

HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH, BOSTON, MA

'OMICS: ADVANCES, APPLICATIONS, AND TRANSLATION IN
NUTRITION AND EPIDEMIOLOGY- 3RD ANNUAL SYMPOSIUM

HEALTH APPLICATION OF TYPE 2 DIABETES GENETICS

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MASSACHUSETTS
GENERAL HOSPITAL



Harvard Medical
School



BROAD
INSTITUTE



FRAMINGHAM
HEART STUDY

JBM Disclosures and Acknowledgments

- NIH
 - NIDDK U01 DK078616
 - NIDDK K24 DK080140
 - NHLBI Framingham Heart Study N01-HC-25195
- American Diabetes Association
 - ADA Mentored Fellowship Grant
- Industry
 - Quest Diagnostics



Themes for Today

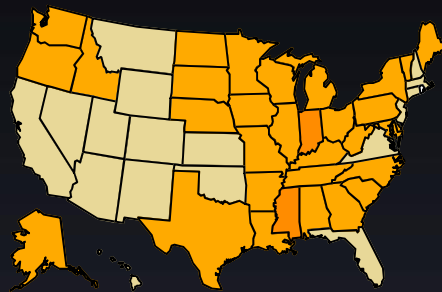
- Discoveries over 15 years in T2D genetics
- Predicting future T2D using T2D genetics
- Screening for T2D influenced by HbA1c genetics

Themes for Today

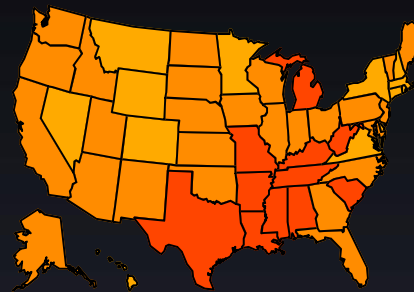
- Discoveries over 15 years in T2D genetics

Obesity and T2D Prevalences in the US Have Increased Inexorably and in Tandem for >16 Years

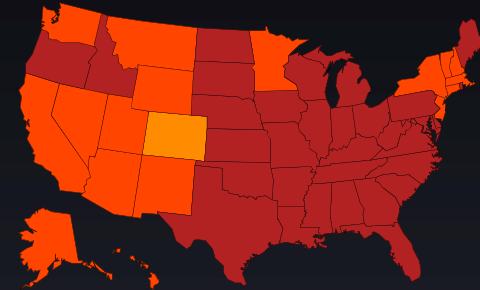
Obesity (BMI ≥ 30 kg/m²)
1994



2000



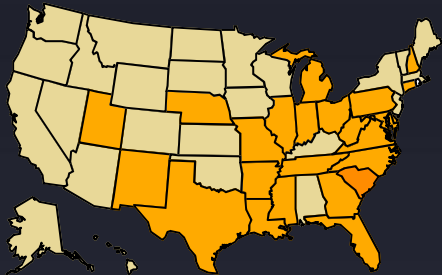
2010



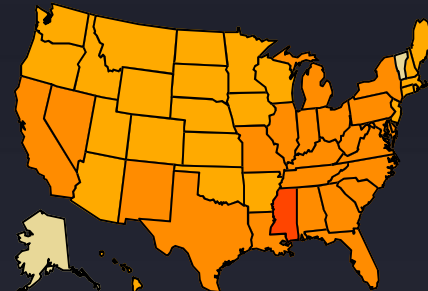
■ No Data ■ <14.0% ■ 14.0-17.9% ■ 18.0-21.9% ■ 22.0-25.9% ■ ≥26.0%

Diabetes

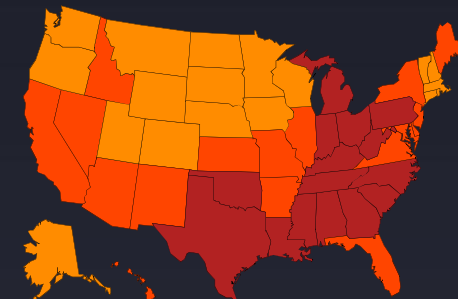
1994



2000



2010



■ No Data ■ <4.5% ■ 4.5-5.9% ■ 6.0-7.4% ■ 7.5-8.9% ■ ≥9.0%

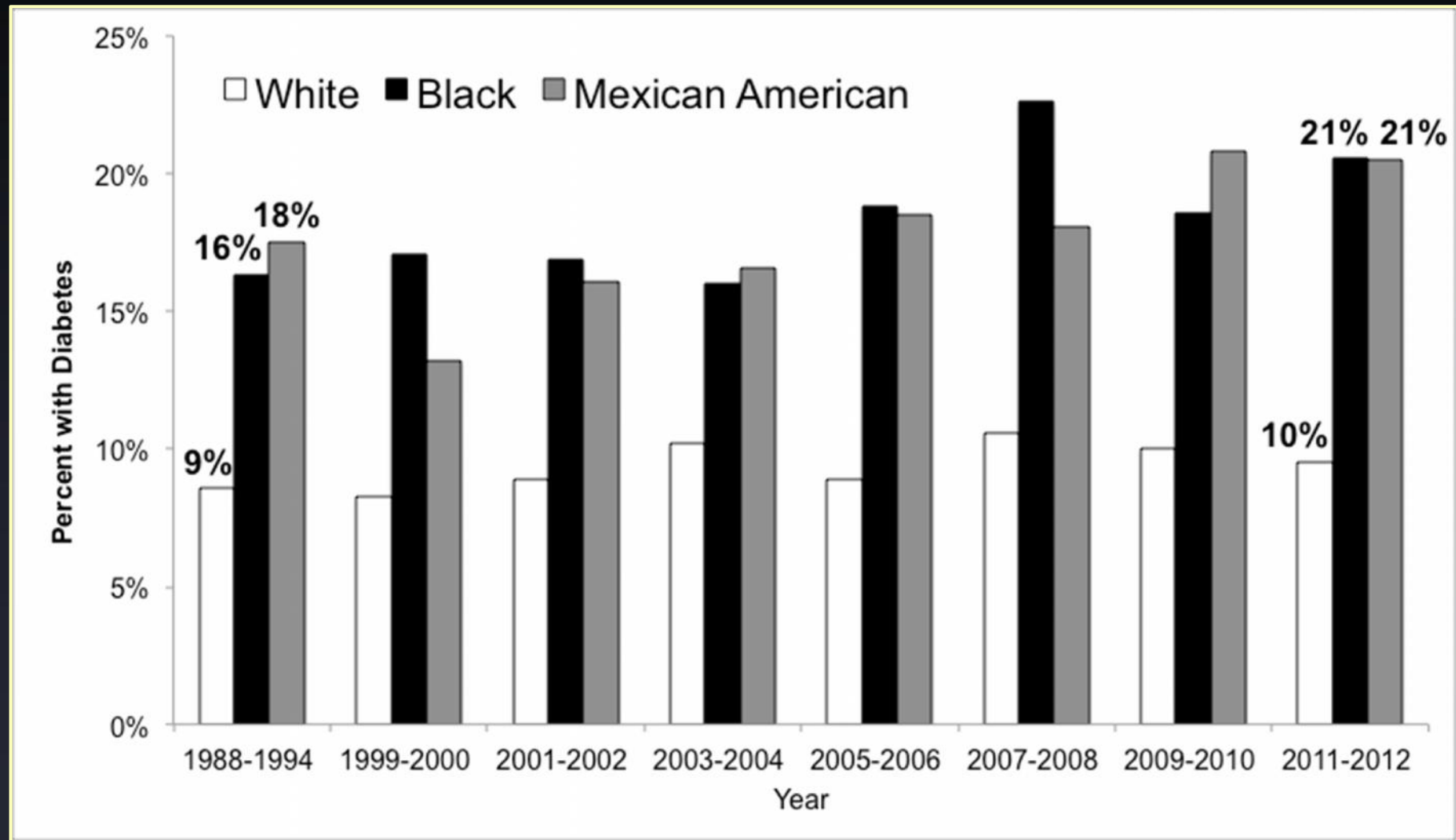


CDC's Division of Diabetes Translation. National Diabetes Surveillance System available at <http://www.cdc.gov/diabetes/statistics>



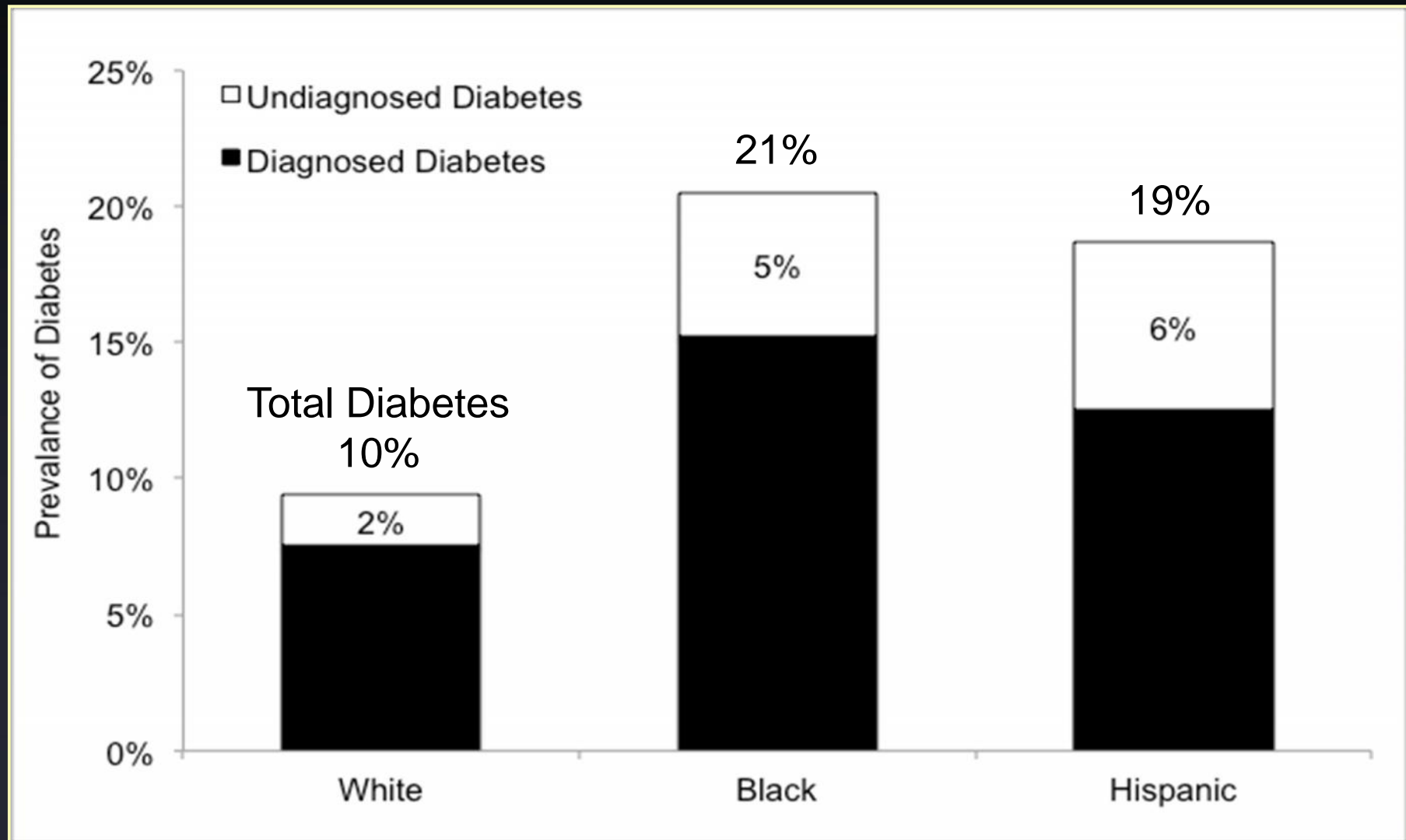
Increasing T2D Prevalence Disproportionately Impacts U.S. Black and Mexican American Communities

NHANES Adults 1988-2012, Dx by HbA1c or FPG



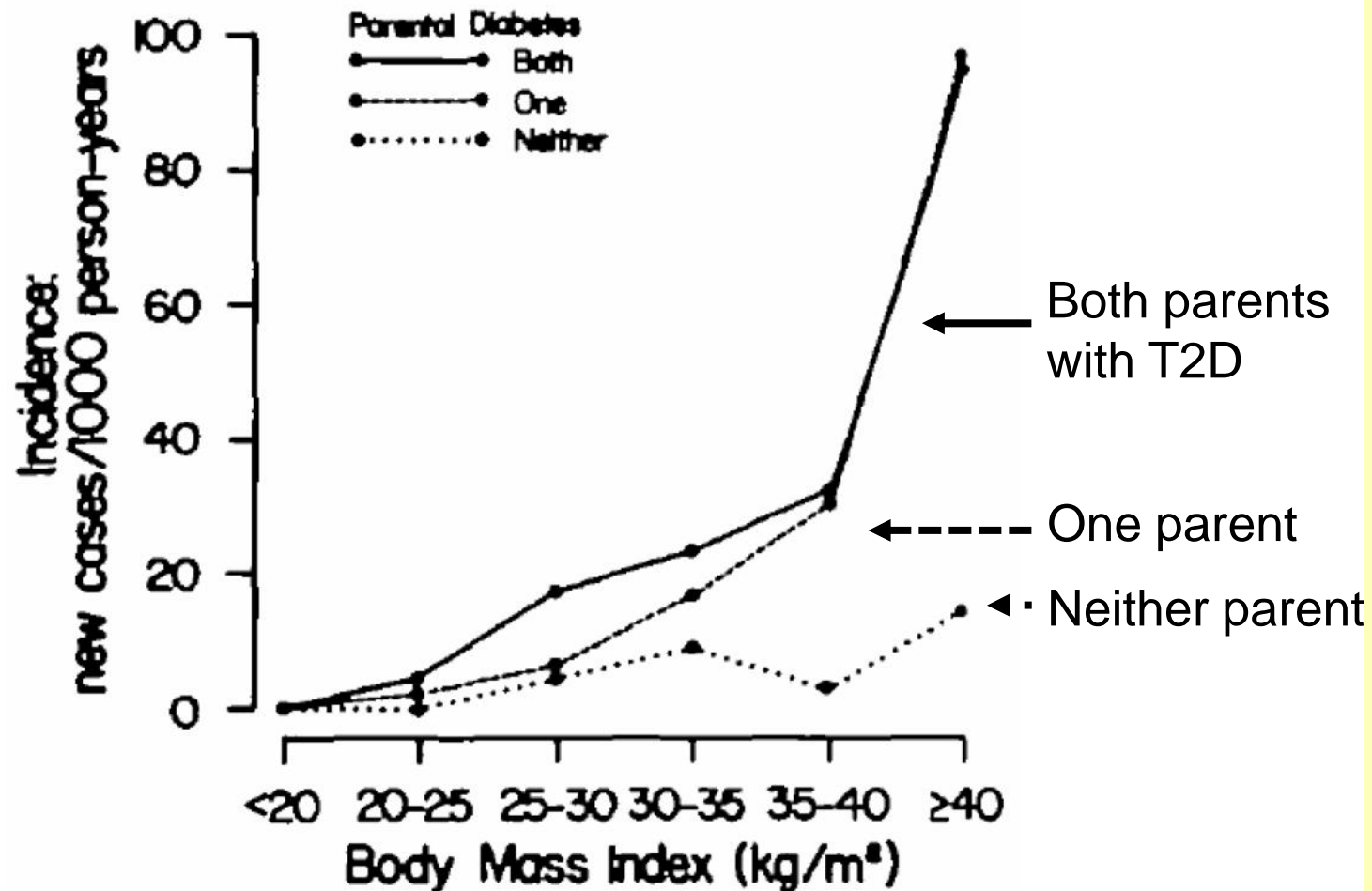
Undiagnosed T2D Disproportionately Impacts U.S. Black and Mexican American Communities

