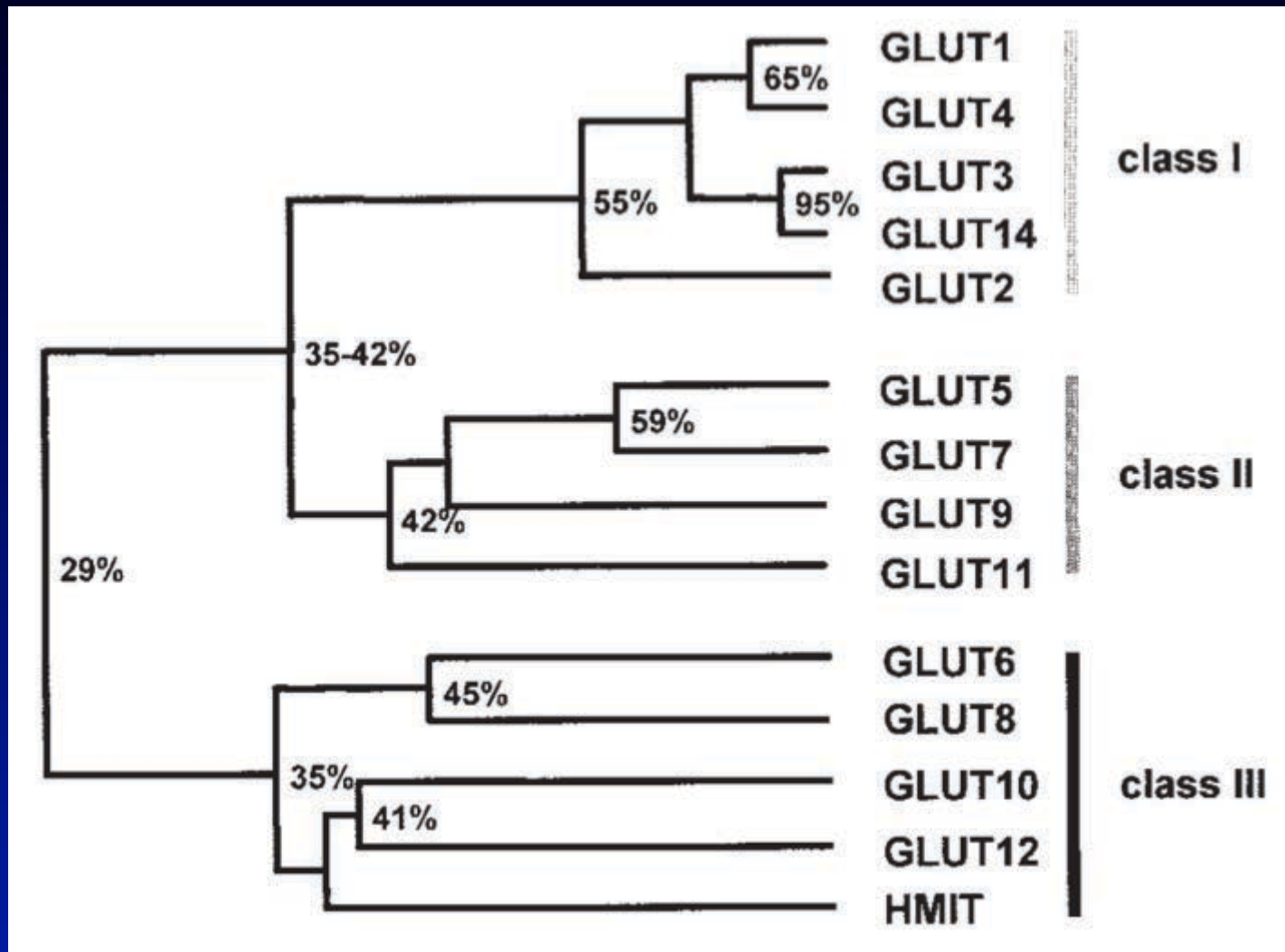
Metabolic Substrate Utilization



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Facilitative Glucose Transporters: GLUTs

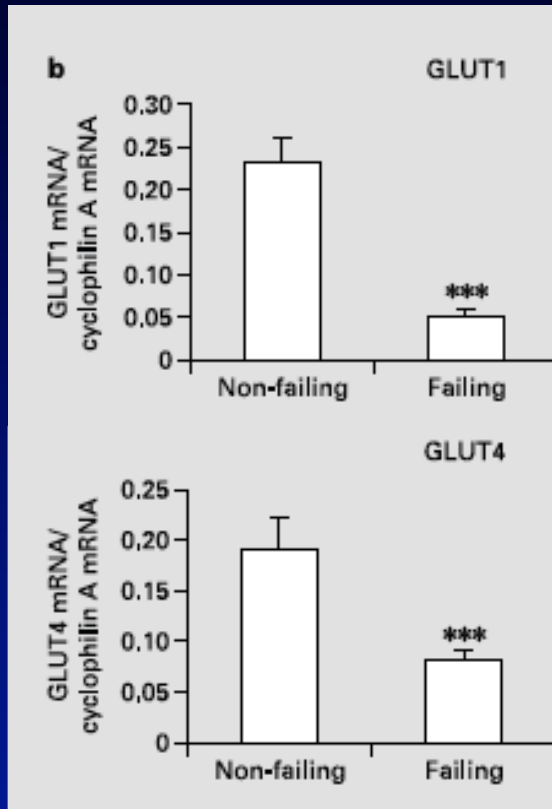
“Solute Carrier Family, SLC2A”



Changes in Human Heart GLUT Levels

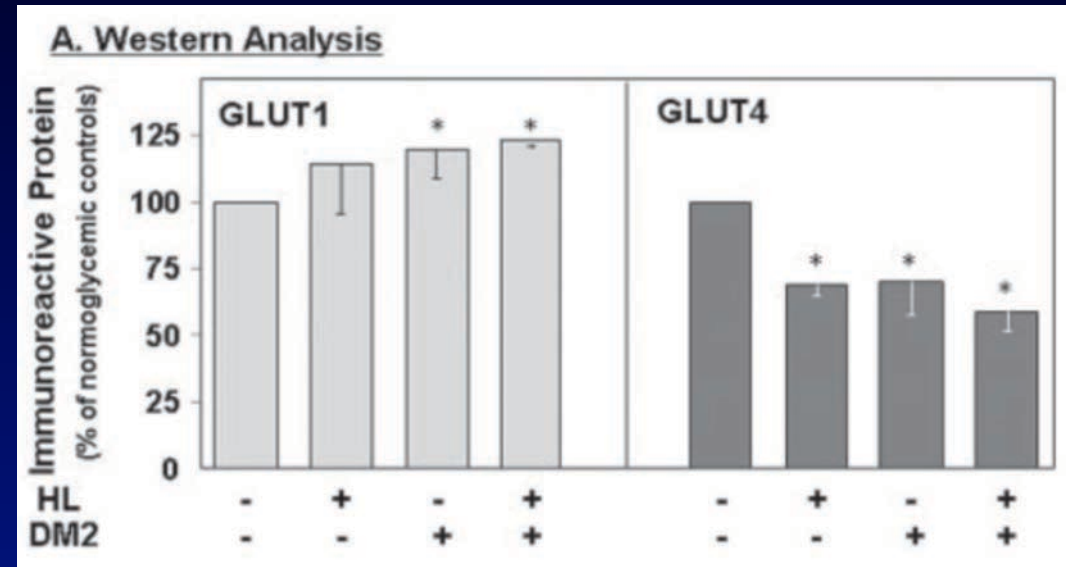
RNA

Human heart failure



Protein

Human heart diabetes



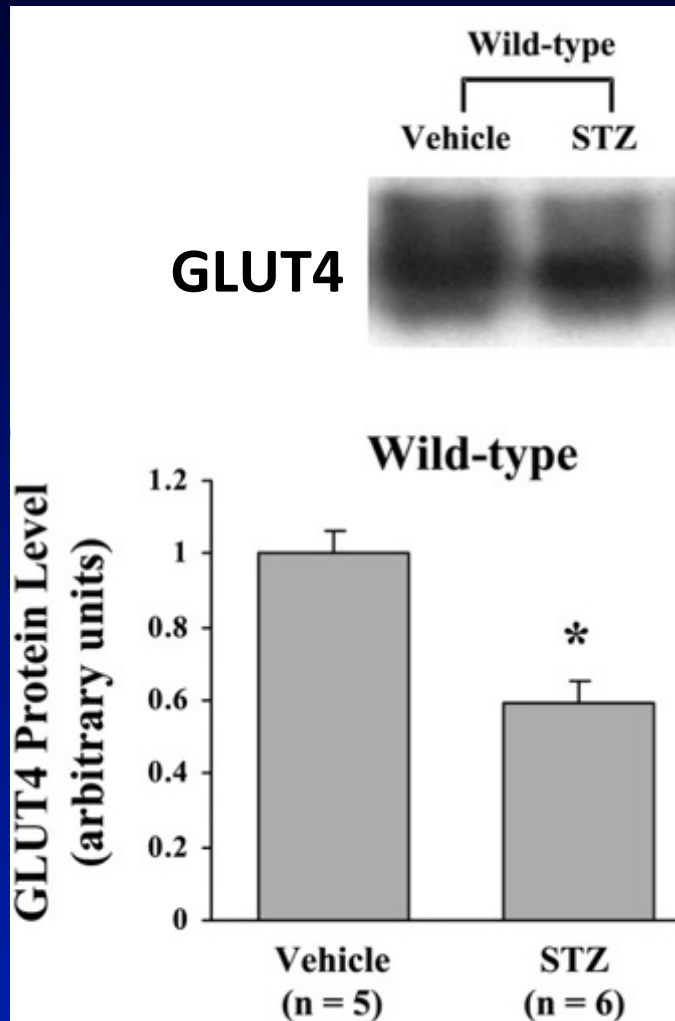
Biopsies obtained during coronary bypass surgery
 HL = hyperlipidemia
 DM2 = diabetes mellitus type 2

Razeghi ... Taegtmeyer 2002 *Cardiology* 280(41):34786

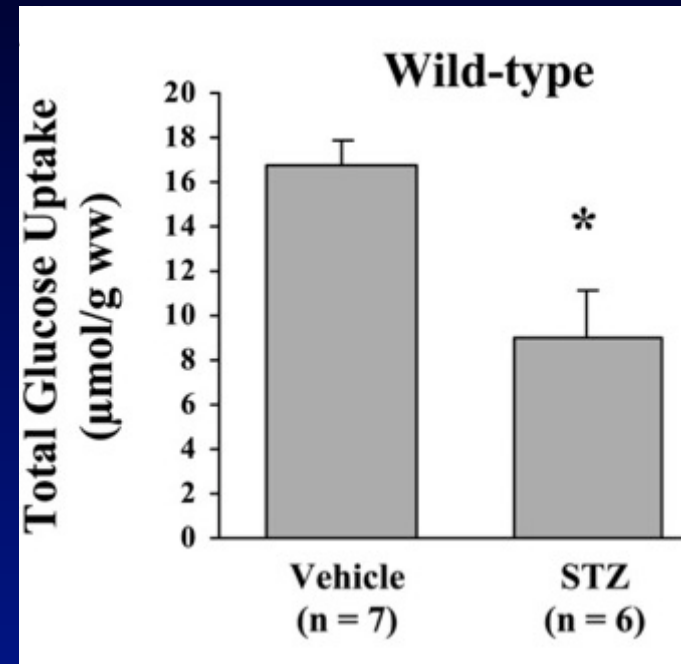
Armoni ... Karnieli 2005 *J Biol Chem* 280(41):34786

Glucose Utilization and Rodent Models of Type 1 Diabetes

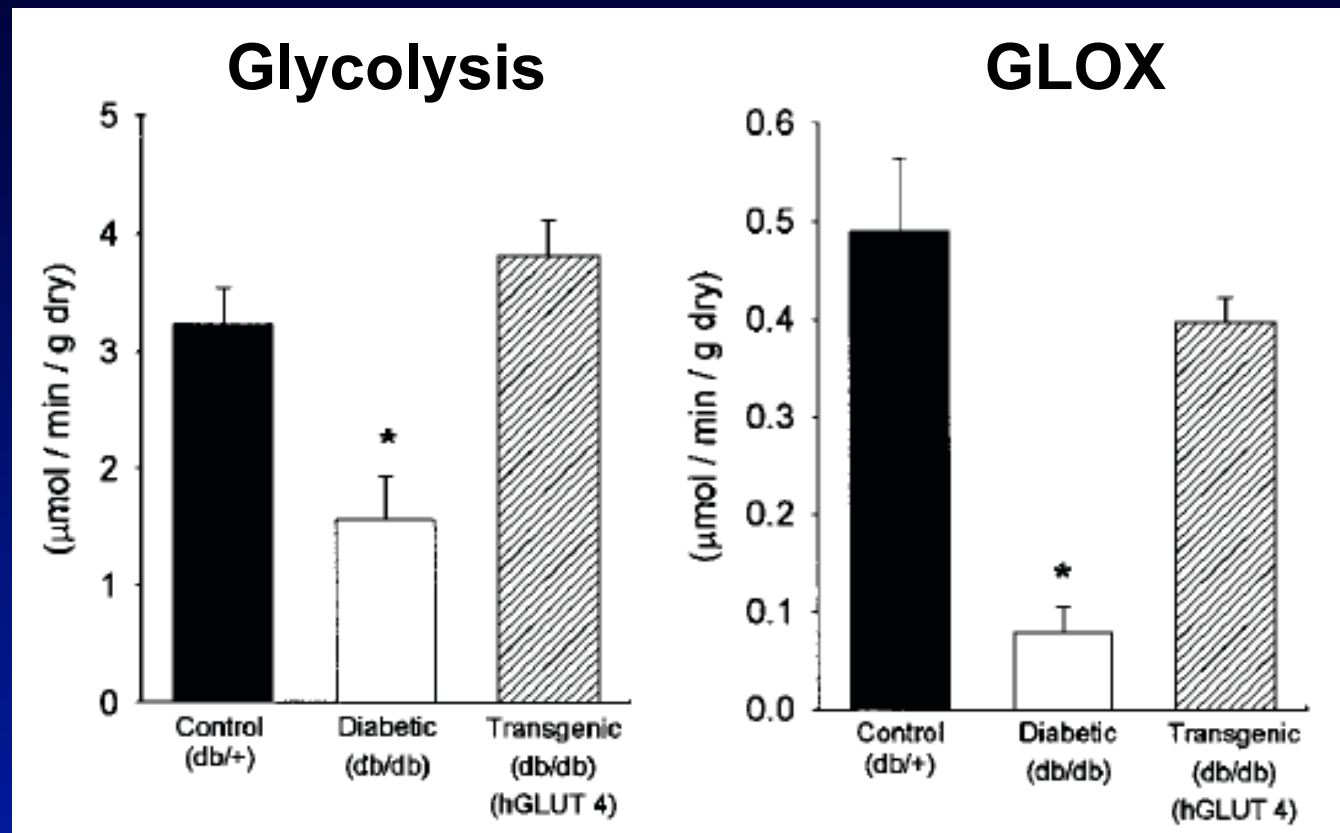
Protein
Diabetic Mouse Heart



Glucose Uptake
Diabetic Mouse Heart



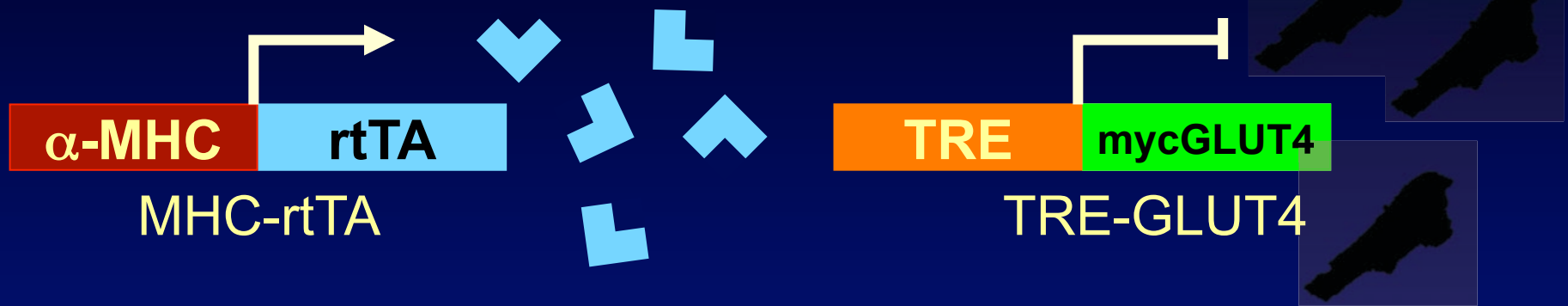
Constitutive GLUT4 Expression Prevents Development of Glucose Utilization Defects



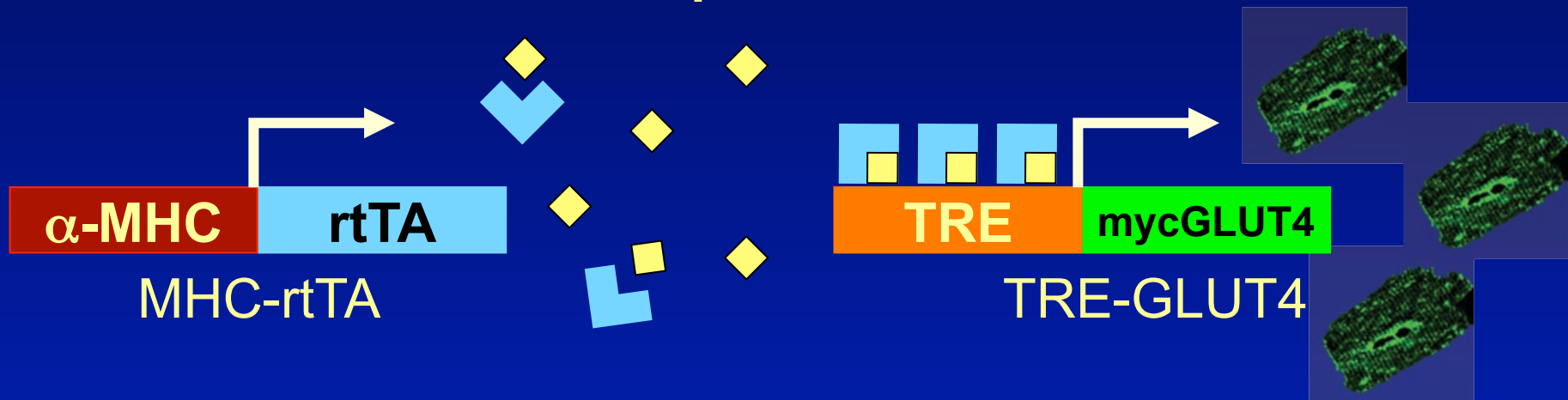
Question: Is the change in
cardiac metabolic
substrate flexibility
adaptive or maladaptive?

Inducible Cardiomyocyte-Specific GLUT4 Expression (mG4H)

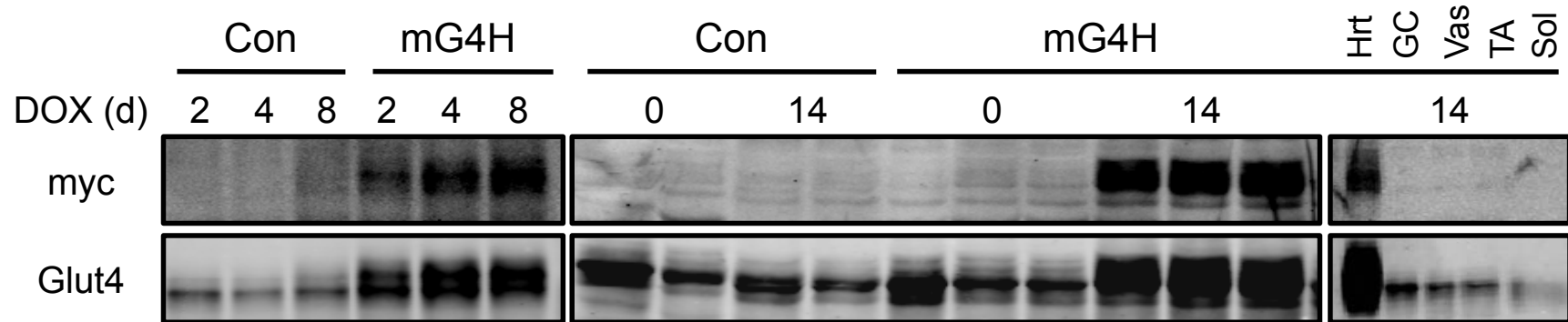
DOX absent = OFF



DOX present = ON



mG4H Mice Exhibit Inducible Cardiac-Specific Expression of GLUT4



Hrt = Heart

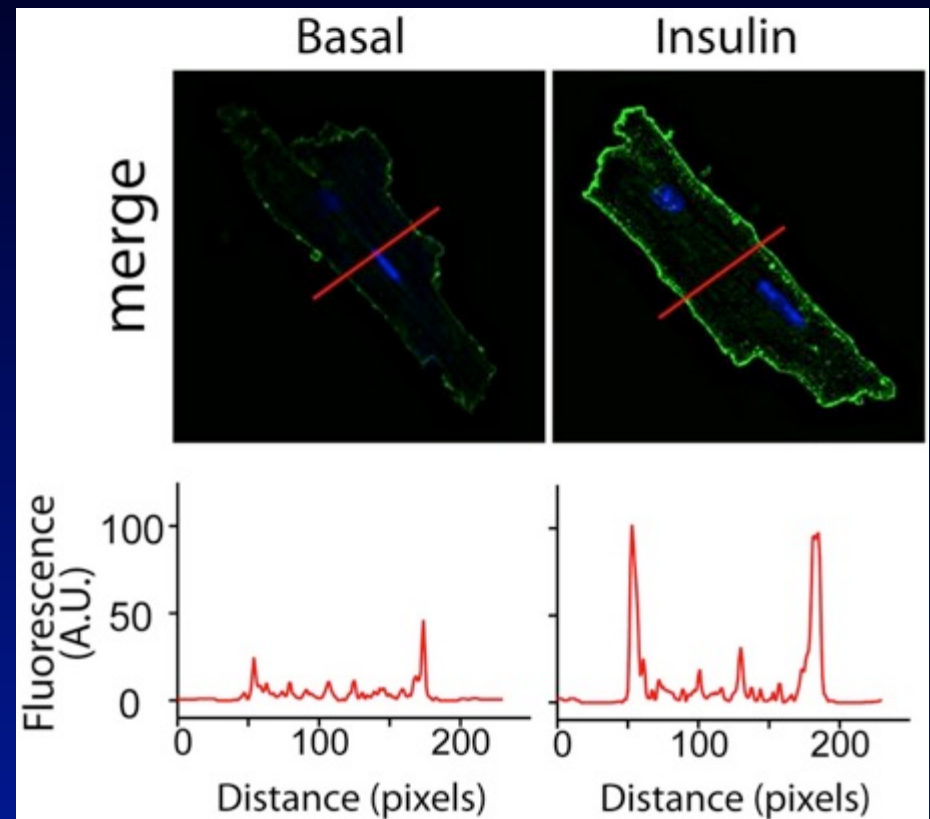
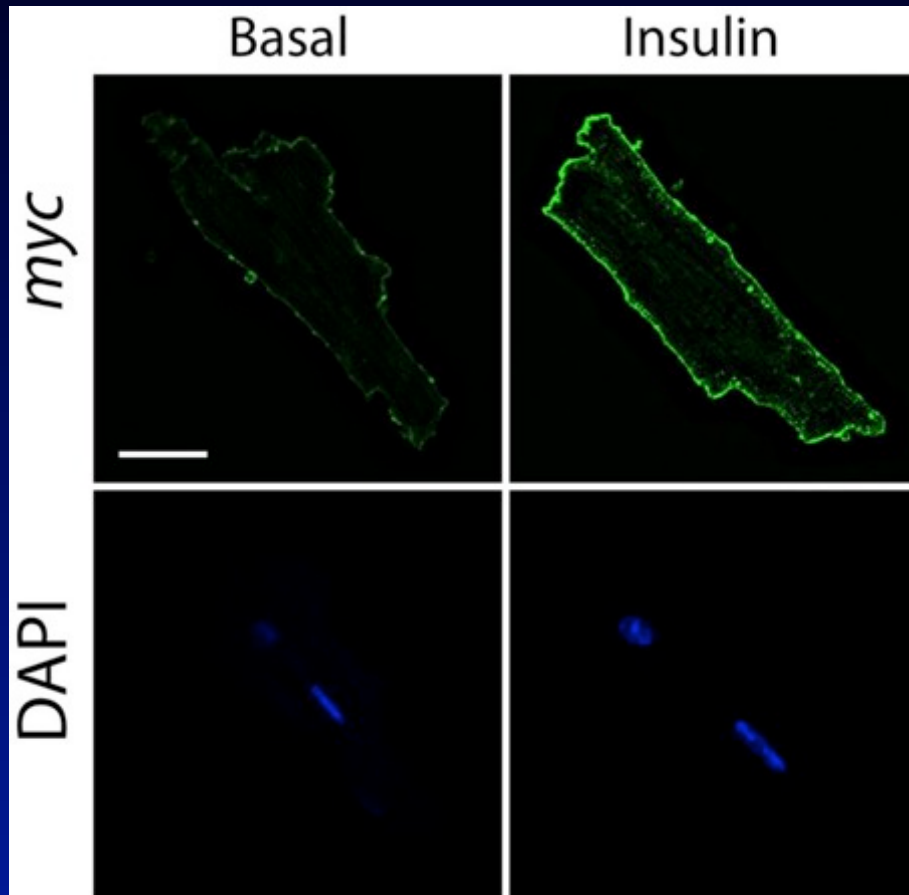
GC = Gastrocnemius

Vas = Vastus lateralis

TA = Tibialis anterior

Sol = Soleus

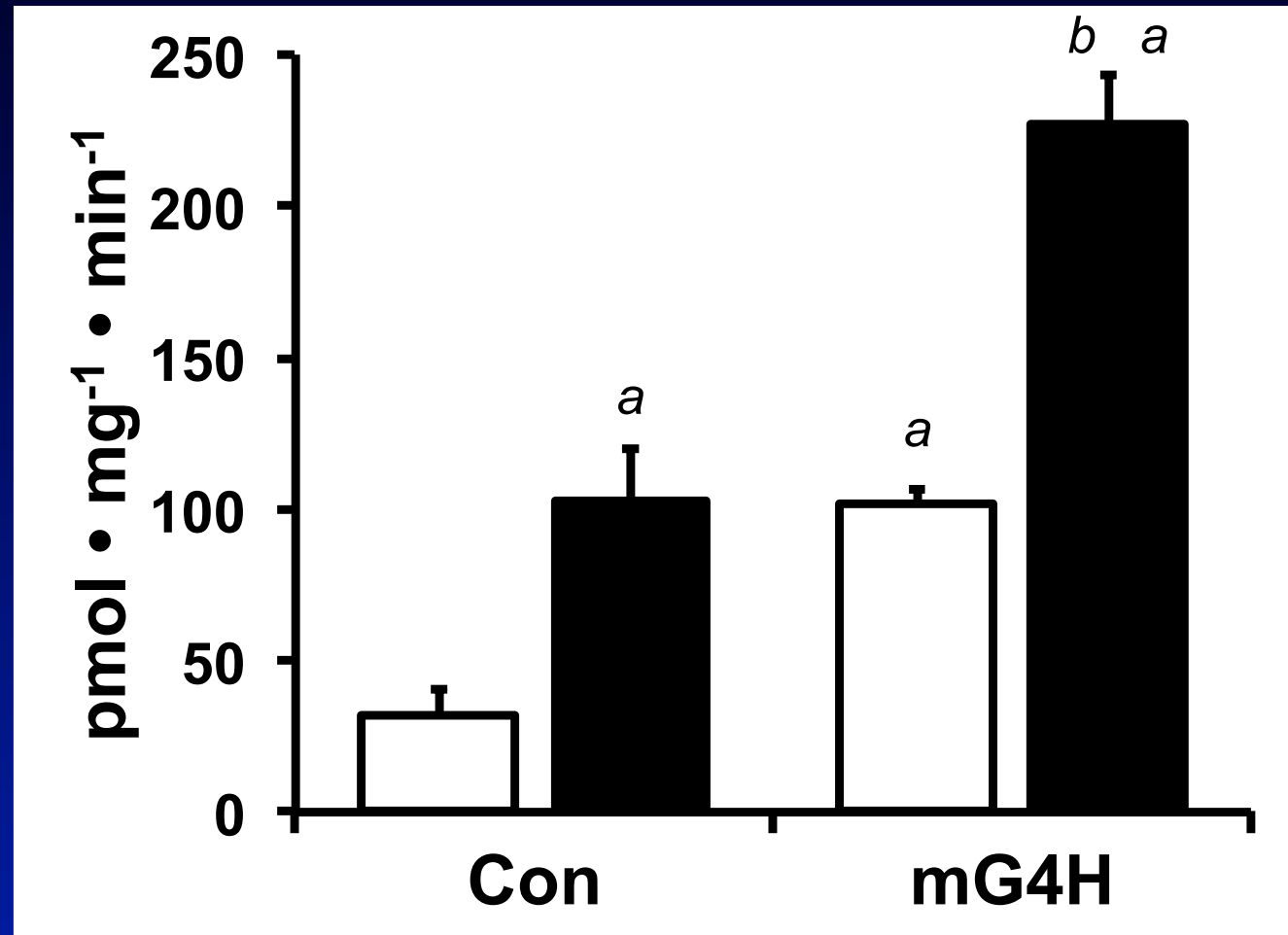
Insulin-induced GLUT4 Vesicle Fusion and Exofacial Myc-Epitope Exposure



