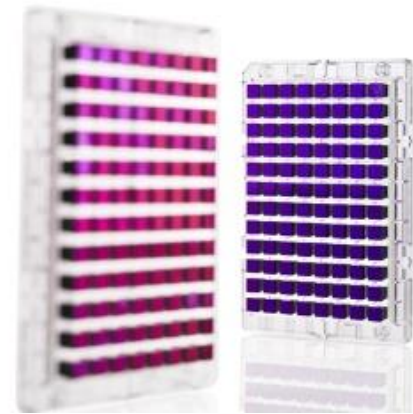


Genome-wide association studies (GWAS) – still continued!

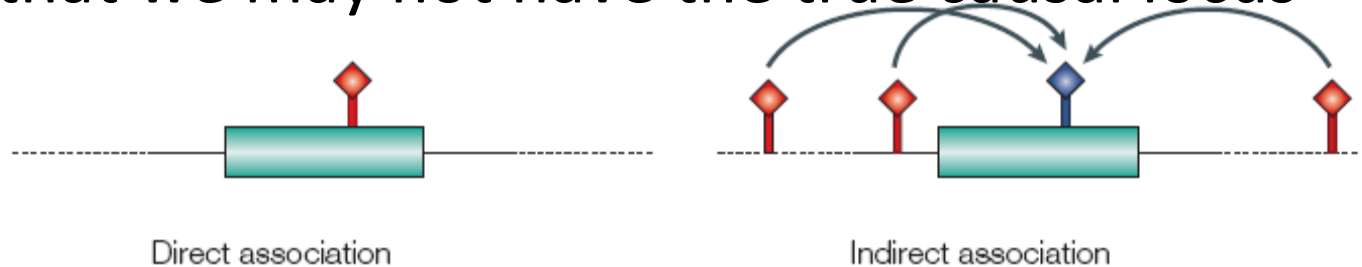


Outline for GWAS

- Following up on hits
- eQTLs & Transcriptome-wide association studies (TWAS)
- Limitations, heritability, and “missing heritability”, Genetic risk scores
- Enriching weak signals?:
Gene/pathways/polygenic models

What after we've discovered (and replicated) a novel variant?

- Recall that we may not have the true causal locus



- Fine mapping vs. imputed genotypes
 - UKB paper you read on # of variants to follow-up on...
- Tie-in to biology
- A lot of work has been done to characterize SNPs and prioritize what should be followed up on
- Functional studies

Refining GWAS SNPs: Haploreg

- <http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>

Build Query

Set Options

Documentation

Use one of the three methods below to enter a set of variants. If an r^2 threshold is specified (see the Set Options tab), results for each variant will be shown in a separate table along with other variants in LD. If r^2 is set to NA, only queried variants will be shown, together in one table.

Query
(comma-delimited
list of
rsIDs OR
a single
region as
chrN:start-end):

rs6544713, rs1800562

or, upload
a text file
(one
refSNP ID
per line):

Browse...

 No file selected.

or, select
a GWAS:

Submit Query

Haploreg further options (r^2 , 1000 Genomes population)

[Build Query](#) [Set Options](#) [Documentation](#)

LD threshold, r^2 (select NA to only show query variants):

1000G Phase 1 population for LD calculation: ☐ AFR ☐ AMR ☐ ASN ☒ EUR

Source for epigenomes:

Mammalian conservation algorithm: ☐ GERP ☒ SiPhy-omega ☐ both

Show position relative to: ☒ GENCODE genes ☐ RefSeq genes ☐ both

Condense lists in table longer than:

Condense indel oligos longer than:

Output mode: ☒ HTML ☐ Text

[Submit Query](#)

Which one is causal / biological mechanism?

- Don't know for certain, can do some exploration:

(Talk about eQTLs later today)



Query SNP: **rs1800562** and variants with $r^2 \geq 0.8$

chr	pos (hg38)	LD (r ²)	LD (D')	variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	SiPhy cons	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	dbSNP func annot
6	26072764	0.89	0.97	rs144861591	C	T	0.00	0.03	0.00	0.05						7 altered motifs			12 hits	15kb 5' of HFE	
6	26092913	1	1	rs1800562	G	A	0.00	0.02	0.00	0.05		BLD	4 tissues	BLD		5 altered motifs	32 hits	5 hits	20 hits	HFE	missense
6	26098246	1	1	rs79220007	T	C	0.00	0.02	0.00	0.05						NRSF			14 hits	HFE	
6	26123274	0.83	0.94	rs115740542	T	C	0.01	0.02	0.00	0.05		23 tissues		53 tissues	29 bound proteins	YY1			11 hits	HIST1H2BC	

- Likely will not know for certain, may prioritize for functional work

Which one is causal / biological mechanism?

- ?