NHANES Adults 2011-2012, Dx by HbA1c or FPG



Obesity Increases Risk Most in Pimas w Parental T2D

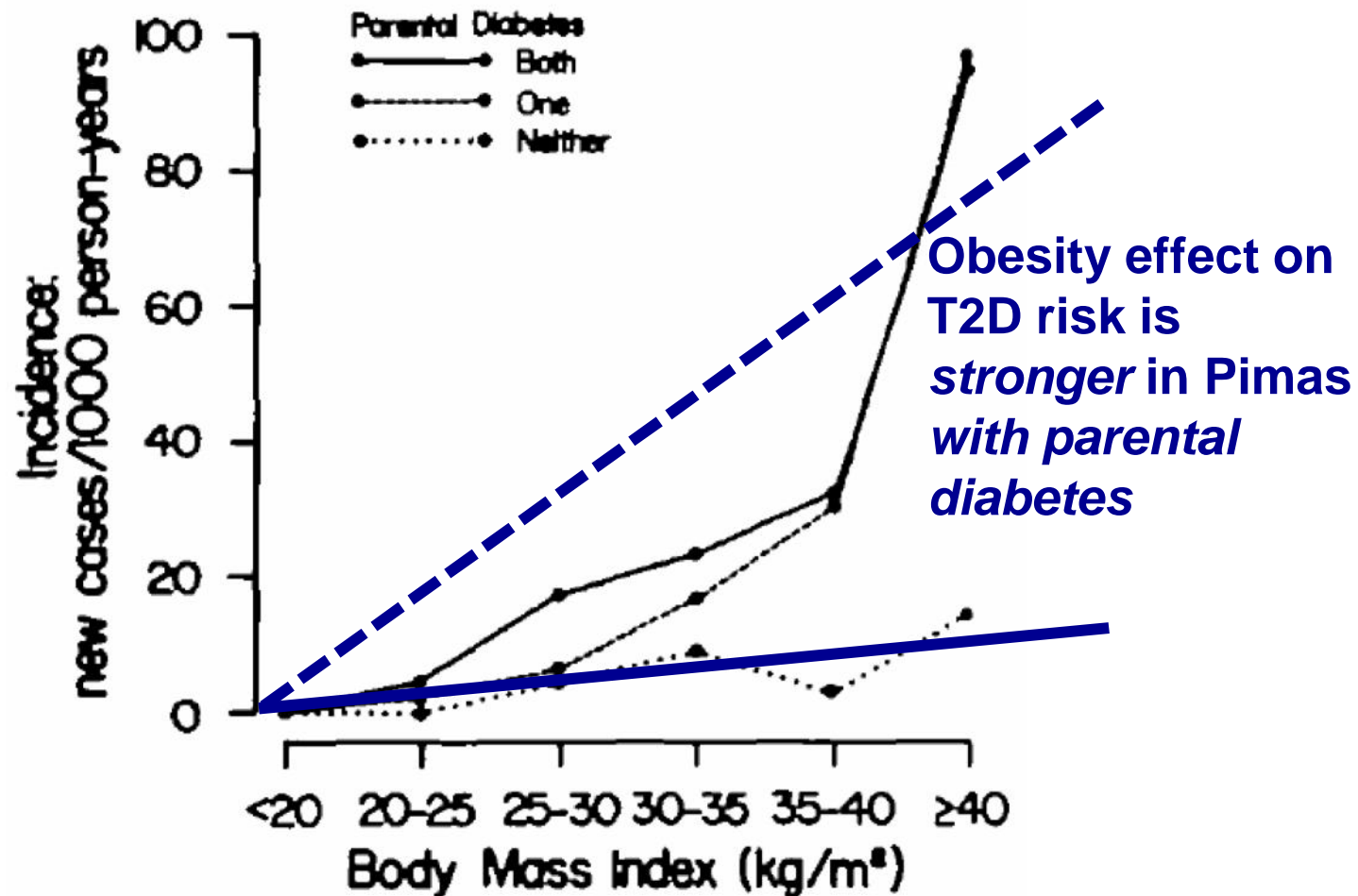
Parental T2D = Genetic Effects Causing T2D



3137 Pima Indians followed with periodic examinations

Obesity Increases Risk Most in Pimas w Parental T2D

Genetic Studies Unmask Causation of T2D



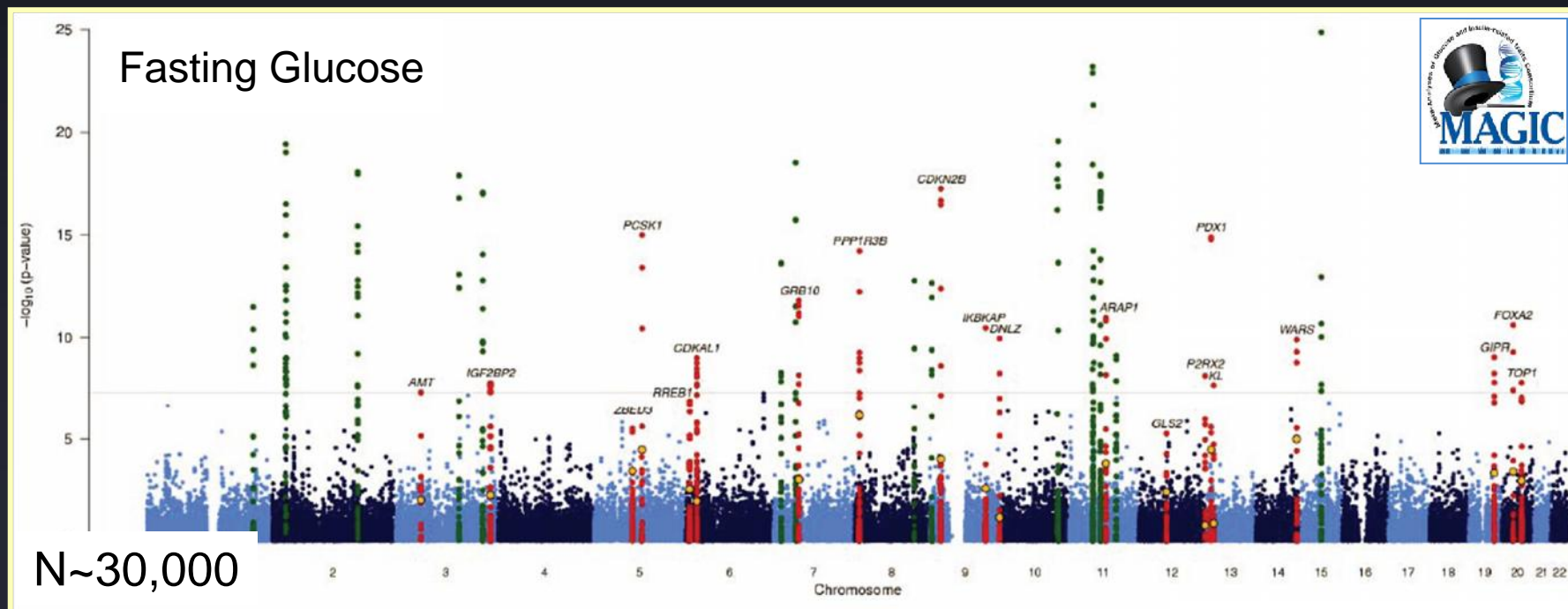
3137 Pima Indians followed with periodic examinations

Mendel's Laws – Segregation and Independent Assortment

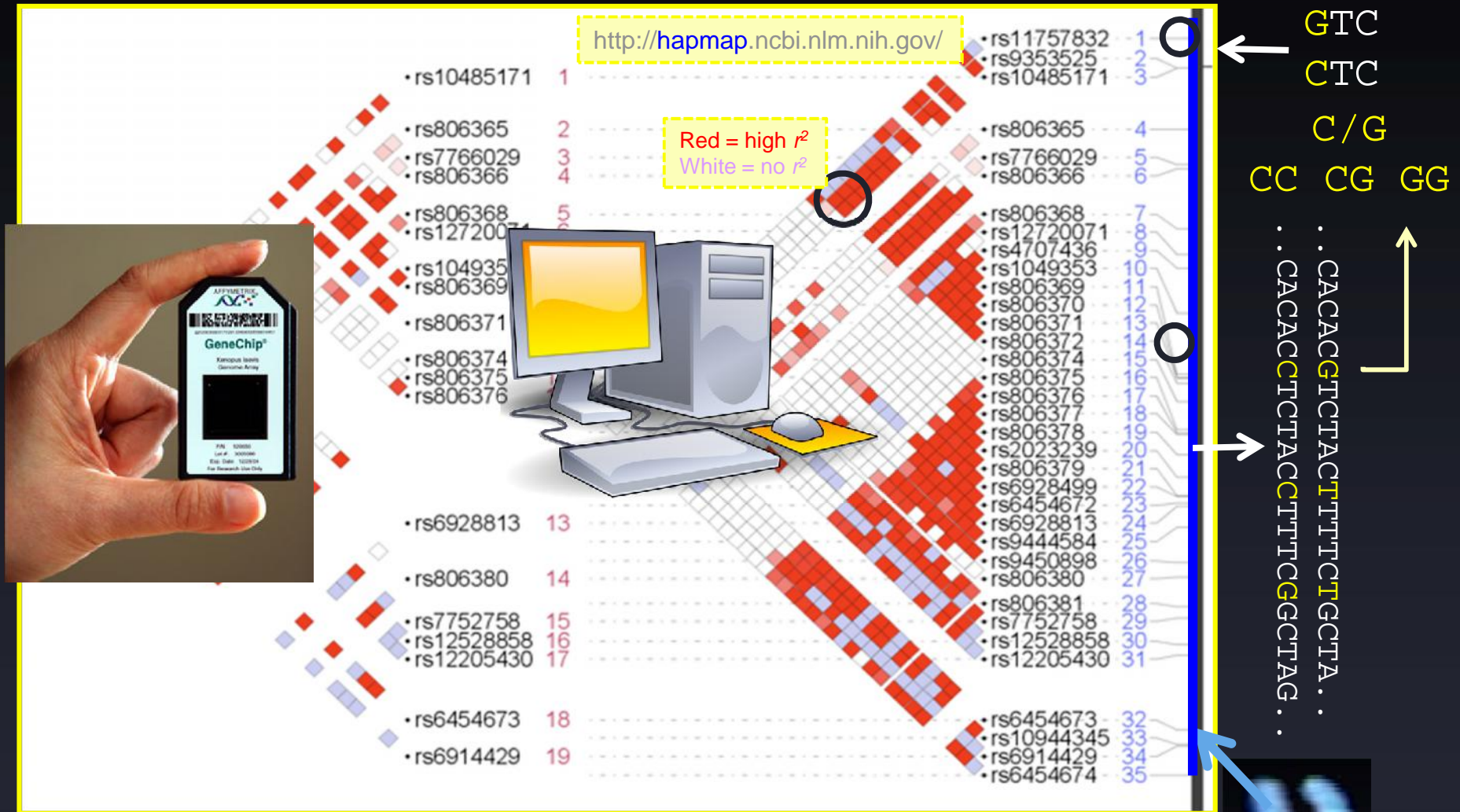
	Flower color	Flower position	Seed color	Seed shape	Pod shape	Pod color	Stem length
P	Purple × White	Axial × Terminal	Yellow × Green	Round × Wrinkled	Inflated × Constricted	Green × Yellow	Tall × Dwarf
F ₁	Purple	Axial	Yellow	Round	Inflated	Green	Tall

N~30,000

GWAS – from Peas to Human Complex Trait Genetics



Array SNPs, Linkage Disequilibrium, Imputation



Imputation for MAF > 0.05%

500K to 15M SNPs

Fruitful Collaboration in T2D-QT Genetics Consortia

Framingham Heart Study
N ~ 6,500, longitudinal



Fruitful Collaboration in T2D-QT Genetics Consortia

MAGIC v3 133,010
CHARGE 60,564
FHS SHARE 6,479



Quantitative Traits

Fasting Glucose

Fasting Insulin

HbA_{1c}

2hr OGTT glucose

Proinsulin



Fruitful Collaboration in T2D-QT Genetics Consortia

Type 2 Diabetes
Case/Control



DIAGRAM v5
47,979 T2D cases
187,595 non-T2D controls

MAGIC v3 133,010
CHARGE 60,564
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Quantitative Traits

Fasting Glucose

Fasting Insulin

HbA_{1c}

2hr OGTT glucose

Proinsulin



Fruitful Collaboration in T2D-QT Genetics Consortia

- Large numbers
- Physiology data
- Populations, over time
- Lab functional experiments

MAGIC v3 133,010
CHARGE 60,564
FHS SHARE 6,479



Quantitative Traits

Fasting Glucose
Fasting Insulin
HbA_{1c}
2hr OGTT glucose
Proinsulin

Type 2 Diabetes Case/Control



DIAGRAM v5
47,979 T2D cases
187,595 controls



CHARGE



T2D-GENES Consortium

39,339 T2D and controls
Five ancestry groups
Exome data

AAGILE

30,305 African
American non-diabetes
with Glycemic QTs

MEDIA

8,284 AA T2D cases
and 15,543 controls

African American
T2D and QTs

ACCELERATING MEDICINES PARTNERSHIP (AMP)

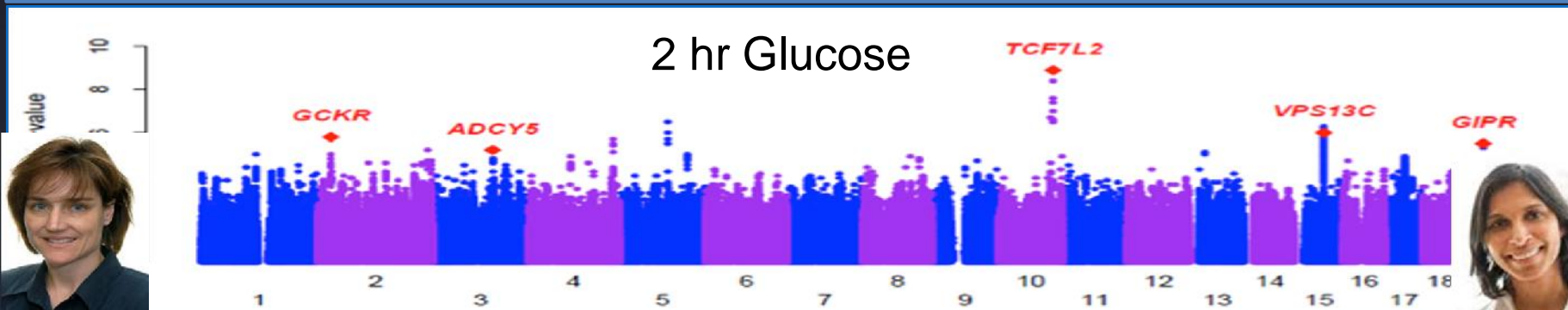
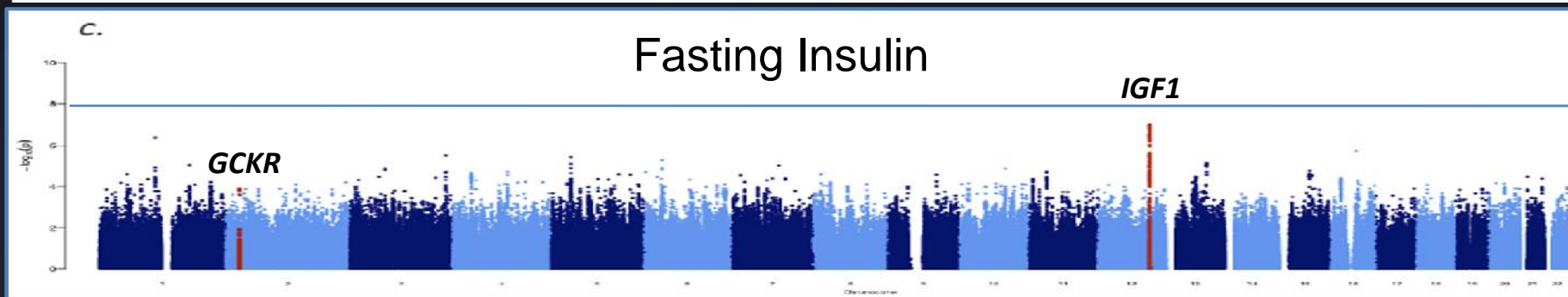
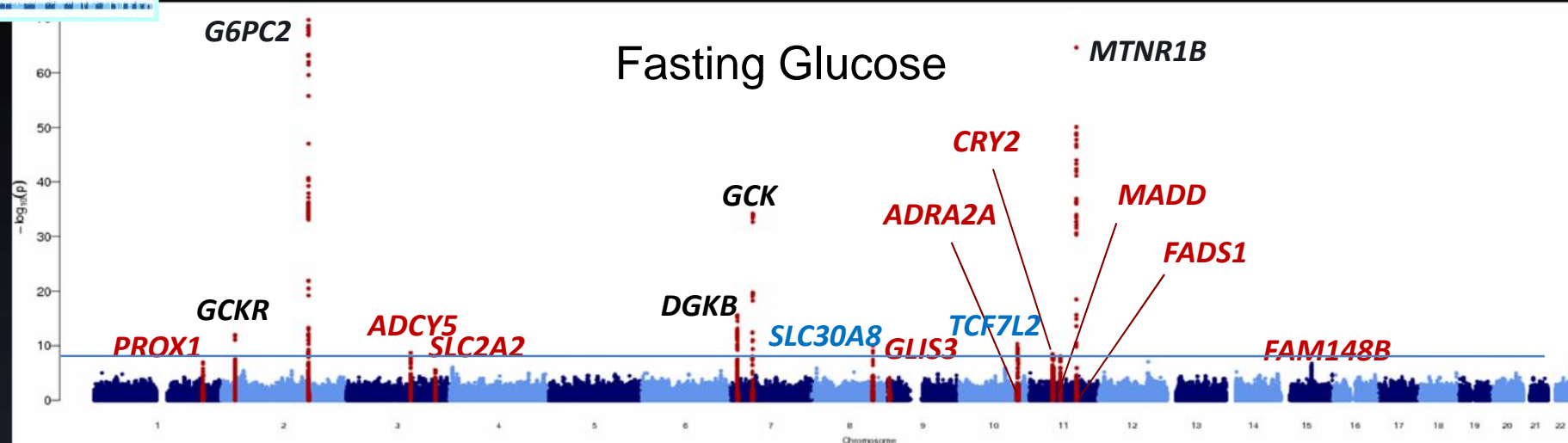
TYPE 2 DIABETES KNOWLEDGE PORTAL