GLUT4 Induction Increases Basal and Insulin-Stimulated Glucose Uptake

Cardiac
Myocytes
2-DG
Uptake

□ Basal
■ 0.1 nM Ins



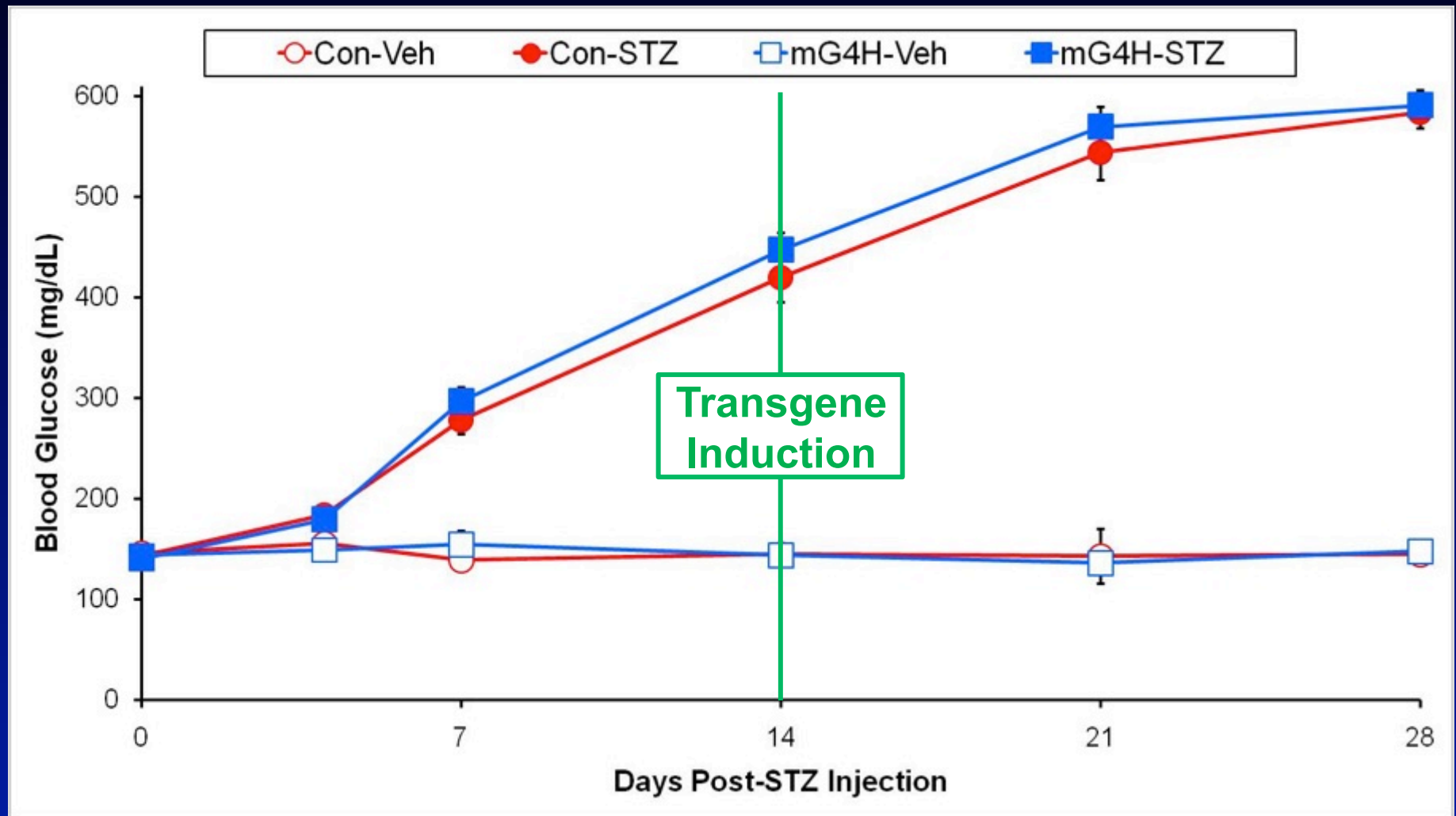
$n = 3 - 4$

a $P < 0.01$ vs. Con-Basal

b $P < 0.001$ vs. All

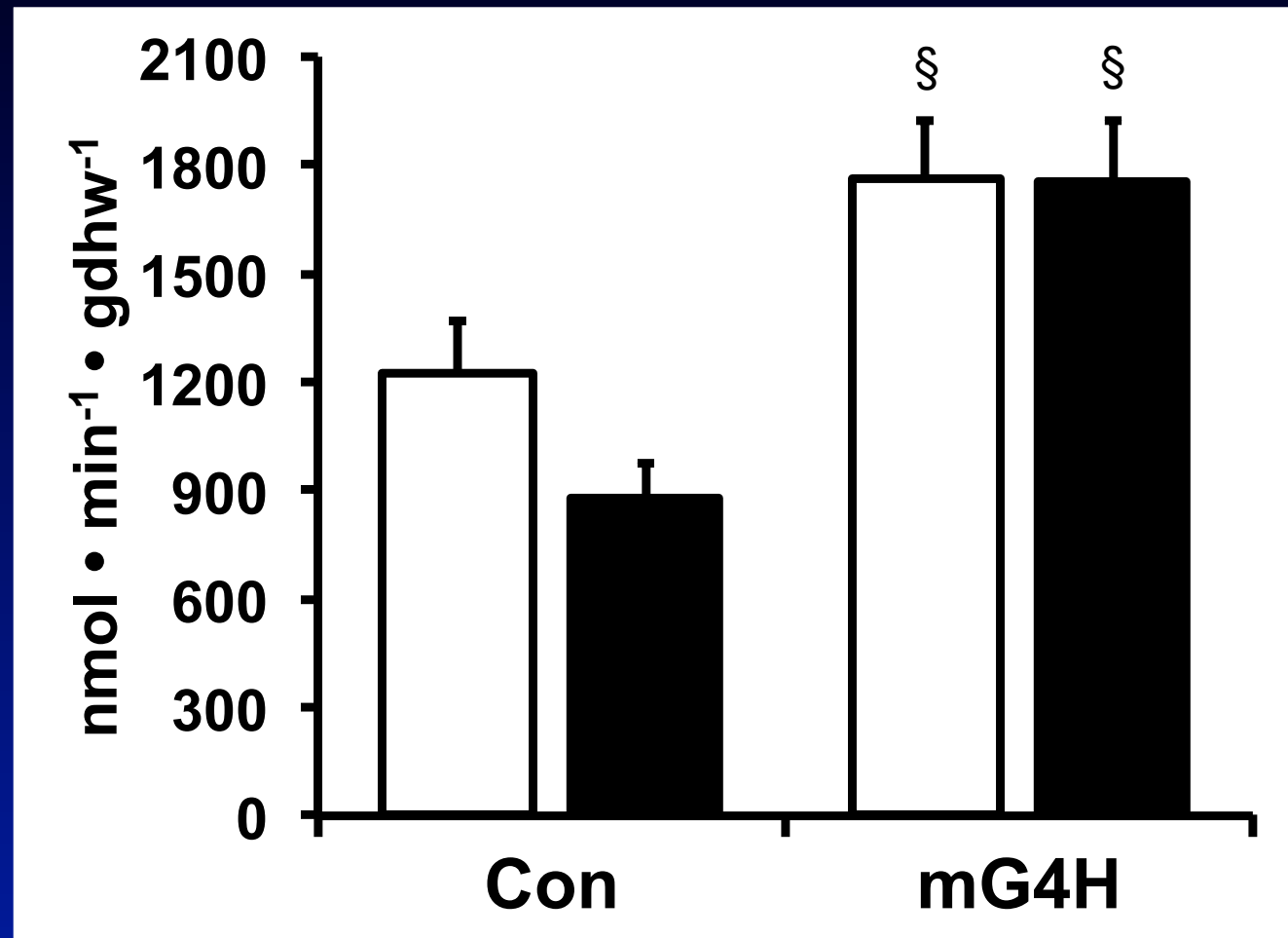
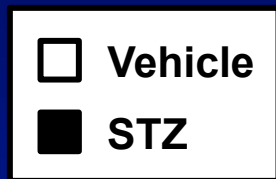
Renata O. Pereira

Streptozotocin (STZ)-Induced Hyperglycemia is Not Altered by Transgene Induction



GLUT4 Induction Increases Glycolysis and Rescues Diabetic Cardiac Glycolytic Defects

Isolated
Working
Hearts
Glycolysis



$n = 6 - 10$

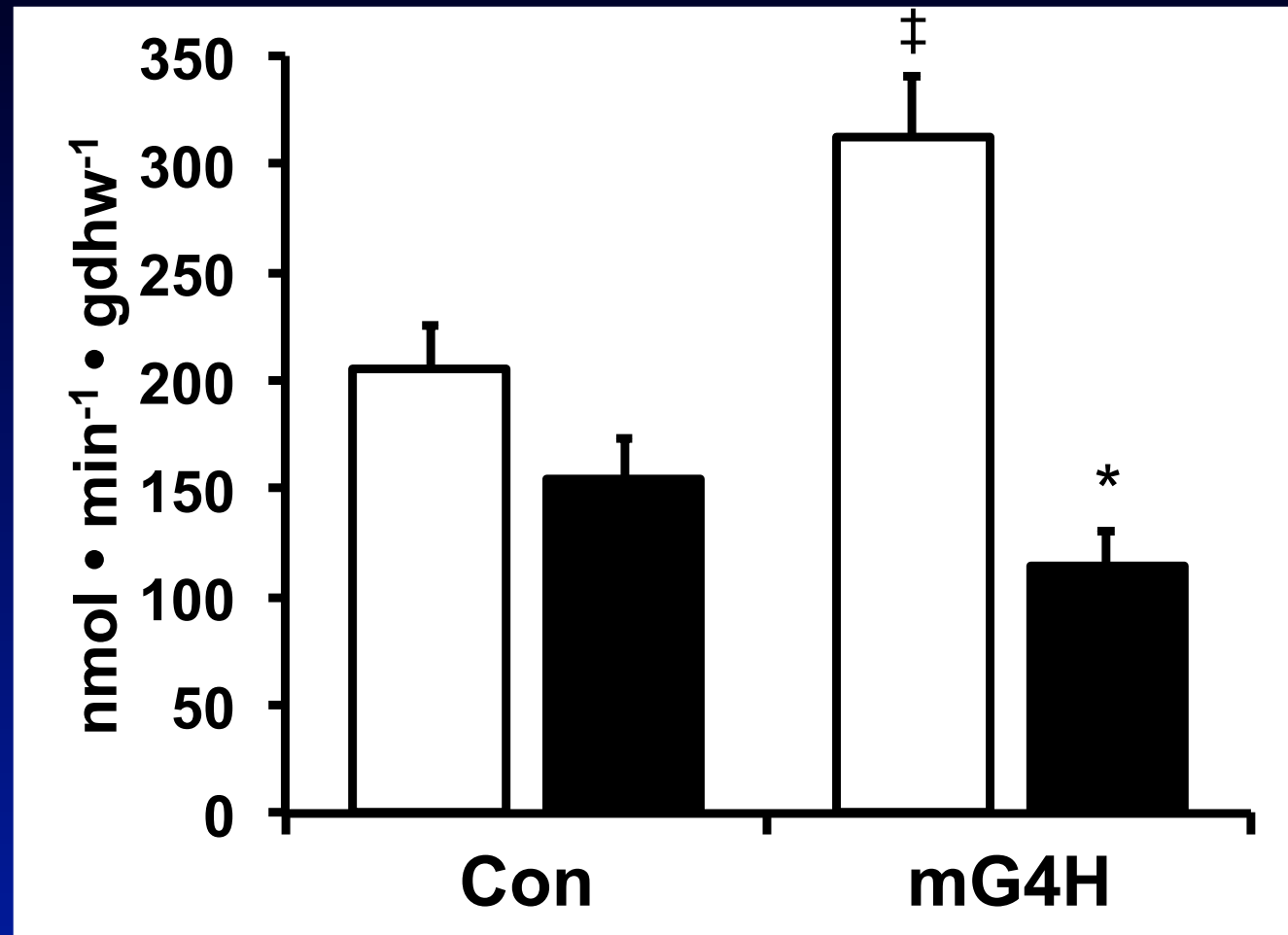
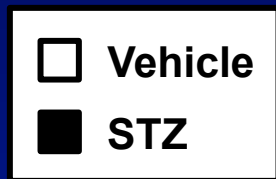
§ $P < 0.01$ vs. Con

ARW

Joseph Tuinei
Wende ... Abel *in prep*

GLUT4 Induction Increases GLOX but Accelerates Diabetic Cardiac GLOX Defects

Isolated Working Hearts
Glucose Oxidation (GLOX)



$n = 6 - 10$

‡ $P < 0.001$ vs. All

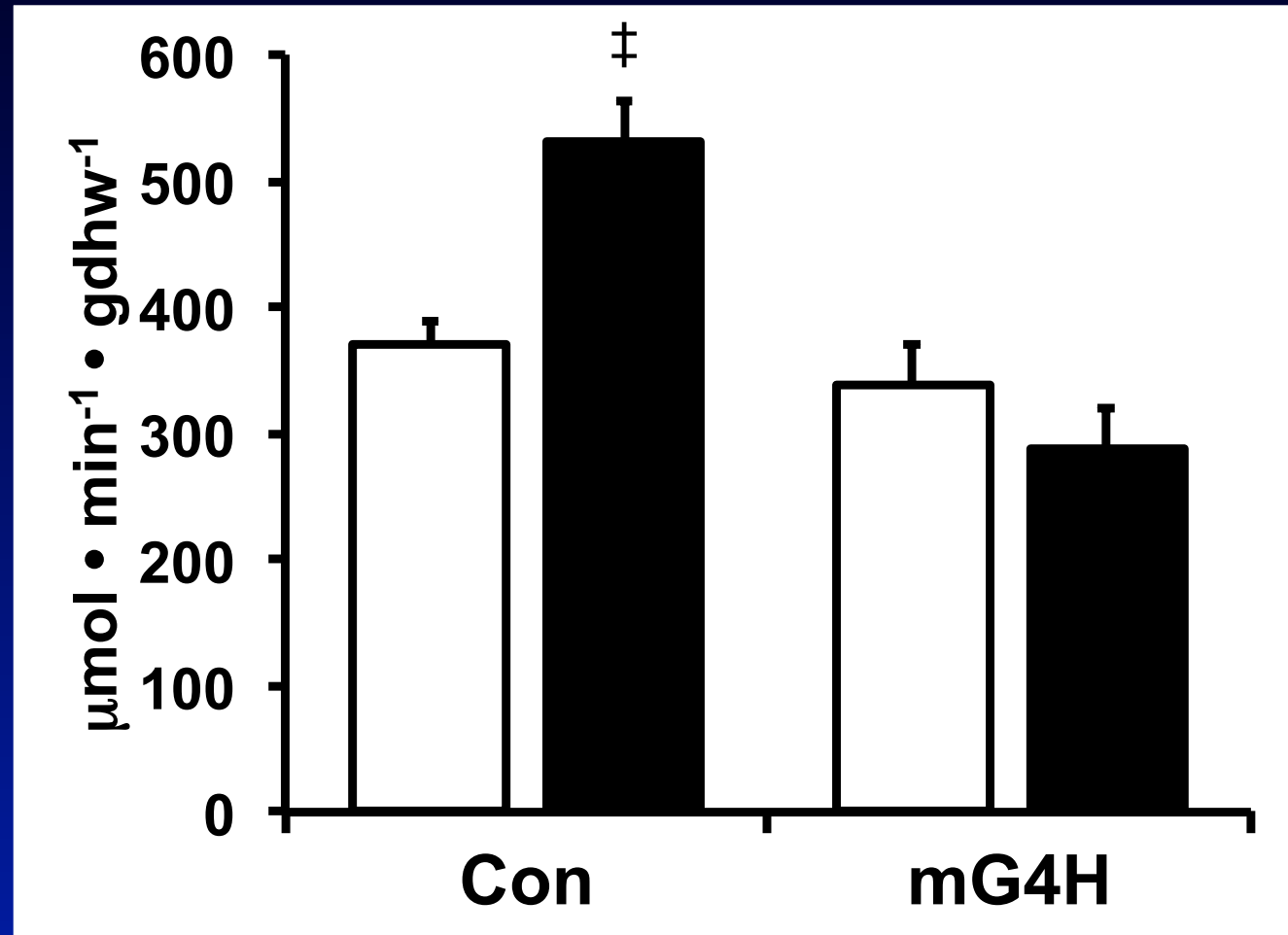
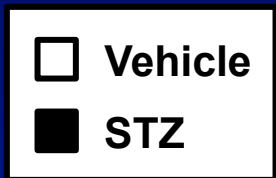
* $P < 0.01$ vs. Veh

ARW

Joseph Tuinei
Wende ... Abel *in prep*

GLUT4 Induction Prevents Increased Cardiac POX in Diabetes

Isolated Working Hearts
Palmitate Oxidation (POX)



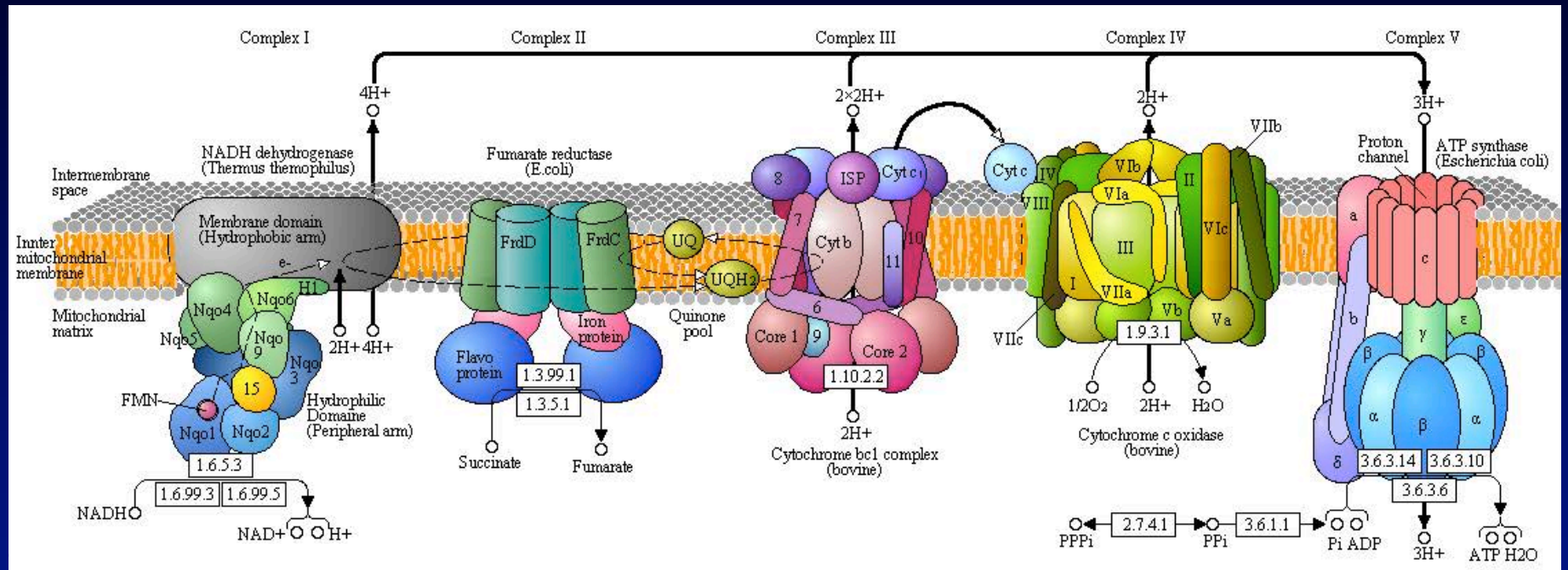
$n = 5 - 13$

‡ $P < 0.001$ vs. All

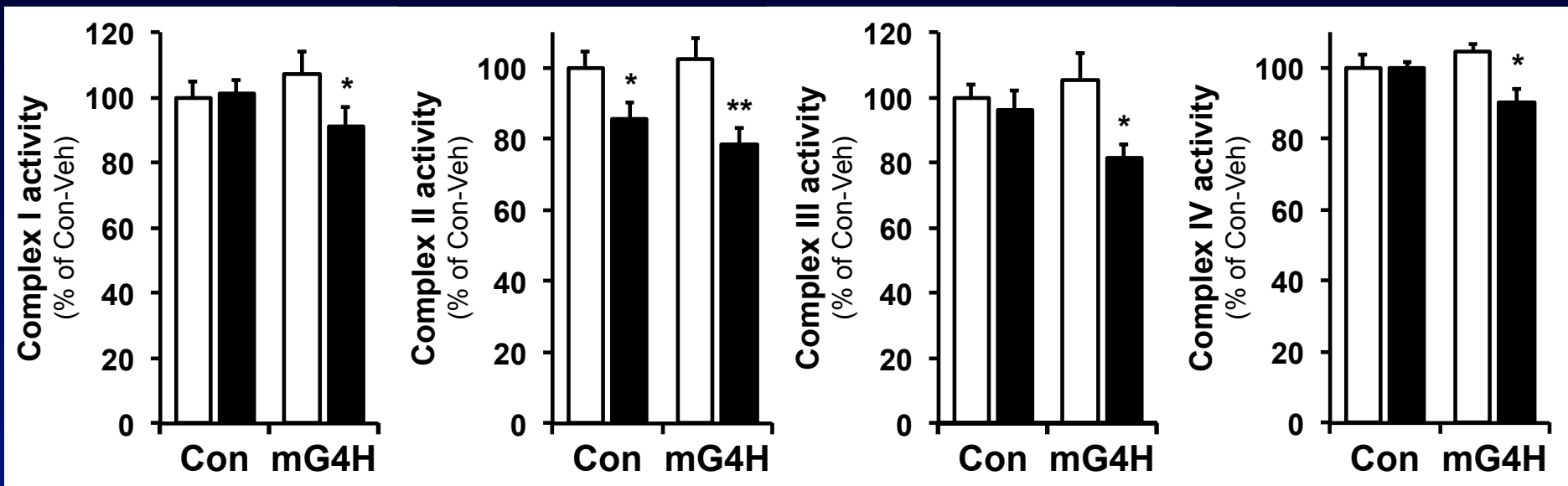
ARW

Joseph Tuinei

Oxidative Phosphorylation



GLUT4 Induction Accelerates Development of Mitochondrial Dysfunction



$n = 3 - 4$
* $P < 0.05$

ARW

Oleh Khalimonchuk
Wende ... Abel *in prep*

Conclusion – Part 1

In the context of diabetes,
enhancing glucose delivery by
expression of GLUT4
accelerates the progression of
mitochondrial dysfunction.

Diabetic Cardiomyopathy

“Death by a Thousand Cuts...”

Insulin resistance

Inflammation

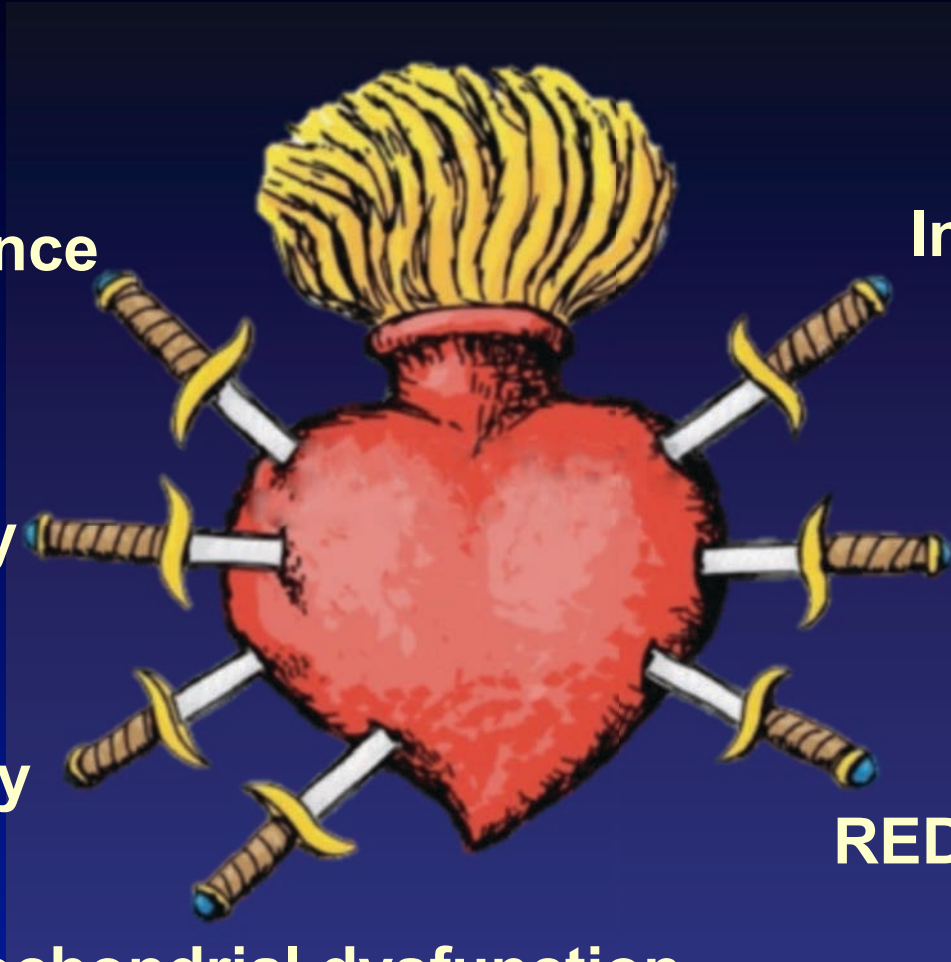
Lipotoxicity

ER stress

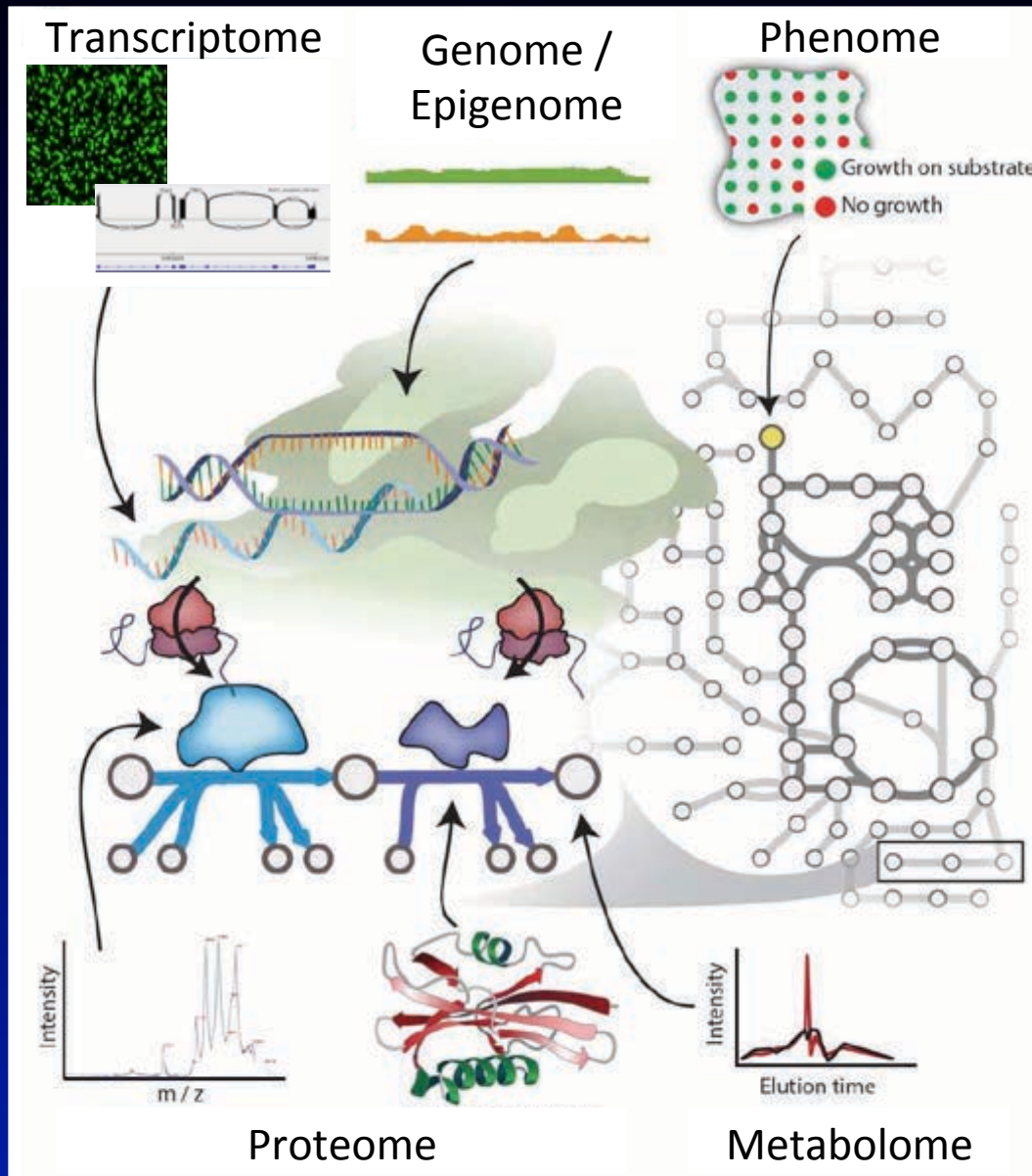
Glucotoxicity

REDOX Imbalance

Mitochondrial dysfunction



Systems Biology



Phenome

Obesity, diabetes, heart failure, BHI, etc.