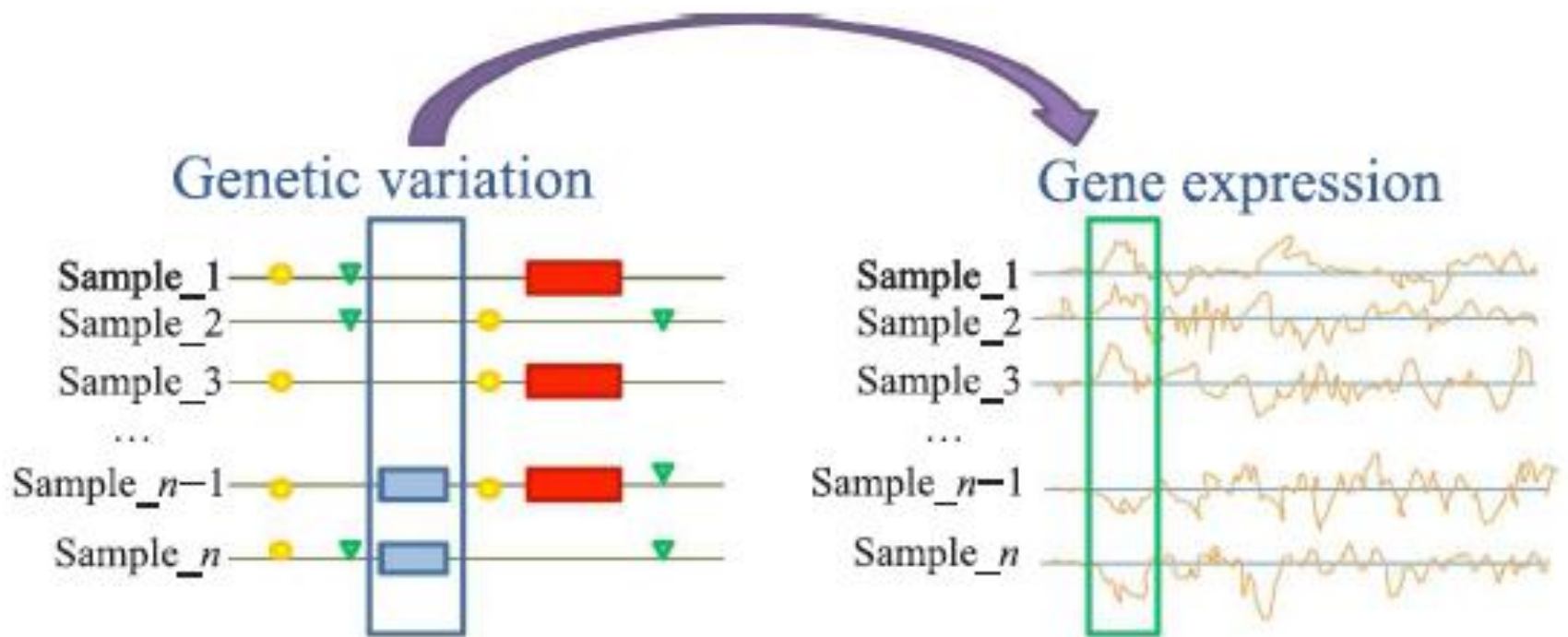
Query SNP: **rs6544713** and variants with $r^2 \geq 0.8$

chr	pos (hg38)	LD (r ²)	LD (D')	variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	SiPhy cons	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	dbSNP func annot
2	43845437	0.96	0.99	rs4299376	G	T	0.85	0.78	1.00	0.70			LIV, GI				5 hits	1 hit	1 hit	ABCG8	intronic
2	43846742	1	1	rs6544713	T	C	0.85	0.78	1.00	0.71			LIV, GI			Pou2f2	1 hit	2 hits	1 hit	ABCG8	intronic
2	43847292	0.99	1	rs4245791	C	T	0.87	0.78	1.00	0.70			LIV, GI	GI		7 altered motifs	2 hits	1 hit	1 hit	ABCG8	intronic
2	43864927	0.84	0.99	rs4603816	C	T	0.93	0.79	1.00	0.74						Cdx,Mef2,Nanog			1 hit	ABCG8	intronic
2	43869000	0.83	0.98	rs6740545	G	A	0.91	0.79	1.00	0.73						BCL				ABCG8	intronic
2	43869120	0.84	0.99	rs6544716	T	G	0.91	0.79	1.00	0.74										ABCG8	intronic
2	43869197	0.83	0.98	rs6755809	T	A	0.92	0.79	1.00	0.73									1 hit	ABCG8	intronic
2	43869263	0.83	0.98	rs6544717	G	A	0.97	0.81	1.00	0.73						Pax-5			1 hit	ABCG8	intronic
2	43869631	0.83	0.97	rs4952688	T	A	0.94	0.80	1.00	0.73						Zfp105			1 hit	ABCG8	intronic
2	43870228	0.82	0.98	rs4953026	C	T	0.91	0.79	1.00	0.74						CACD,TFII-I				ABCG8	intronic

Outline for GWAS

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- Limitations, heritability, and “missing heritability”, Genetic risk scores
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Gene/pathways/polygenic models

What is an eQTL?



What is an eQTL?