<http://www.type2diabetesgenetics.org>



MAGIC 2010: 55 Cohorts with 122,744 non-diabetic EA

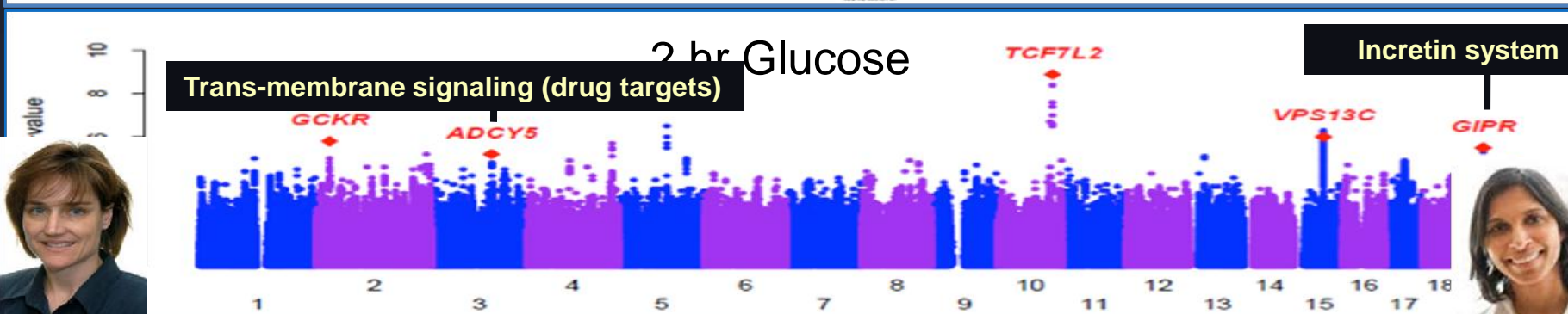
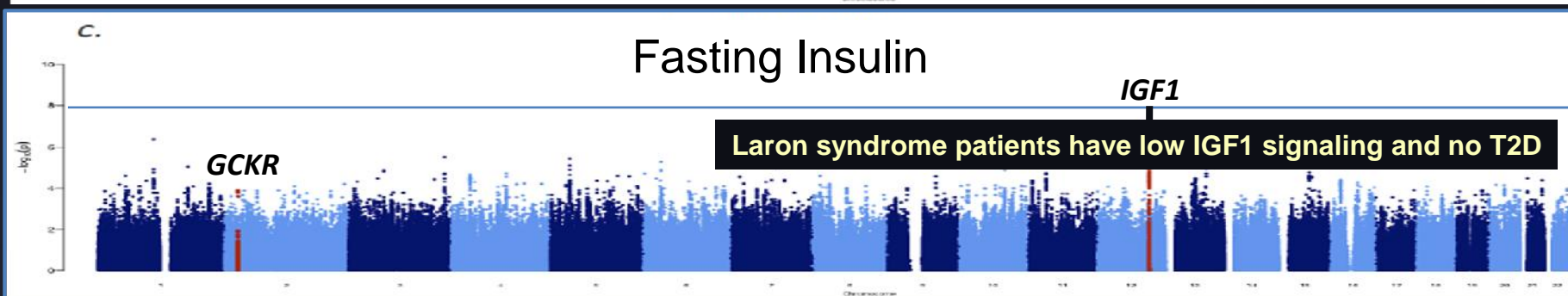
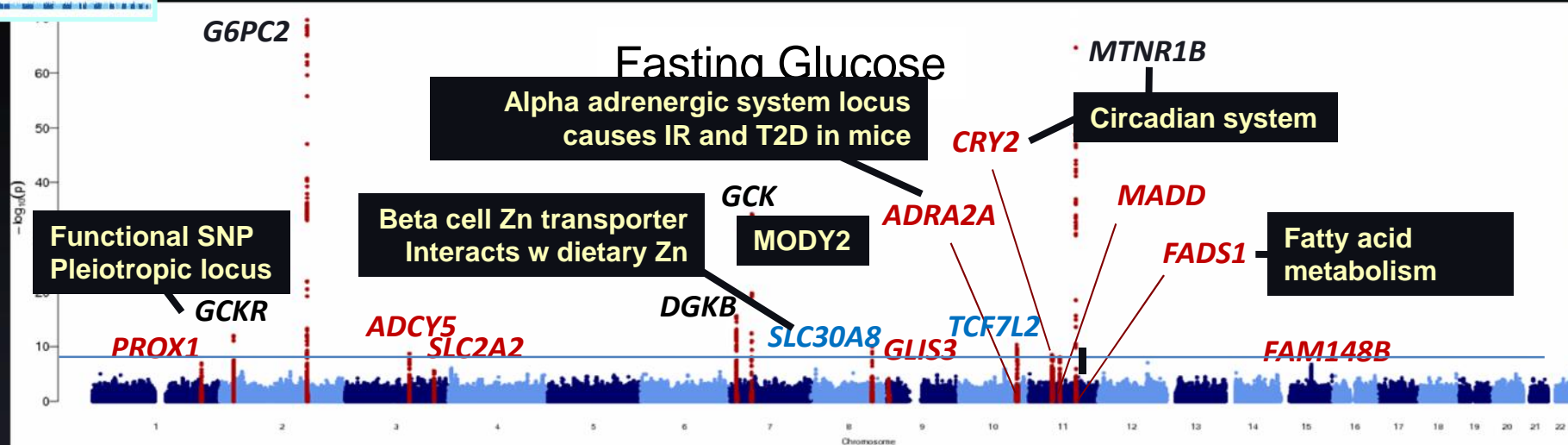
14 Genetic Loci Associated with FG, 2 w FI, 5 w 2hrG





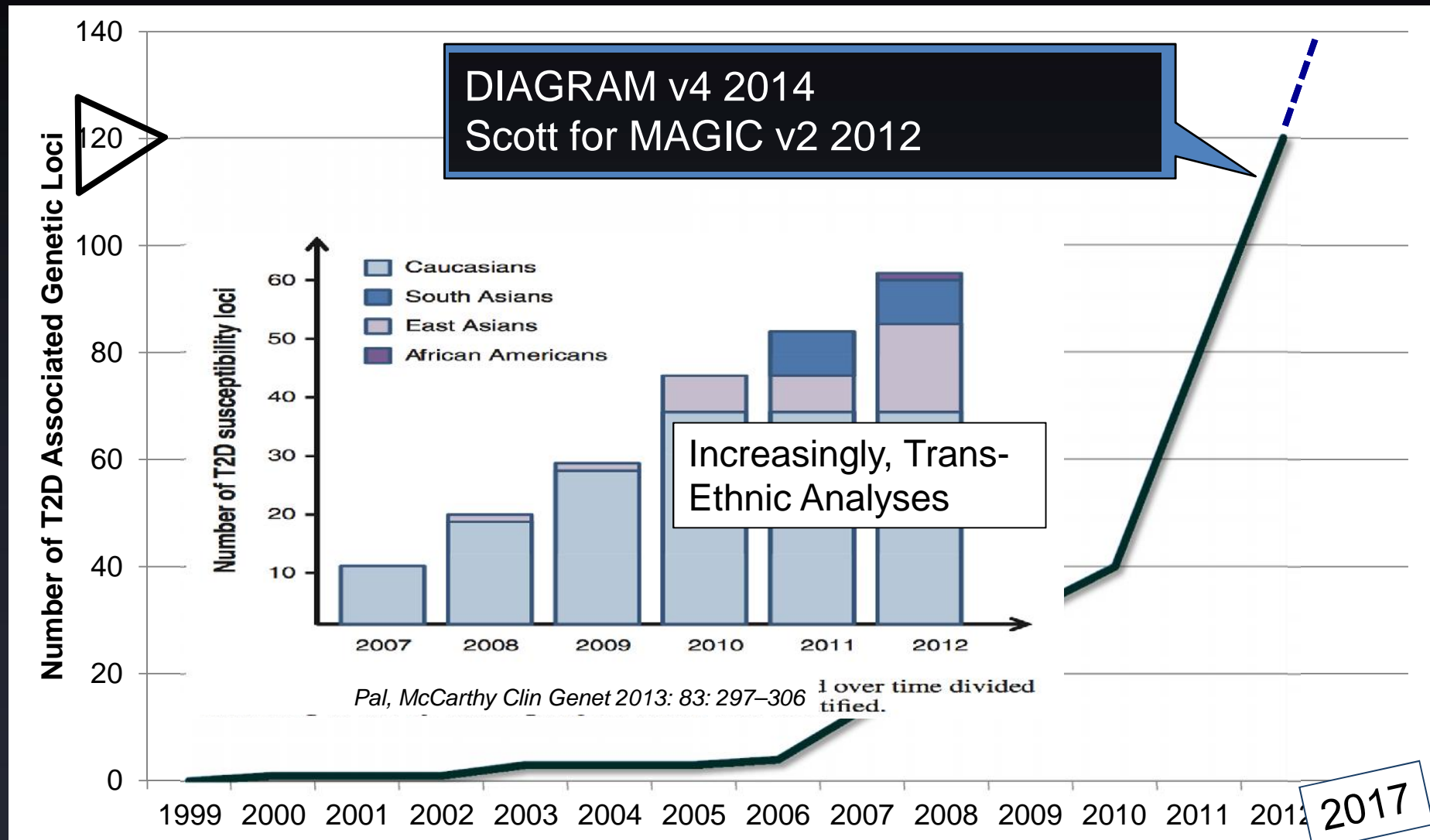
MAGIC GWAS of T2D-Related Quantitative Traits

Abundant New Biology, New Hypotheses

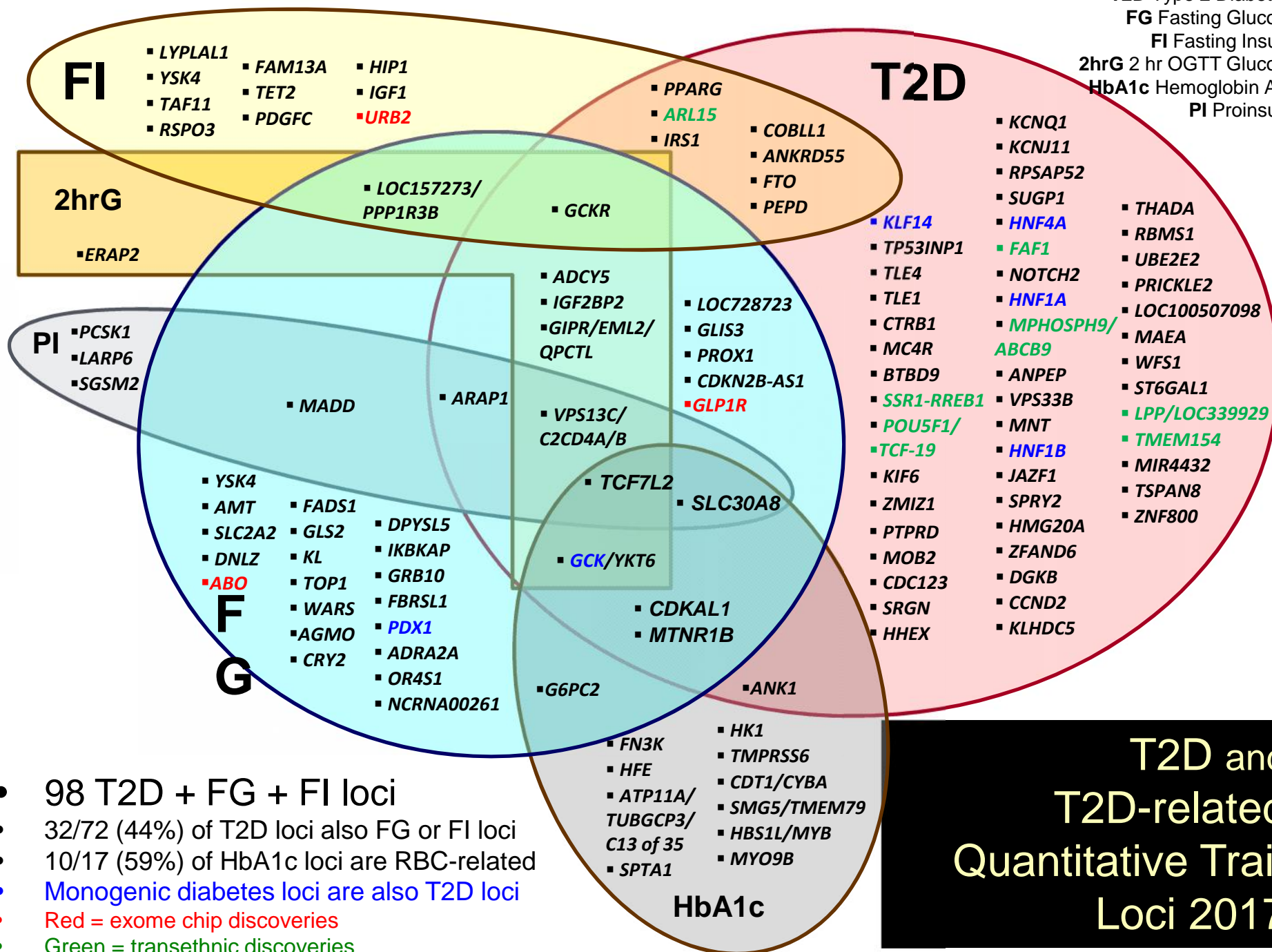


>120 SNPs at >110 T2D/QT-Associated Loci

T2D-QT Genetics @ June, 2017



T2D Type 2 Diabetes
 FG Fasting Glucose
 FI Fasting Insulin
 2hrG 2 hr OGTT Glucose
 HbA1c Hemoglobin A1c
 PI Proinsulin



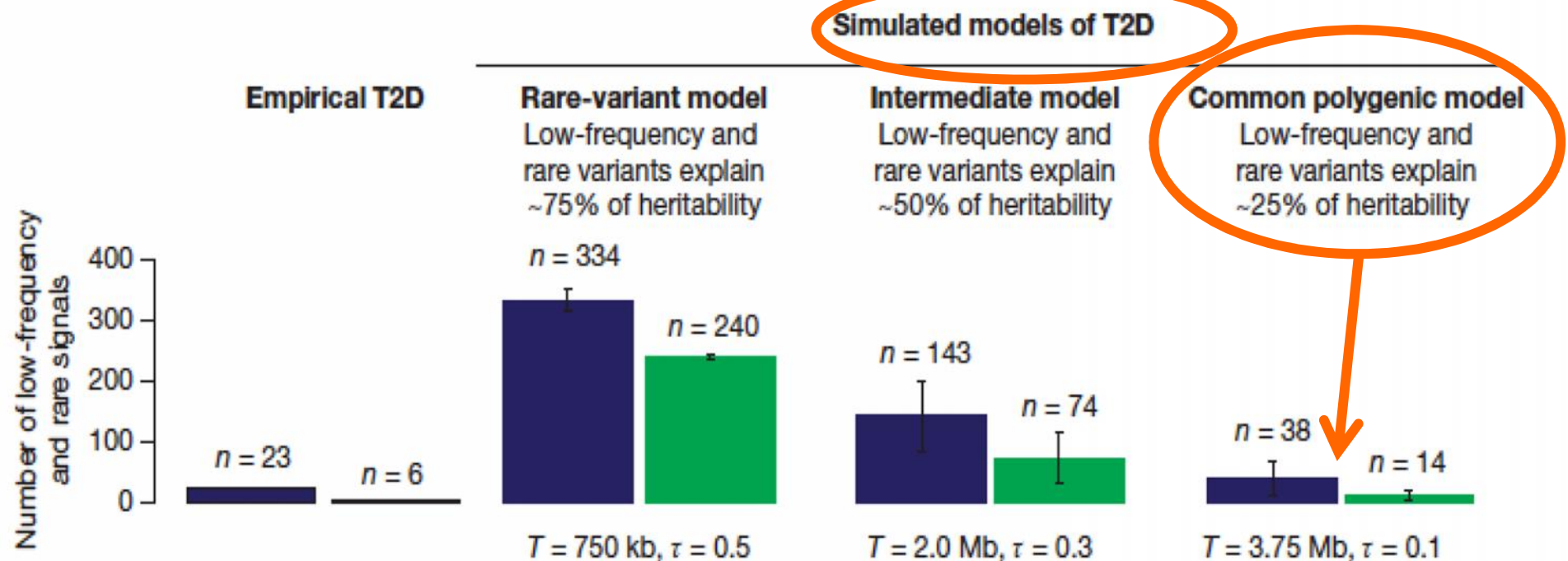
- 98 T2D + FG + FI loci
- 32/72 (44%) of T2D loci also FG or FI loci
- 10/17 (59%) of HbA1c loci are RBC-related
- Monogenic diabetes loci are also T2D loci
- Red = exome chip discoveries
- Green = transethnic discoveries