Transcriptome

Northerns, qPCR, microarray
RNA-seq, miR, lncRNA, etc.

Proteome

Mass spec, western blot, Co-IP,
IHC, PTMs, etc.

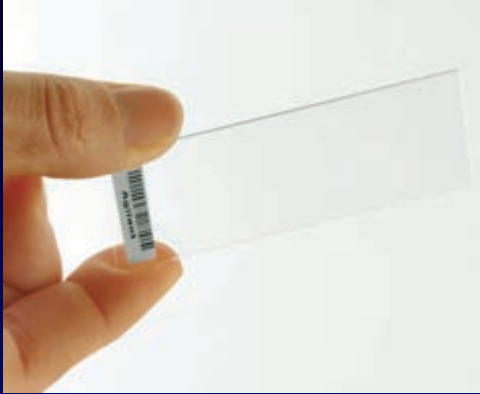
Metabolome

Glucometer, ELISA, GC-MS,
HPLC, NMR, fluxomics, etc.

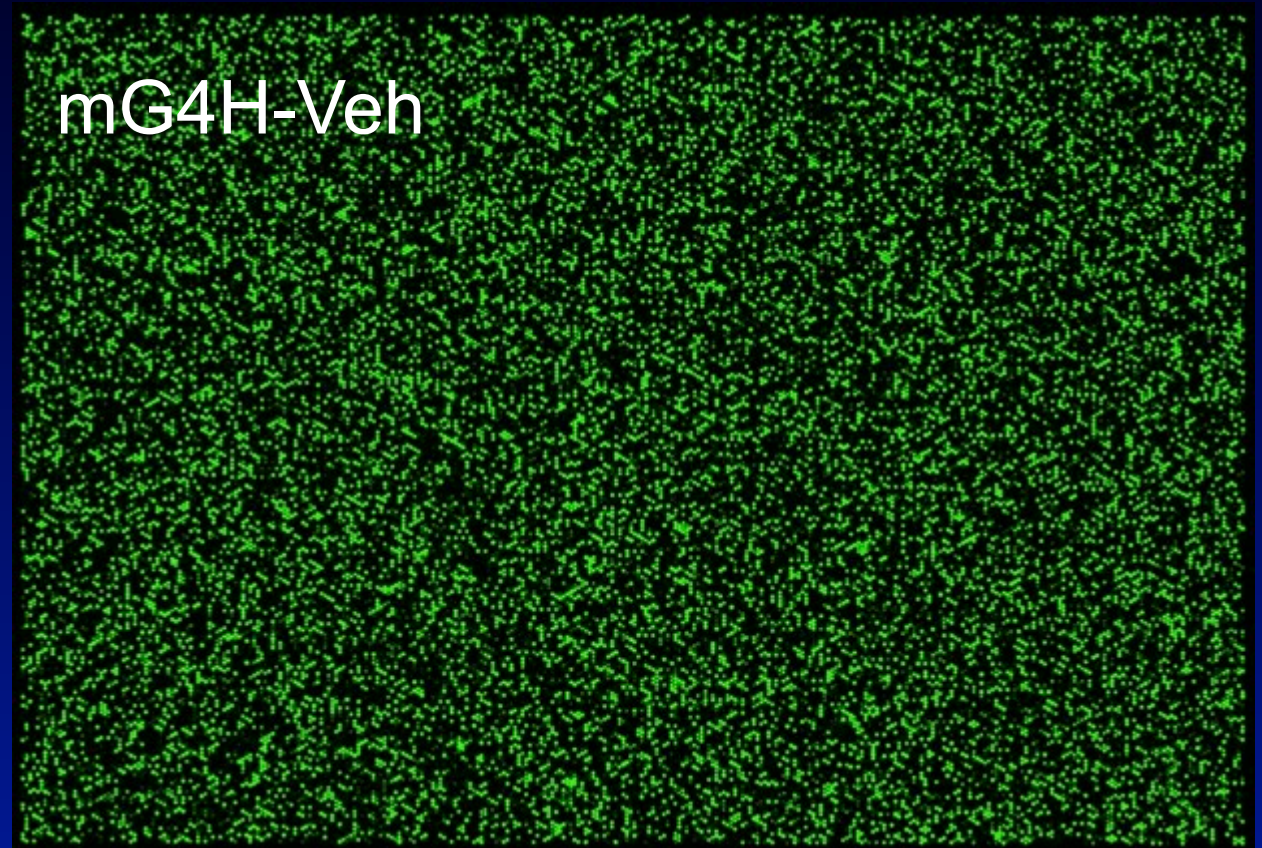
Genome / Epigenome

Southerns, sequencing,
GenBank, ENCODE,
ChIP-seq, bsDNA-seq, etc.

Transcriptomic Analysis Using the Agilent SurePrint G3 60K Microarray

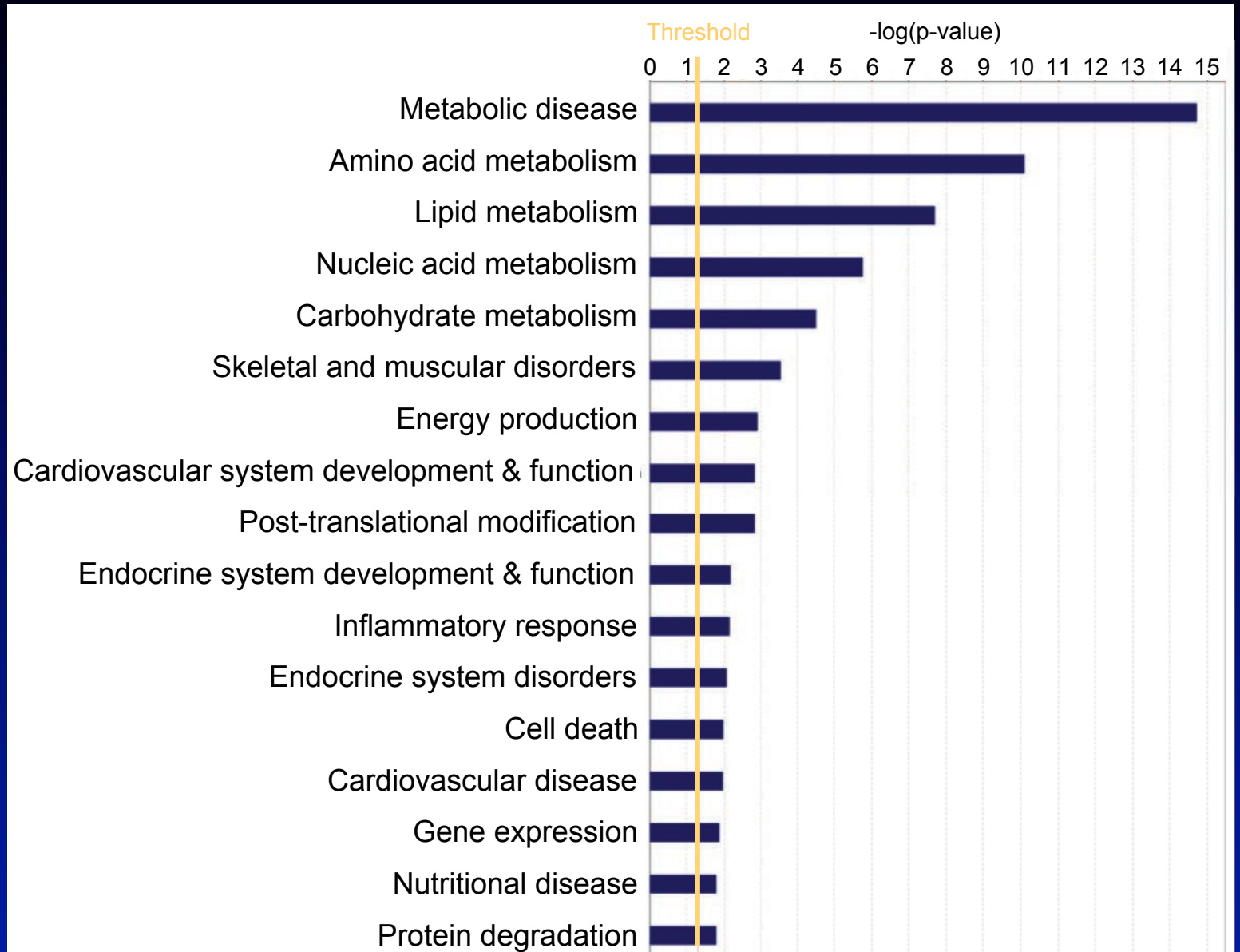


181.9 MB



Microarray and Bioinformatic cores – Brian Dalley and Brett Milash
Wende ... Abel *in prep*

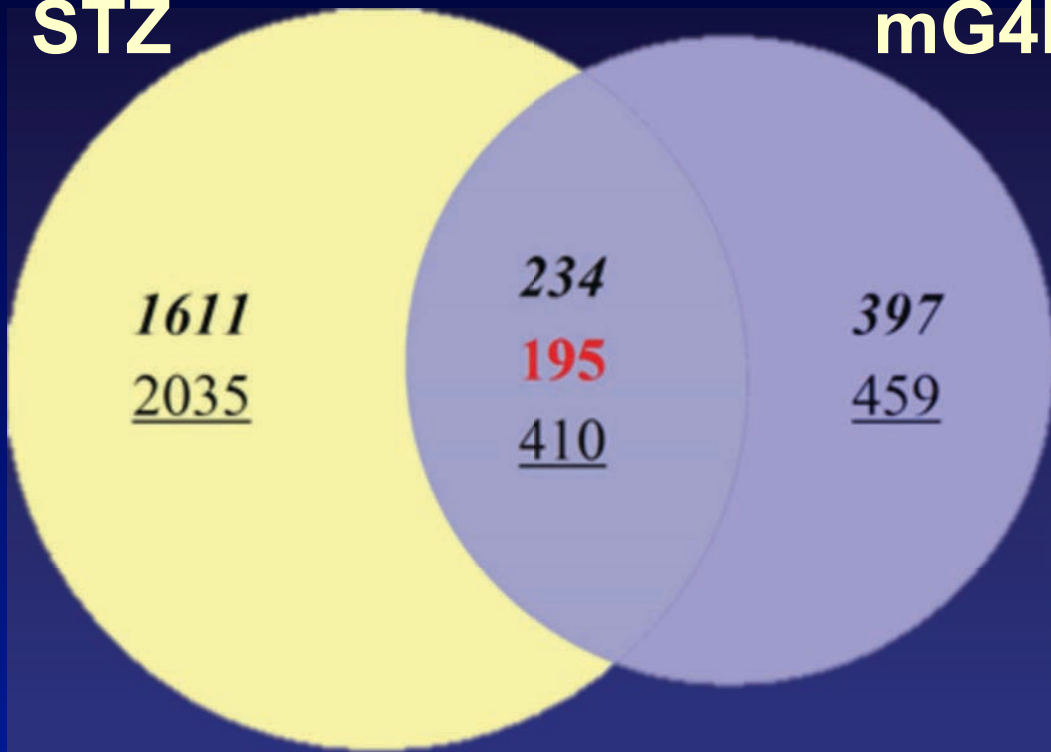
Pathway Analysis of Microarray



Glucose Regulated Gene Expression

Mouse
STZ

Mouse
mG4H



0 = *up-regulated*

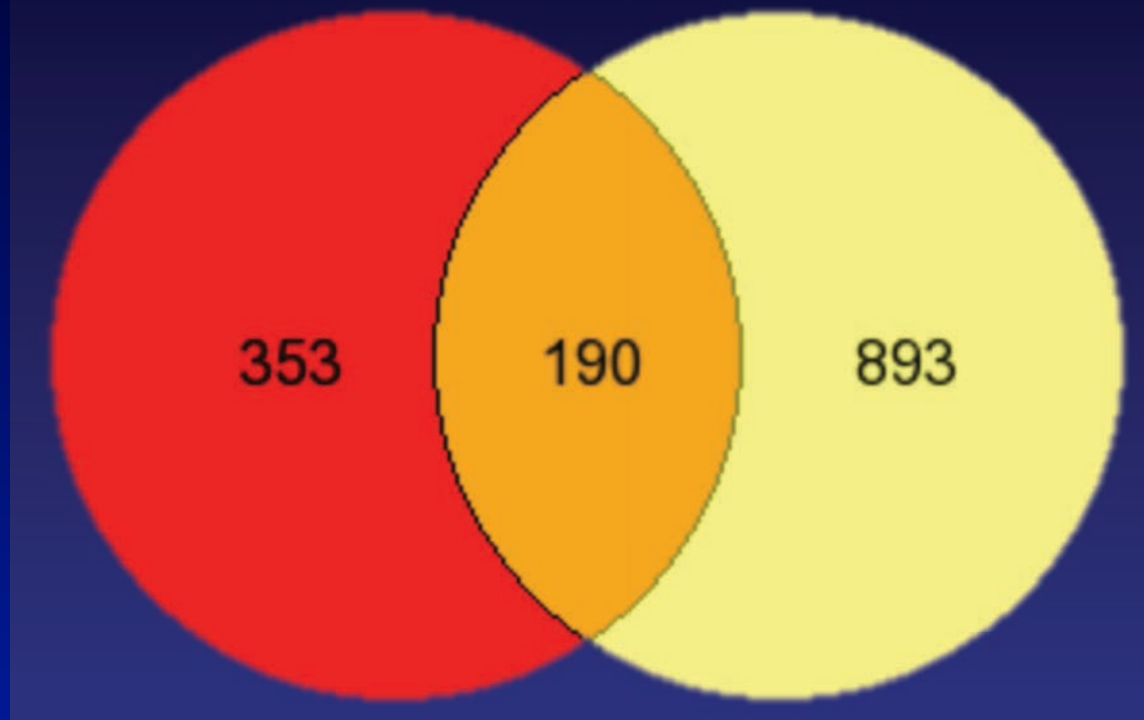
0 = **contra-regulated**

0 = down-regulated

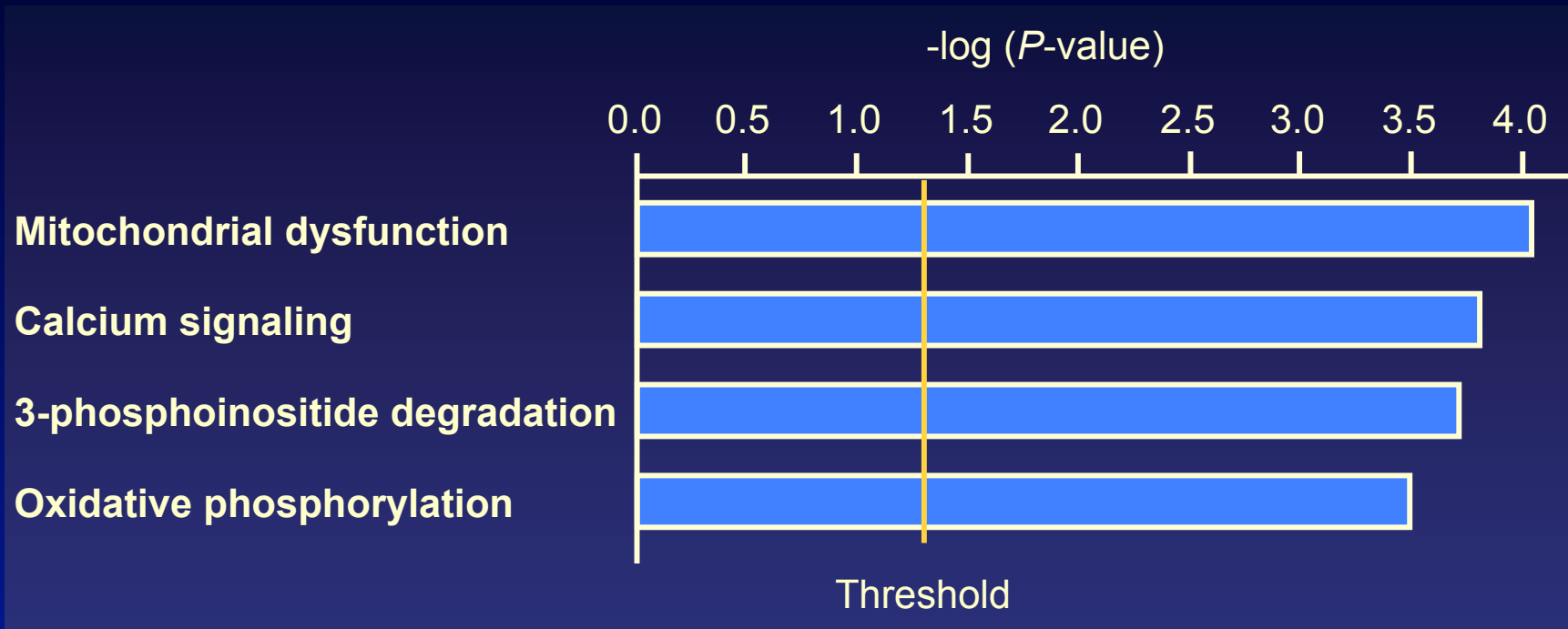
Species Conservation of Gene Expression Changes in Diabetes

Human
T1D

Mouse
T1D

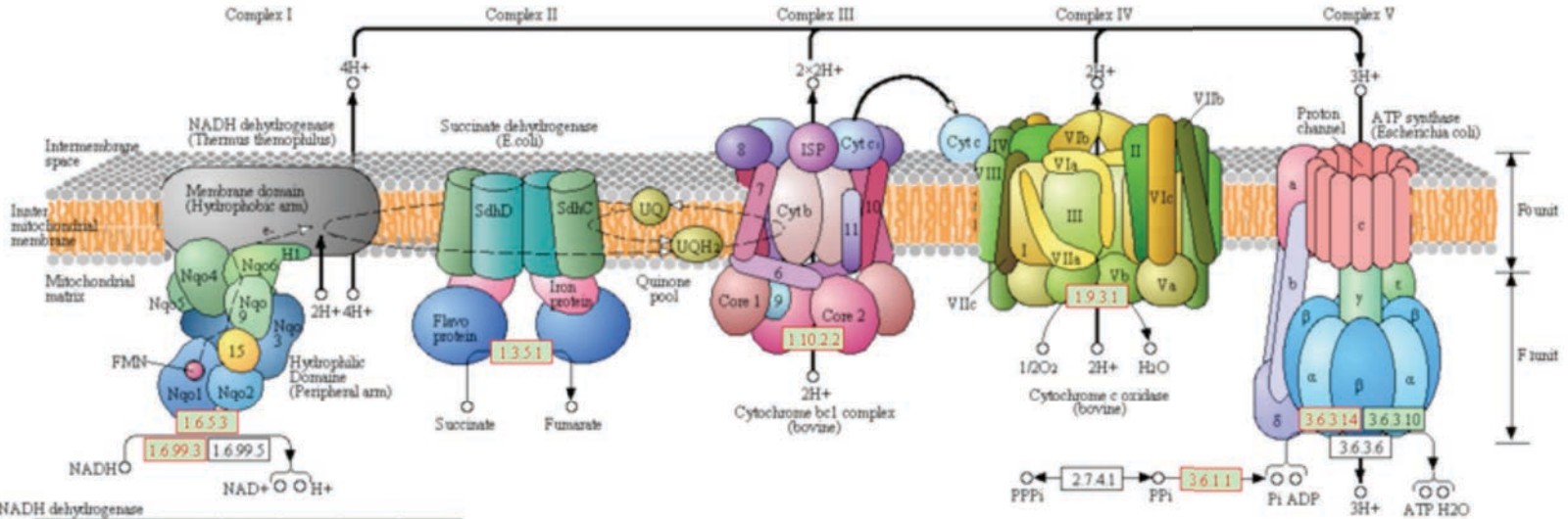


Species Conservation of Gene Expression Changes in Diabetes



Oxidative Phosphorylation

OXIDATIVE PHOSPHORYLATION



NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6										
E	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3						
B/A	NuoA	NuoB	NuoC	NuoD	NuoE	NuoF	NuoG	NuoH	NuoI	NuoJ	NuoK	NuoL	NuoM	NuoN			
B/A	NdhC	NdhK	NdhJ	NdhH	NdhA	NdhI	NdhG	NdhE	NdhF	NdhD	NdhB	NdhL	NdhM	NdhN	HoxE	HoxF	HoxU
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9	Ndufa10	Ndufab1	Ndufa11	Ndufa12	Ndufa13			
E	Ndub1	Ndub2	Ndub3	Ndub4	Ndub5	Ndub6	Ndub7	Ndub8	Ndub9	Ndub10	Ndub11	Ndufc1	Ndufc2				

Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB				
B/A	SdhC	SdhD	SdhA	SdhB	FrdA	FrdB	FrdC	FrdD

Cytochrome c oxidase

E	COX10	COX3	COX1	COX2	COX4	COX5A	COX5B	COX6A	COX6B	COX6C	COX7A	COX7B	COX7C	COX8	COX11	COX15	COX17
B/A	CyoE	CyoD	CyoC	CyoB	CyoA	CoxD	CoxC	CoxA	CoxB	QoxD	QoxC	QoxB	QoxA	CytA	CytB		

Cytochrome c reductase

E/B/A	ISP	Cytb	Cyt1	QOR1	QOR2	QOR6	QOR7	QOR8	QOR9	QOR10
-------	-----	------	------	------	------	------	------	------	------	-------

Cytochrome c oxidase, dbb3-type

B	I	II	IV	III
---	---	----	----	-----

Cytochrome bd complex

B/A	CytA	CytB
-----	------	------

F-type ATPase (Bacteria)

alpha	beta	gamma	delta	epsilon
a	b	c		

F-type ATPase (Eukaryotes)

alpha	beta	gamma	delta	epsilon	
OSCP	a	b	c	d	e
f	g	f6/h	j	k	g

V/A-type ATPase (Bacteria, Archaea)

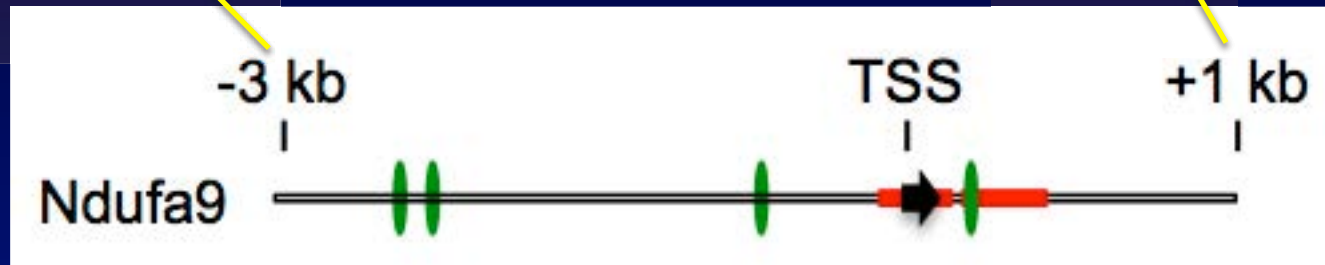
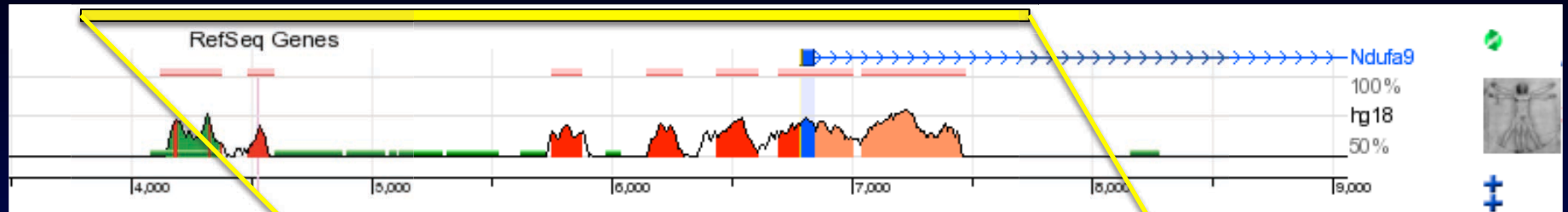
A	B	C	D	E	F	G/H
I	K					

V-type ATPase (Eukaryotes)

A	B	C	D	E	F	G	H
a	c	d	e	S1			

00190 5/7/14
(c) Kanehisa Laboratories

Ndufa9 Gene Promoter Structure



KEY

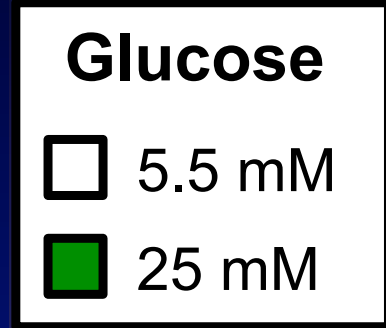
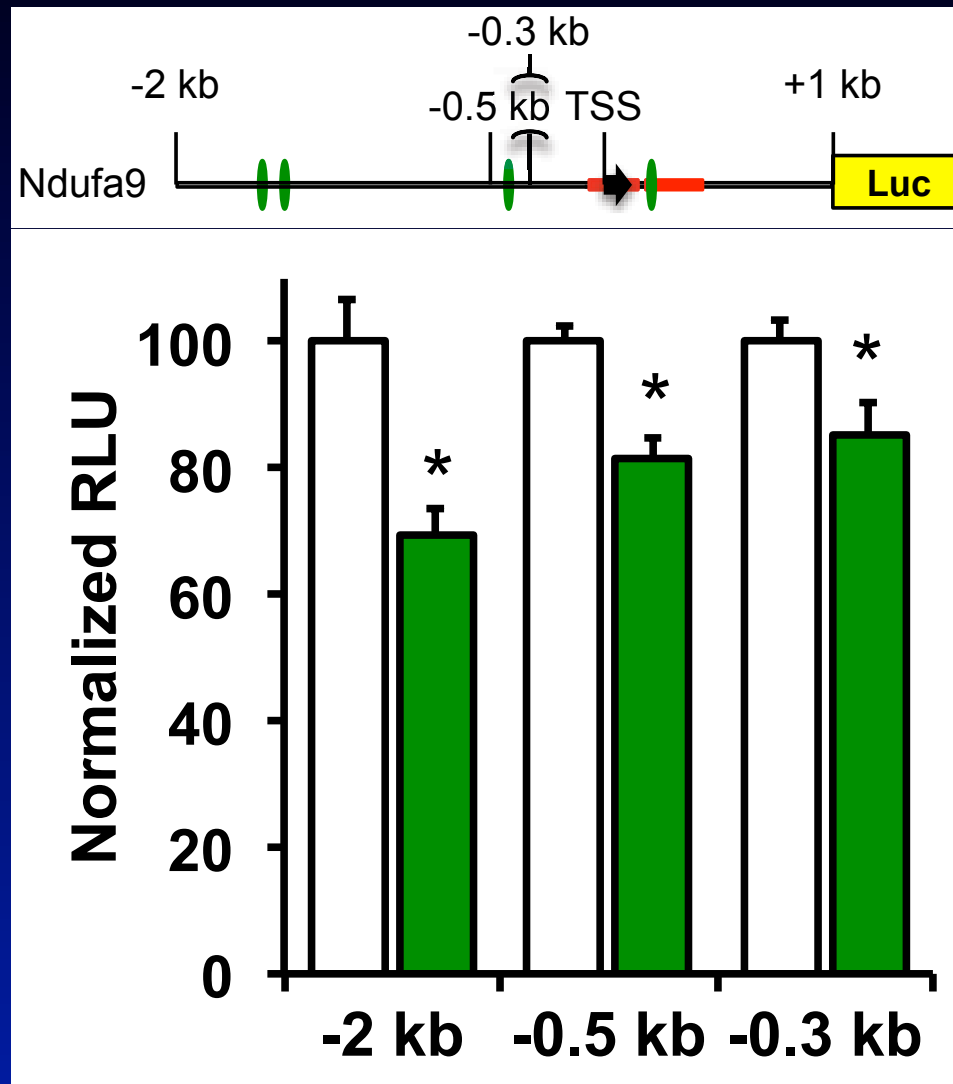
TSS = Transcription start site