Cis-eQTL

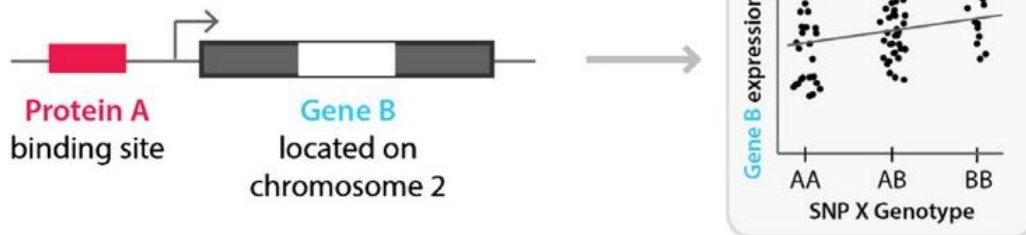
SNP X has an effect on local Gene A



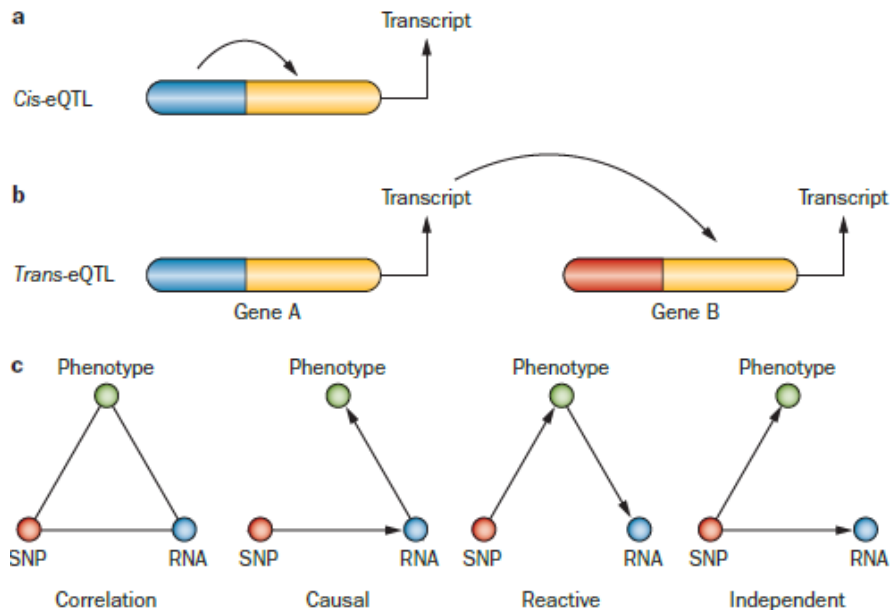
Altered **Protein A** levels,
effect on the binding to
the transcription factor
binding sites of
downstream genes

Trans-eQTL

SNP X has an effect on distant Gene B through an intermediary factor (such as a transcription factor)



What is an eQTL?



E.g. of cis-eQTL –
transcription factor

Figure 2 | Principles of eQTL analysis. Loci that control transcript levels are referred to as eQTL. Typically, eQTL analysis of humans or mice reveals thousands of eQTL, which are classified as either 'local' or 'distant', depending on the distance of the locus from the gene that an eQTL regulates. **a** | A local eQTL most likely acts in *cis*, meaning it affects the expression of a gene on the same chromosome (for example, an eQTL in a promoter only influences expression of the contiguous gene). **b** | Distal loci act in *trans*, affecting both copies of the genes they regulate (for example, an eQTL may encode a transcription factor that controls the expression of the regulated gene on both chromosomes). **c** | This panel illustrates possible causal relationships between a SNP, a transcript (RNA) and a physiological or pathologic trait (phenotype). Using the SNP as a 'causal anchor', causal relationships between the three can be modeled.⁷¹ Abbreviations: eQTL, expression quantitative trait locus; SNP, single nucleotide polymorphism.

What is an eQTL?

Cis-eQTL

SNP X has an effect on local Gene A



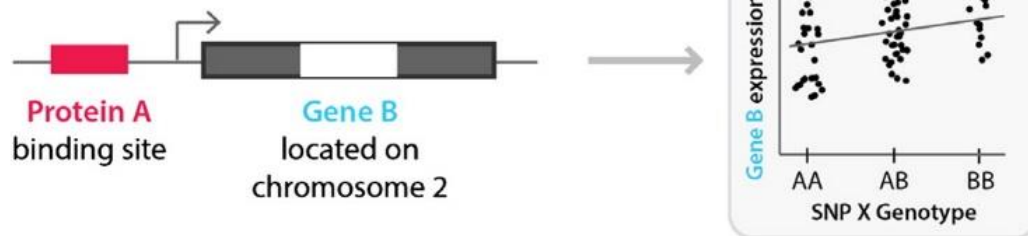
CLASS EXERCISE

- Design an eQTL study!
- (Assume that the expression of each gene has been quantified. Or sort of. This is expensive.)

Altered **Protein A** levels, effect on the binding to the transcription factor binding sites of downstream genes

Trans-eQTL

SNP X has an effect on distant Gene B through an intermediary factor (such as a transcription factor)



What is an eQTL?

Cis-eQTL

SNP X has an effect on local Gene A

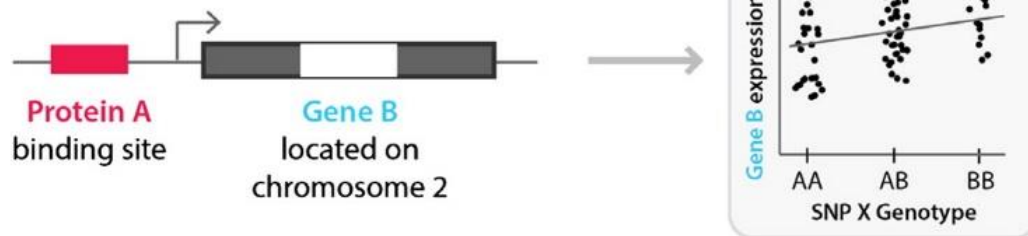


CLASS EXERCISE

- Design an eQTL study!
- (Assume that the expression of each gene has been quantified. Or sort of. This is expensive.)
- What kind of genotyping method? LD?
- Advantages / Disadvantages to testing only cis, only trans, both? How many tests?
- How far up/downstream of each gene?