The genetic architecture of type 2 diabetes

A list of authors and affiliations appears in the online version of the paper

GoT2D and T2D-GENES

- Whole-genome sequencing in 2,657 European individuals with and without diabetes
- Exome sequencing in 12,940 individuals from five ancestry groups
- GWAS and EWAS genotyping and imputation in a further 111,548 subjects



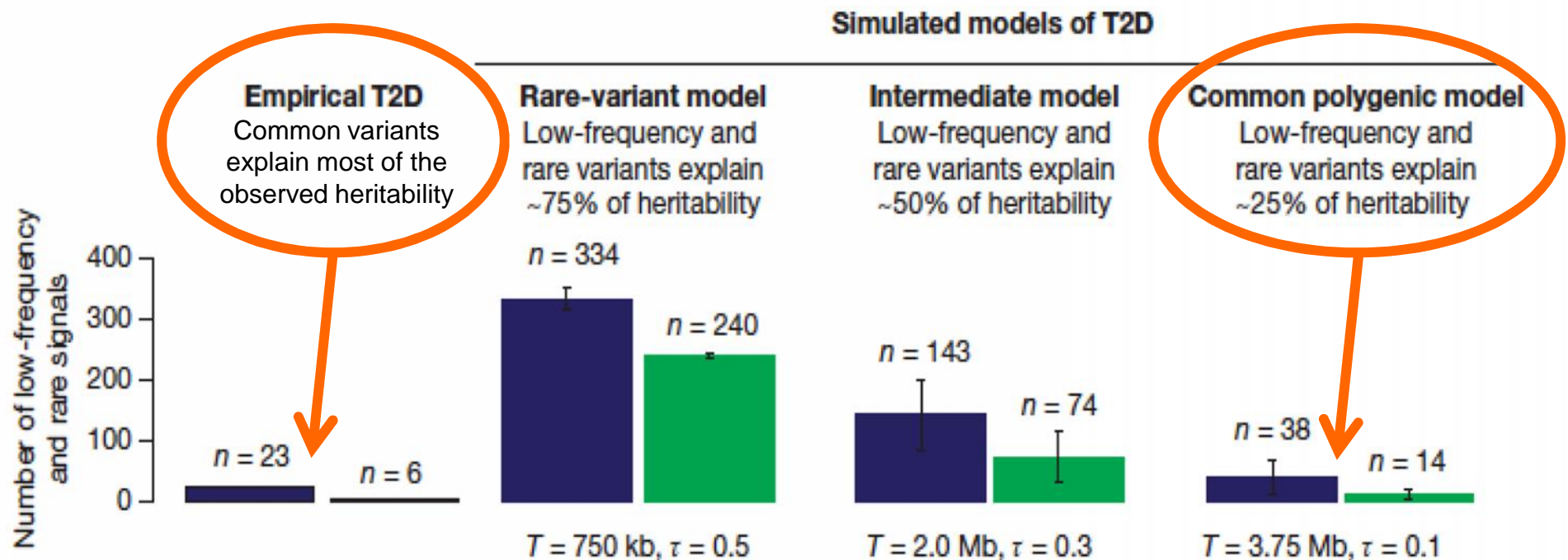
T2D-GENES Consortium

The genetic architecture of type 2 diabetes

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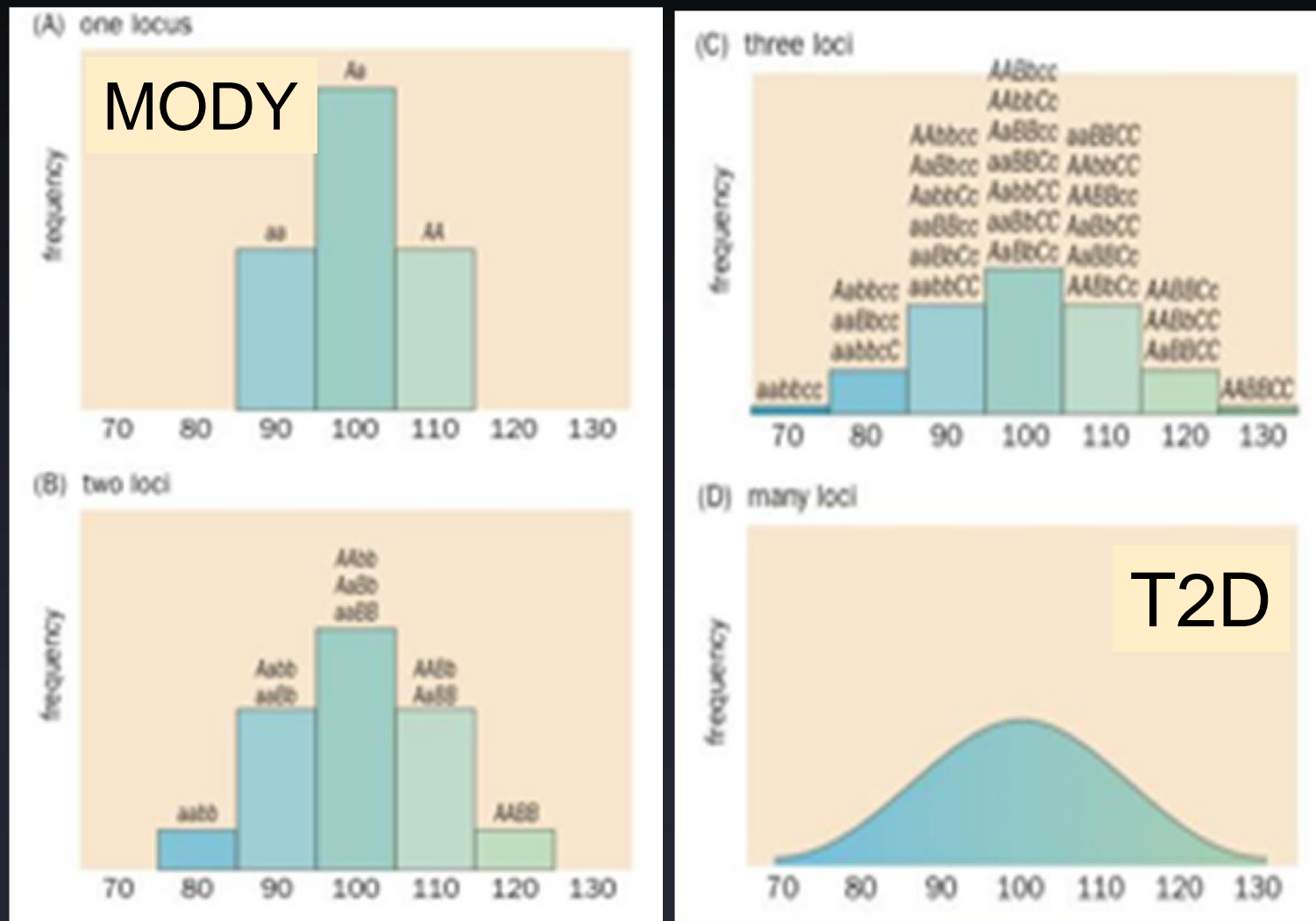
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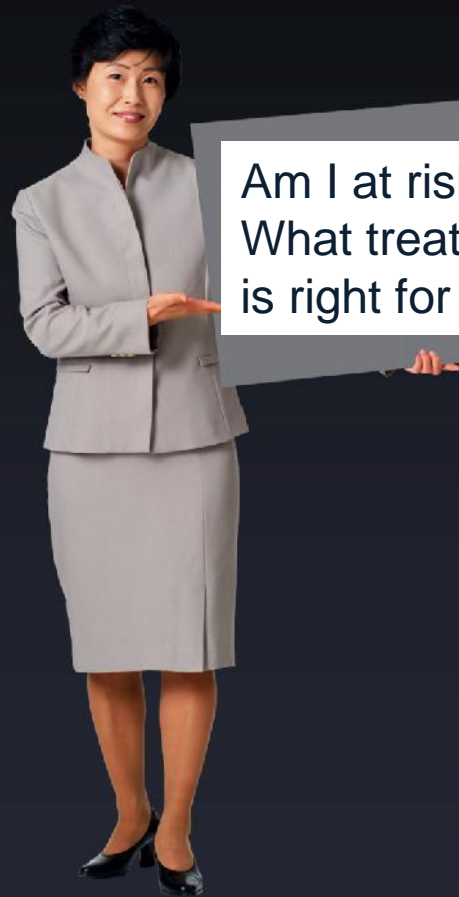
T2D-GENES Consortium

MODY: Monogenic Disorders Have ~2 Risk States
T2D Polygenic Risk ~ a Bell Shaped Distribution



Clinical Application of T2D Genetics

Personal and Population Health



Am I at risk?
What treatment
is right for me?



Which people are at risk?
Are all treatments right for everyone?

Clinical Application of T2D Genetics

Personal and Population Health



Am I at risk?
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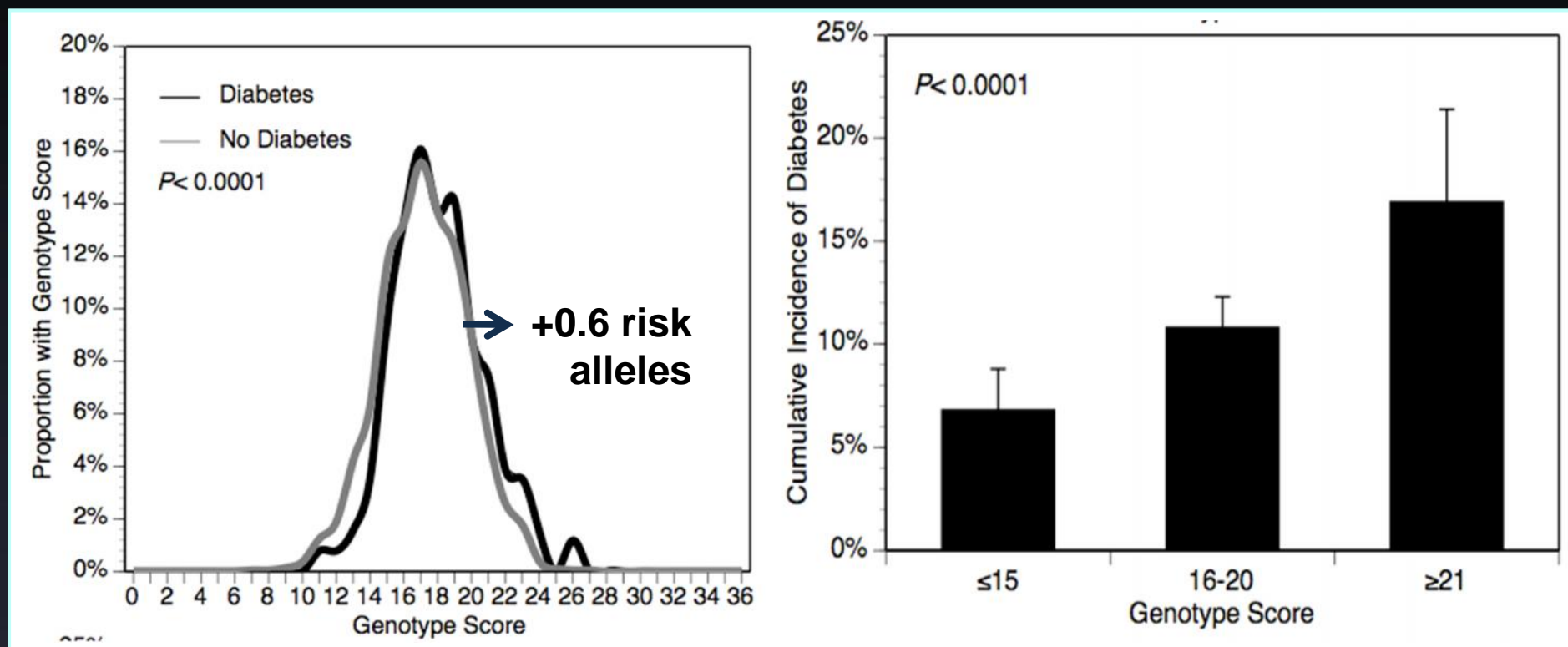
Which people are at risk?

Are all treatments right for everyone?

Predicting Future T2D using T2D Genetics

18 SNP Genotype Score Predicts New Cases of T2D

0 risk allele = 0, 1 risk allele = 1, 2 risk alleles = 2; range 0-36



Mean genotype score:

Diabetes: 17.7

No diabetes: 17.1

($P < 0.0001$)

% of Pop.

25%

64%

11%

RR

1.0

1.6

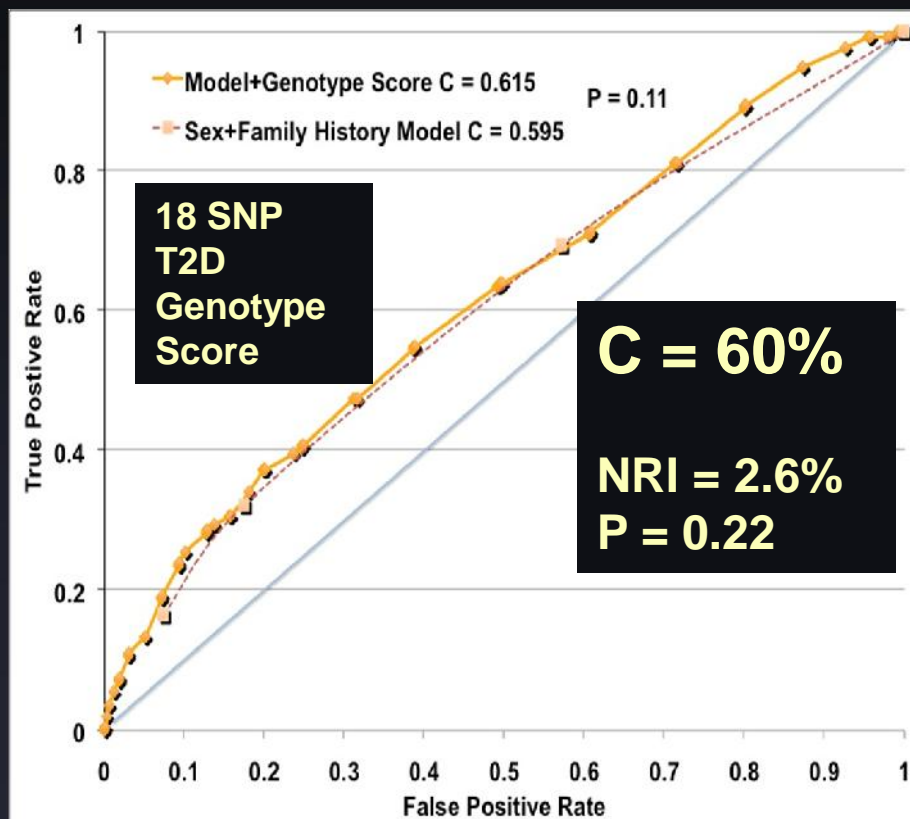
2.5

Meigs et al N Engl J Med 2008;359:2208-19

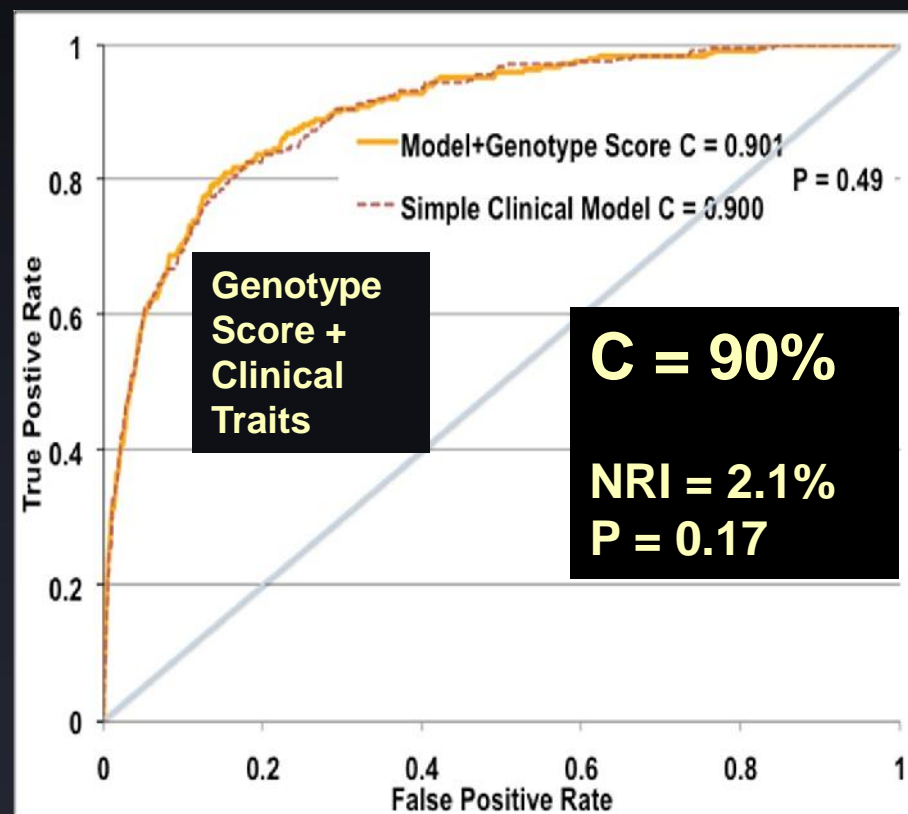
T2D Genotype Scores Predict Incident T2D in Adults