— = CpG island

● = Sp1 RE

Ndufa9 Gene Promoter Mapping

Transient Transfection Promoter Activity



C₂C₁₂ Myotubes
n = 9

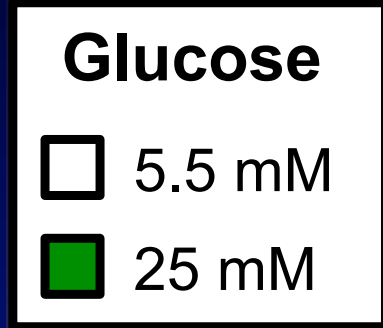
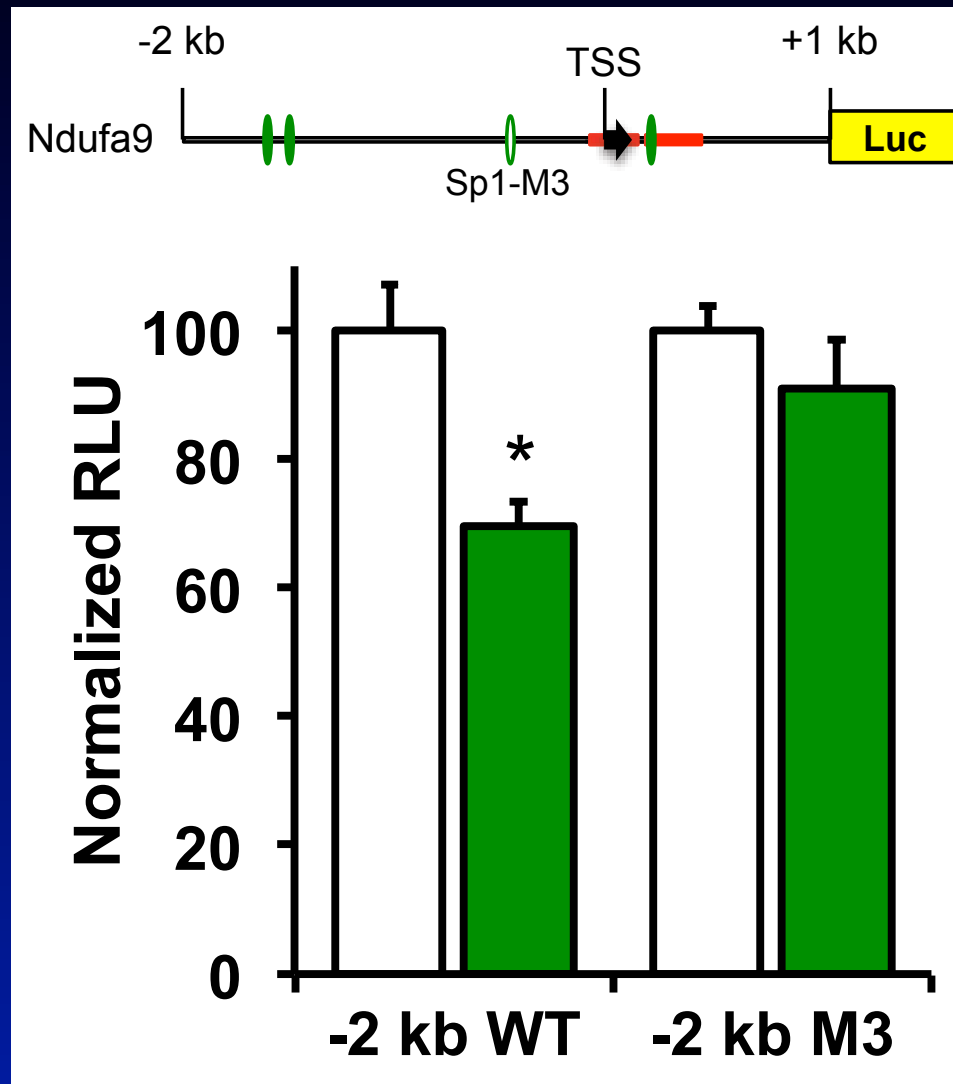
* P < 0.05

ARW

Wende ... Abel in prep

Ndufa9 Gene Promoter Mapping

Transient Transfection Promoter Activity



C₂C₁₂ Myotubes
n = 9

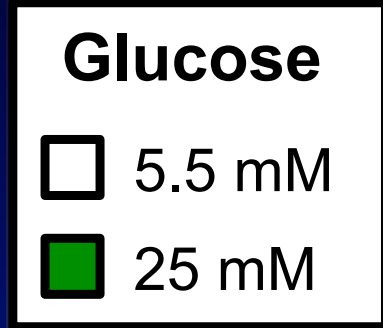
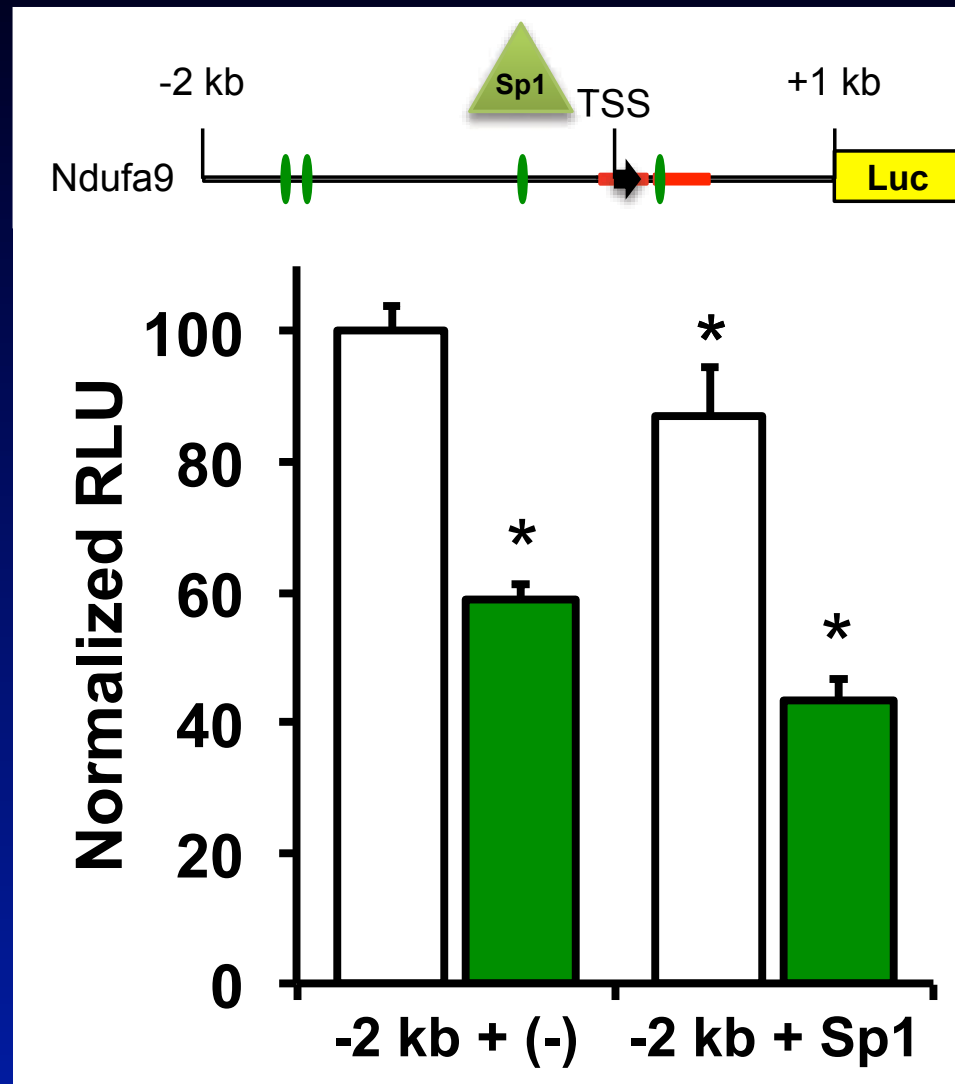
* P < 0.05

ARW

Wende ... Abel *in prep*

Ndufa9 Gene Promoter Mapping

Transient Transfection Promoter Activity



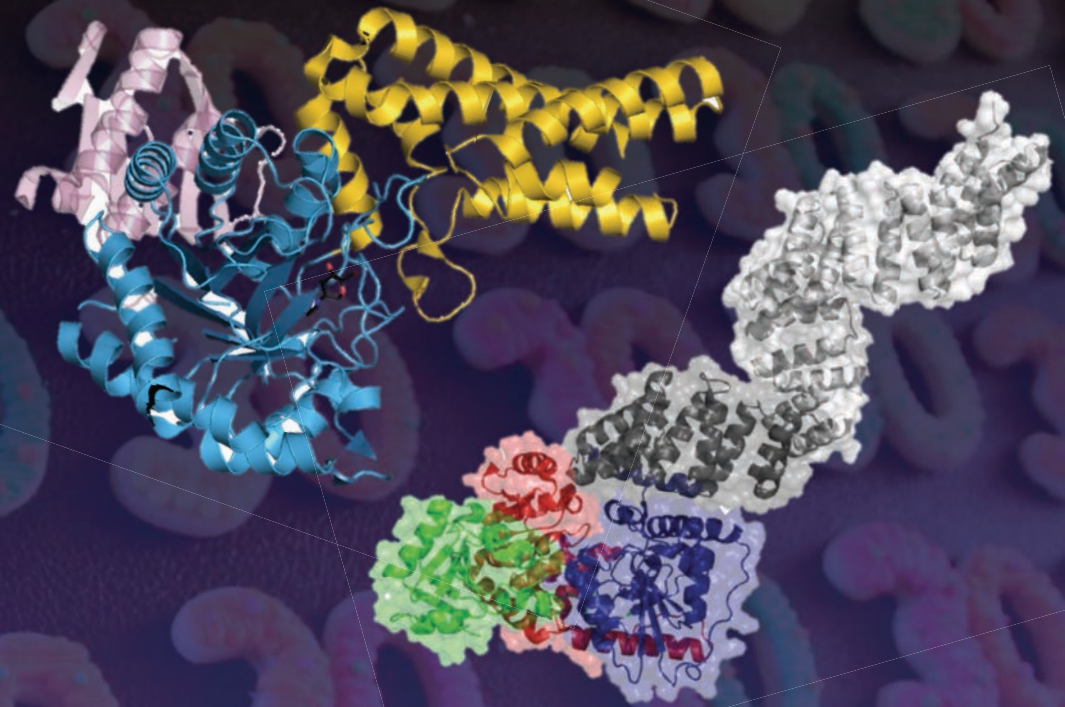
C₂C₁₂ Myotubes
n = 9

* P < 0.05

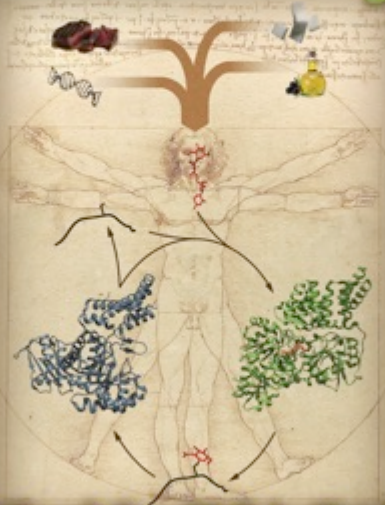
ARW

Wende ... Abel in prep

O-GlcNAcylation



the journal of biological chemistry
jbc
2014
THEMATIC
MINIREVIEW
SERIES



**Nutrient Regulation of Cellular Metabolism
& Physiology by O-GlcNAcylation**

ASBMB AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY



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Research Topic

30 years old: O-GlcNAc reaches age of reason - Regulation of cell signaling and metabolism by O-GlcNAcylation.

Submission closed.

Like Comment Share

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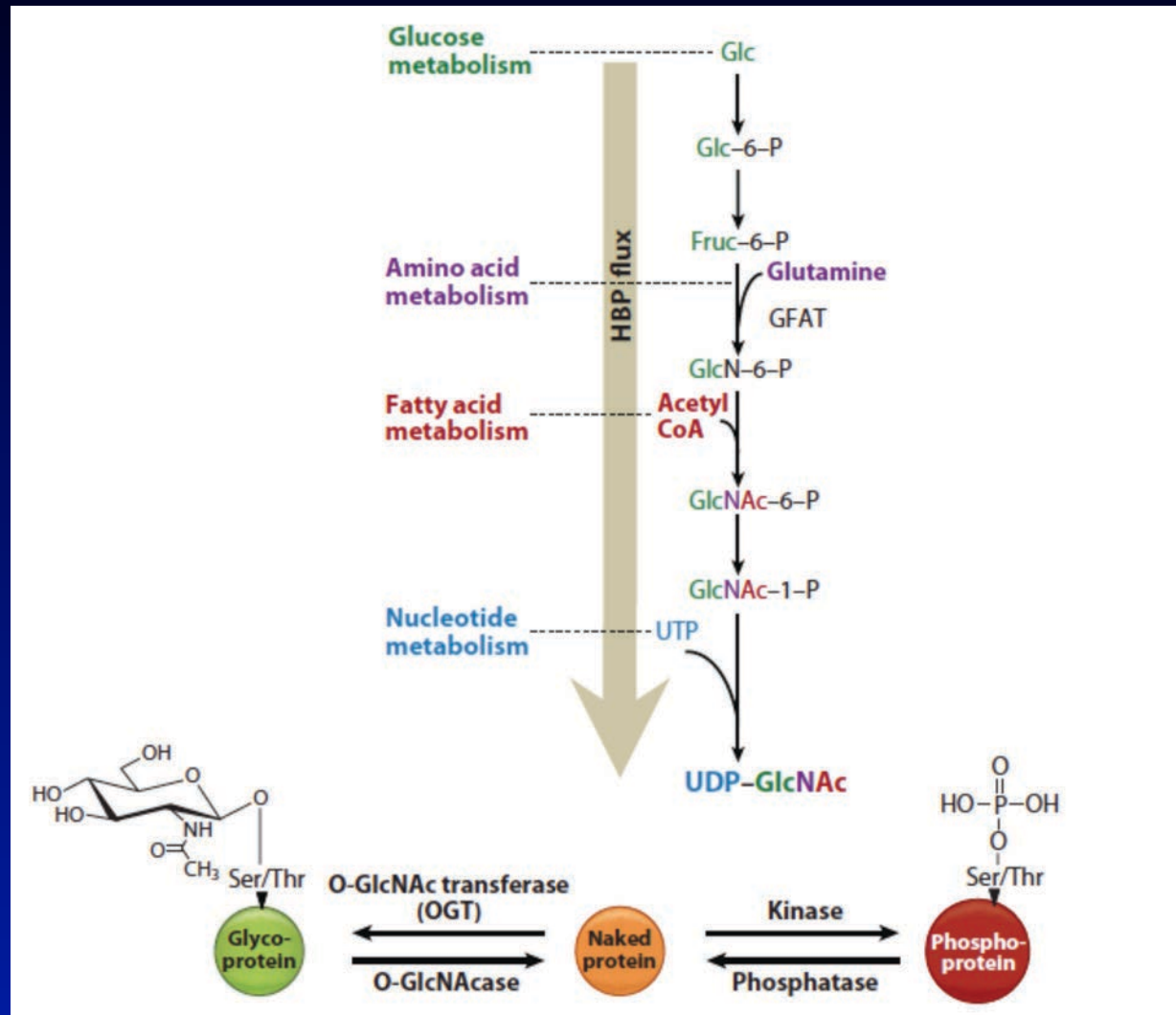
f 19 | t 1 | g+ 0 | in 0 | < 50

Overview 13 Articles 63 Authors Impact Comments

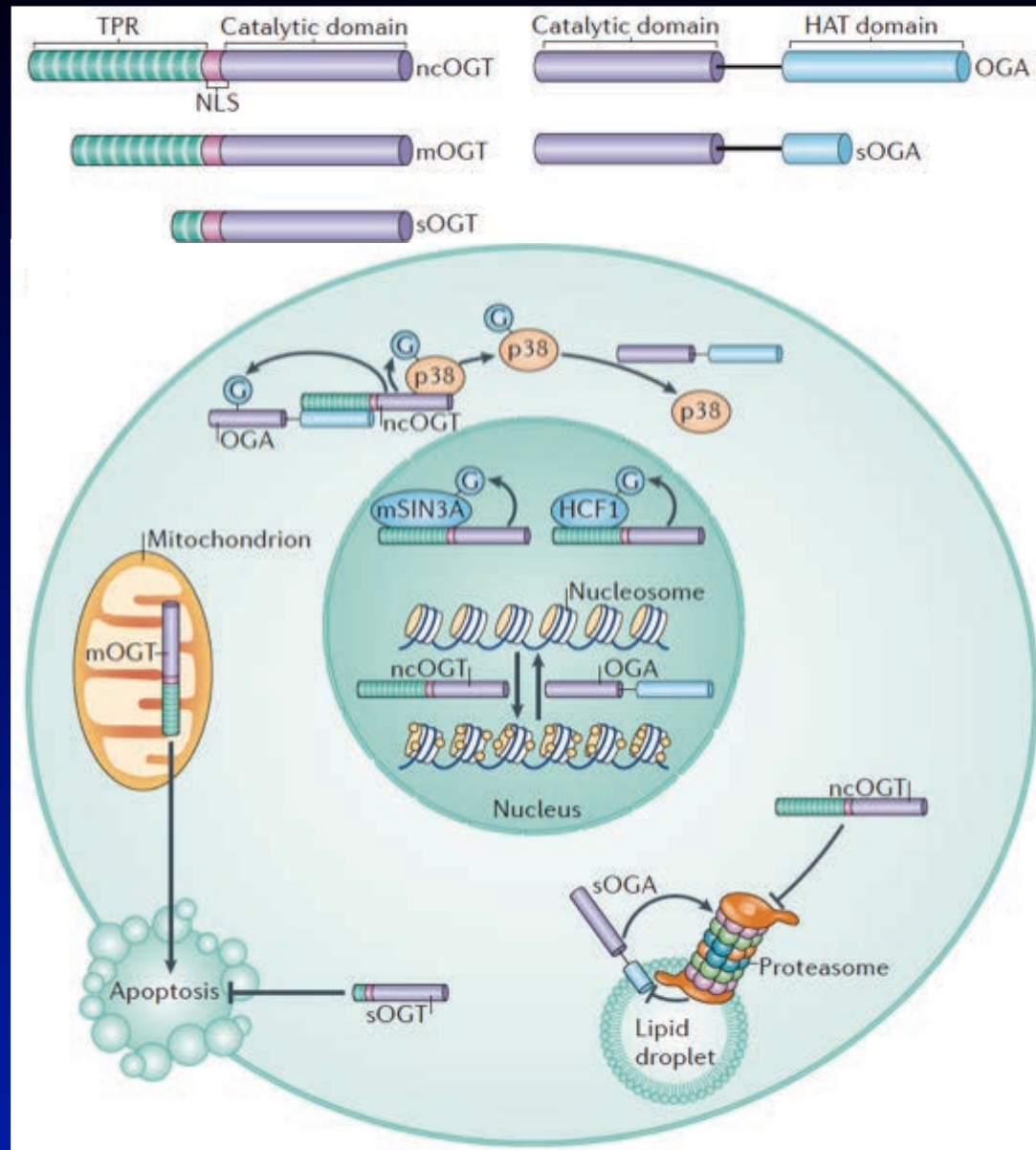
views

13,483

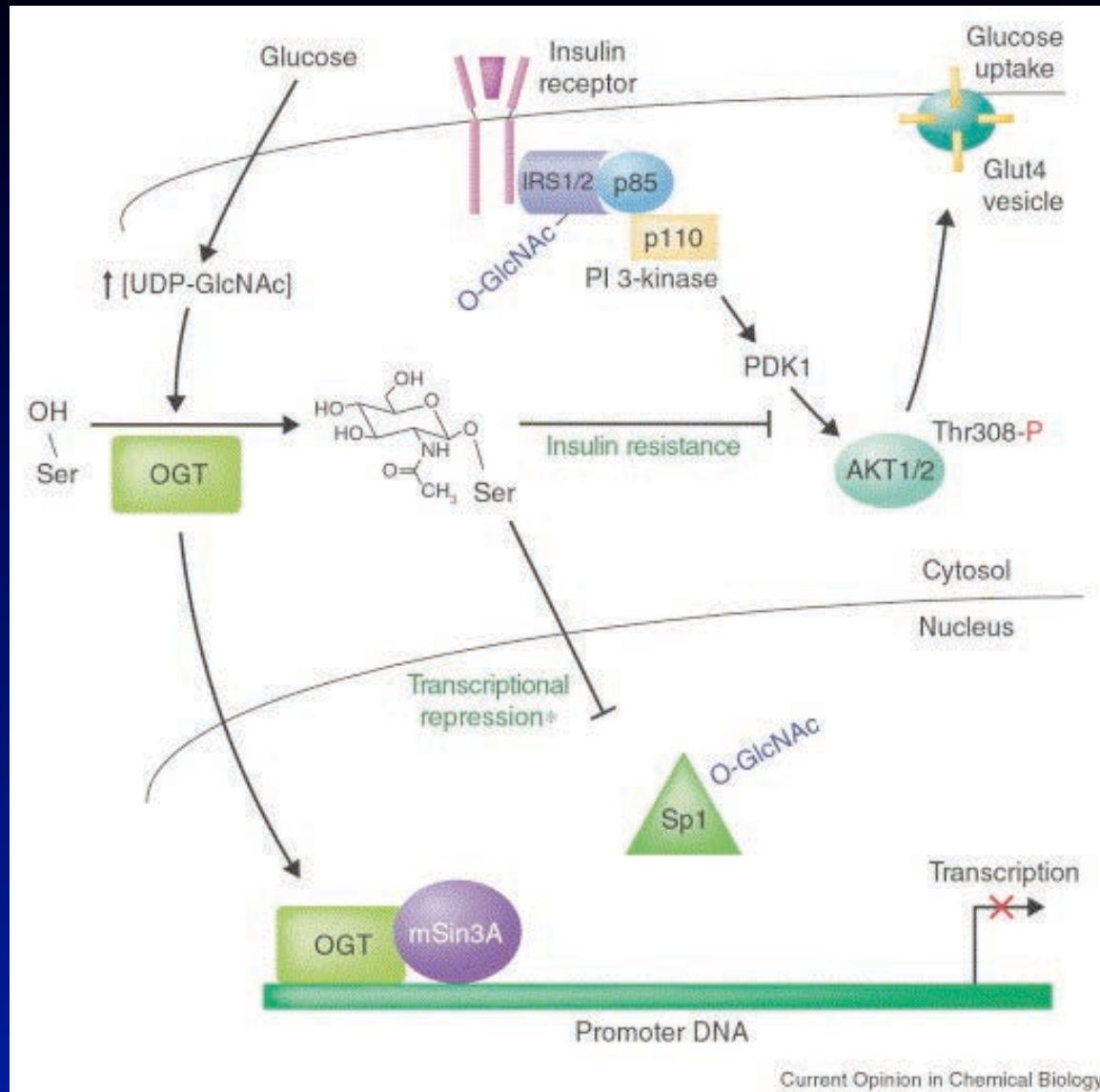
Metabolic Integration: Protein O-GlcNAcylation



O-GlcNAc Cycling

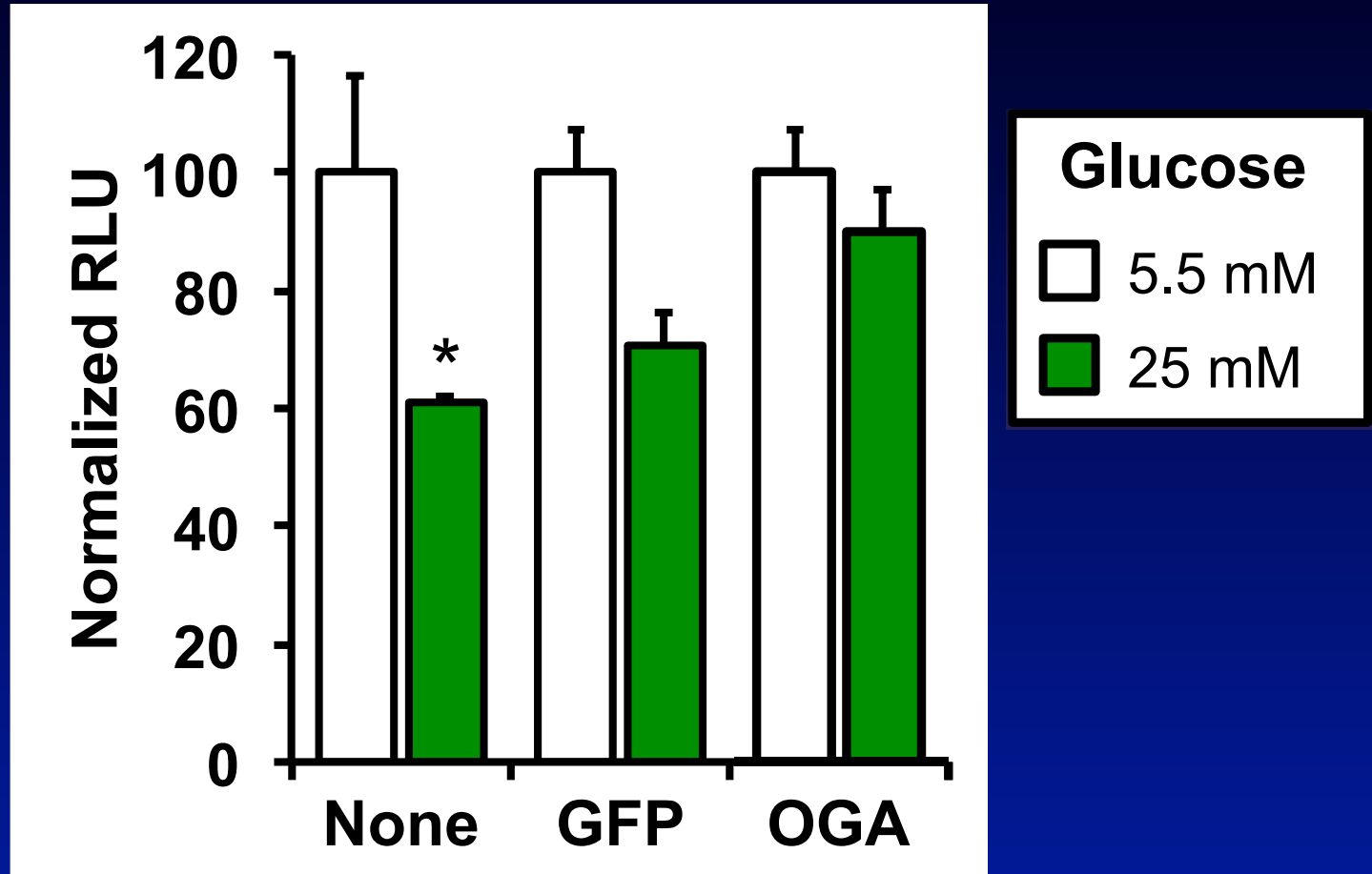


GlcNAc Regulation of Sp1



GlcNAcylation Regulates *Ndufa9* Gene Expression

Transient
Transfection
Promoter
Activity



C₂C₁₂ Myotubes

n = 3

* P < 0.05

ARW

Li Wang

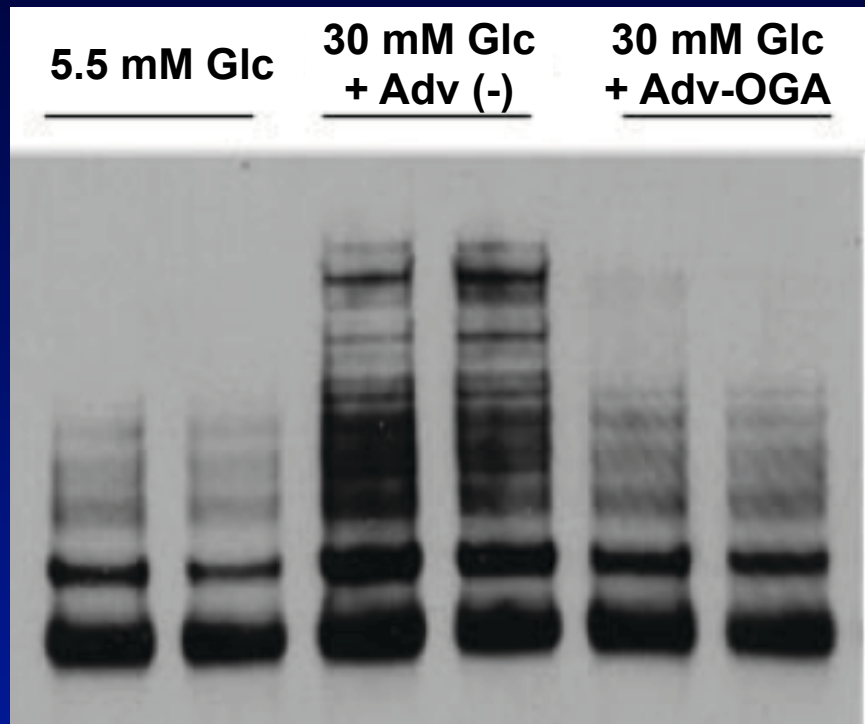
Wende ... Abel *in prep*

Conclusion – Part 2

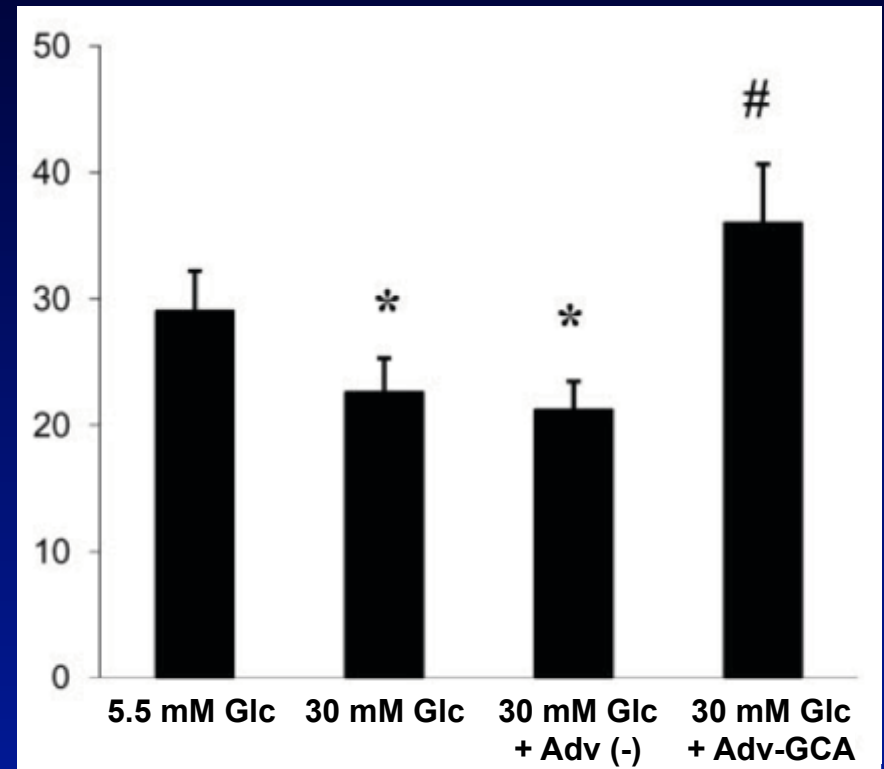
Enhanced glucose delivery regulates oxidative capacity via transcriptional mechanisms including GlcNAcylation of transcription factors.