Trans-eQTL

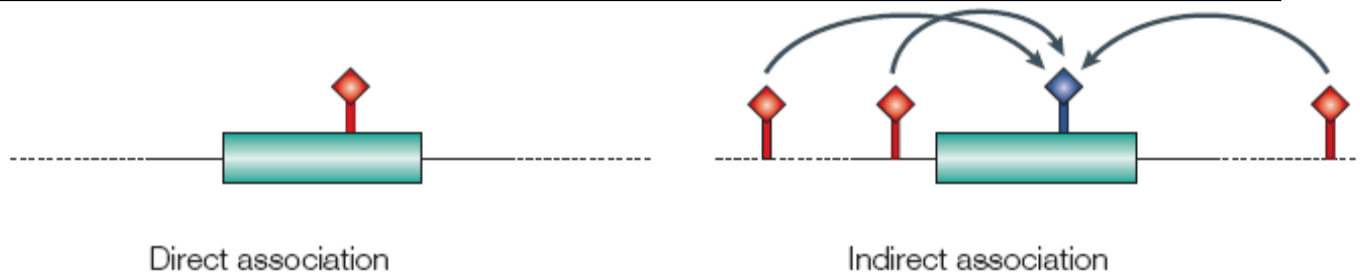
SNP X has an effect on distant Gene B through an intermediary factor (such as a transcription factor)



Altered **Protein A** levels, effect on the binding to the transcription factor binding sites of downstream genes

What is an eQTL?

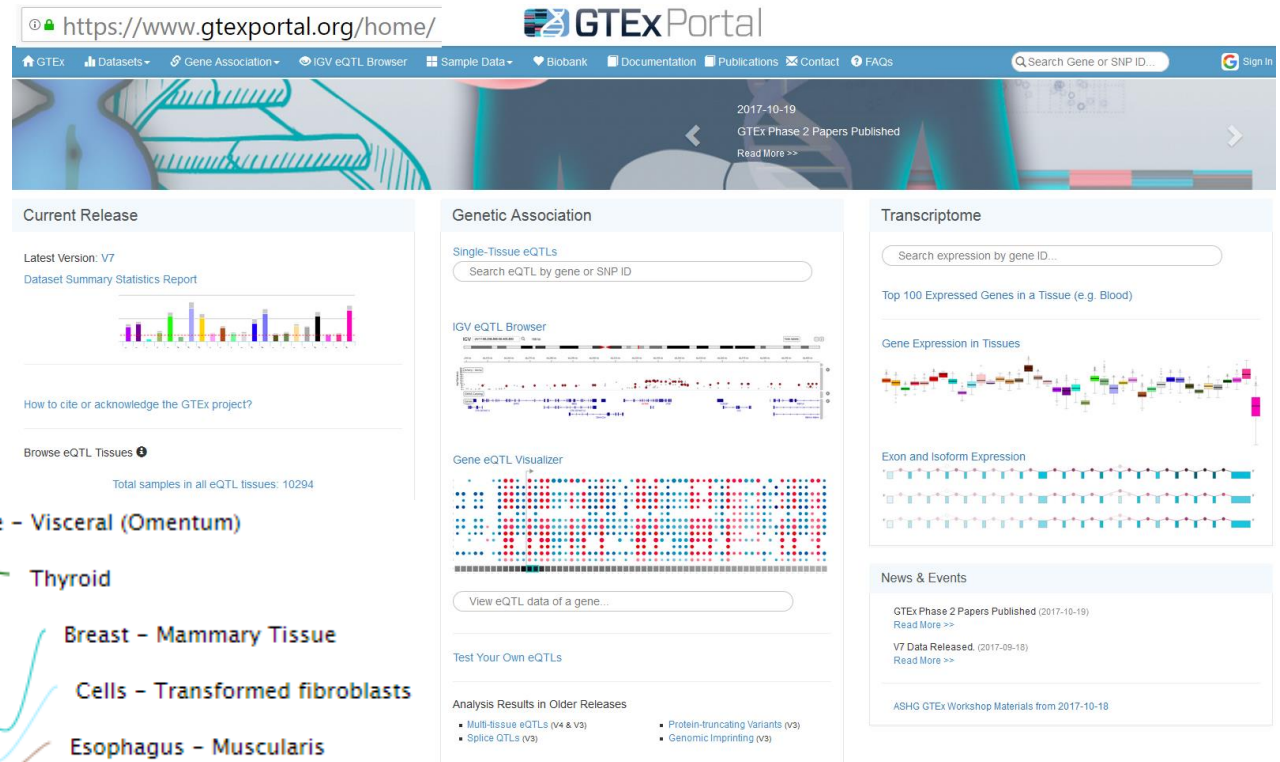
- The expression of a gene can be viewed as a quantitative trait.
- Test the SNPs around the gene for association with the expression of the gene.
- Does the SNP affect expression?
- ***The same problem still applies, don't know causal locus!***



- Might differentiate between which gene is being expressed, if between or amongst more than one.

cis eQTLs: GTeX

- Database of SNP associations with gene expression in humans



Transcriptome-Wide Association Studies (TWAS)

- We have used reference panel sequence data to fill in missing genotypes.
- We have talked about eQTLs, testing for correlation between SNPs and the genotype expression
- But what about predicting/imputing what the expression data was based on the genotypes?
 - And then test that for correlation with the trait instead?
 - Guided gene-based test, if you will

Class Exercise!: Express yourself (or at least someone else)!