... so do Clinical Risk Factors

T2D Genetics Alone



T2D Genetics + Clinical Risk Factors



T2D Genetic Risk Increases All-Cause Mortality

1,556 of 6,501 NHANES Mortality Follow-Up participants died over 17 years

Estimated mortality risk per T2D risk allele by ethnicity

OR (95% CI)

All ethnicities

BMI model

1.04 (1.00, 1.07)

Modifiable risk factors model

1.04 (1.01, 1.08)

Non-Hispanic Whites

BMI model

1.04 (1.00, 1.09)

Modifiable risk factors model

1.05 (1.00, 1.10)

Non-Hispanic Blacks

BMI model

1.04 (1.01, 1.06)

Modifiable risk factors model

1.03 (1.00, 1.06)

Mexican Americans

BMI model

0.95 (0.90, 1.01)

Modifiable risk factors model

0.95 (0.89, 1.02)

.8 .9 1 1.1 1.2
Odds ratio (OR) per T2D risk allele



Patients Say that Genetic Testing Would Increase Motivation to Change Lifestyle

152 MGH 1^o Care Patients

Imagine that your PCP tells you that there is an approved genetic test to help predict whether you have a 'high' or 'low' chance of getting diabetes. It is a simple blood test at no cost to you.

> If the test result indicated that you had a 'high' chance of developing diabetes, how would this result change your motivation to make recommended lifestyle changes?

More motivated **99%**

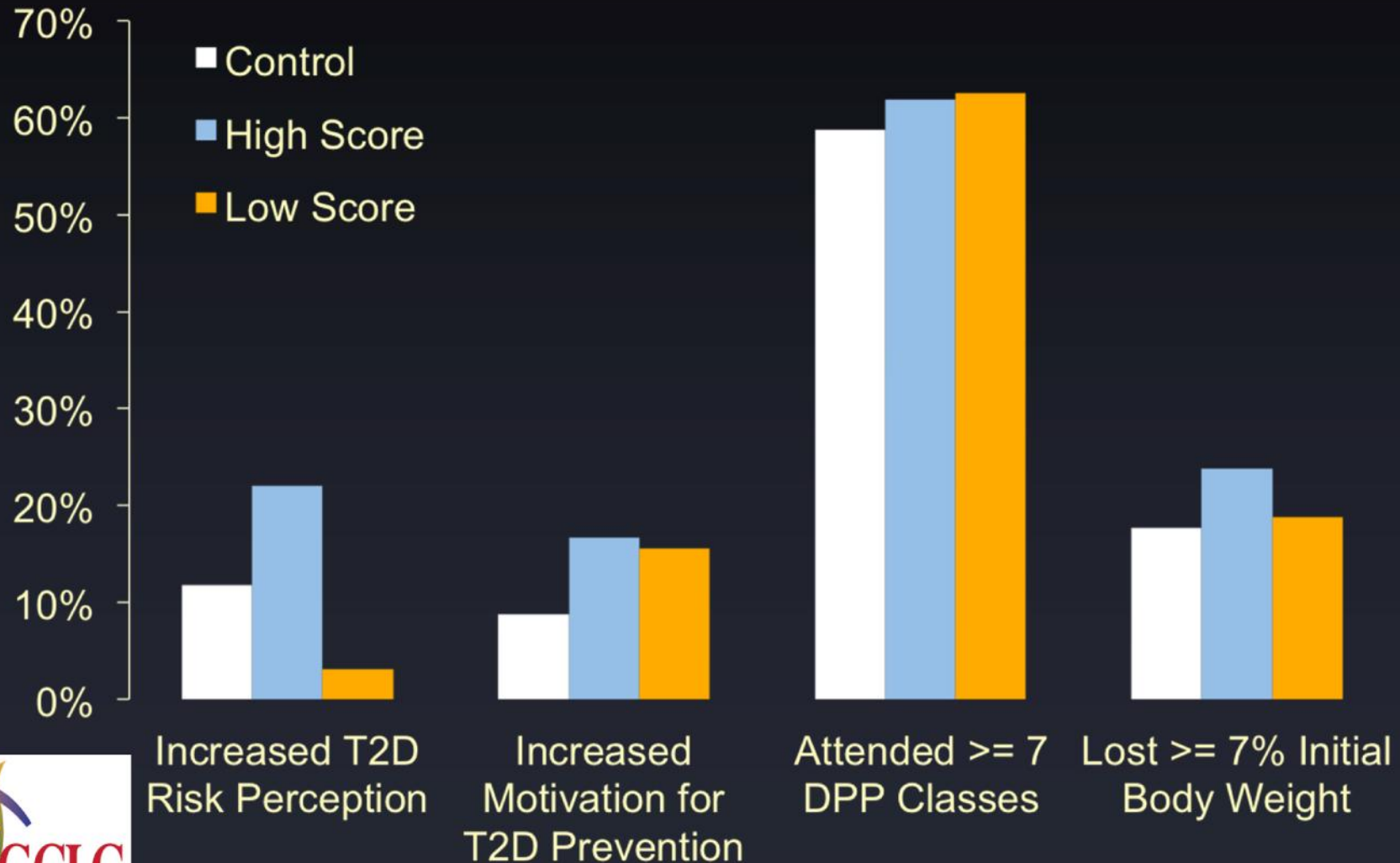
> If the test result indicated that you had a 'low' chance of developing diabetes, how would this result change your motivation to make recommended lifestyle changes?

Less motivated
or No Change **59%**



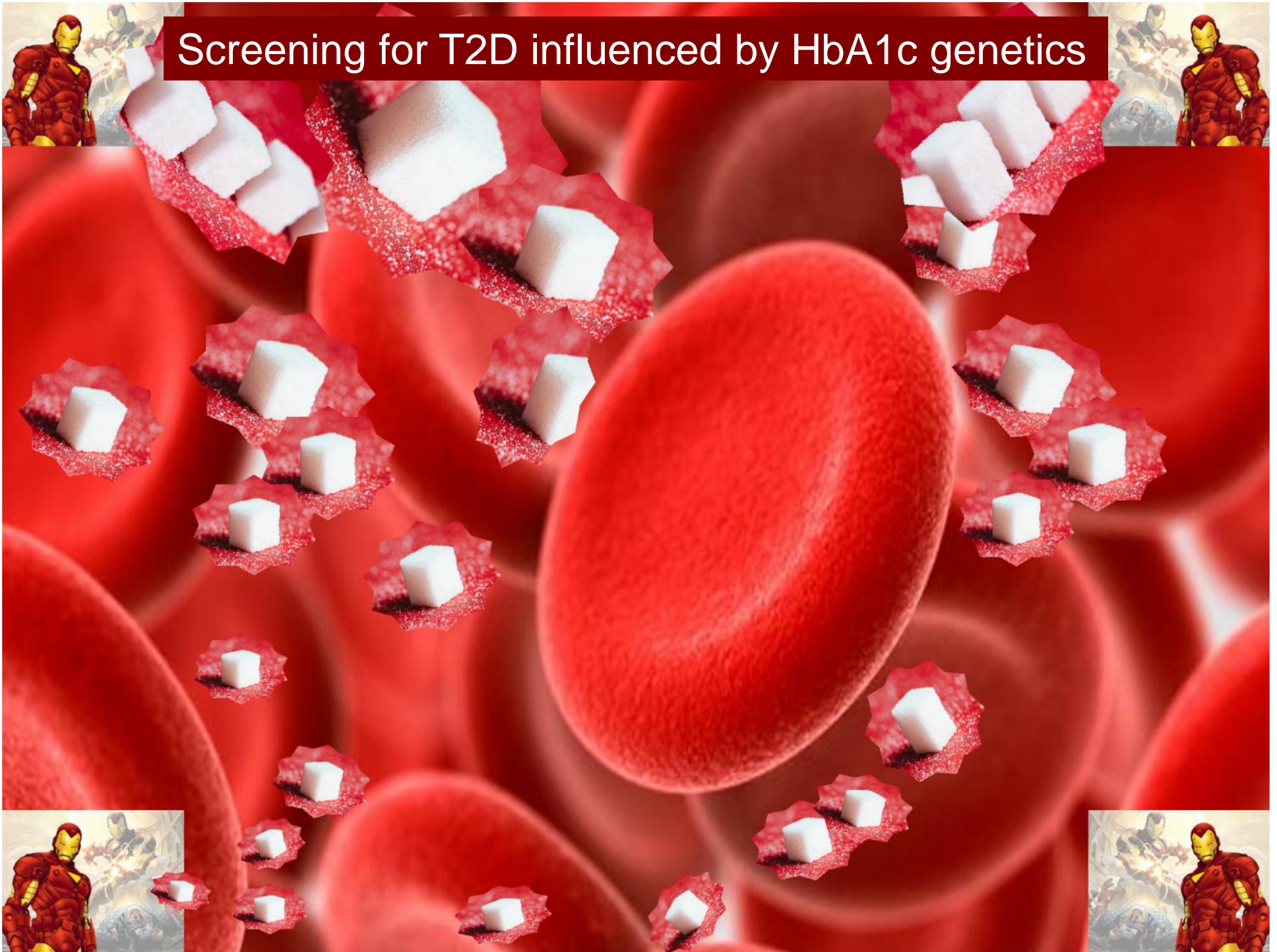
(No) Effects of Genetic Counseling for Lifestyle Change in 116 People with MetS Randomized to Genetic Testing or No Testing

N = 44 High Risk, 34 Low Risk, 38 Control



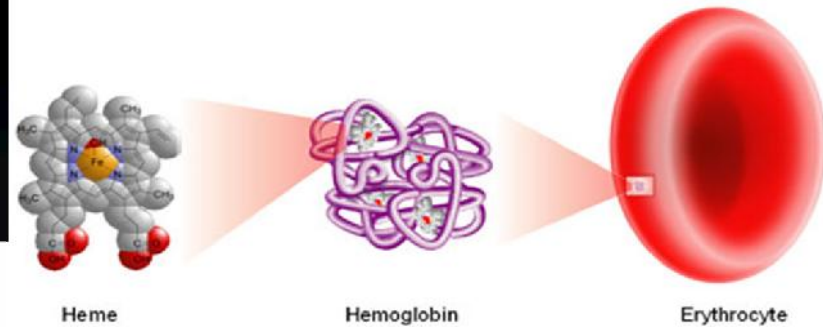
Grant et al Diabetes Care. 2013 PMID: 22933432

Screening for T2D influenced by HbA1c genetics



Hemoglobin A_{1c}

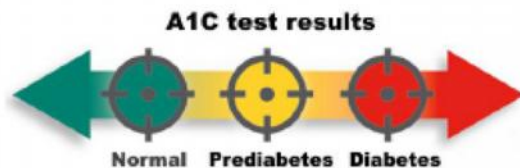
A1C & T2D DIAGNOSIS



WHAT?

HbA_{1c} (A1C) test

- Measures the proportion of glycated hemoglobin in the blood (*irreversible chemical modification by blood glucose*)



👍 Reflects average glycemia over the life of RBC (2-3 months)

WHY?

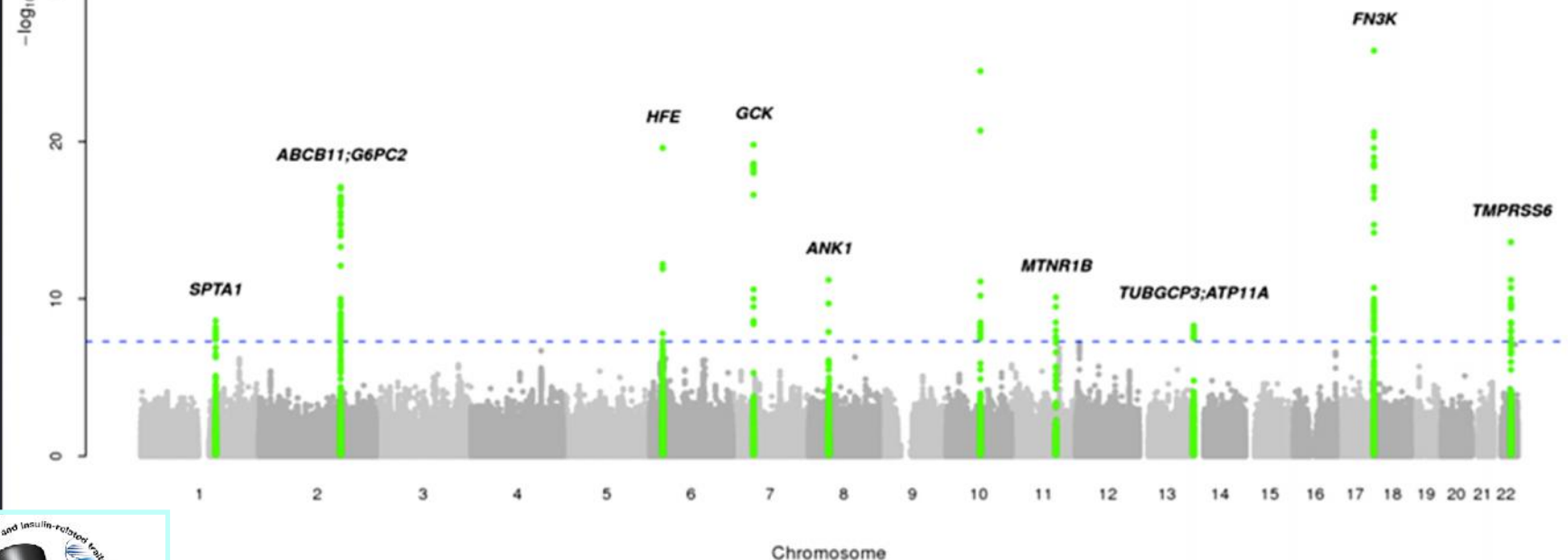
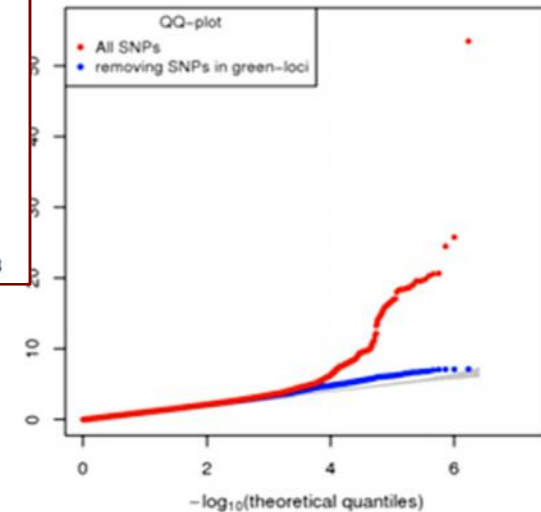
A1C testing in diagnosing Type 2 diabetes

- Only test for T2D that is not directly a measurement of blood glucose
- Non-glycemic factors are known to influence the diagnostic accuracy for T2D
- Some of these non-glycemic factors may be genetically determined