Mitochondrial Protein O-GlcNAcylation and Neonatal Cardiomyocyte Metabolic Function

Mitochondrial Protein O-GlcNAcylation



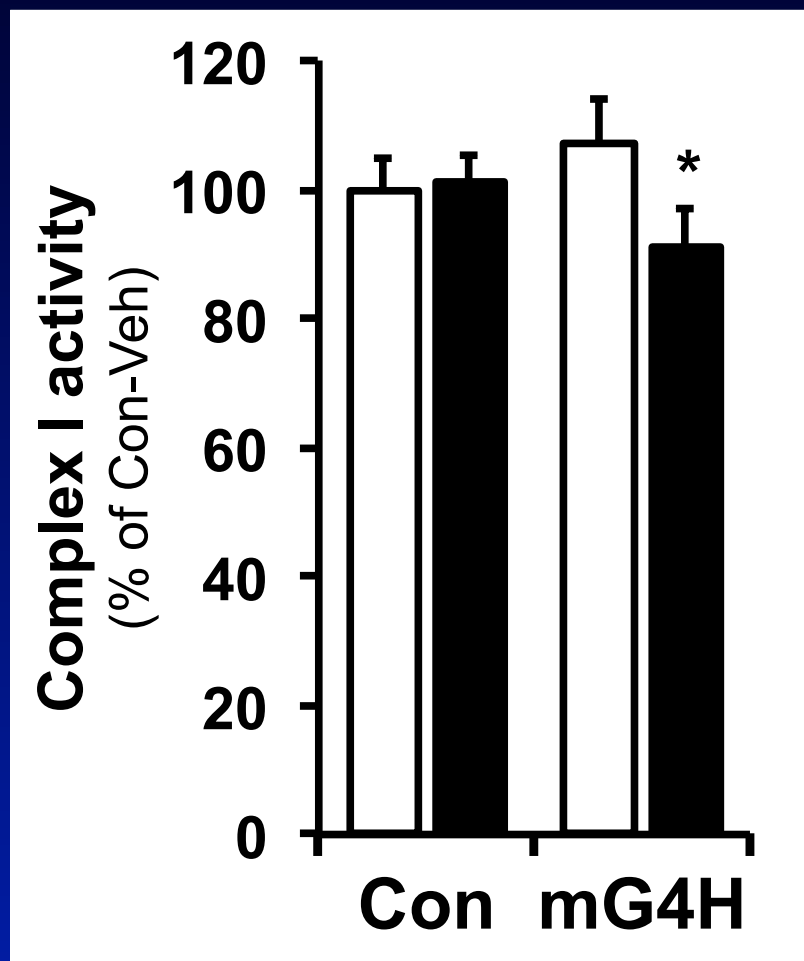
Complex I Activity



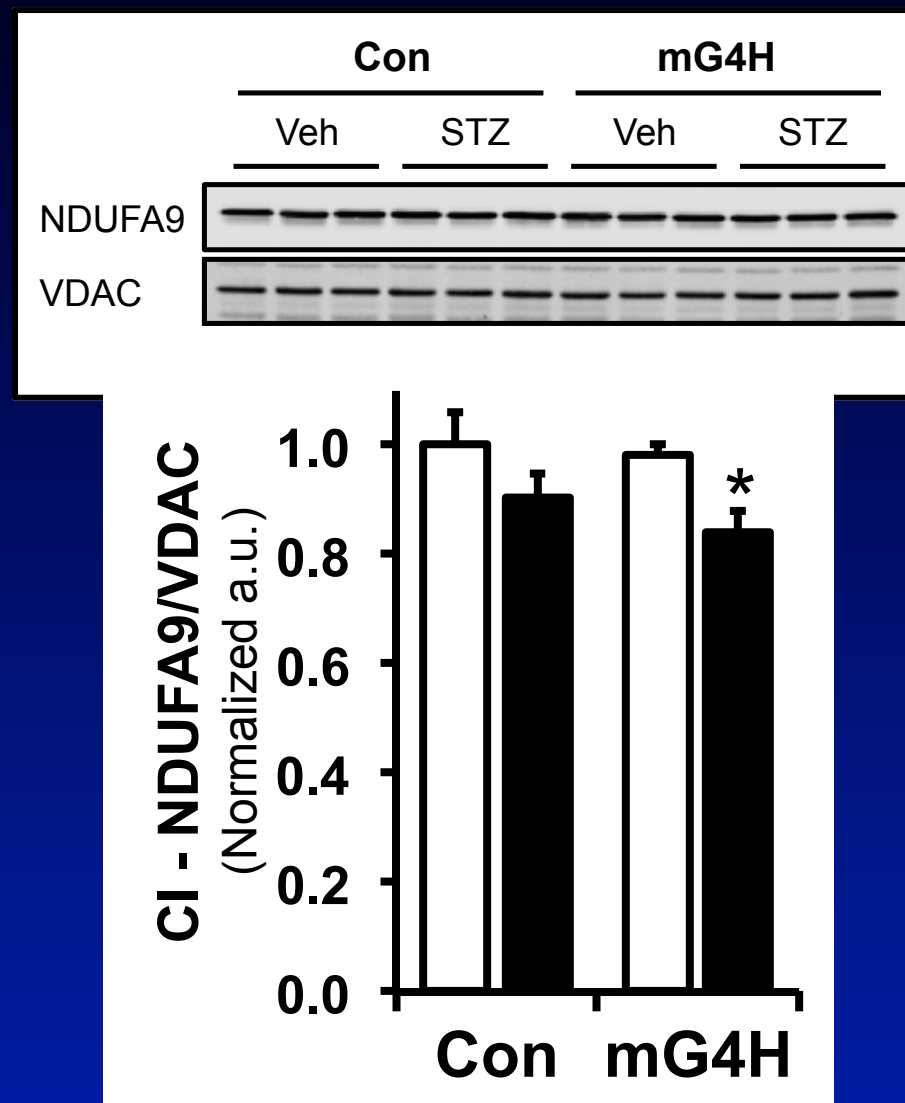
O-GlcNAcylation of NDUFA9

NDUFA9 – Complex I

OXPPOS
Activity

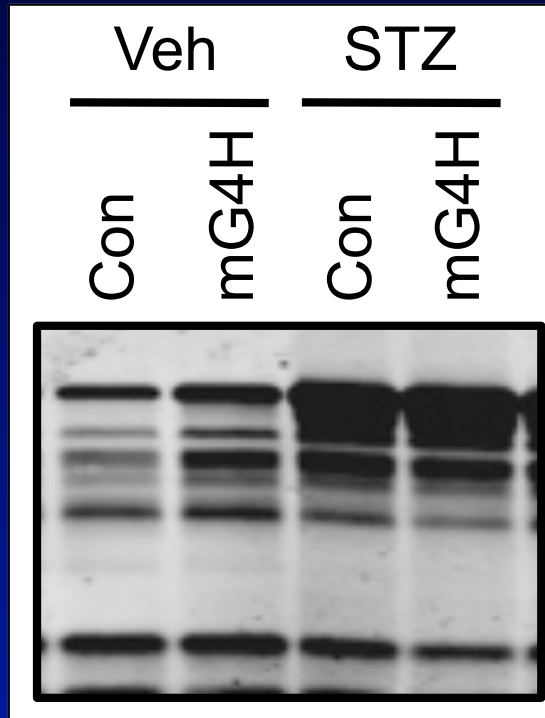


Western Blot

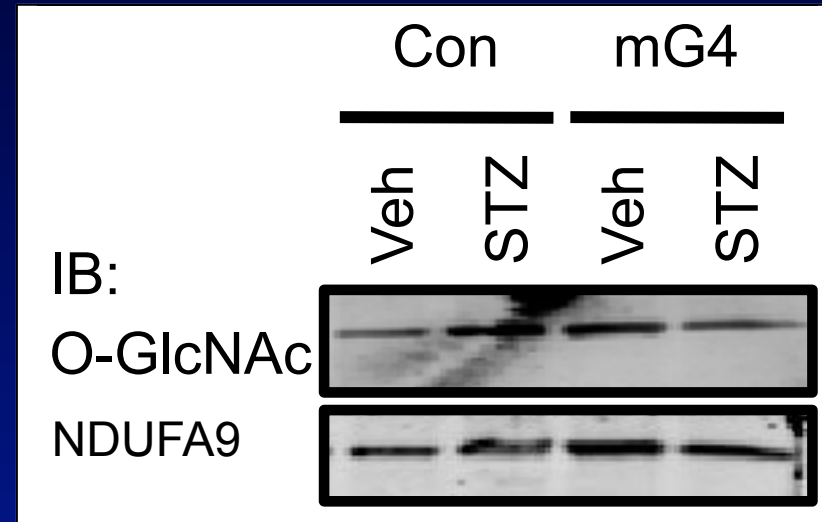


GLUT4 Induction Alters Mitochondrial Protein O-GlcNAcylation

Mitochondrial Protein O-GlcNAcylation

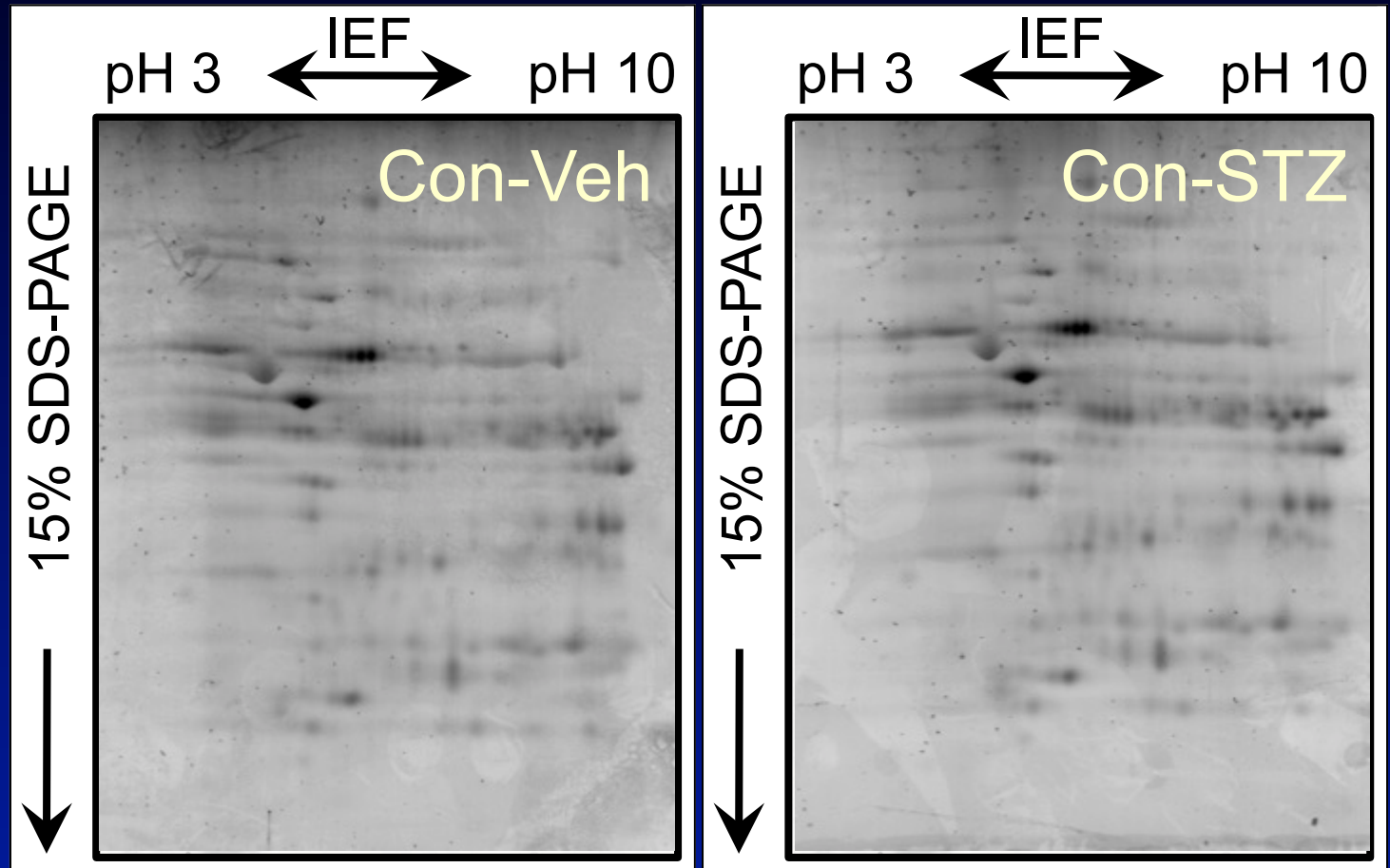


NDUFA9 Immunoprecipitation



GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome

Isolated
Mitochondria
2D-PAGE
Pro-Q
Emerald



Hansjörg Schwertz
Wende, unpublished

GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome

Symbol	Description	Gene ID	O-GlcNAc Target	LC-MS/MS PTM	Pathway
ATP5A1	ATP synthase F1 complex, α subunit 1	11946	known ^{1,2}	Ac-	OXPHOS
ATP5H	ATP synthase F0 complex, subunit d	71679	novel	Ac-	OXPHOS
ATP5O	ATP synthase F1 complex, O subunit	28080	novel		OXPHOS
ETFB	Electron transferring flavoprotein, β polypeptide	110826	novel	Ac-	OXPHOS
UQCRC1	Ubiquinol-cytochrome c reductase core protein 1	22273	known ¹		OXPHOS
UQCRFS1	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	66694	novel		OXPHOS
MDH2	Malate dehydrogenase 2, NAD (mitochondrial)	17448	novel	Ac-	TCA
OGDH	Oxoglutarate dehydrogenase (lipoamide)	18293	known ³	P-	TCA
SUCLA2	Succinate-Coenzyme A ligase, ADP-forming, β subunit	20916	novel	Ac-, P-	TCA
DLAT	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	235339	known ¹		Glycolysis/ TCA
ACADL	Acyl-Coenzyme A dehydrogenase, long-chain	11363	novel	P-	FAO
HADHB	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), β subunit	231086	novel	P-	FAO

PTM = post-translational modification; Ac- = acetylation; P- = phosphorylation; OXPHOS = Oxidative phosphorylation; TCA = Tricarboxylic acid cycle; FAO = Fatty acid β -oxidation

¹Clark et al 2008 J Am Chem Soc 130(35): 11576; Previously identified modification by O-GlcNAc in rat brain and HeLa cells.

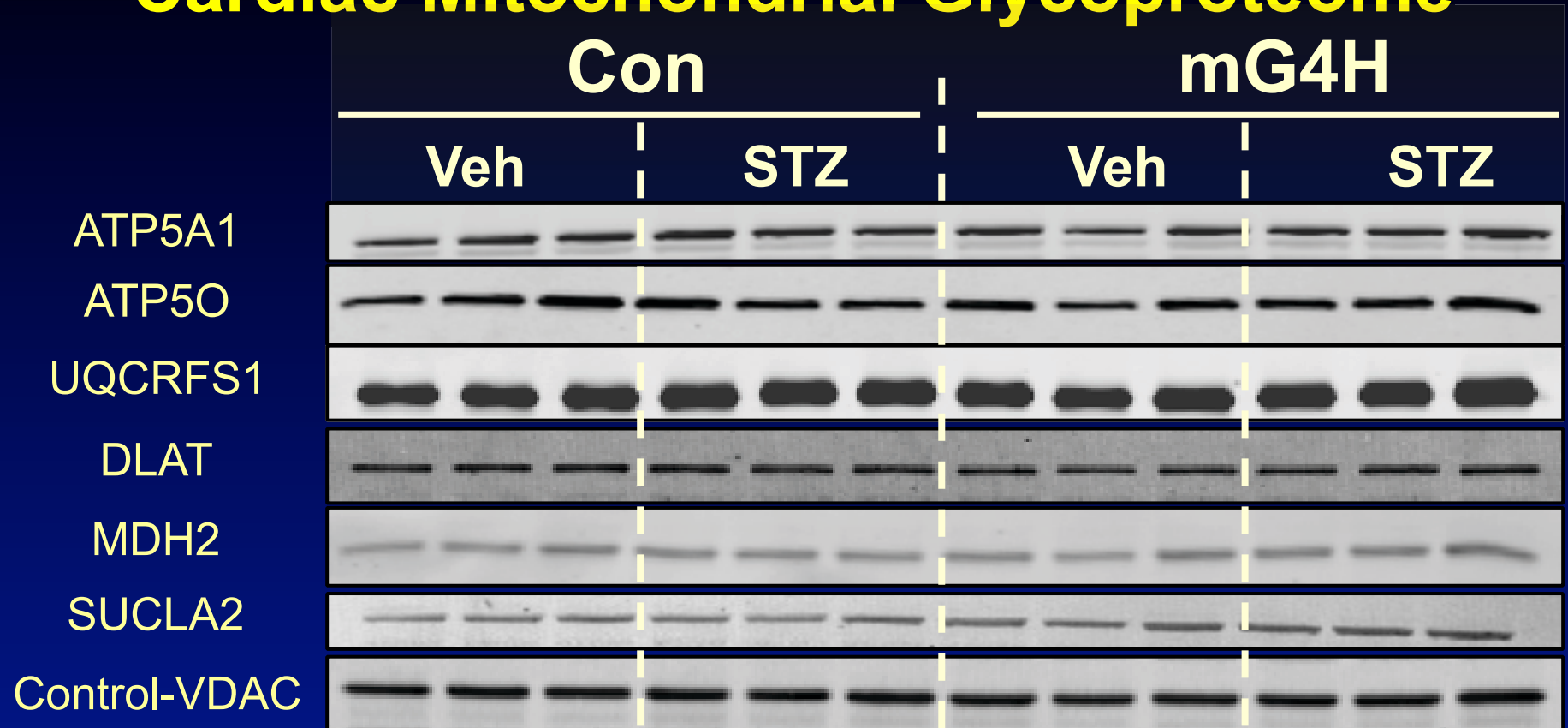
²Teo et al 2010 Nat Chem Biol 6(5):338; Previously identified modification by O-GlcNAc in rat liver.

³Nandi et al 2006 Anal Chem 78(2):452; Previously identified modification by O-GlcNAc in HeLa cells.

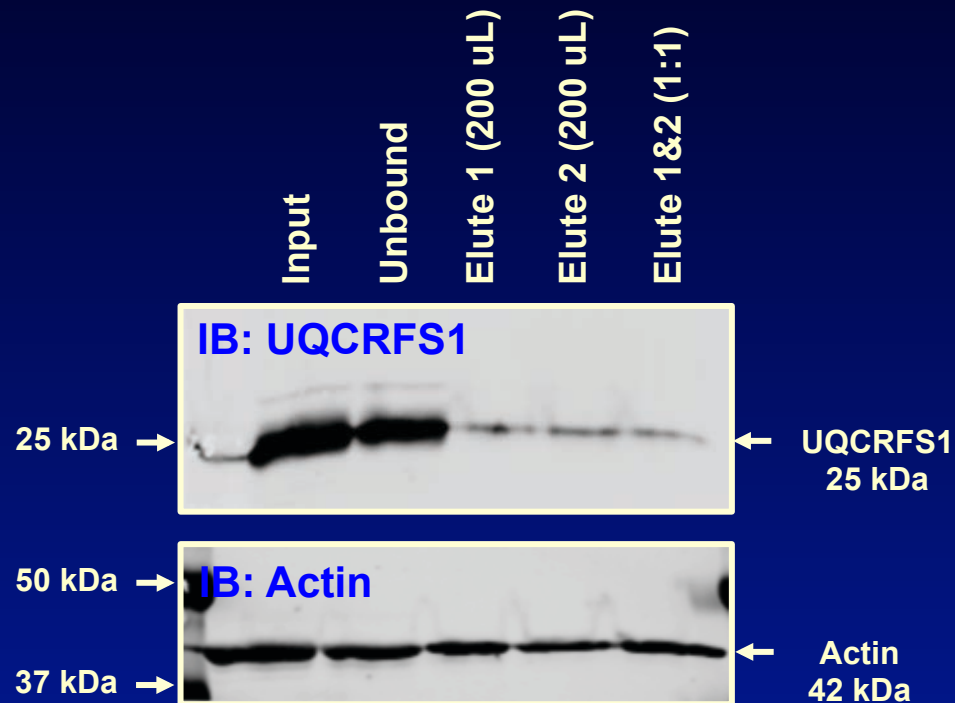
Wende, unpublished

dbOGAP <http://cbsb.lombardi.georgetown.edu> and YinOYang www.cbs.dtu.dk

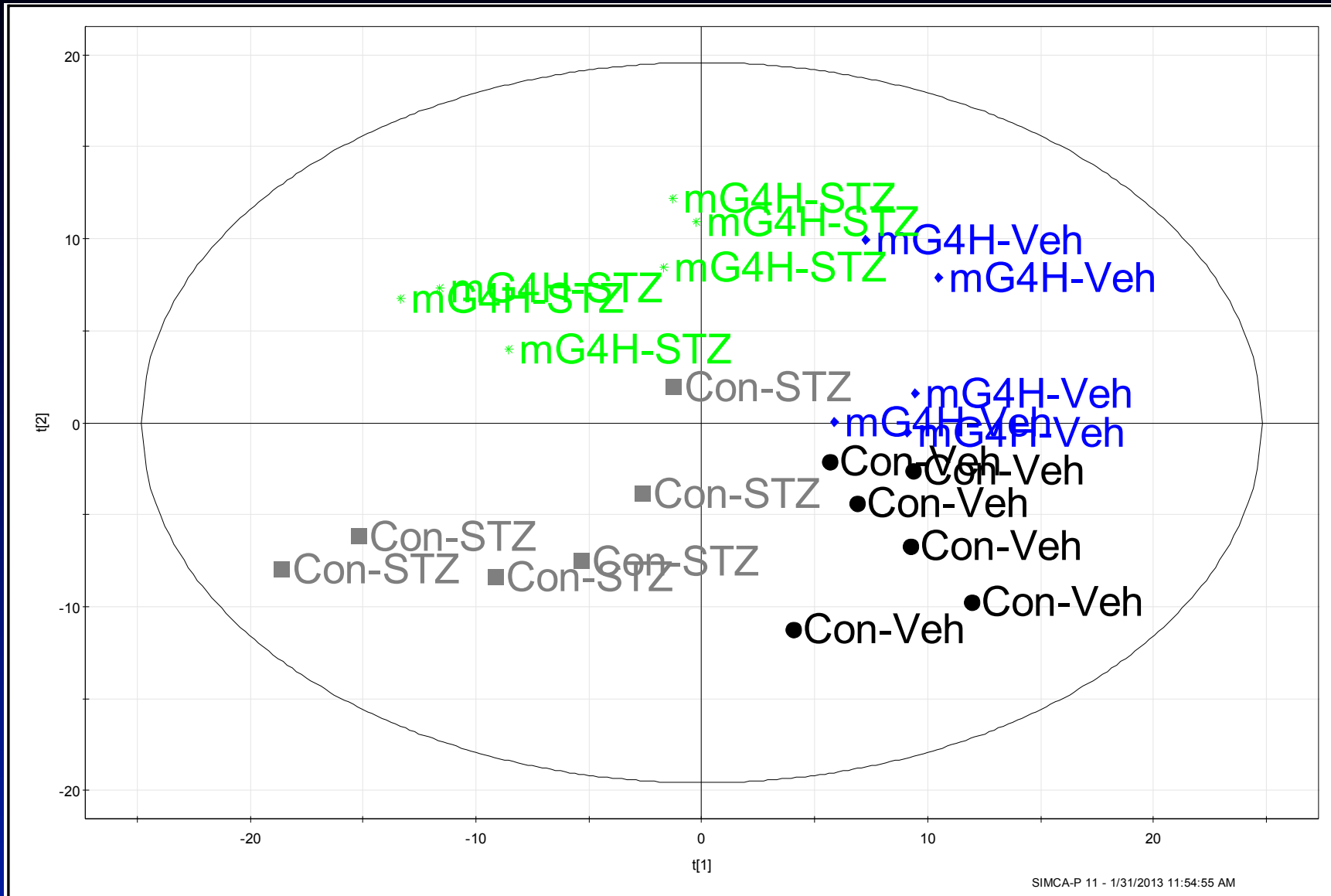
GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome



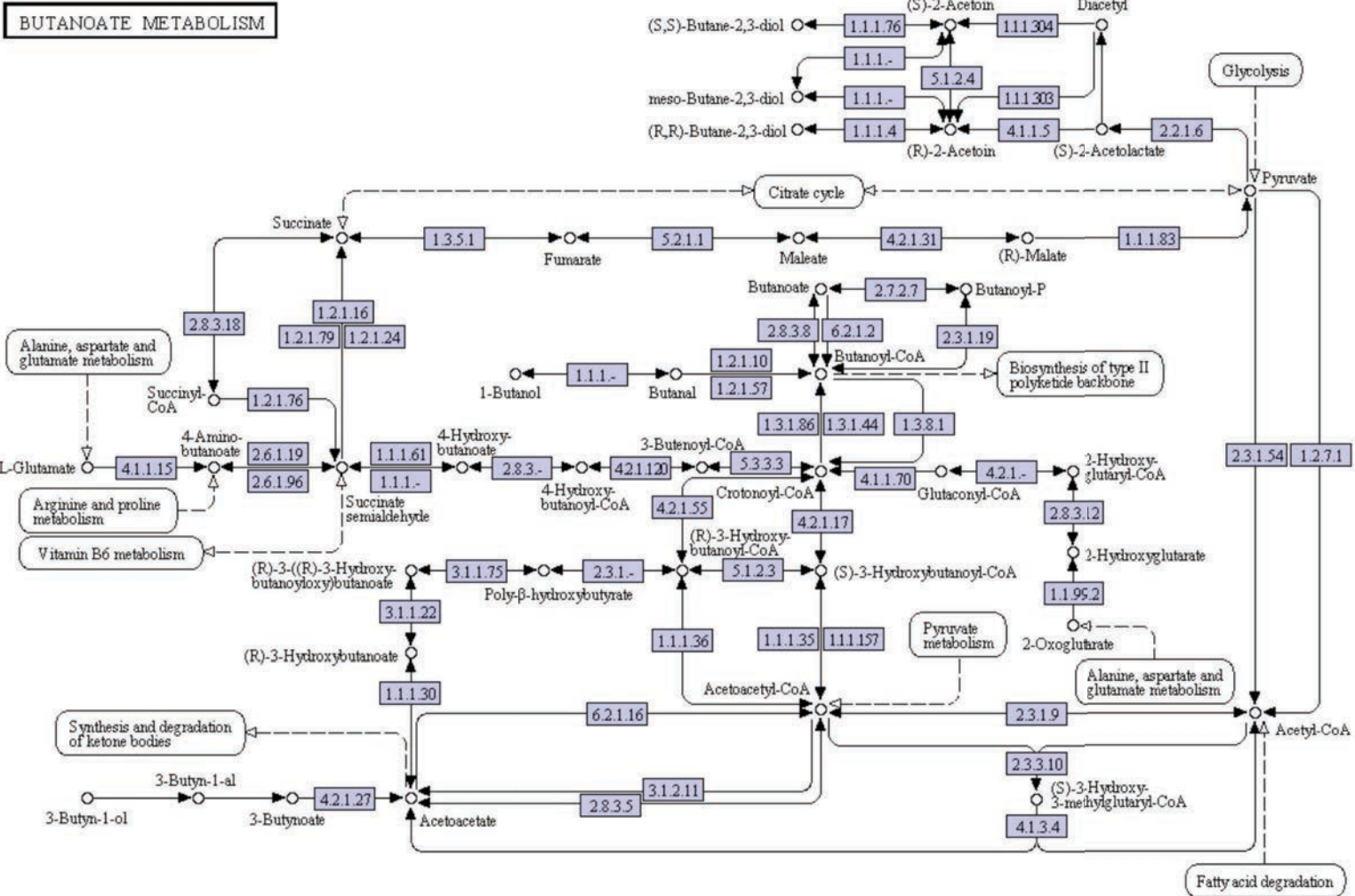
GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome



Metabolomics

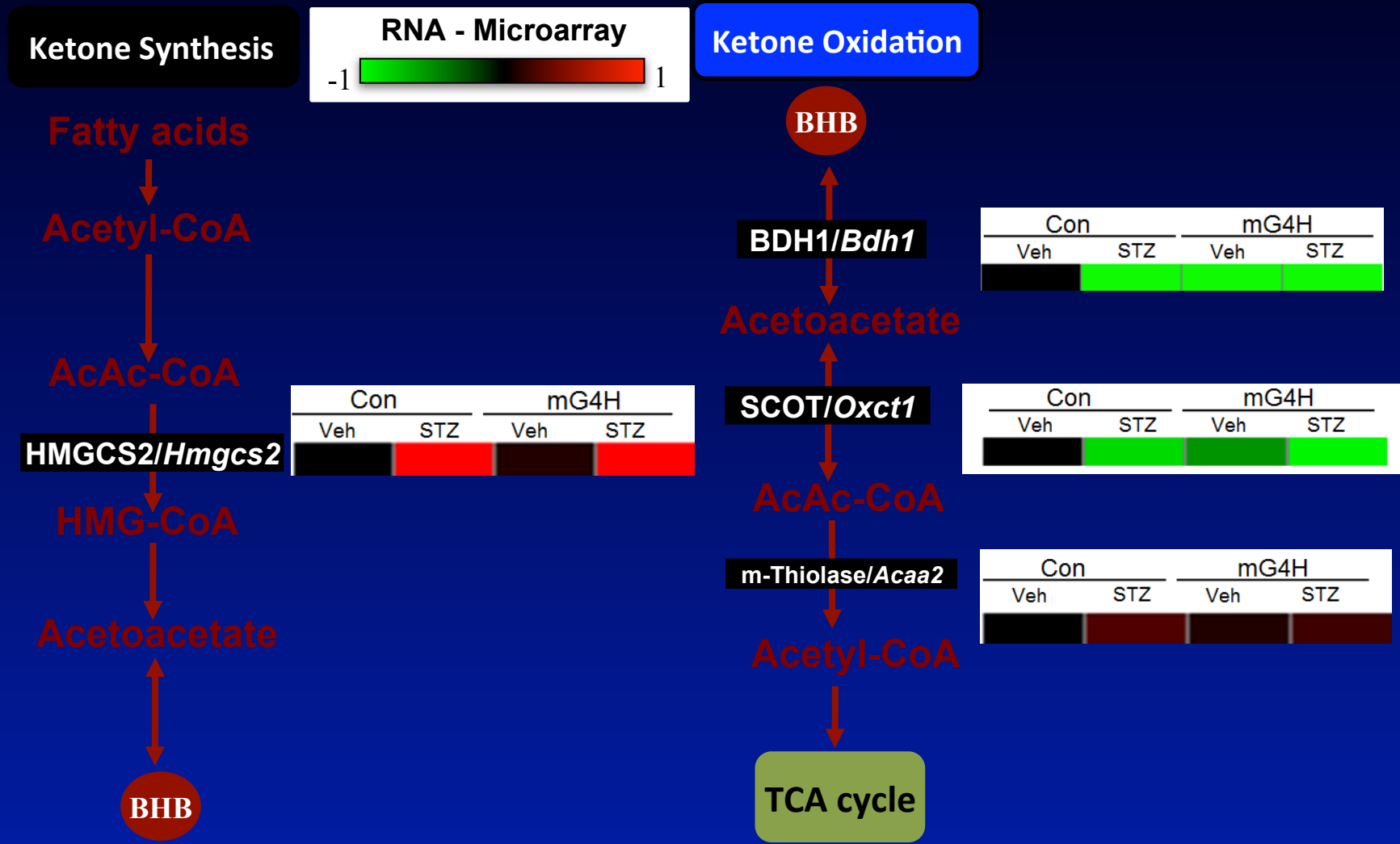


Metabolomics

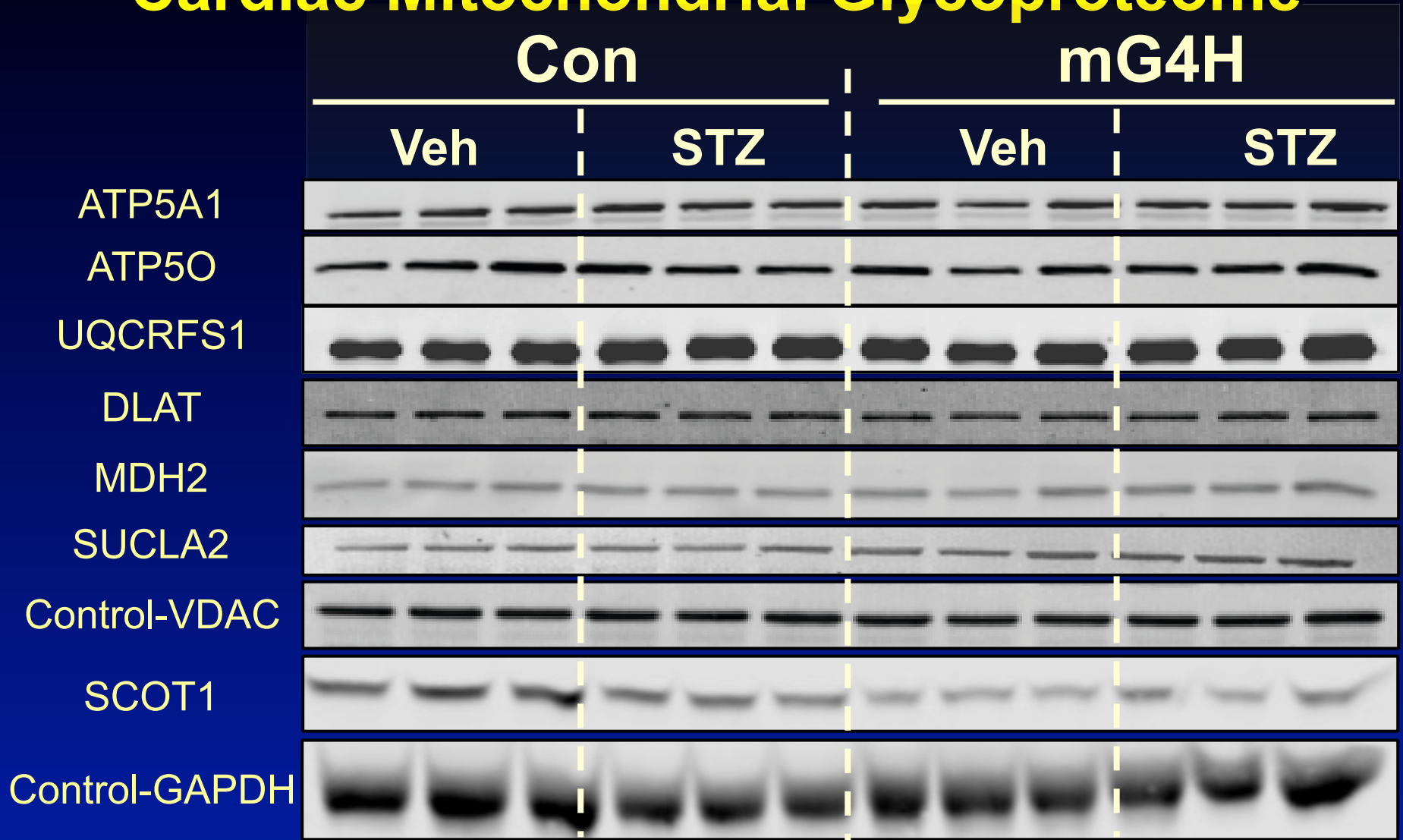


00650 6/24/14
 (c) Kanehisa Laboratories

GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome

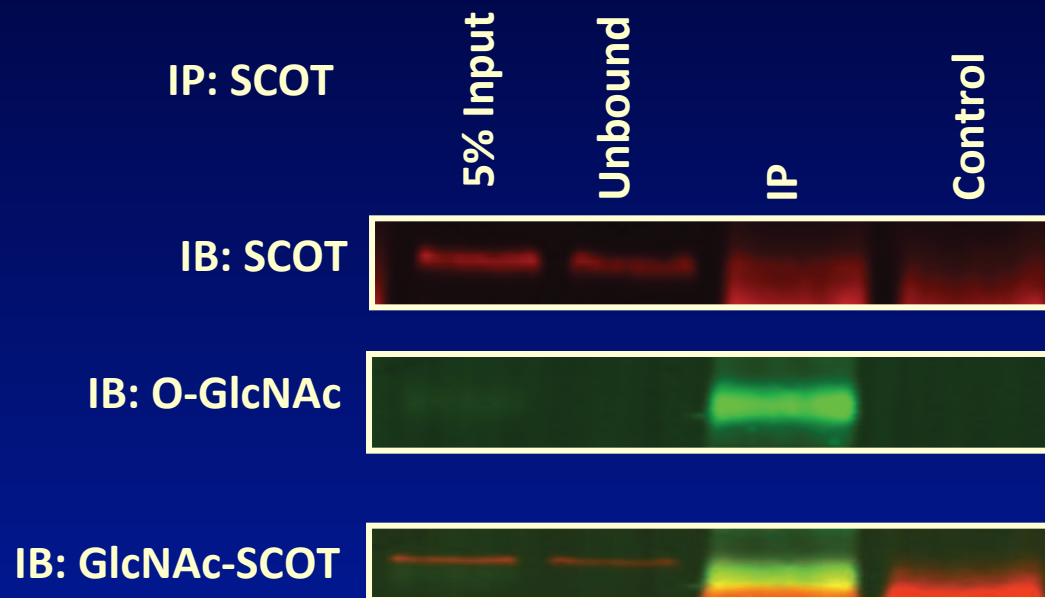


GLUT4 Induction Alters the Cardiac Mitochondrial Glycoproteome



GLUT4 Induction Alters Mitochondrial Protein O-GlcNAcylation

SCOT immunoprecipitation
from LV of 24h fasted mice



Conclusion – Part 3

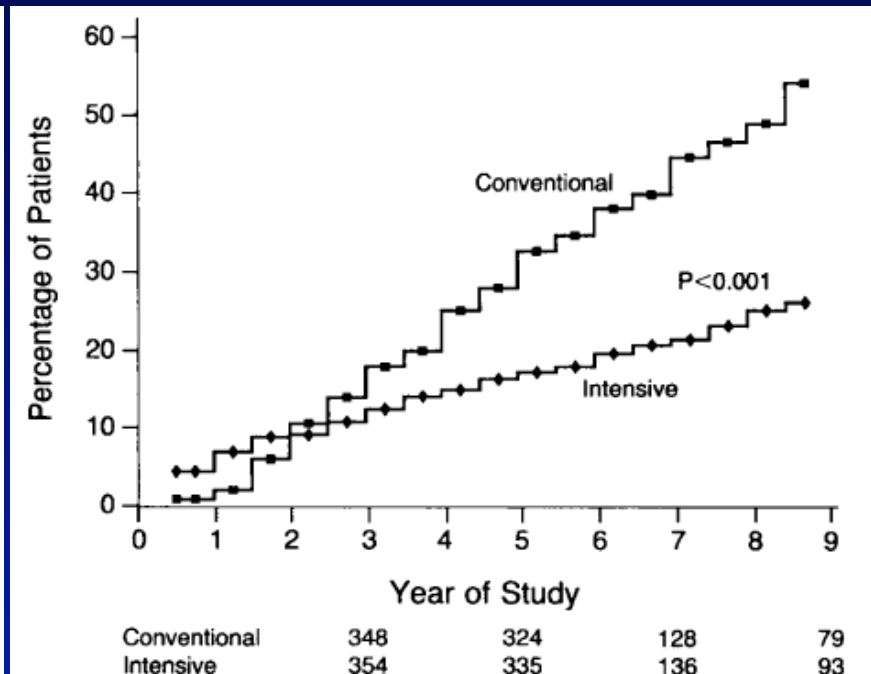
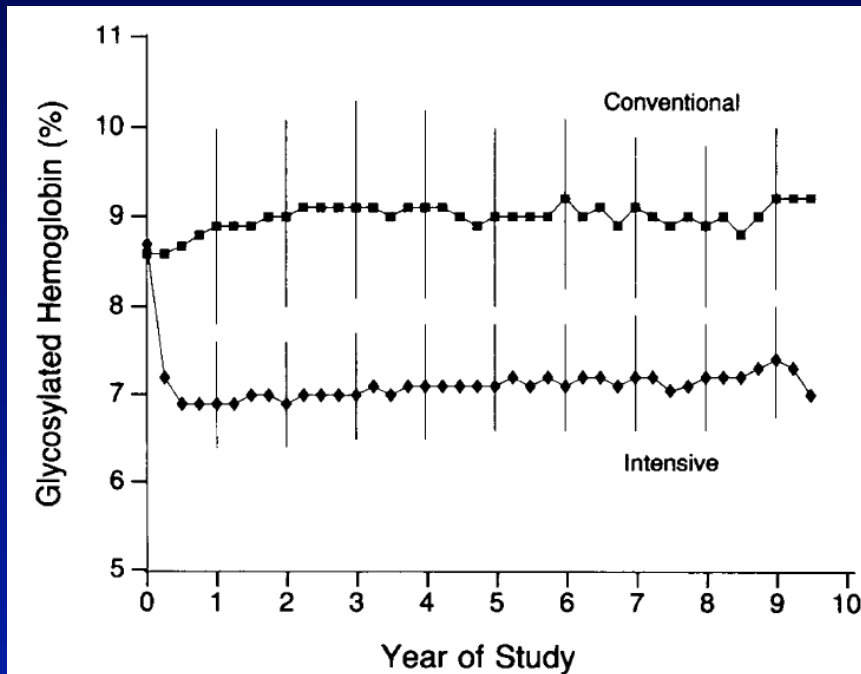
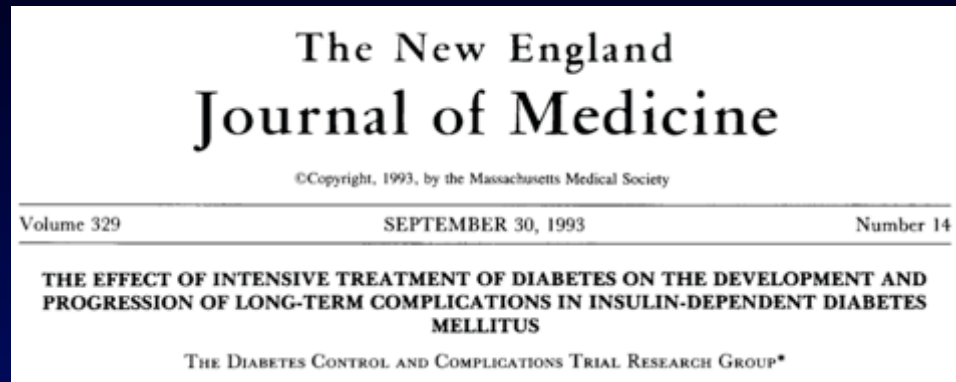
Enhanced cardiac glucose delivery alters metabolic flux through other pathways and regulates the mitochondrial proteome via O-GlcNAcylation.

From Human to Mouse and Back Again



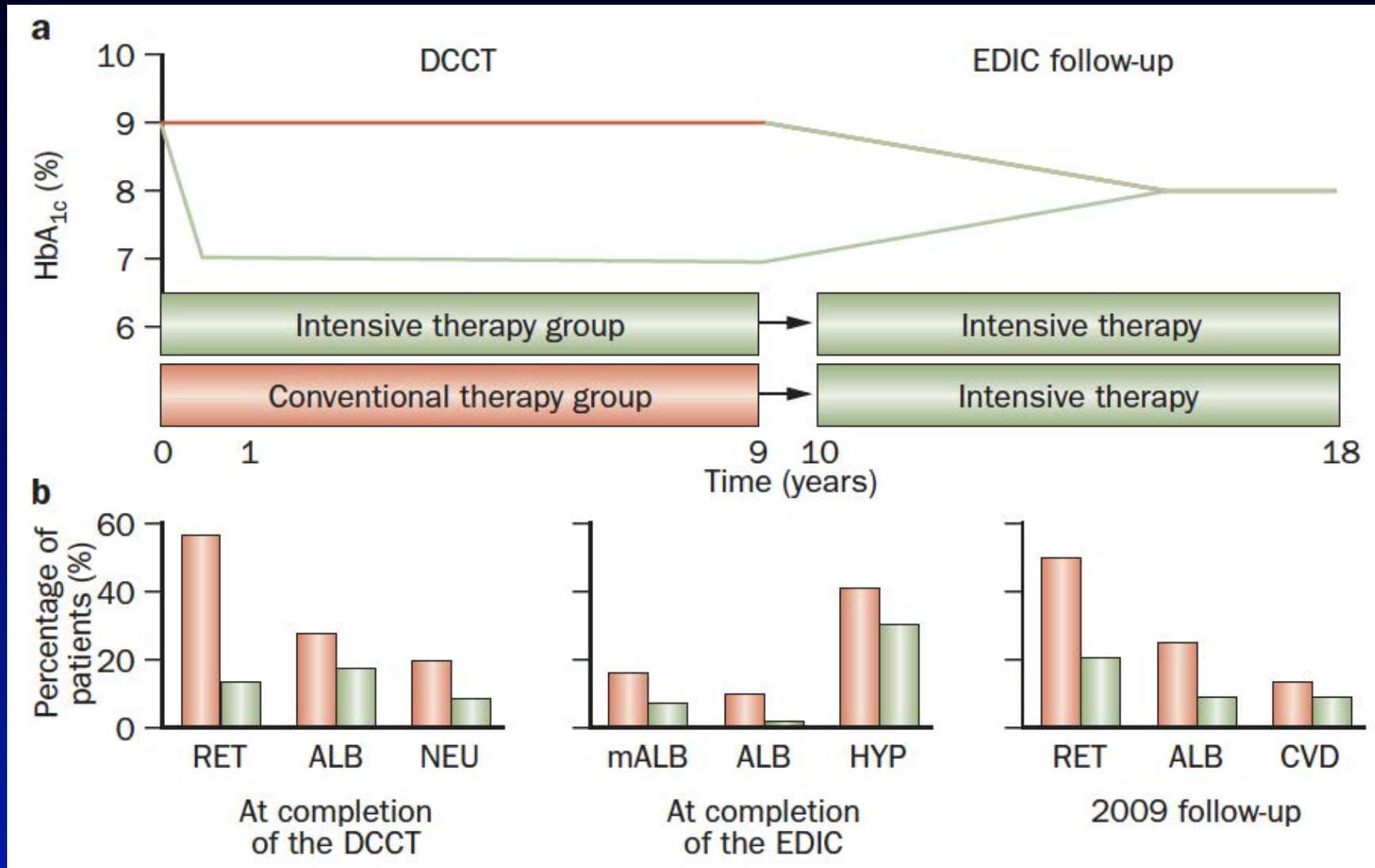
Epigenetics - Programming

DCCT: Diabetes Control and Complications Trial

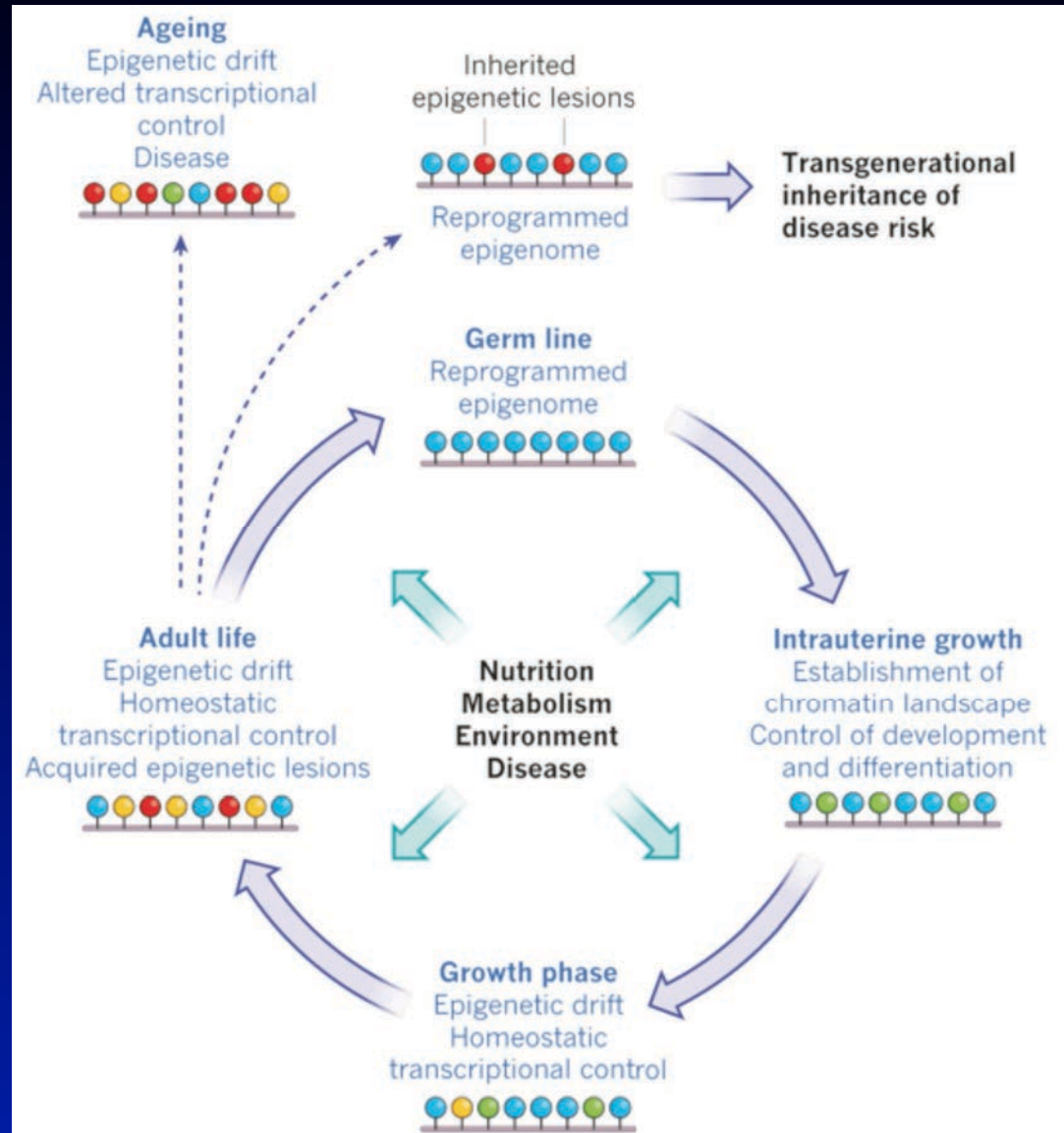


Epigenetics - Memory

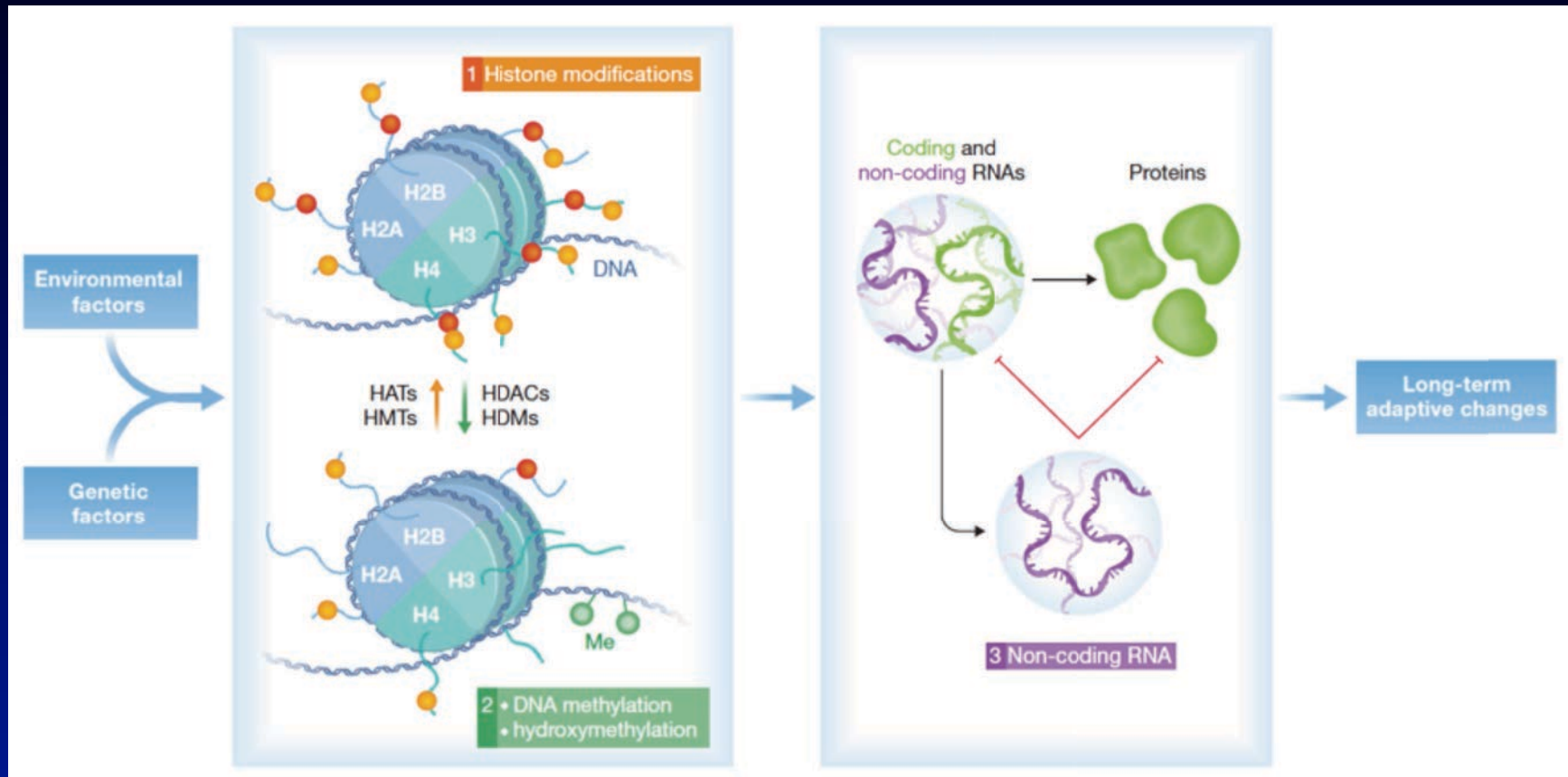
EDIC: Epidemiology of Diabetes Interventions Trial



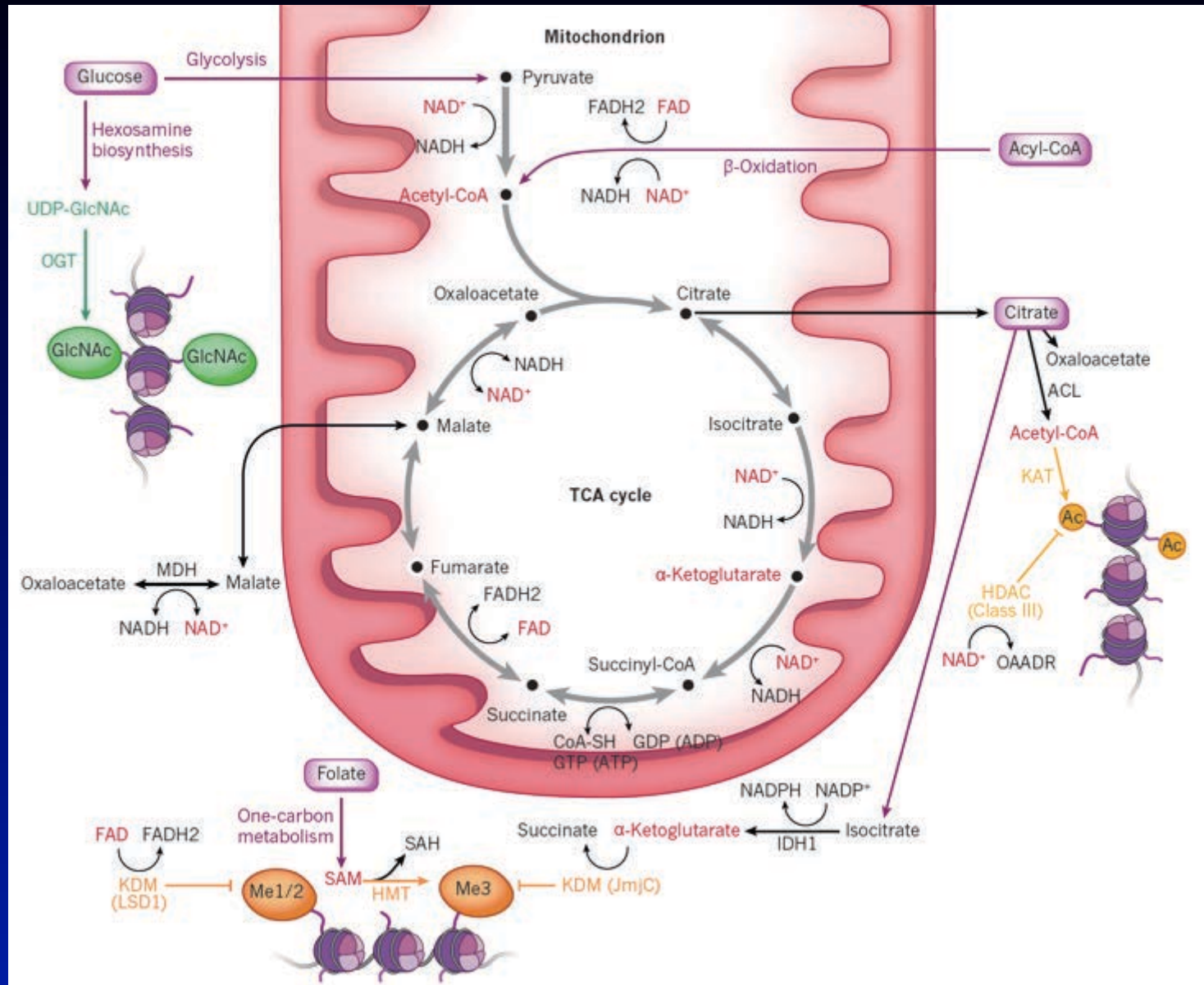
Epigenetics: Transgenerational and Drift