Reference population

<u>Person</u>	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	Expression
Ref-001	AA	AA	TT	TT	TT	0.98
Ref-002	AA	AA	TC	TG	TG	0.90
Ref-003	GG	GG	TC	TG	TG	0.10
Ref-004	GG	GG	CC	TT	TG	0.12
Ref-005	GG	GG	CC	TT	GG	0.05

How is this similar/different to genotype imputation?

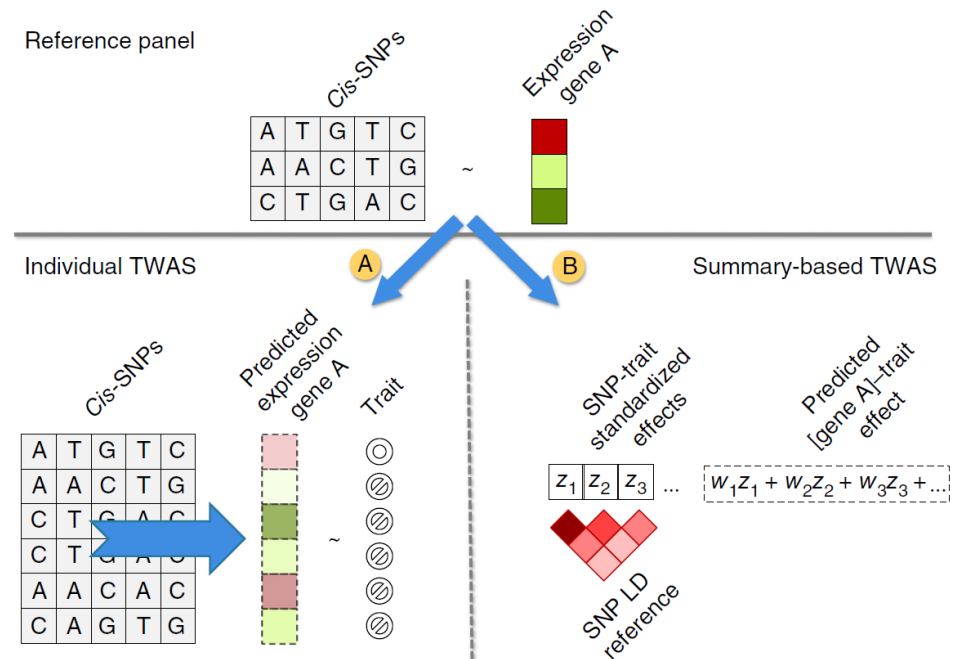
Target population

<u>Person</u>	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	Expression
Target-001	AA	AA	TT	TT	TT	~
Target-002	GG	GC	CC	CC	GG	~

TWAS – cis expression

- GTEx eQTL data
- Model that predicts expression data using the GWAS SNPs (instead of testing for association between those SNPs and expression)
- Test that expression for association with trait
- Repeat for each of the 44 GTEx tissues
- Software Predixcan

Figure 1 Schematic of the TWAS approach. Top, estimate gene expression effect sizes in the reference panel either directly (eQTL), modeling all SNPs (BLUP), or modeling SNPs and effect sizes (BSLMM). Path A: predict expression directly for genotyped samples using the effect sizes from the reference panel and measure the association between predicted expression and a trait. Path B: indirectly estimate association between predicted expression and a trait as the weighted linear combination of SNP-trait standardized effect sizes while accounting for LD among SNPs.