Common Variants at 10 Genomic Loci Influence Hemoglobin A_{1c} Levels via Glycemic and Nonglycemic Pathways

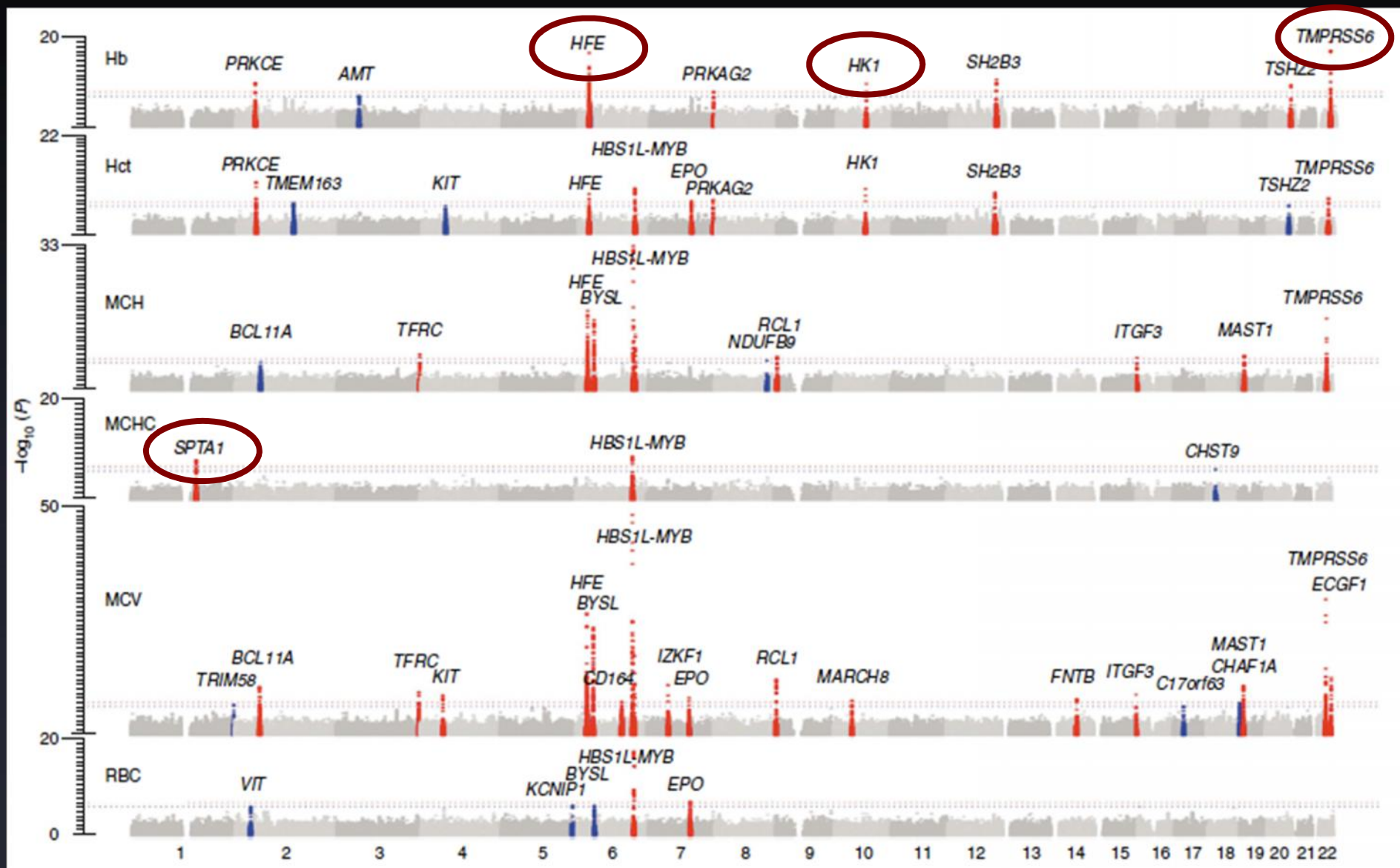
Nicole Soranzo,^{1,2} Serena Sanna,³ Eleanor Wheeler,¹ Christian Gieger,⁴ Dörte Radke,⁵ Josée Dupuis,^{6,7} Nabila Bouatia-Naji,⁸ Claudia Langenberg,⁹ Inga Prokopenko,^{10,11} Elliot Stolerman,^{12,13,14} Maniinder S. Sandhu,^{9,15,16} Matthew M. Heenev,¹⁷ Joseph M. Devaney.¹⁸

>46,000 individuals, 31 cohorts
10 Loci $P < 5 \times 10^{-8}$, 6 Novel



CHARGE GWAS of Hematology Traits

Shares Loci with HbA1c Loci



>2/3 of 10 HbA1c-associated SNPs are in Non-Glycemic Biologic Pathways

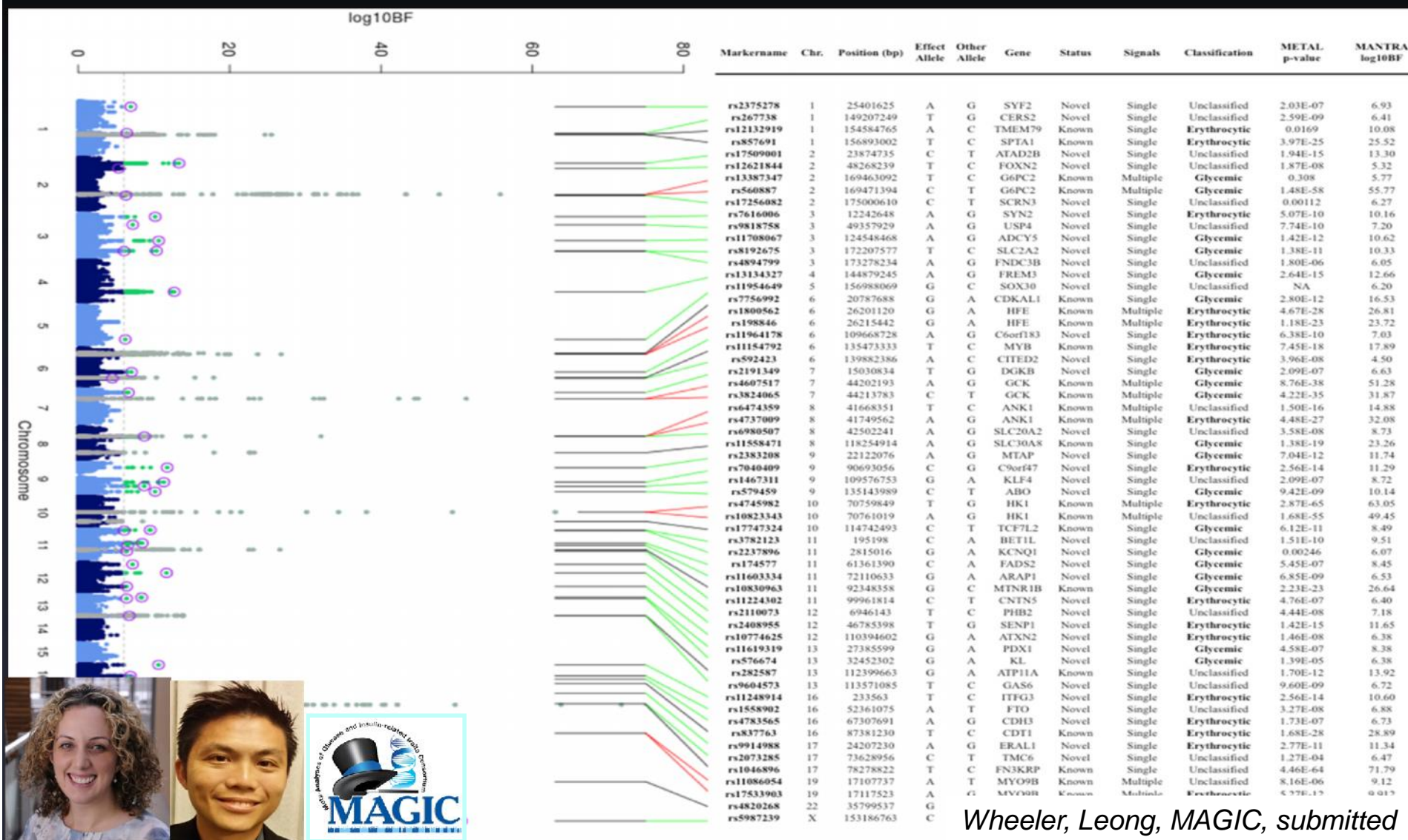


Locus	Name	Chr	Pathway	Heme GWAS
<i>G6PC2</i>	glucose-6-phosphatase, catalytic, 2	2	Glycemic	
<i>GCK</i>	glucokinase	7	Glycemic, T2D	
<i>MTNR1B</i>	melatonin receptor 1B	11	Glycemic, T2D	
<i>FN3K</i>	fructosamine 3-kinase	17	Deglycation	
<i>HFE</i>	hemochromatosis	6	Iron	MCV, Hb
<i>TMPRSS6</i>	transmembrane protease, serine 6	22	Iron	MCV, MCHC
<i>HK1</i>	erythrocyte hexokinase 1	10	Eythrocyte	MCV, Hb
<i>SPTA1</i>	spectrin, alpha, erythrocytic 1	1	Eythrocyte	MCV, Hb
<i>ANK1</i>	ankyrin 1, erythrocytic	8	Eythrocyte	
<i>ATP11A</i>	ATPase type 11A	13	Erythrocyte	



New GWAS of Hemoglobin A_{1c}

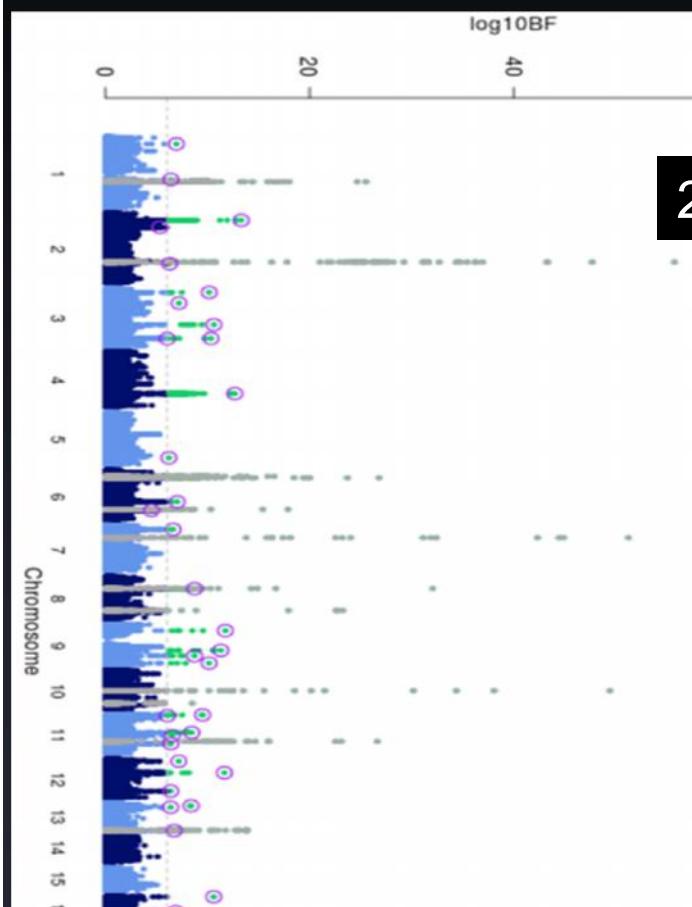
185,000 People without Diabetes from >50 cohorts and 7 ancestral groups
60 Loci, 43 new, 65 independent SNPs



Wheeler, Leong, MAGIC, submitted

New GWAS of Hemoglobin A_{1c}

185,000 People without Diabetes from >50 cohorts and 7 ancestral groups
60 Loci, 43 new, 65 independent SNPs



20 Erythrocytic SNPs

20 Glycemic SNPs

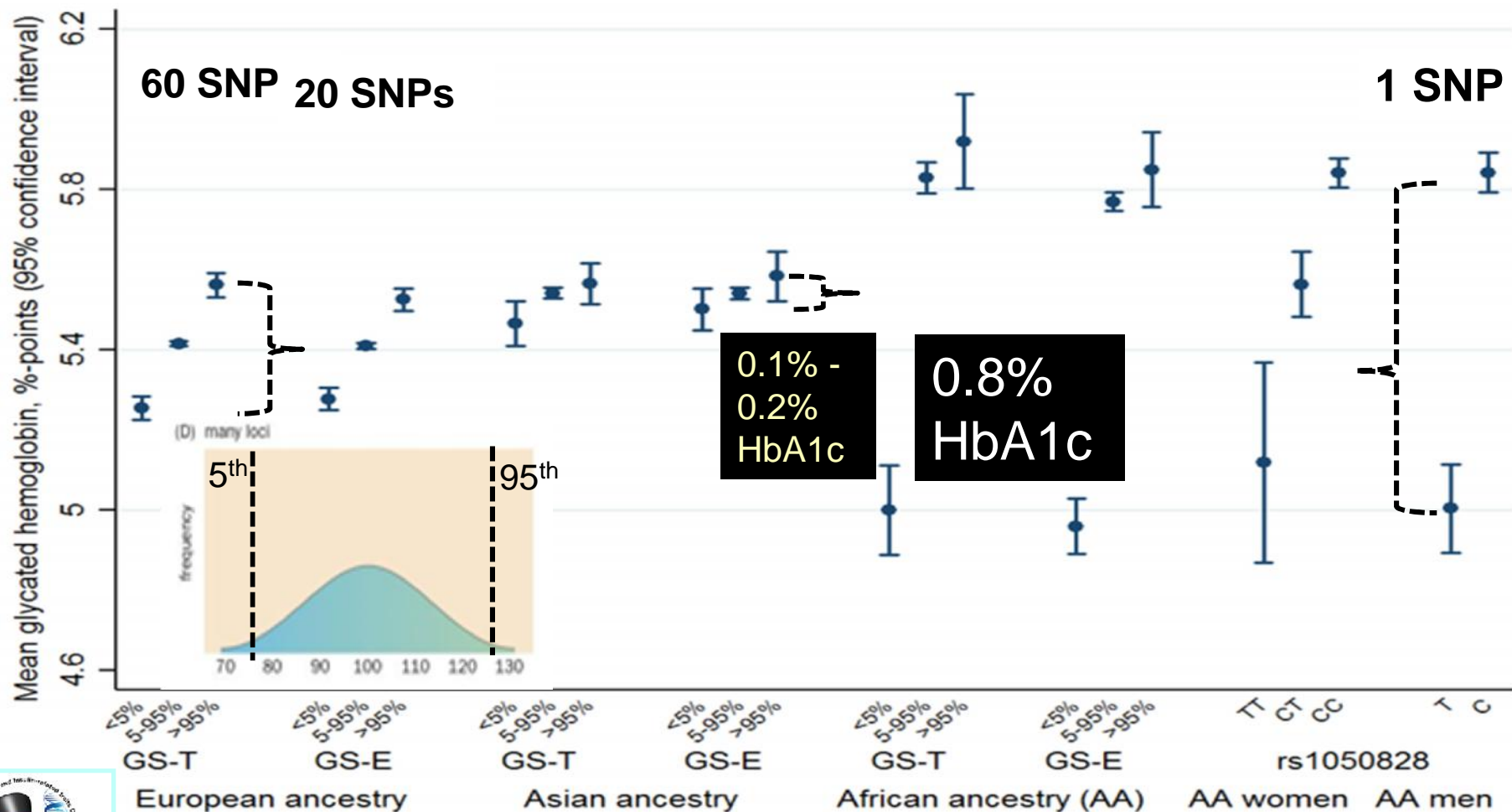
Gene	Known	Single	Glycemic	2.80E-12	16.53	TAL	MANTRA
CDKAL1	Known	Single	Glycemic	2.80E-12	16.53	value	log10BF
HFE	Known	Multiple	Erythrocytic	4.67E-28	26.81		
HFE	Known	Multiple	Erythrocytic	1.18E-23	23.72	1E-07	6.93
			Erythrocytic	6.38E-10	7.03	9E-09	6.41
			Erythrocytic	7.45E-18	17.89	9169	10.08
			Erythrocytic	3.96E-08	4.50	7E-25	25.52
CITED2	Novel	Single	Erythrocytic	3.96E-08	4.50	4E-15	13.30
DGKB	Novel	Single	Glycemic	2.09E-07	6.63	7E-08	5.32
			Glycemic	8.76E-38	51.28	308	5.77
			Glycemic	4.22E-35	31.87	4E-58	55.77
ANK1	Known	Multiple	Unclassified	1.50E-16	14.88	0112	6.27
ANK1	Known	Multiple	Erythrocytic	4.48E-27	32.08	7E-10	10.16
SLC20A2	Novel	Single	Unclassified	3.58E-08	8.73	4E-10	7.20
SLC30A8	Known	Single	Glycemic	1.38E-19	23.26	2E-12	10.62
MTAP	Novel	Single	Glycemic	7.04E-12	11.74	4E-11	10.33
C9orf47	Novel	Single	Erythrocytic	2.56E-14	11.29	9E-06	6.05
KLF4	Novel	Single	Unclassified	2.09E-07	8.72	4E-15	12.66
ABO	Novel	Single	Glycemic	9.42E-09	10.14	1A	6.20
HK1	Known	Multiple	Erythrocytic	2.87E-65	63.05	9E-12	16.53
HK1	Known	Multiple	Unclassified	1.68E-55	49.45	7E-28	26.81
TCF7L2	Known	Single	Glycemic	6.12E-11	8.49	4E-23	23.72
BET1L	Novel	Single	Unclassified	1.51E-10	9.51	4E-10	7.03
KCNQ1	Novel	Single	Glycemic	0.00246	6.07	9E-18	17.89
FADS2	Novel	Single	Glycemic	5.45E-07	8.45	9E-08	4.50
ARAP1	Novel	Single	Glycemic	6.85E-09	6.53	9E-07	6.63
MTNR1B	Known	Single	Glycemic	2.23E-23	26.64	9E-38	51.28
CNTN5	Novel	Single	Erythrocytic	4.76E-07	6.40	2E-35	31.87
						9E-16	14.88
						3E-27	32.08
						9E-08	8.73
						9E-19	23.26
						4E-12	11.74
						9E-14	11.29
						9E-07	8.72
						2E-09	10.14
						7E-65	63.05
						9E-55	49.45
						2E-11	8.49
						1E-10	9.51
						0246	6.07
						9E-07	8.45
						9E-09	6.53
						1E-23	26.64
						9E-07	6.40
						9E-08	7.18
						2E-15	11.65
						9E-08	6.38
						9E-07	8.38
						9E-05	6.38
						9E-12	13.92
						9E-09	6.72
						4E-14	10.60
						7E-08	6.88
						1E-07	6.73
						4E-28	28.89
						7E-11	11.34
						7E-04	6.47
						4E-64	71.79
						8.16E-06	9.12
						6.37E-15	0.015