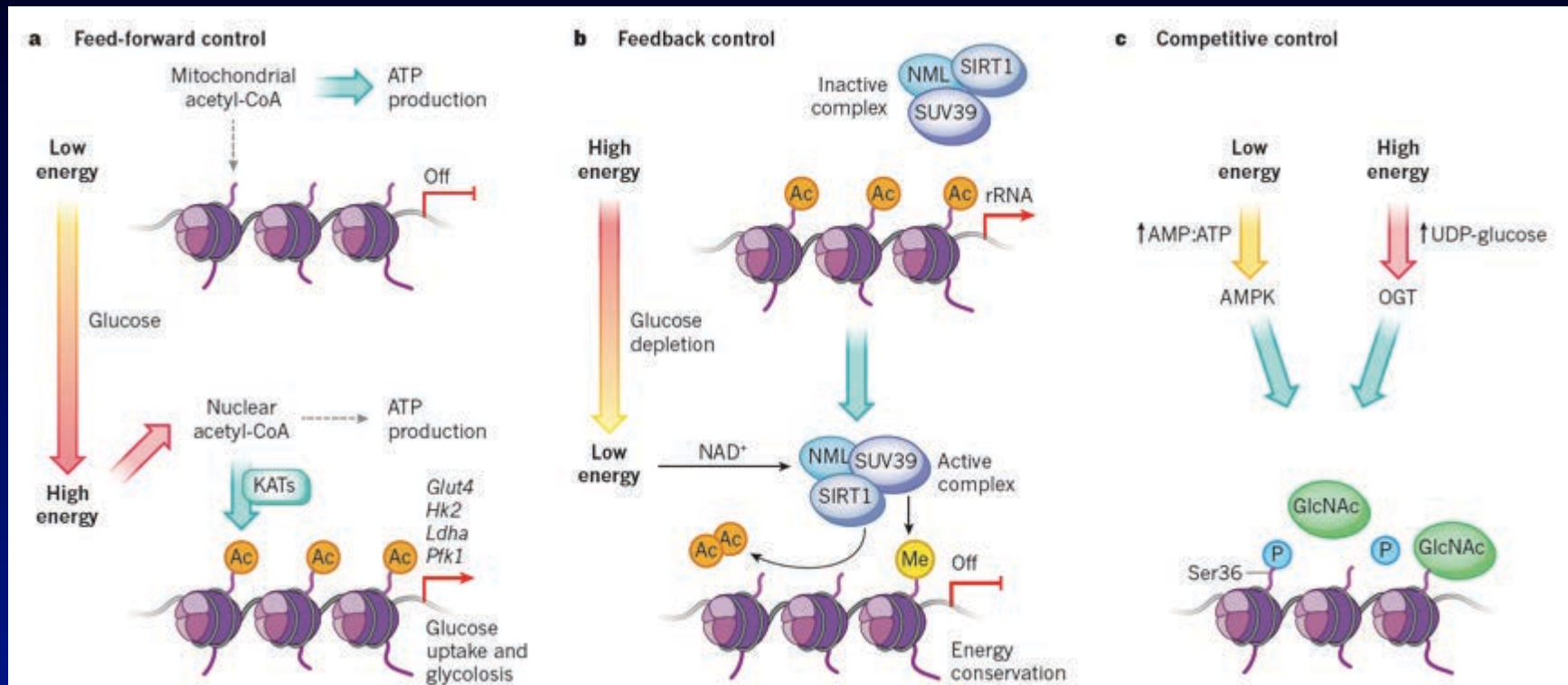
Epigenetic Code



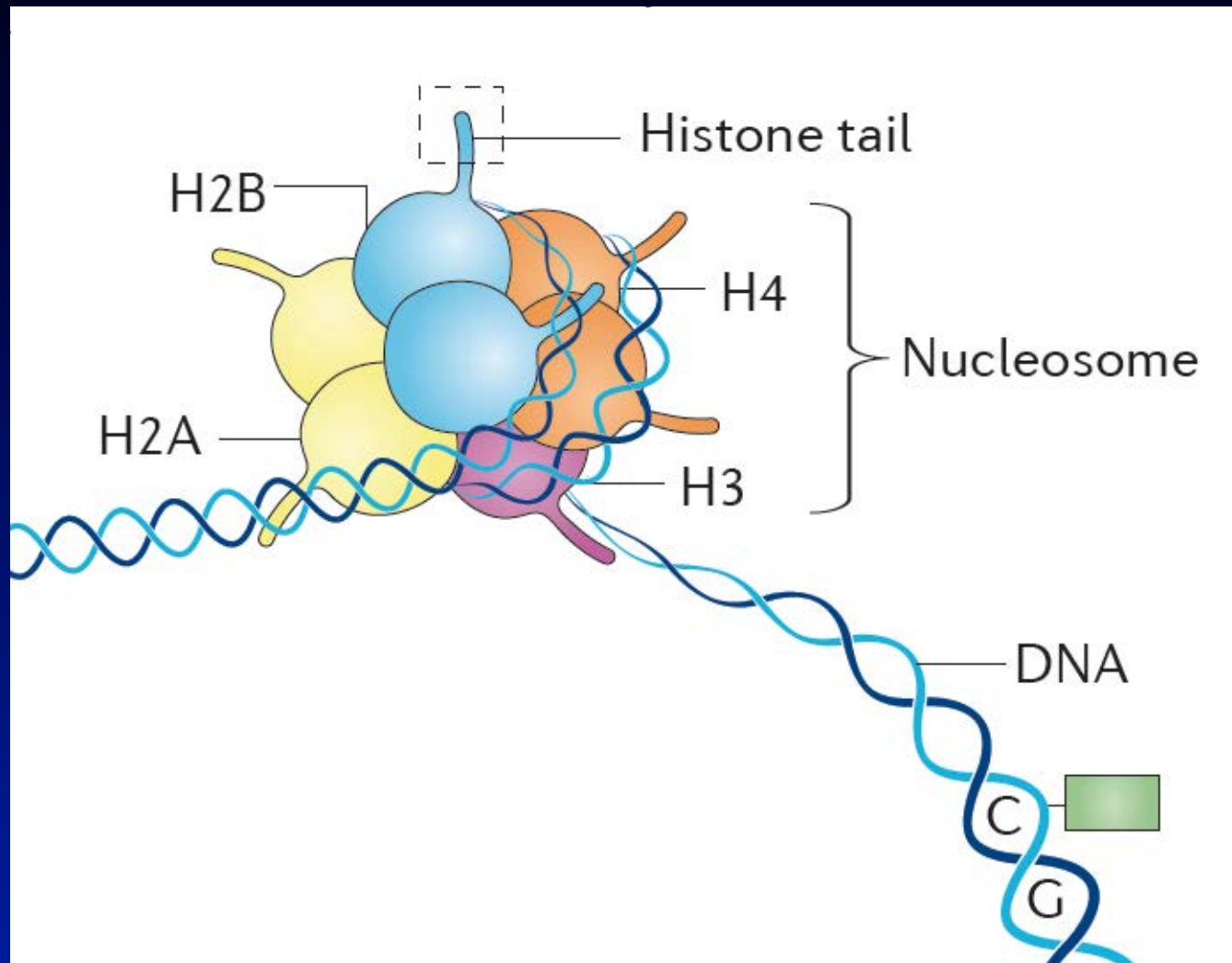
Metabolite Signaling to Chromatin



How does GlcNAc fit in?



Chromatin Regulation



How does GlcNAc fit in?

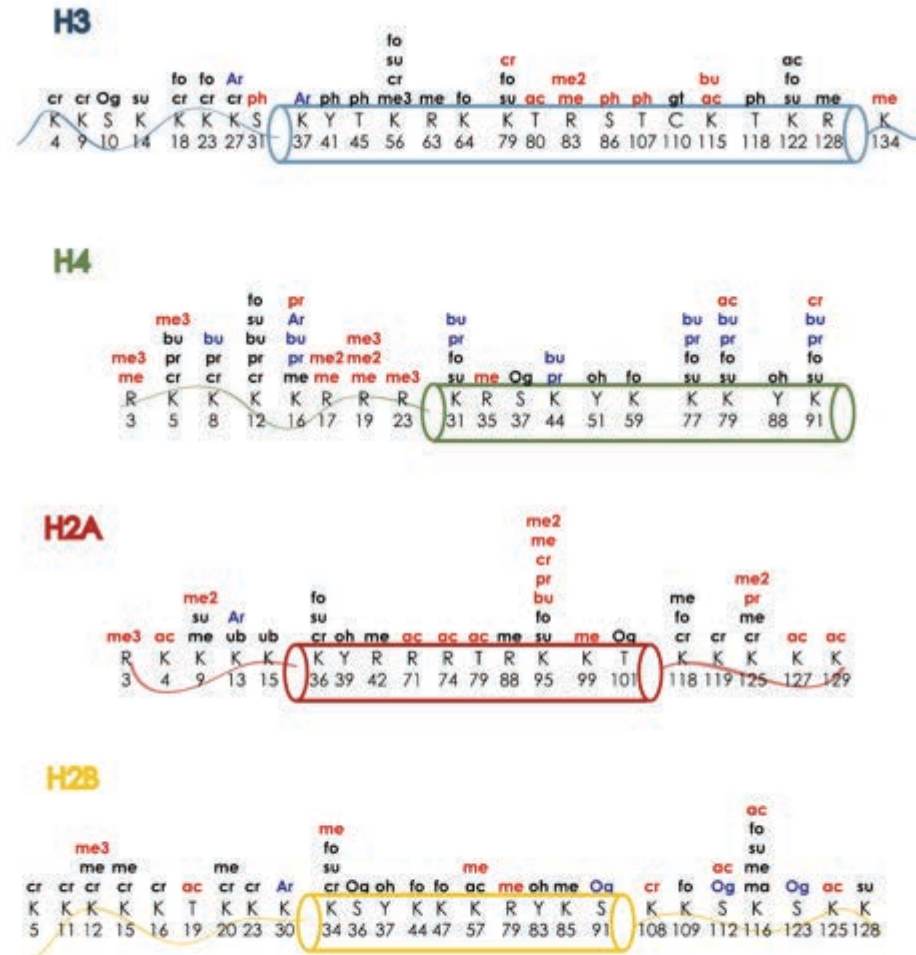
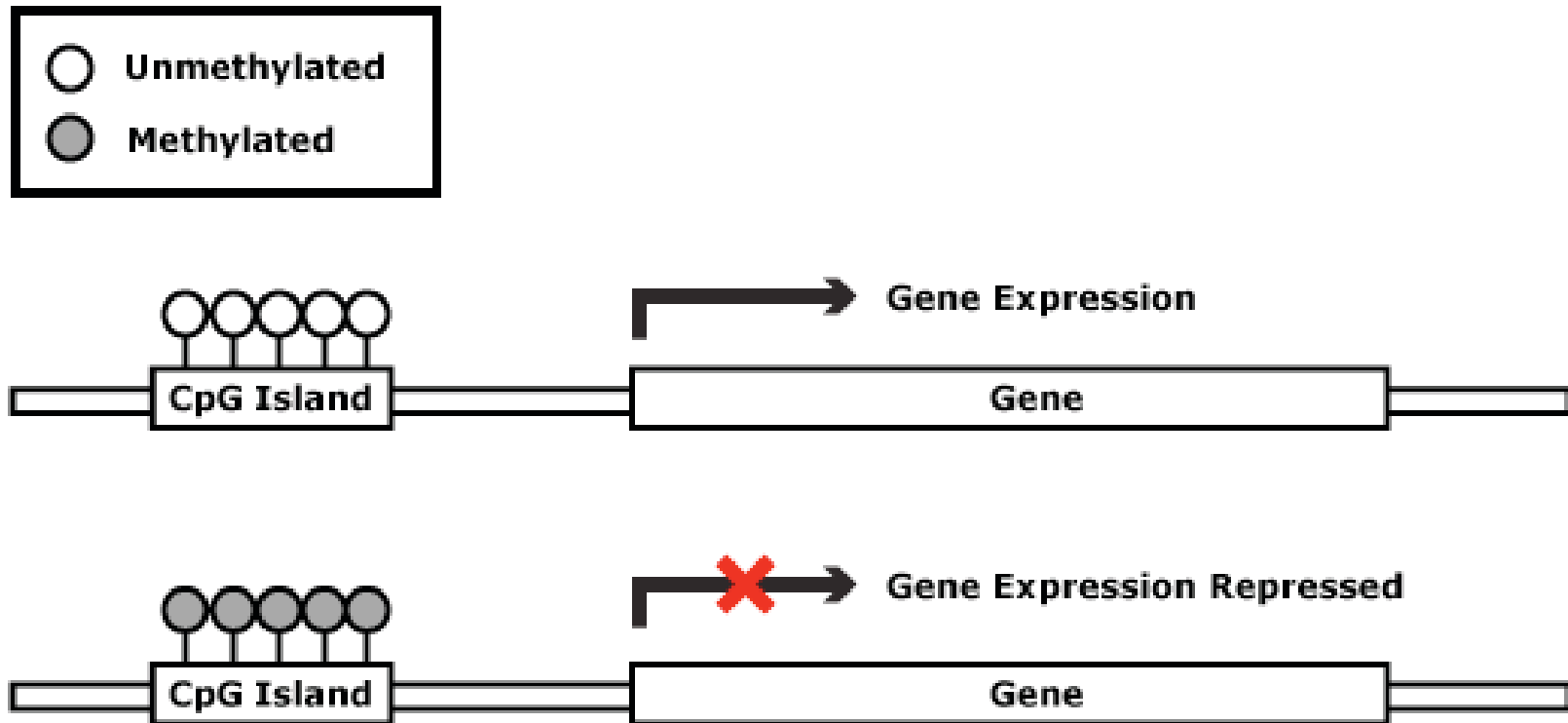
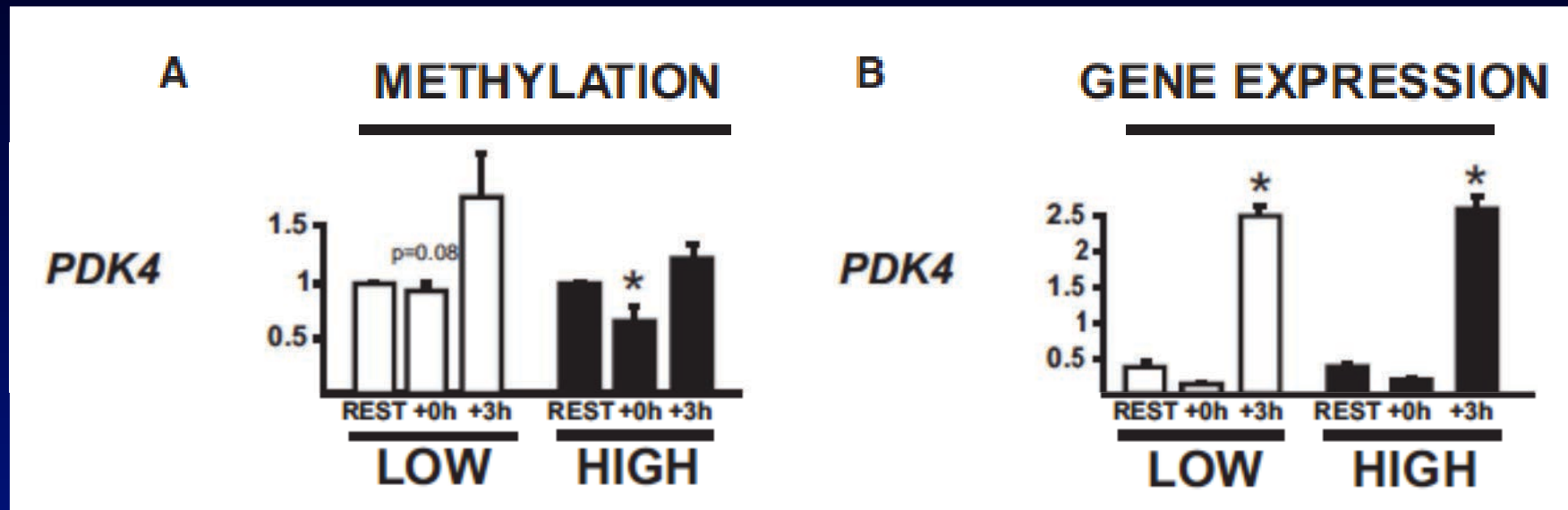


Figure 1 Recently identified modifications on the core histones. Black, modifications found *in vivo* in human; red, modifications found in mouse brain; blue, modifications found *in vitro*. ac, acetylation; Ar, ADP-ribosylation; bu, butyrylation; cr, crotonylation; fo, formylation; gt, glutathionylation; ma, malonylation; me, methylation; Og, O-glcNAcylation; oh, hydroxylation; pr, propionylation; su, succinylation; ph, phosphorylation; ub, ubiquitination.

DNA Methylation 101



Exercise Alters DNA Methylation of Key Metabolic Genes

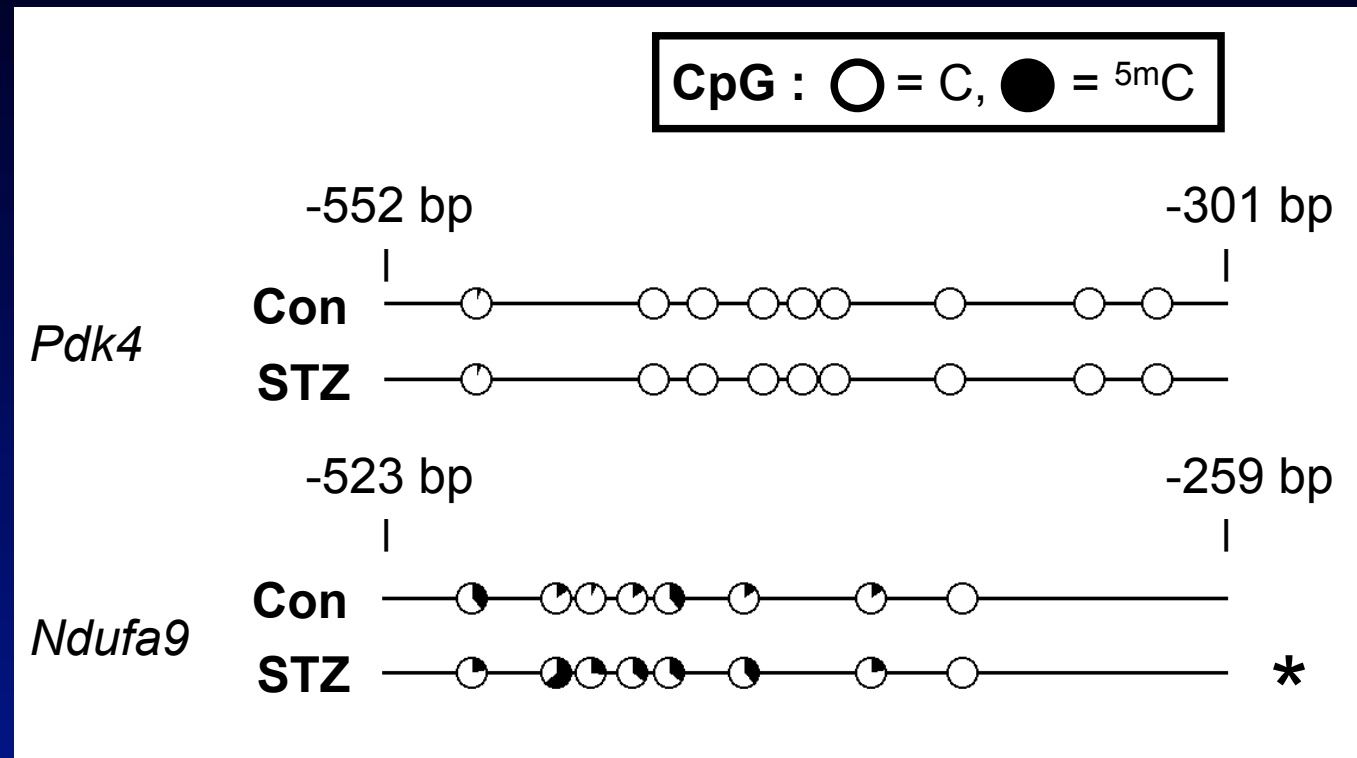
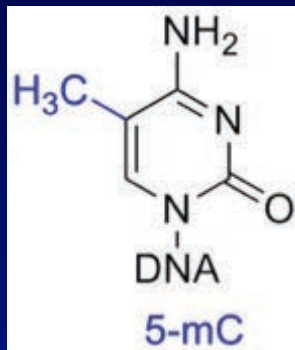


Low = 40% VO_{2peak} High = 80% VO_{2peak}

Subjects fasted overnight and then consumed a high carbohydrate diet 4 hr prior to exercise.

Diabetes Regulated Cardiac DNA Methylation

Targeted
bsDNA-seq
5-mCpG



Heart, LV

$n = 10$

* $P < 0.05$

ARW

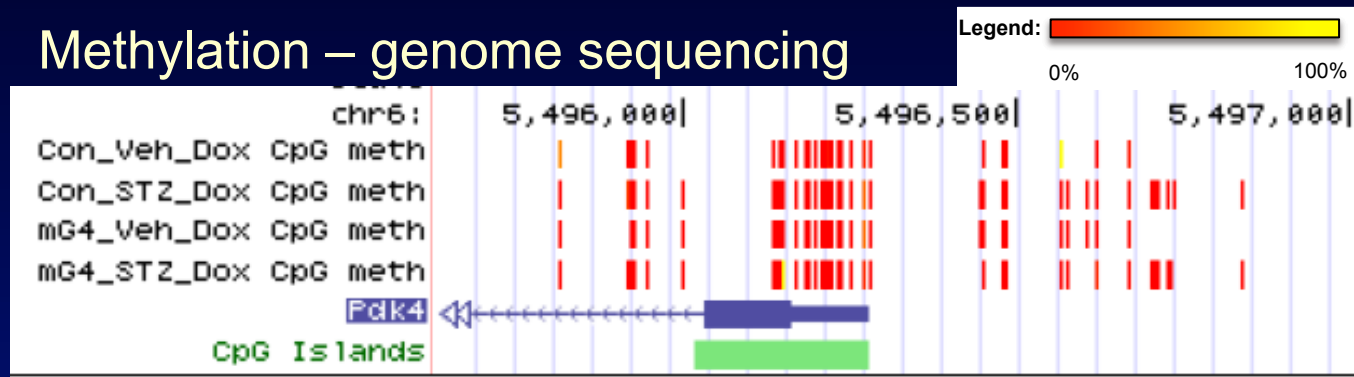
Wende, unpublished

Methylation and Expression

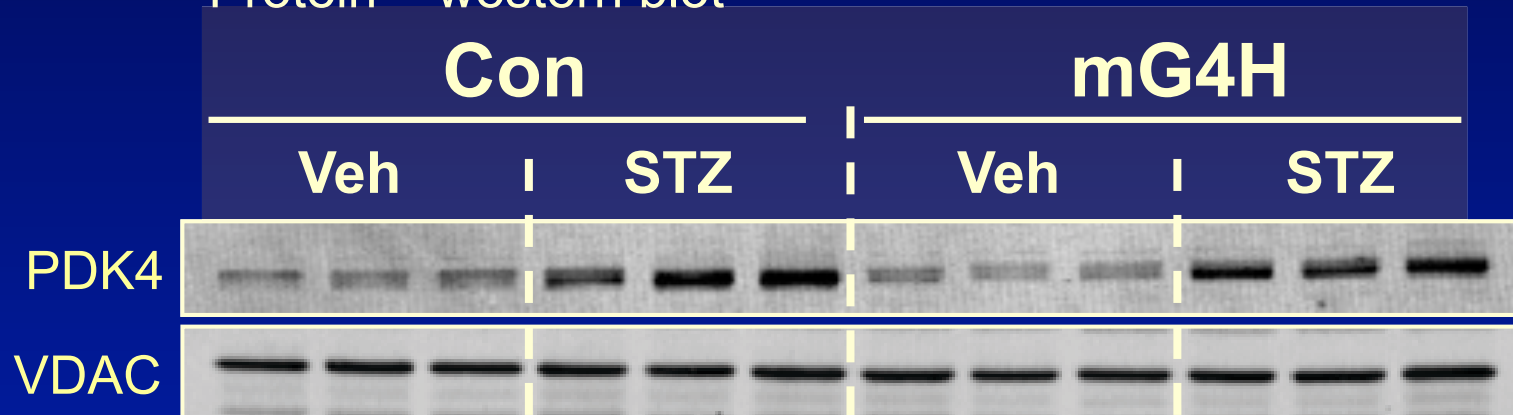
RNA – microarray



Methylation – genome sequencing



Protein – western blot



Other Human/Mouse Comparisons



Genetics Of Lipid Lowering Drugs And Diet Network

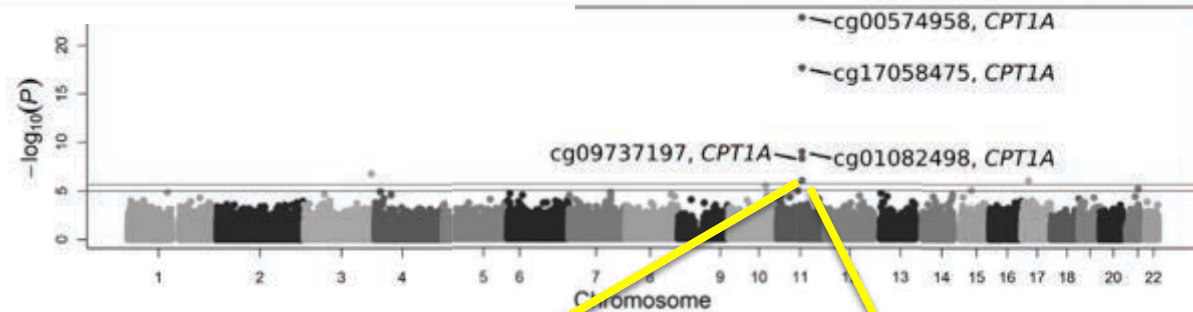


Figure 2. Epigenome-wide association Manhattan plot for VLDL-C in the discovery dataset (n=991). VLDL-C indicates very-low-density lipoprotein cholesterol.

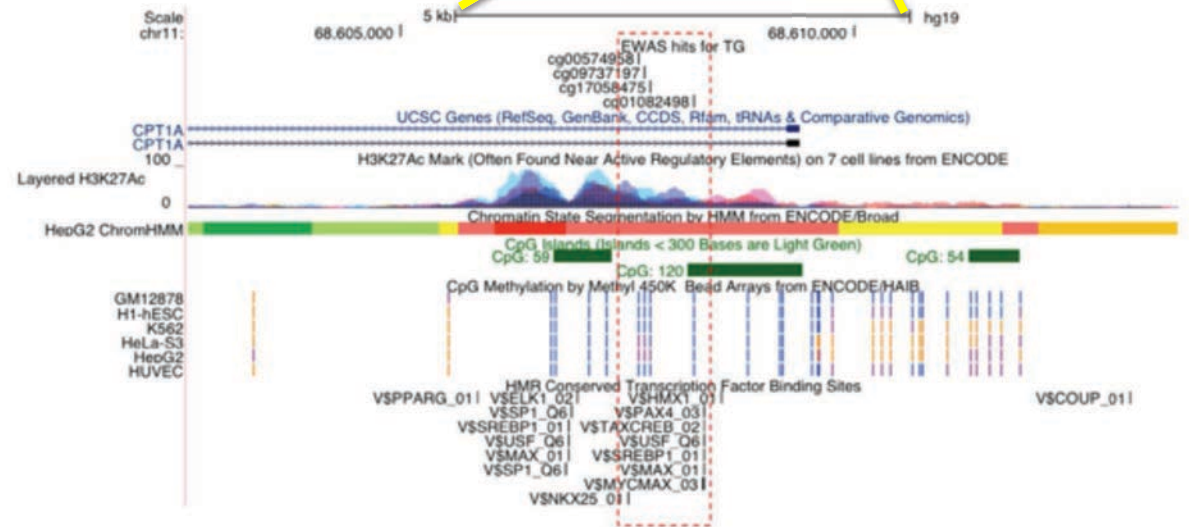


Figure 3. ENCODE annotation of the promoter region and intron 1 of *CPT1A*. Top CpGs for TG are positioned within the gene along with CpG islands, cell line chromatin state (ChromHMM), cell line methylation at CpG sites on the Methy450 Beadchip according to Hudson Alpha Institute for Biotechnology (HAIB; note blue, purple, and orange highlights correspond to low, medium and high methylation state, respectively), and HMR conserved transcription factor binding sites. CpG indicates cytosine-(phosphate)-guanine; and TG, triglyceride.