TWAS results

Table 1 TWAS significant genes with no known GWAS risk variants within 500 kb

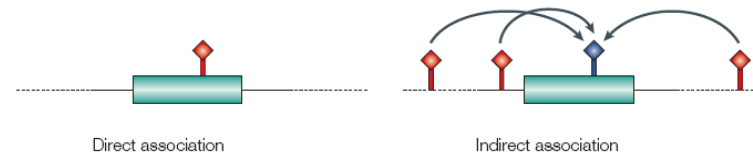
GWAS	Training expression	Gene	Chr.	Locus start	Locus end	P value			
						TWAS	Permuted	Best <i>cis</i> -SNP	
LOCKE.BMI	Omnibus	<i>INO80E</i>	16	29,506,615	30,517,114	3×10^{-9}	3×10^{-7}	3×10^{-6}	*
LOCKE.BMI	Omnibus	<i>FTSJ3</i>	17	61,396,793	62,407,372	1×10^{-7}	5×10^{-6}	9×10^{-7}	*
LOCKE.BMI	Omnibus	<i>PAM</i>	5	101,589,685	102,866,809	3×10^{-7}	4×10^{-9}	3×10^{-3}	*
LOCKE.BMI	YFS	<i>GGNBP2</i>	17	34,400,737	35,446,278	1×10^{-6}	7×10^{-5}	3×10^{-6}	*
LOCKE.BMI	YFS	<i>MYO19</i>	17	34,351,477	35,399,284	3×10^{-6}	4×10^{-5}	3×10^{-6}	*
LOCKE.BMI	Omnibus	<i>OPRL1</i>	20	62,211,526	63,231,996	3×10^{-6}	9×10^{-5}	2×10^{-5}	*
LOCKE.BMI	NTR	<i>RABGAP1</i>	9	125,203,287	126,367,145	4×10^{-6}	3×10^{-5}	1×10^{-5}	*
LOCKE.BMI	YFS	<i>SMARCD2</i>	17	61,409,444	62,420,425	5×10^{-6}	9×10^{-5}	9×10^{-7}	*
LOCKE.BMI	METSIM	<i>ALO49840.1</i>	14	103,677,607	104,679,149	5×10^{-6}	5×10^{-5}	1×10^{-7}	*
LOCKE.BMI	Omnibus	<i>LPAR2</i>	19	19,234,477	20,239,739	6×10^{-6}	3×10^{-5}	4×10^{-6}	*
WILLER.HDL	YFS	<i>MRPS18B</i>	6	30,085,486	31,094,172	1×10^{-7}	2×10^{-2}	4×10^{-6}	
WILLER.LDL	Omnibus	<i>PAM</i>	5	101,589,685	102,866,809	4×10^{-15}	9×10^{-12}	2×10^{-3}	*
WILLER.LDL	Omnibus	<i>ITIH4</i>	3	52,346,991	53,365,495	8×10^{-9}	4×10^{-6}	3×10^{-5}	*
WILLER.LDL	Omnibus	<i>WARS</i>	14	100,300,125	101,343,142	1×10^{-8}	6×10^{-7}	3×10^{-5}	*
WILLER.LDL	Omnibus	<i>MAN2C1</i>	15	75,148,133	76,160,971	1×10^{-8}	1×10^{-5}	6×10^{-5}	*
WILLER.LDL	YFS	<i>DHRS13</i>	17	26,724,799	27,730,089	6×10^{-7}	4×10^{-4}	2×10^{-6}	*
WILLER.LDL	YFS	<i>ERAL1</i>	17	26,681,956	27,688,085	8×10^{-7}	9×10^{-4}	2×10^{-6}	
WILLER.LDL	YFS	<i>HCG27</i>	6	30,665,537	31,671,745	2×10^{-6}	7×10^{-3}	7×10^{-8}	
WILLER.LDL	YFS	<i>VAR52</i>	6	30,376,019	31,394,236	3×10^{-6}	2×10^{-2}	1×10^{-5}	
WILLER.LDL	Omnibus	<i>PEX6</i>	6	42,431,608	43,446,958	5×10^{-6}	3×10^{-5}	4×10^{-4}	*
WILLER.LDL	Omnibus	<i>CSK</i>	15	74,574,398	75,595,539	6×10^{-6}	1×10^{-4}	1×10^{-5}	*
WILLER.TC	Omnibus	<i>PAM</i>	5	101,589,685	102,866,809	9×10^{-15}	3×10^{-13}	5×10^{-3}	*

Outline for GWAS

- Following up on hits
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- Limitations, heritability, and “missing heritability”, Genetic risk scores
- Enriching weak signals?:
Gene/pathways/polygenic models

Limitations of GWAS

- Not very predictive
- Explain little heritability, generally, but improving
- Focus on common variation, but getting rarer
- Many associated variants are not causal



Limitations of GWAS

- Not very predictive

Example:

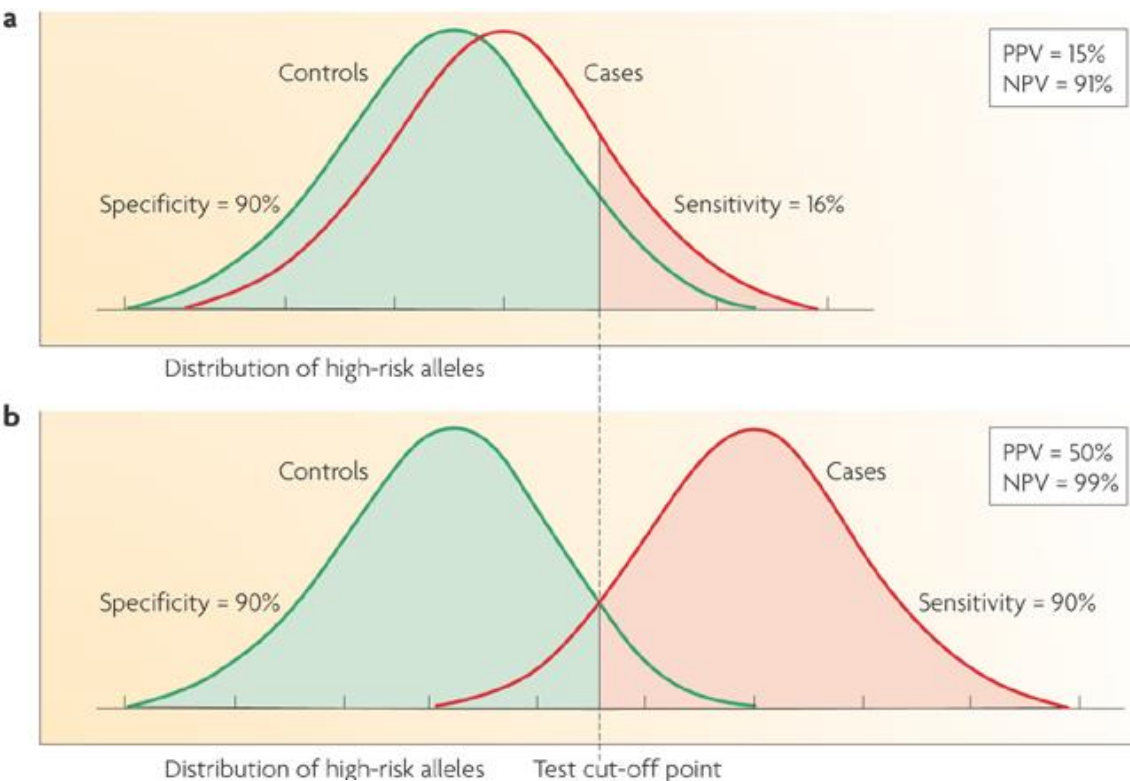
AUC for Breast Cancer Risk

58%: Gail model (# first degree relatives w bc, age menarche, age first live birth, number of previous biopsies) + age, study, entry year

58.9%: SNPs

61.8%: Combined

Wacholder et al., NEJM 2010

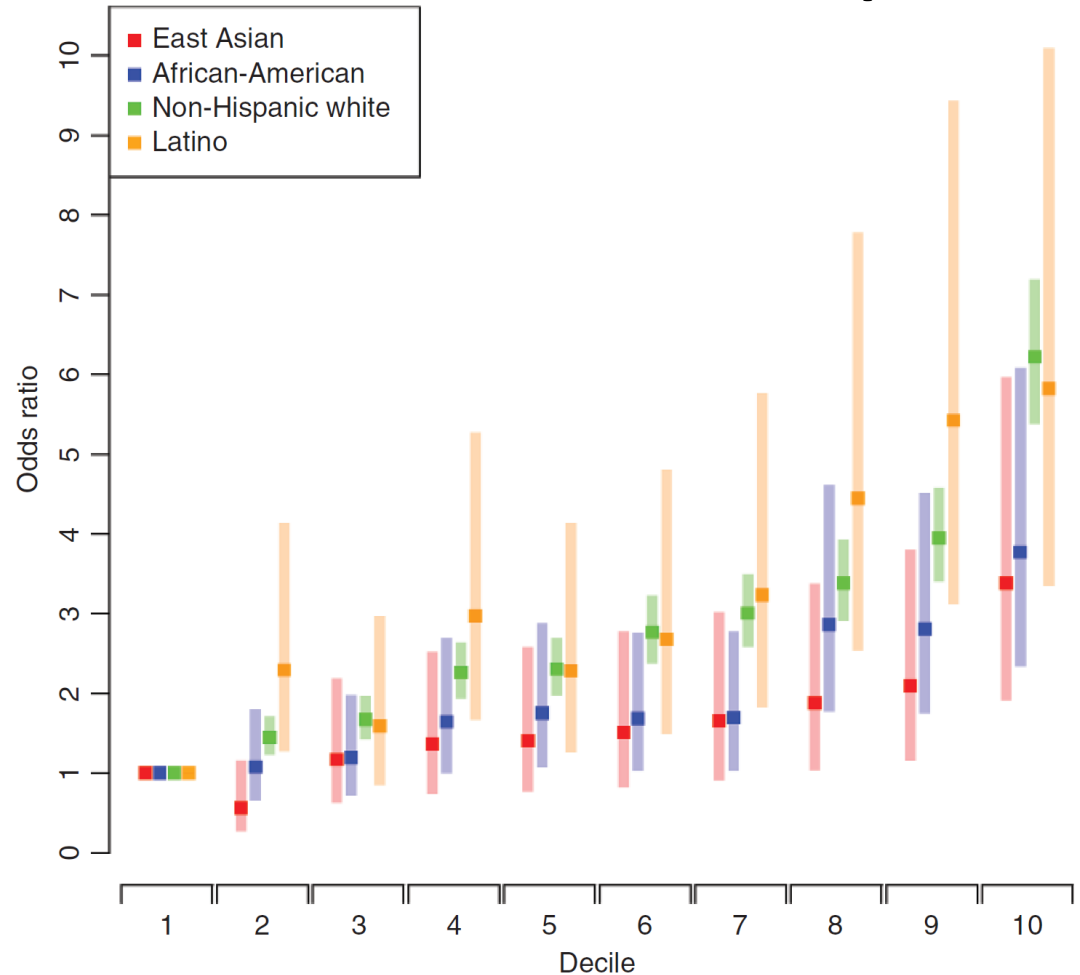


Genetic Risk Score (GRS) – Overall genetic risk; tails show more sep.?