Wheeler, Leong, MAGIC, submitted

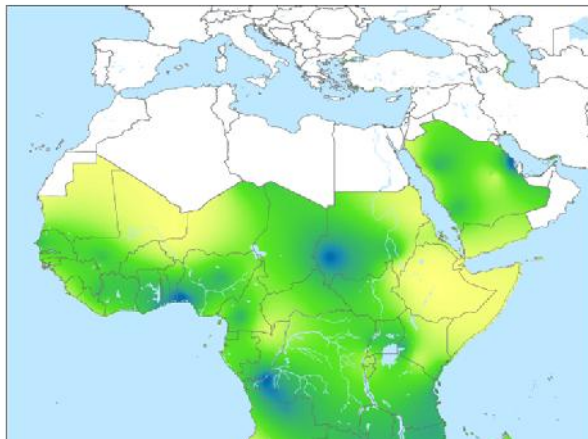
SNP Scores = Small Differences in HbA1c in European, Asian Ancestry

A Single Chromosome X SNP (rs1050828, G202A) in *G6PD* Accounts for a Large Difference in African Ancestry

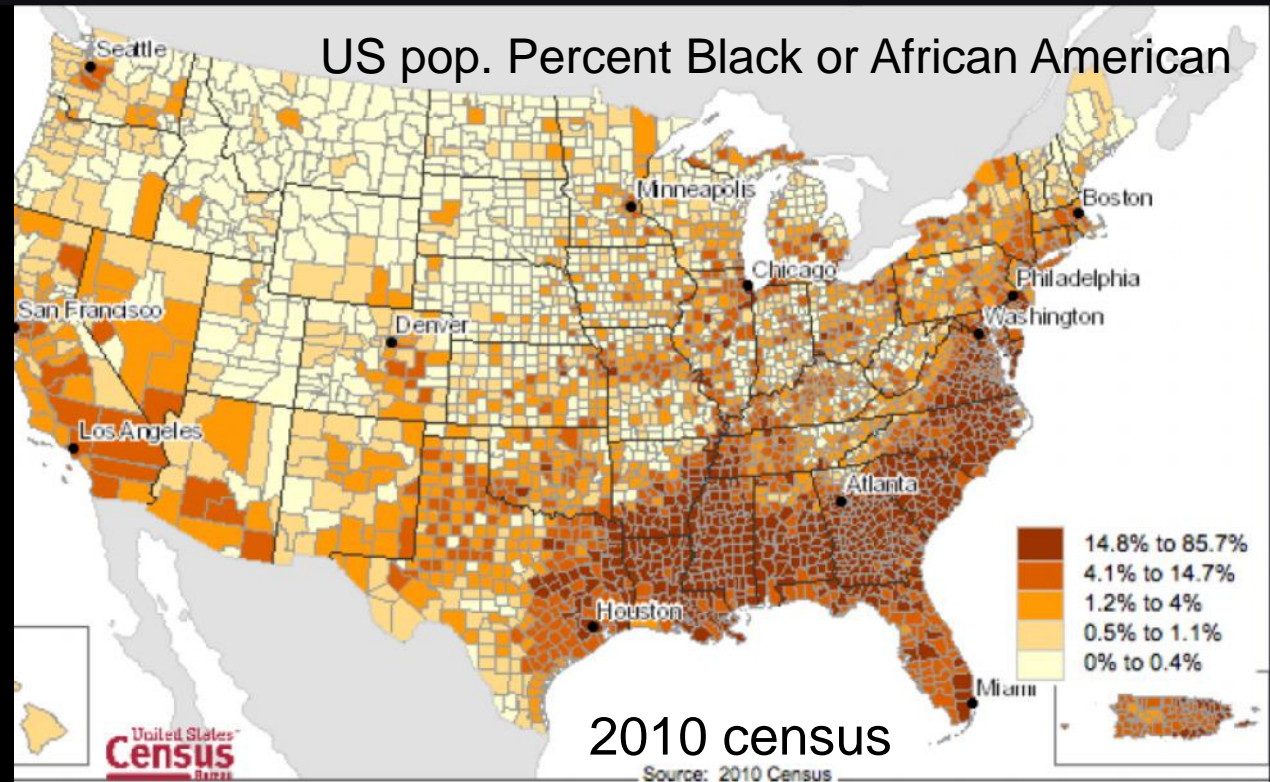
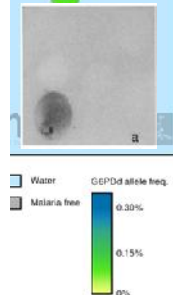


Using NHANES 2013-14, if we tested adult Americans for T2D with HbA1c,
About 2% or 650,000 African Americans would be missed
due to genetically lowered HbA1c

G6PD G202A allele
frequency 11% in African
Americans (0% in whites)



G6PD G202A is
highly prevalent
in West Africa,
where it protects
against severe
malaria



The influence of HbA1c genetics is not distributed
equally in the US

Wheeler, Leong, MAGIC, submitted

Themes for Today

- Discoveries over 15 years in T2D genetics
 - Dramatic expansion in new biology
- Predicting future T2D using T2D genetics
 - Not ready for prime time
- Screening for T2D influenced by HbA1c genetics
 - Opportunity for health application of genetics to reduce T2D disparities?

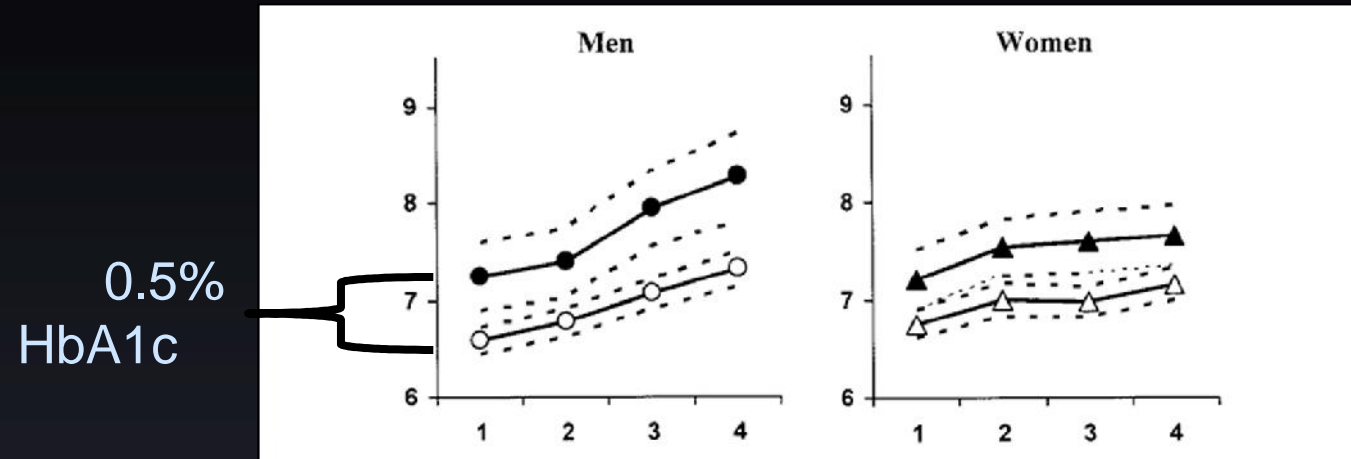
Thank You





African Americans w T2D are More Hyperglycemic at Diagnosis than Whites

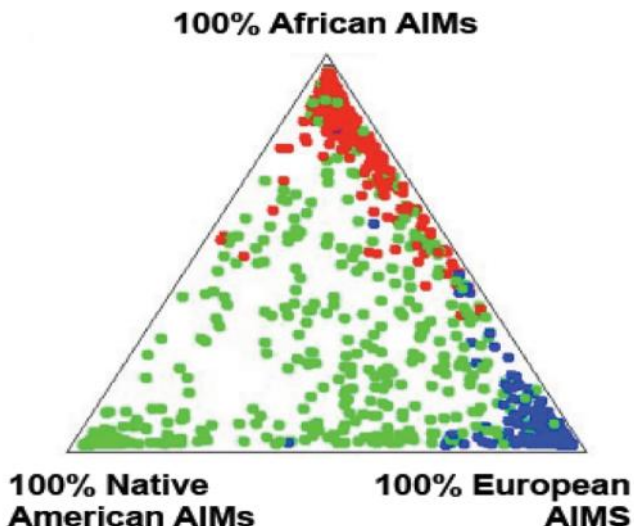
In a health system with equal access to screening, HbA1c was ~0.5 units higher in black (●) vs. white (○) patients at T2D diagnosis. This persisted over time despite equal access and intensity of treatment.



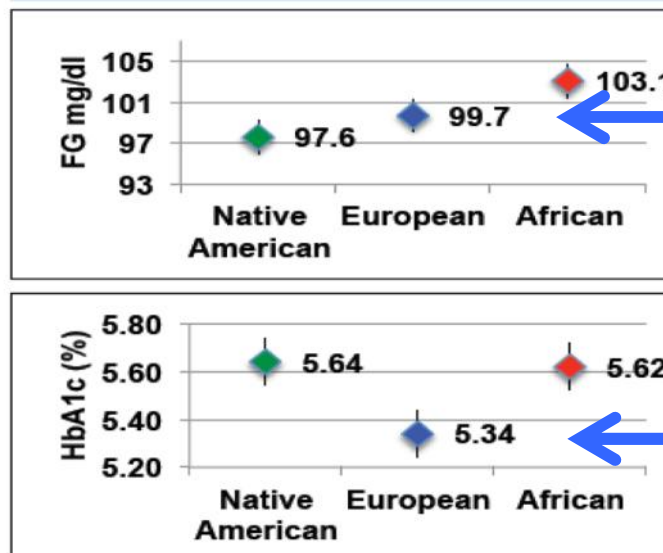
Adams et al Diabetes Care 2005 PMID: 16306543

African American Ancestry → Higher FG and HbA1c vs. European Ancestry

Distribution of AIMS by Self-reported Race



FG and HbA1c Levels if with 100% AIM



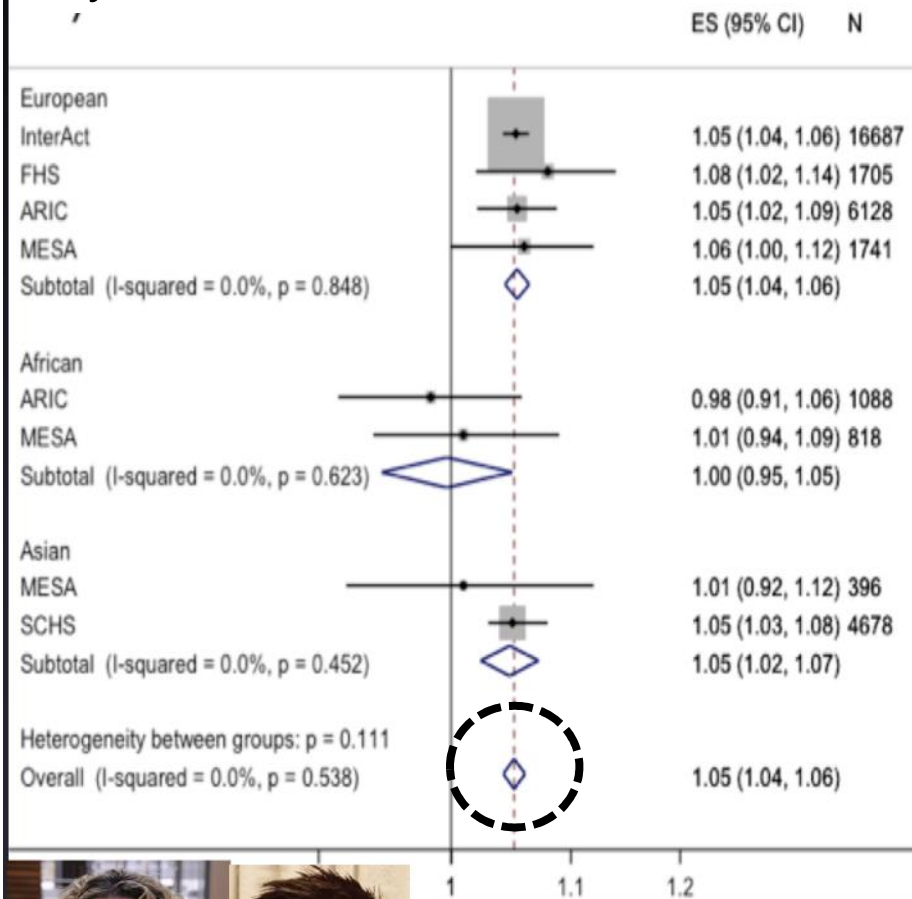
BACH 3, N = 1,387
Differences remained after adjustment for obesity and social inequality variables

0.3% HbA1c

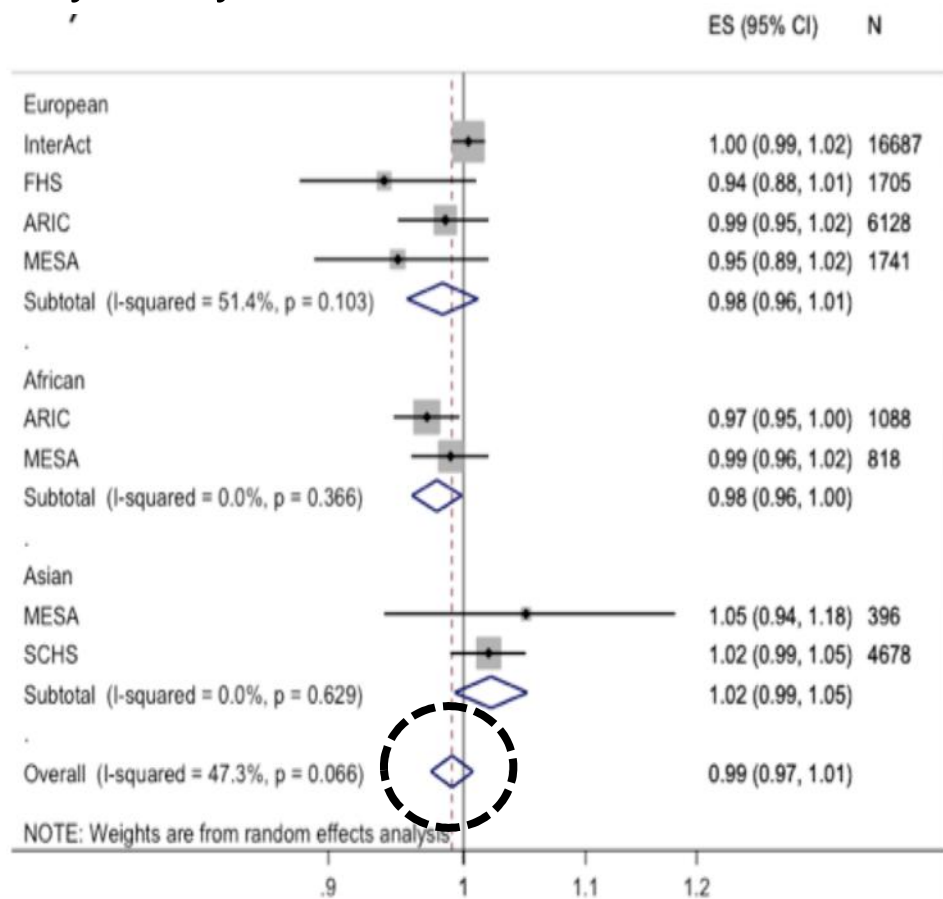
Meigs et al Diabetologia. 2014 PMID: 24942103