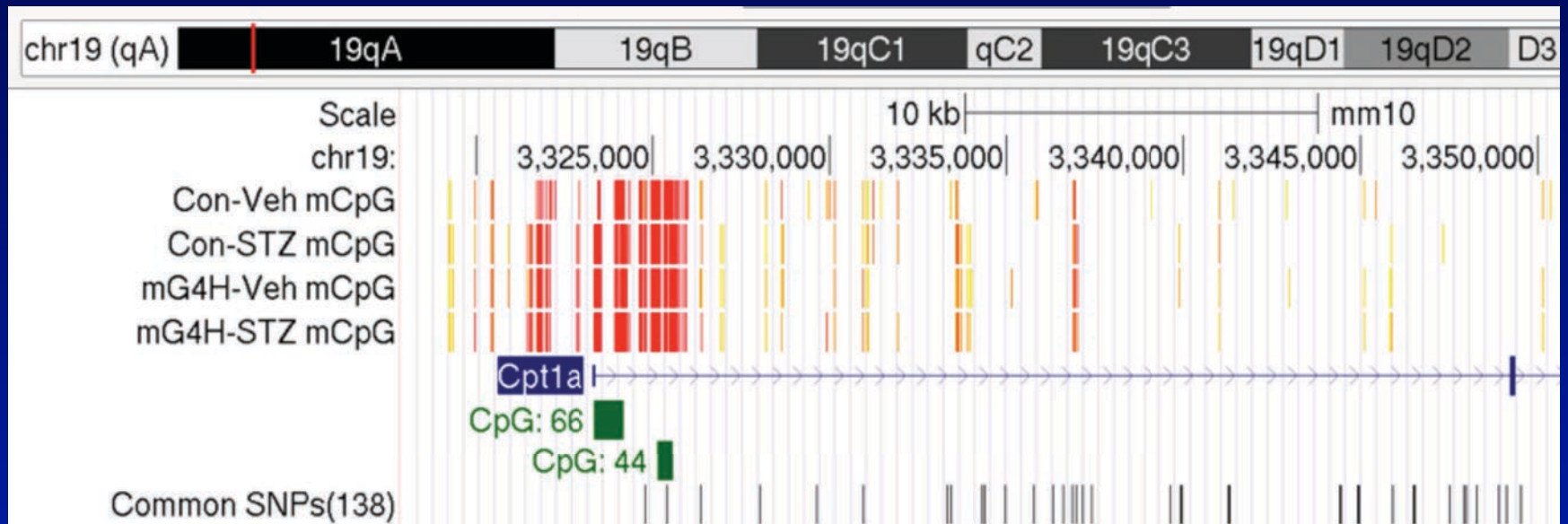
Other Human/Mouse Comparisons

Mouse Gene Expression

Con Veh Con STZ mG4H Veh mG4H STZ GENE

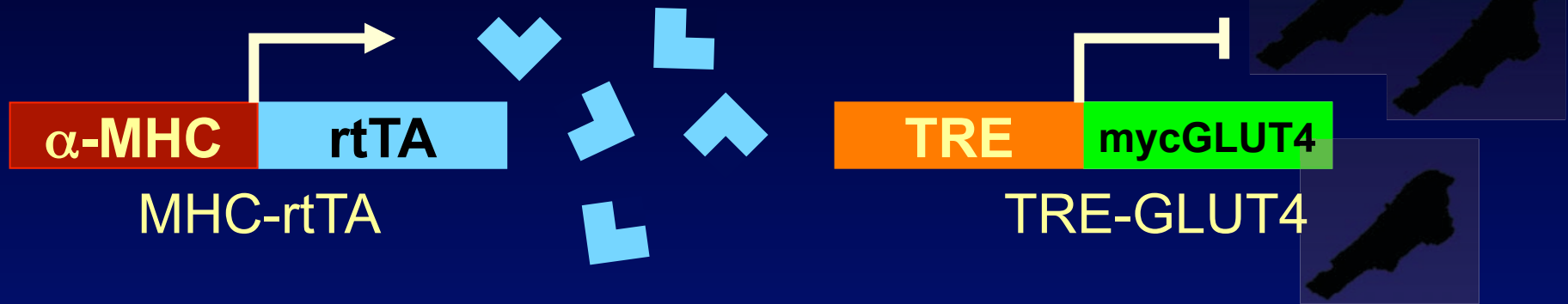


Mouse DNA Methylation

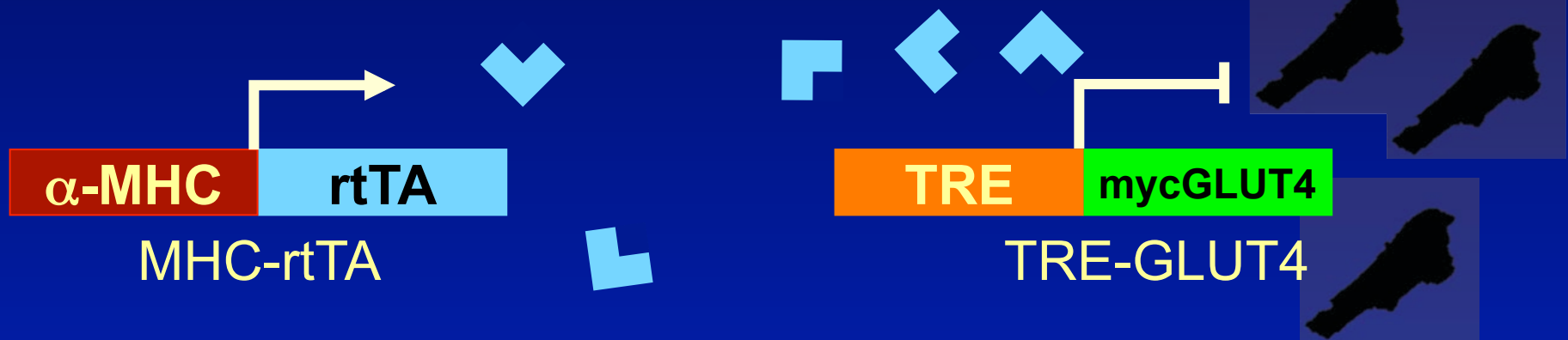


Where Does Glycemic Memory Fit In?

DOX absent = OFF

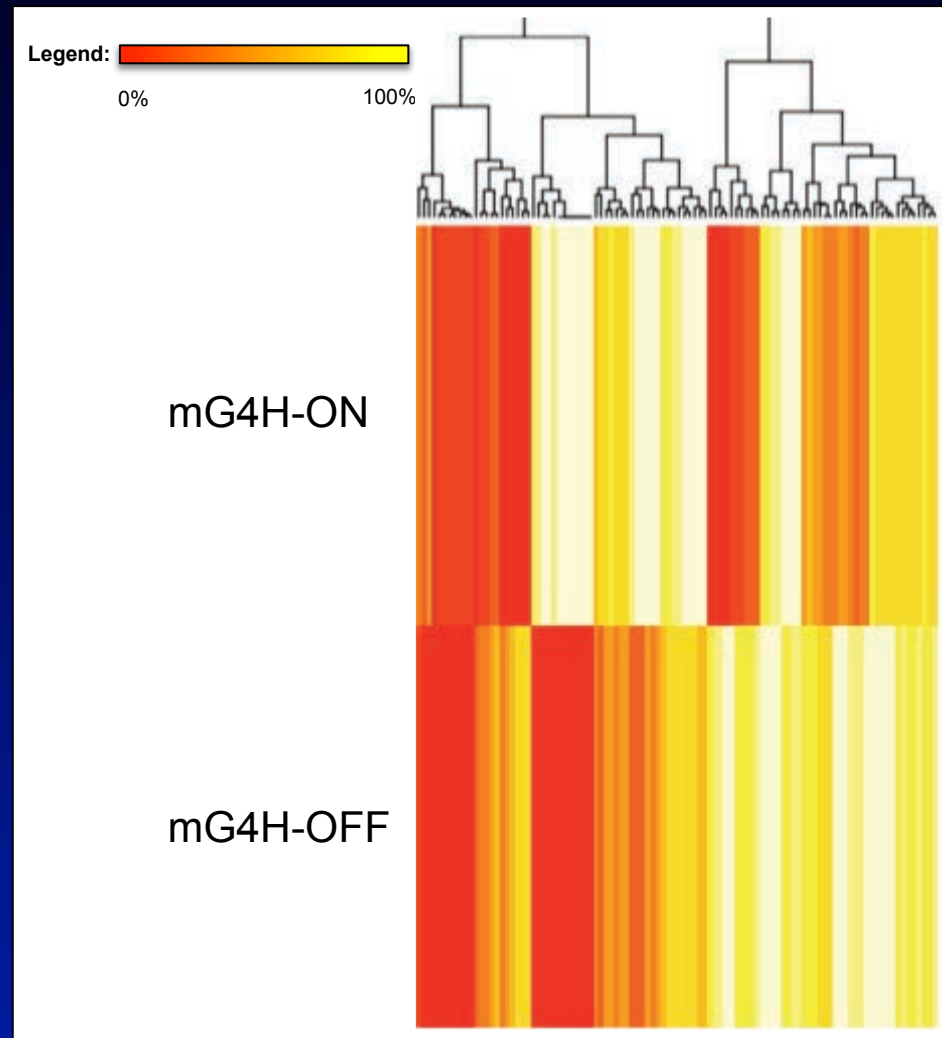
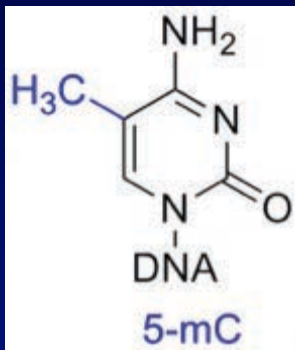


DOX present = ON



Glucose Cycling Alters Epigenetic Programming

Genomewide
bsDNA-seq
5-mCpG

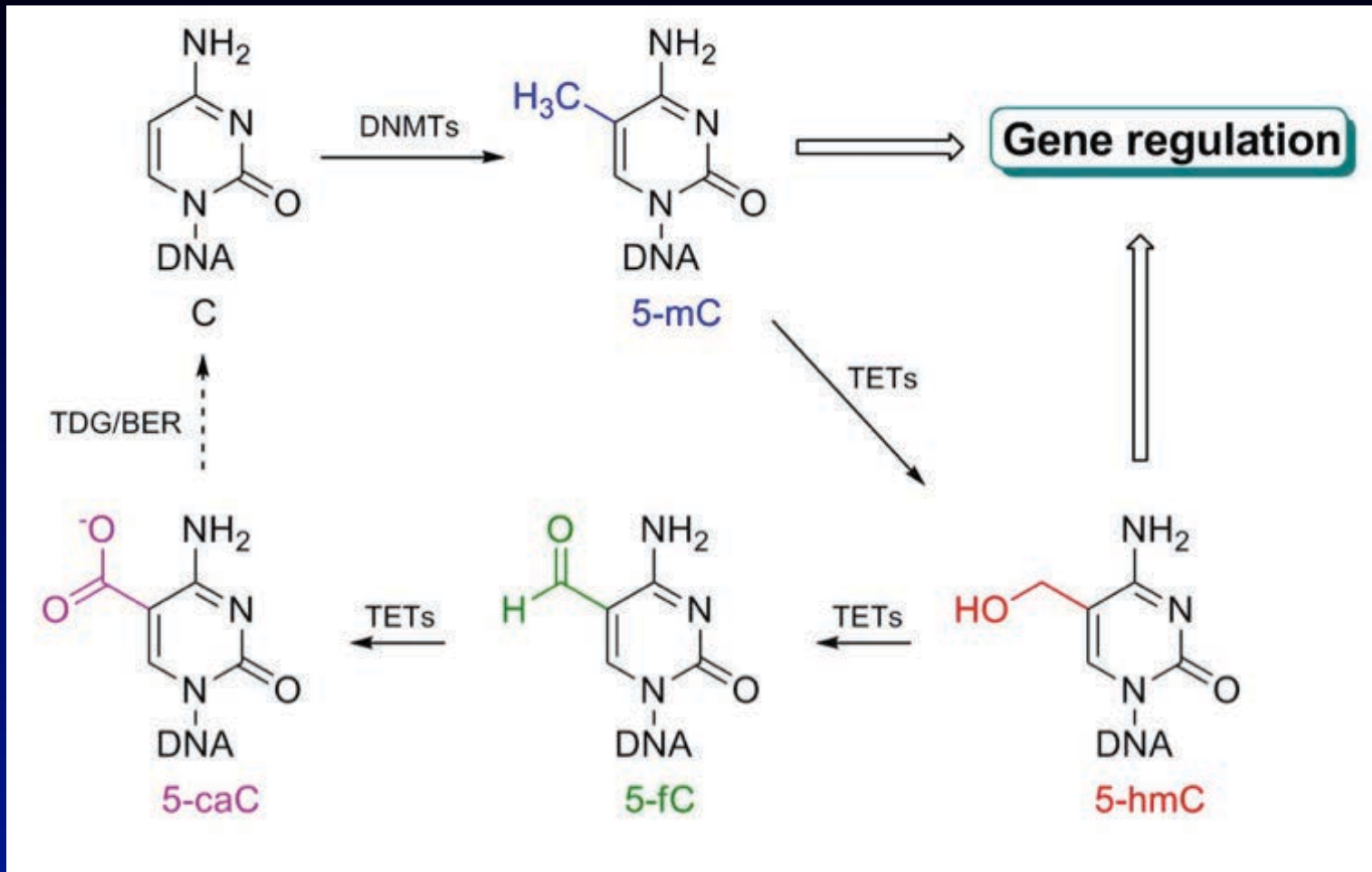


Heart, LV

AKW

Zymo Research
Wende, unpublished

Background



5-hmC

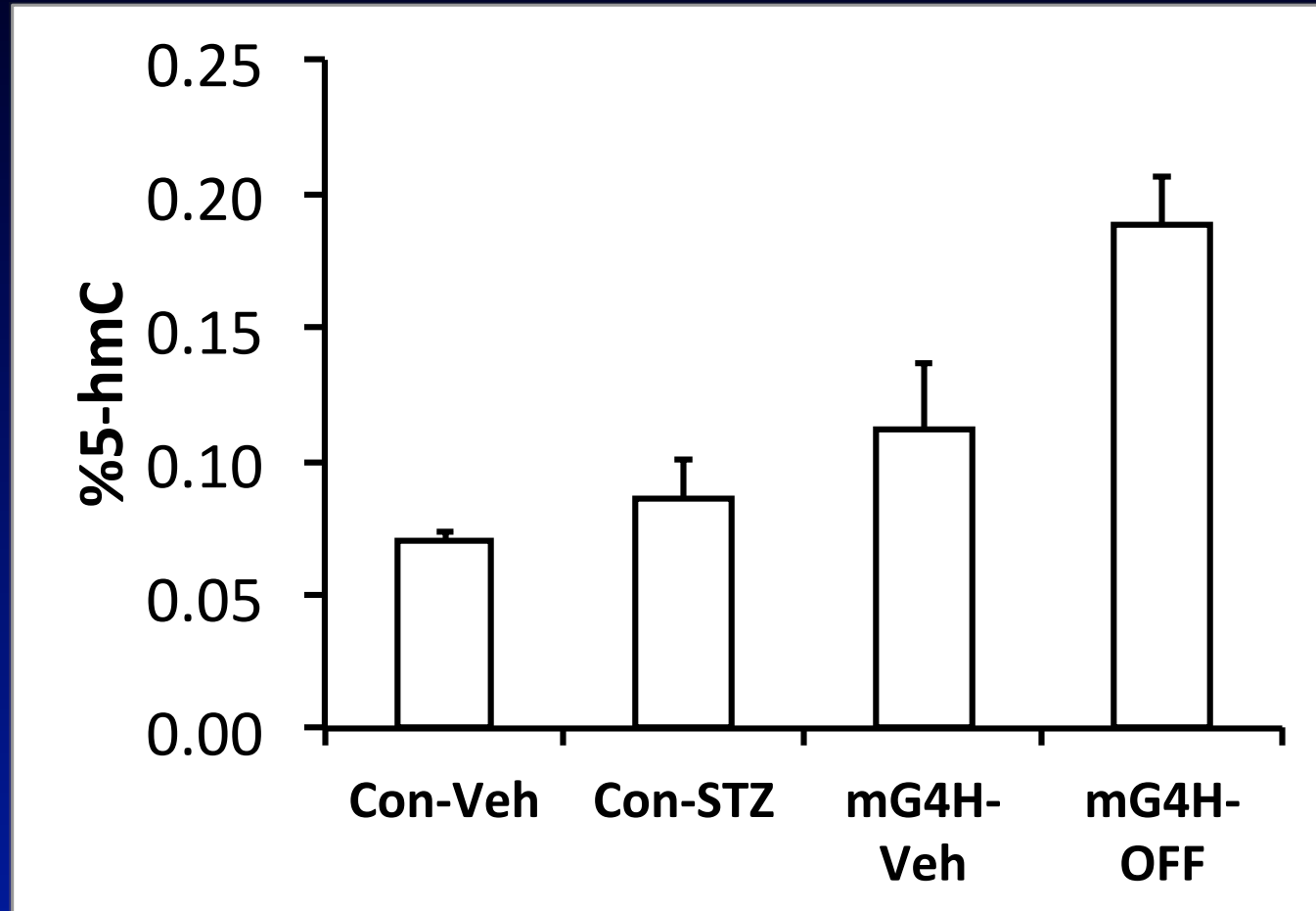
Wyatt and Cohen 1952 *Nature* 170(4338):1072

Kriaucioni and Heintz 2009 *Science* 324(5929):929

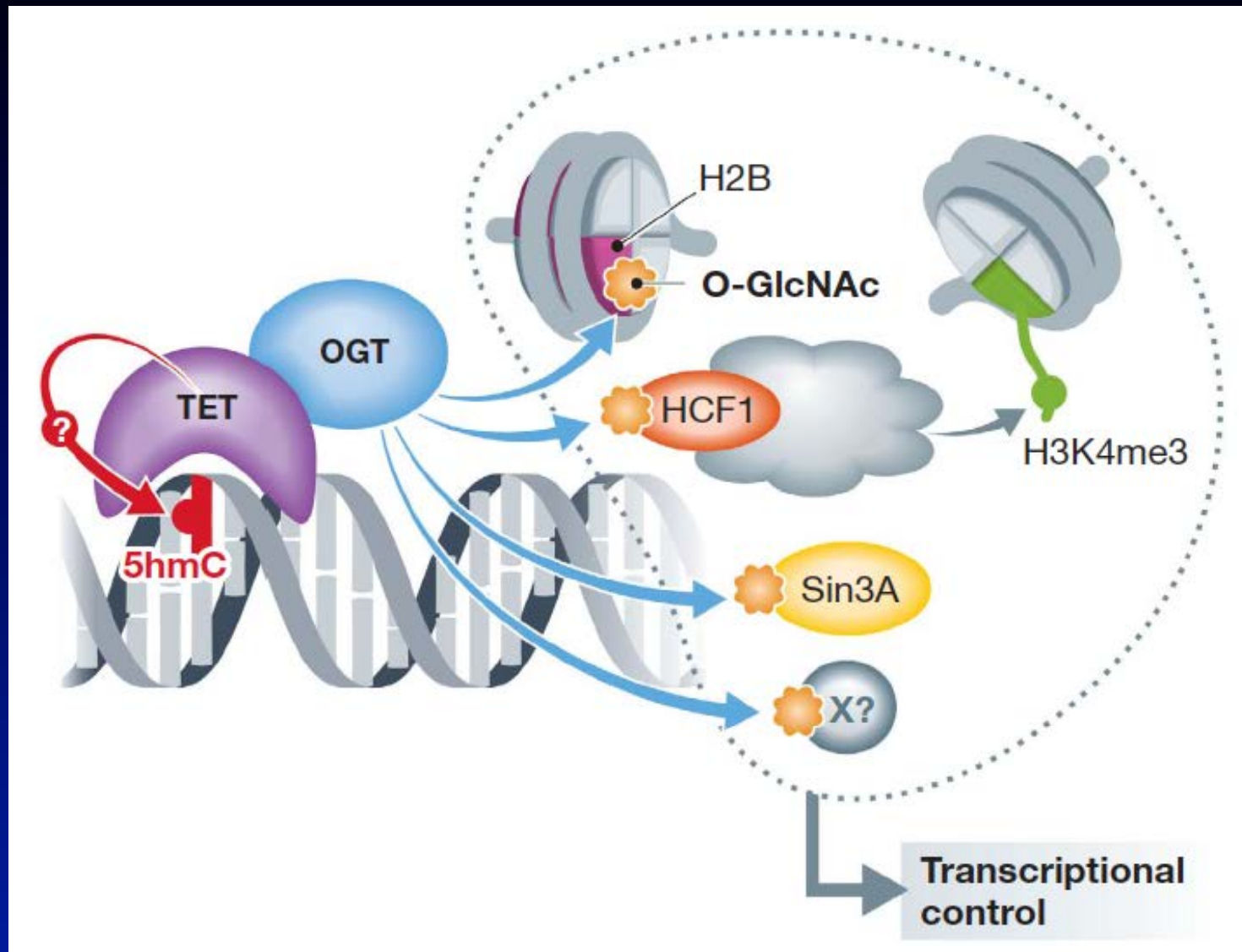
Tahiliani ... Rao 2009 *Science* 324(5929):930

Glucose Cycling Alters Epigenetic Programming

5-hmCpG
ELISA

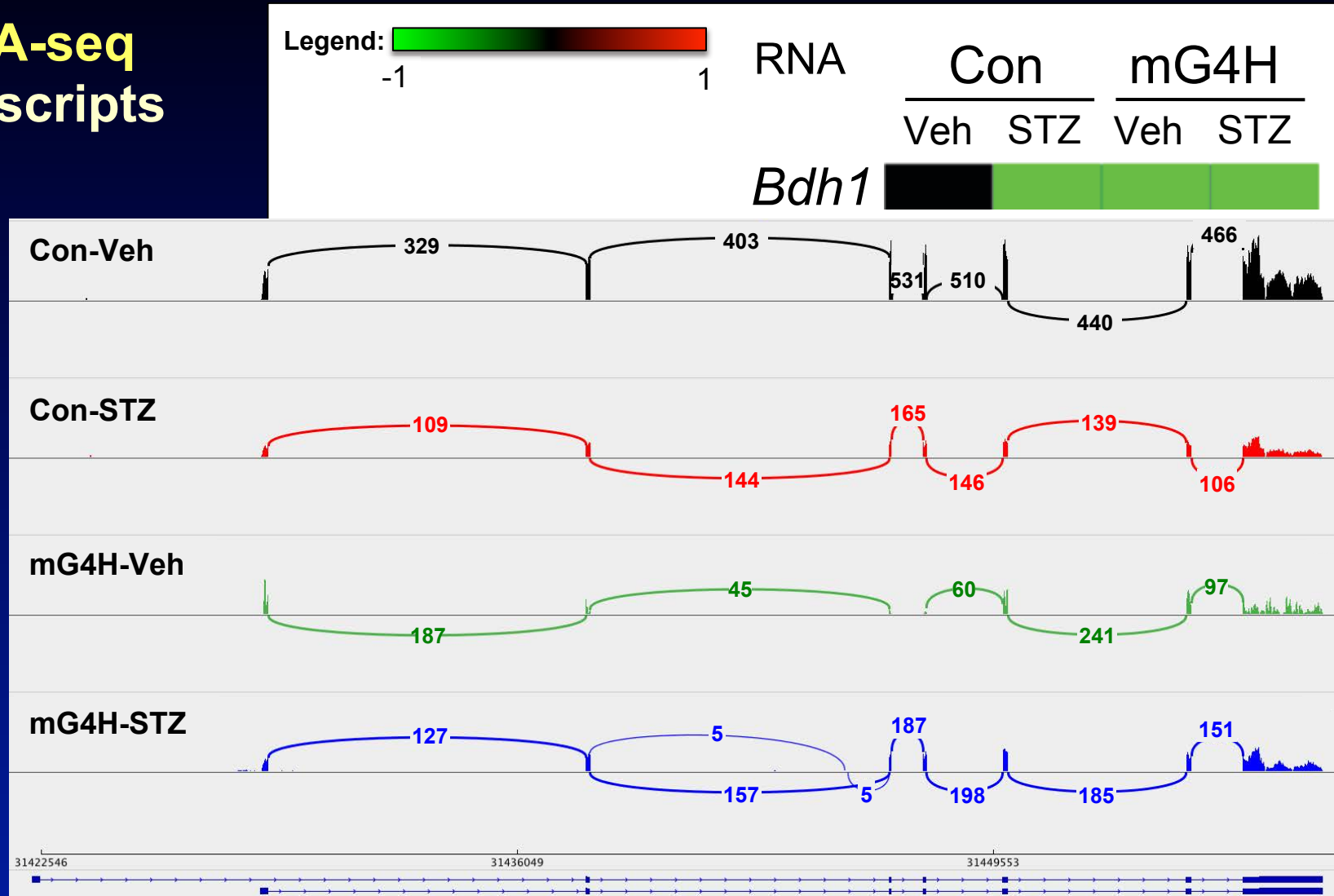


How does GlcNAc fit in?



Tissue Specific Promoter Utilization

RNA-seq Transcripts



Heart, LV
n = 3

Heflin Center for Genomic Sciences, UAB
Nye ... Wende, unpublished

Combined Transcriptome/Methylome

Genomewide bsDNA-seq 5-mCpG



RNA

Con

mG4H

Veh

STZ

Veh

STZ

Bdh1



5-mCpG

Scale
chr16:

10 kb | mm10
31,430,000 | 31,440,000 | 31,450,000

Con-Veh mCpG

Con-STZ mCpG

mG4-Veh mCpG

mG4-STZ mCpG

CpG Islands

CpG Islands (Islands < 300 Bases are Light Green)

RefSeq Genes

Bdh1

Bdh1

GC Percent in 5-Base Windows

GC Percent

Vertebrate Multiz Alignment & Conservation (60 Species)

Placental Cons

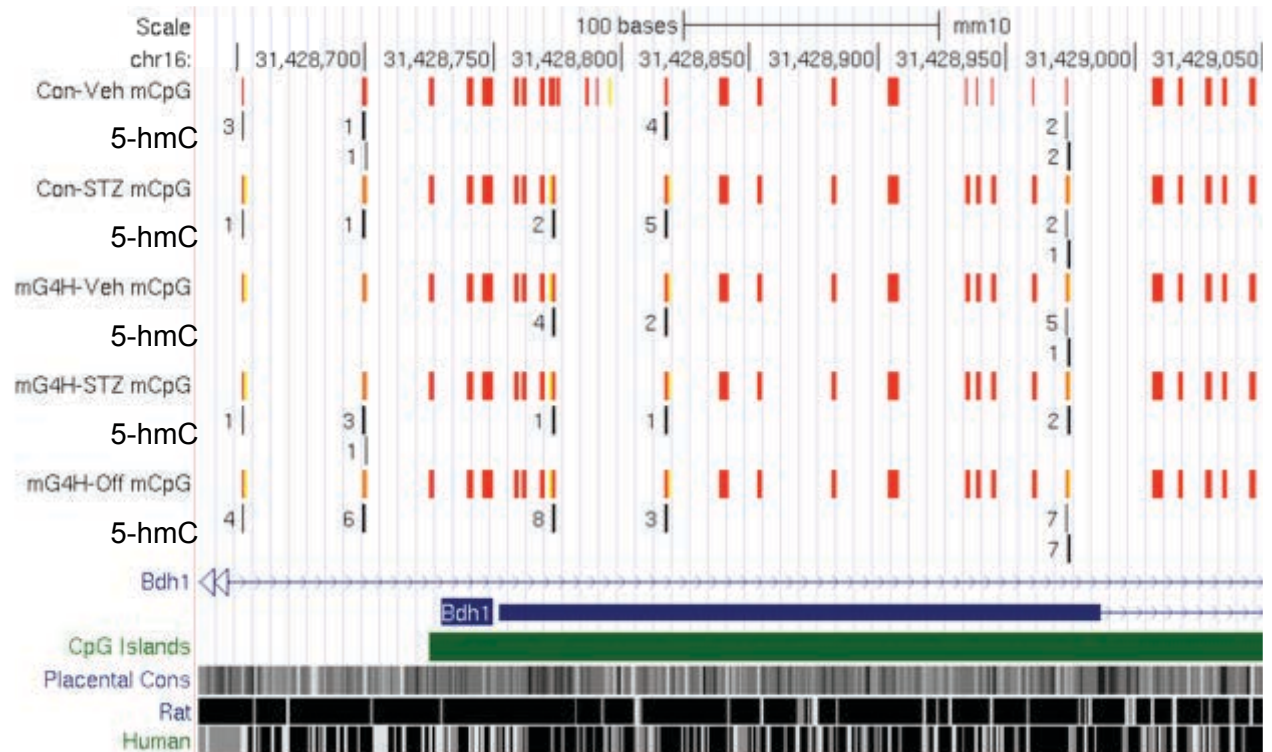
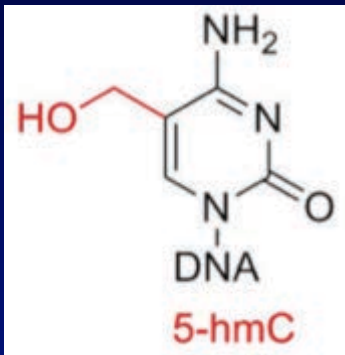
Multiz Align

Heart, LV

Zymo Research and UCSC Genome Browser
Wende, unpublished

Combined Transcriptome/Methylome

Genomewide
RRHP
5-hmCpG



Heart, LV

AKW

Zymo Research and UCSC Genome Browser
Nye ... Wende, unpublished

Conclusion – Part 4

Cellular glucose fluctuations regulates the epigenome via histone modifications and controlling the machinery for DNA methylation.

Sugar Gumming Up the Works



Overall Summary

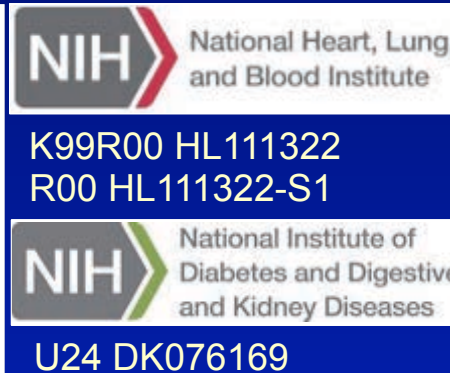
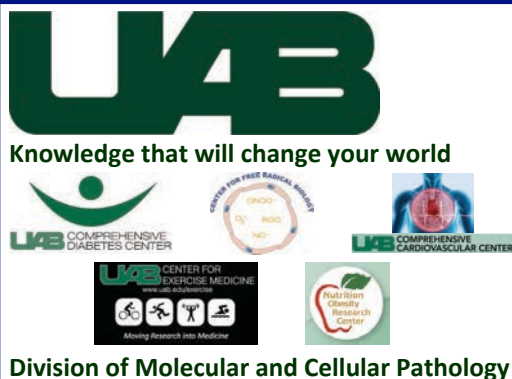
Using combined methylomics, transcriptomics, proteomics, and metabolomics we have begun to define the mechanism of glucotoxicity.

Acknowledgements

Wende Lab



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Manoja K. Brahma – Postdoc; *Bdh1/Oxct1*
Mark C. McCrory – Lab Manager; *Hmgcs2*
Brenna G. Nye – Undergrad; *Pcx*
Mark Pepin – MSTP; *Abat*
Lamario J Williams – Undergrad; *UQCRFS1/ROS*



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David K. Crossman
Steve M. Pogwizd
Martin E. Young

E. Dale Abel

John C. Schell
Joseph Tuinei
many others...

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Nikos A. Diakos

Hansjörg Schwertz

Oleh Khalimonchuk – UNL

Other Colleagues & Mentors
past and present