A Glycemic Genetic Risk Score Predicts Incident T2D... but an Erythrocytic GRS Does Not

Glycemic SNPs GRS

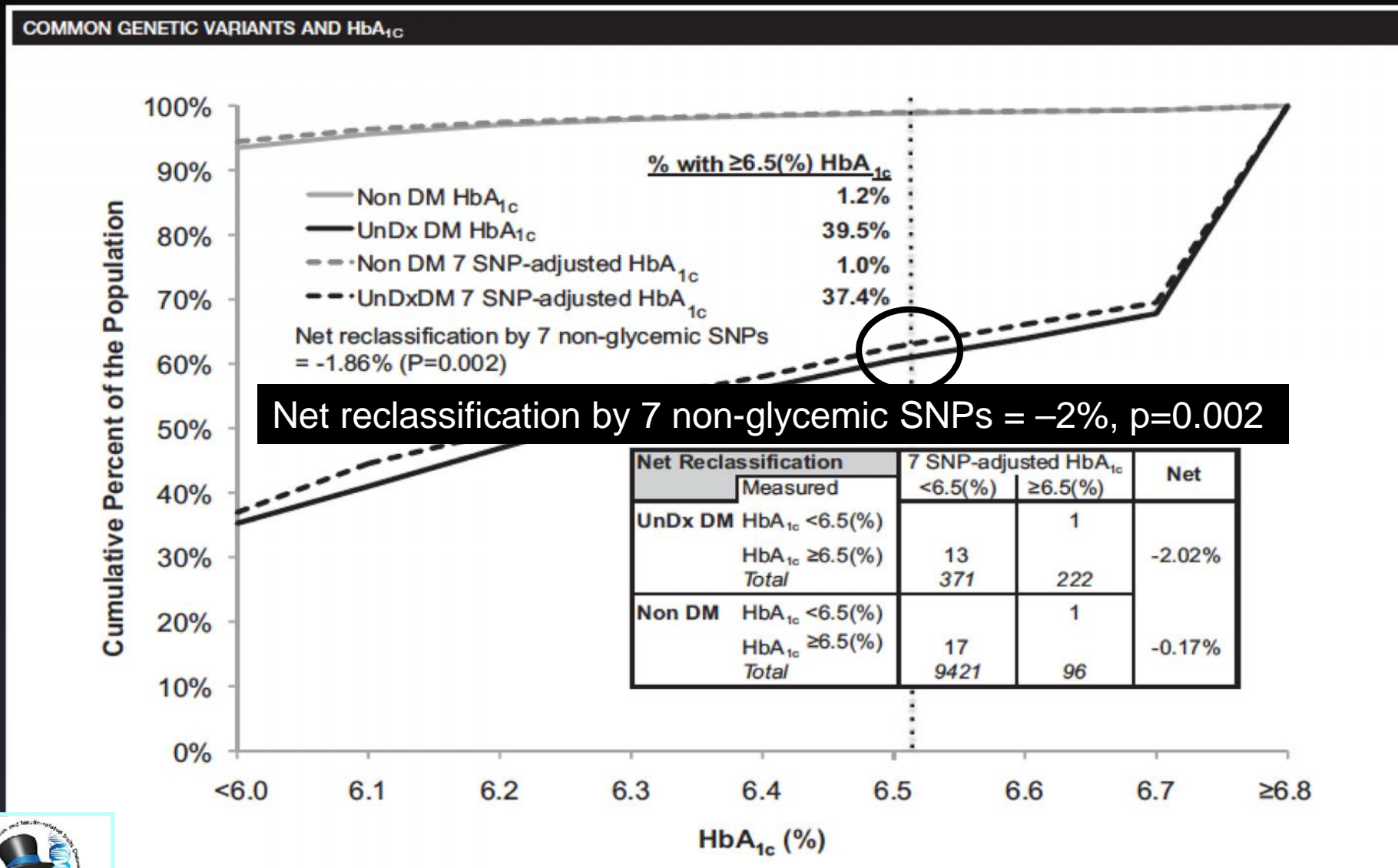


Erythrocytic SNPs GRS

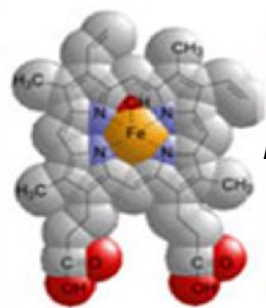
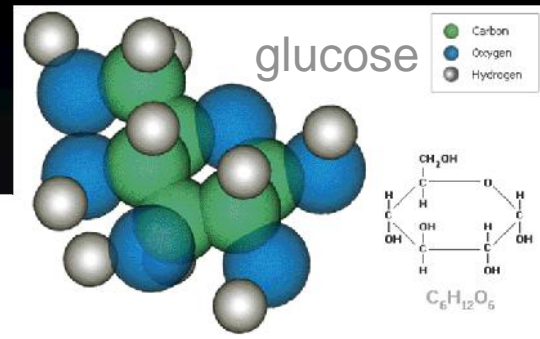


Wheeler, Leong, MAGIC, submitted

Public Health Implications of the *G6PD* Variant on T2D Screening: 2% of whites mis-classified



Genetics Reveals Erythrocyte Pathways that Influence HbA_{1c} Levels



Heme

HFE

TMPRSS6



Hemoglobin



Erythrocyte

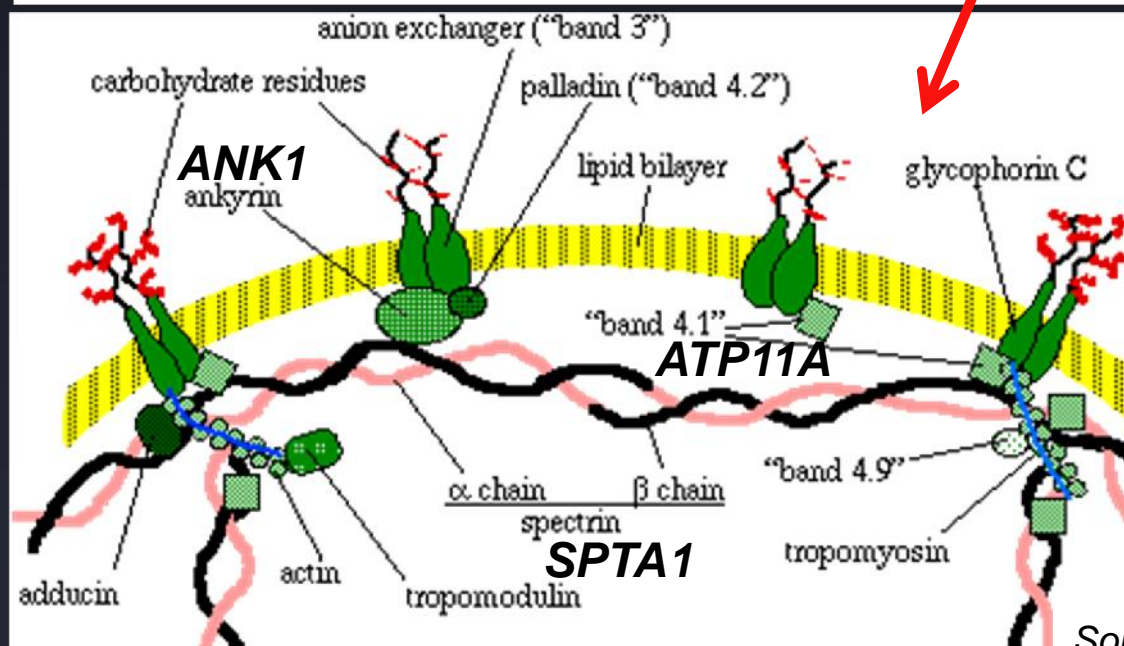
GCK

G6PC2

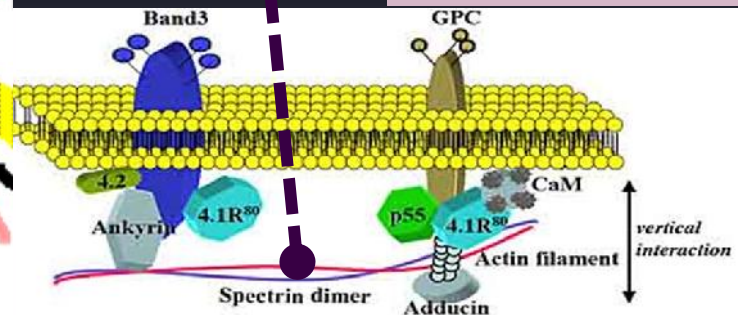
MTNR1B



visuals unlimited



SPTA1:
Hereditary
Elliptocytosis 2,
Pyropoikilocytosis,
African only?



Soranzo et al, Diabetes 2010. PMID: 20858683

G6PD Genetic Variant

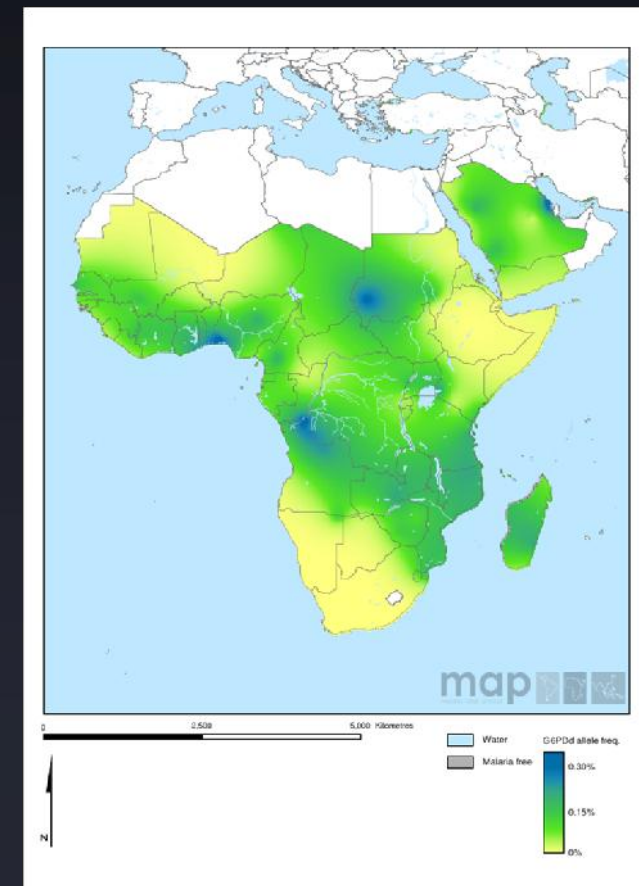
- G6PD-A(-), predominantly in African ancestry (~10%)
 - ▶ Positive selection for G6PD risk alleles associated with protection from severe malaria may explain their higher frequencies in AA
 - ▶ Negative selection from potentially life threatening haemolytic anaemia

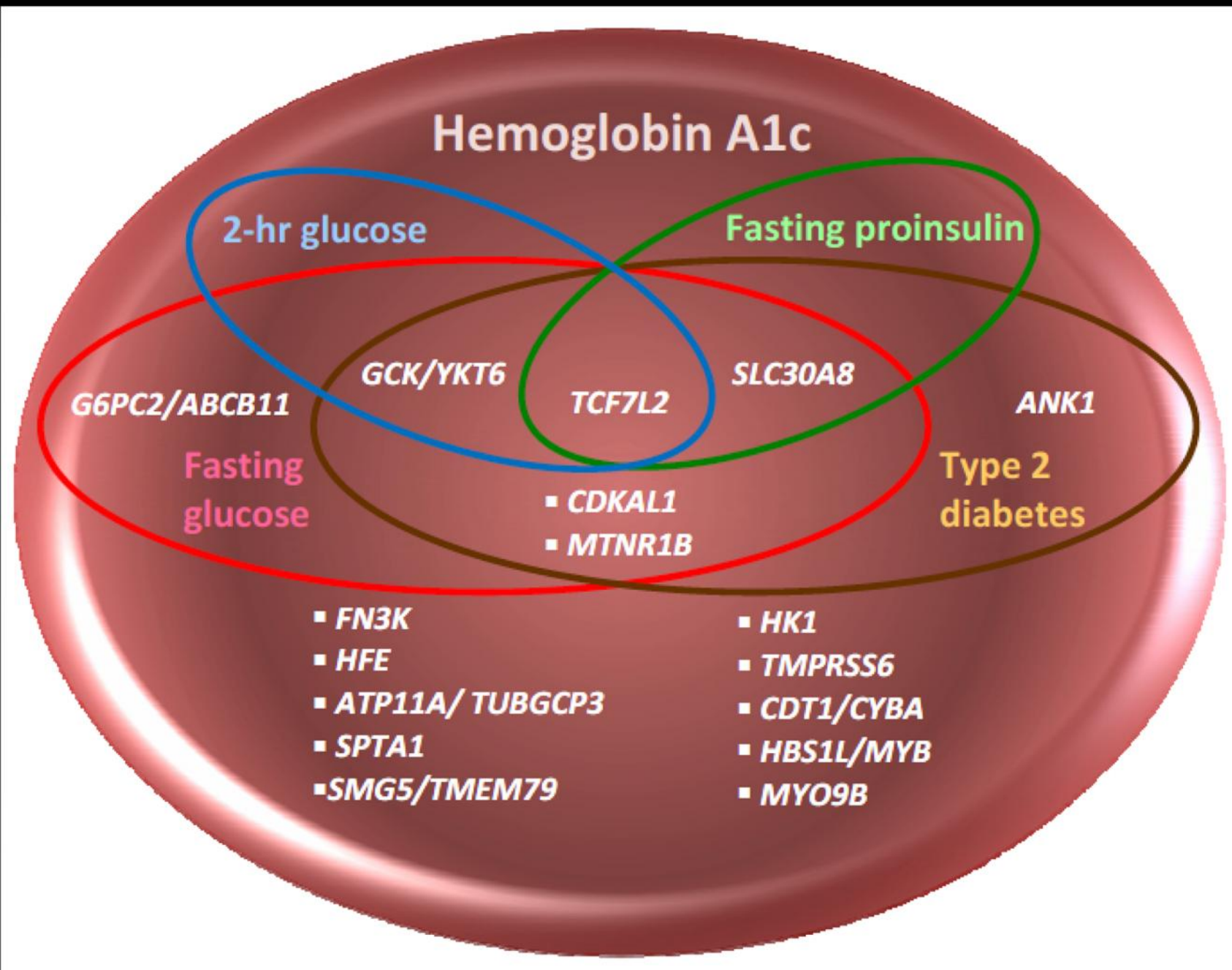
RESEARCH ARTICLE

African Glucose-6-Phosphate Dehydrogenase Alleles Associated with Protection from Severe Malaria in Heterozygous Females in Tanzania

Alphaxard Manjurano¹, Nuno Sepulveda², Behzad Nadjm^{3*}, George Mtove¹, Hannah Wangai¹, Caroline Maxwell¹, Raimos Olomi¹, Hugh Reyburn^{1,2}, Eleanor M. Riley^{1,2‡}, Christopher J. Drakeley^{1,2‡}, Taane G. Clark^{4,5‡*}, MalariaGEN Consortium^{6¶}

Citation: Manjurano A, Sepulveda N, Nadjm B, Mtove G, Wangai H, Maxwell C, et al. (2015) African Glucose-6-Phosphate Dehydrogenase Alleles Associated with Protection from Severe Malaria in Heterozygous Females in Tanzania. PLoS Genet 11 (2): e1004960. doi:10.1371/journal.pgen.1004960





11 A1C GWAS RBC loci
(+/-100kb around lead SNV)

 **EUR**
 **AFR**