Figure 4. Impact of increasing deciles of risk profile scores based on 105 known risk SNPs across different race/ethnicity groups. Risk scores were generated by combining the 105 SNPs into a single score, applying the logs odds ratio estimated by previous studies to our KP study population genotype data. Odds ratios for effect of risk profile scores on prostate cancers calculated within each decile of the scores, using the lowest decile of risk profile scores as the referent category. The non-Hispanic white and Latino groups had substantially higher ORs than the African-American group, and the East Asian group always had the lowest ORs.

$$GRS_j = \frac{\sum_{i=1}^m \ln(OR_i) \times SNP_{ij}}{m}$$

i.e., β_j



Be careful of SNPs in LD... e.g., don't want to include same SNP effectively twice if reported in two studies.

What does it mean to explain little of the heritability, and where is it?

Table 1. Population Variation Explained by GWAS for a Selected Number of Complex Traits

Trait or Disease	h^2 Pedigree Studies	h^2 GWAS Hits ^a	h^2 All GWAS SNPs ^b
Type 1 diabetes	0.9 ⁹⁸	0.6 ^{99, c}	0.3 ¹²
Type 2 diabetes	0.3–0.6 ¹⁰⁰	0.05–0.10 ³⁴	
Obesity (BMI)	0.4–0.6 ^{101,102}	0.01–0.02 ³⁶	0.2 ¹⁴
Crohn's disease	0.6–0.8 ¹⁰³	0.1 ¹¹	0.4 ¹²
Ulcerative colitis	0.5 ¹⁰³	0.05 ¹²	
Multiple sclerosis	0.3–0.8 ¹⁰⁴	0.1 ⁴⁵	
Ankylosing spondylitis	>0.90 ¹⁰⁵	0.2 ¹⁰⁶	
Rheumatoid arthritis	0.6 ¹⁰⁷		
Schizophrenia	0.7–0.8 ¹⁰⁸	0.01 ⁷⁹	0.3 ¹⁰⁹
Bipolar disorder	0.6–0.7 ¹⁰⁸	0.02 ⁷⁹	0.4 ¹²
Breast cancer	0.3 ¹¹⁰	0.08 ¹¹¹	

Von Willebrand factor	0.66–0.75 ^{112,113}	0.13 ¹¹⁴	0.25 ¹⁴
Height	0.8 ^{115,116}	0.1 ¹³	0.5 ^{13,14}
Bone mineral density	0.6–0.8 ¹¹⁷	0.05 ¹¹⁸	
QT interval	0.37–0.60 ^{119,120}	0.07 ¹²¹	0.2 ¹⁴
HDL cholesterol	0.5 ¹²²	0.1 ⁵⁷	
Platelet count	0.8 ¹²³	0.05–0.1 ⁵⁸	

^a Proportion of phenotypic variance or variance in liability explained by genome-wide-significant and validated SNPs. For a number of diseases, other parameters were reported, and these were converted and approximated to the scale of total variation explained. Blank cells indicate that these parameters have not been reported in the literature.

^b Proportion of phenotypic variance or variance in liability explained when all GWAS SNPs are considered simultaneously. Blank cell indicate that these parameters have not been reported in the literature.

^c Includes pre-GWAS loci with large effects.

Revised height variance explained (really not very predictive, or?)

[Hum Mol Genet.](#) 2018 Oct 15;27(20):3641-3649. doi: 10.1093/hmg/ddy271.

Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry.

[Yengo L](#)¹, [Sidorenko J](#)^{1,2}, [Kemper KE](#)¹, [Zheng Z](#)¹, [Wood AR](#)³, [Weedon MN](#)³, [Frayling TM](#)³, [Hirschhorn J](#)⁴, [Yang J](#)^{1,5}, [Visscher PM](#)^{1,5}; [GIANT Consortium](#).

Author information

Abstract

Recent genome-wide association studies (GWAS) of height and body mass index (BMI) in ~250000 European participants have led to the discovery of ~700 and ~100 nearly independent single nucleotide polymorphisms (SNPs) associated with these traits, respectively. Here we combine summary statistics from those two studies with GWAS of height and BMI performed in ~450000 UK Biobank participants of European ancestry. Overall, our combined GWAS meta-analysis reaches N ~700000 individuals and substantially increases the number of GWAS signals associated with these traits. We identified 3290 and 941 near-independent SNPs associated with height and BMI, respectively (at a revised genome-wide significance threshold of $P < 1 \times 10^{-8}$), including 1185 height-associated SNPs and 751 BMI-associated SNPs located within loci not previously identified by these two GWAS. The near-independent genome-wide significant SNPs explain ~24.6% of the variance of height and ~6.0% of the variance of BMI in an independent sample from the Health and Retirement Study (HRS). Correlations between polygenic scores based upon these SNPs with actual height and BMI in HRS participants were ~0.44 and ~0.22, respectively. From analyses of integrating GWAS and expression quantitative trait loci (eQTL) data by summary-data-based Mendelian randomization, we identified an enrichment of eQTLs among lead height and BMI signals, prioritizing 610 and 138 genes, respectively. Our study demonstrates that, as previously predicted, increasing GWAS sample sizes continues to deliver, by the discovery of new loci, increasing prediction accuracy and providing additional data to achieve deeper insight into complex trait biology. All summary statistics are made available for follow-up studies.

Class exercise: Where is it?

NEWS FEATURE PERSONAL GENOMES

NATURE | Vol 456 | 6 November 2008

- Can GWAS find more?
- Are our analysis methods not creative enough?
- Are we missing genetic things?

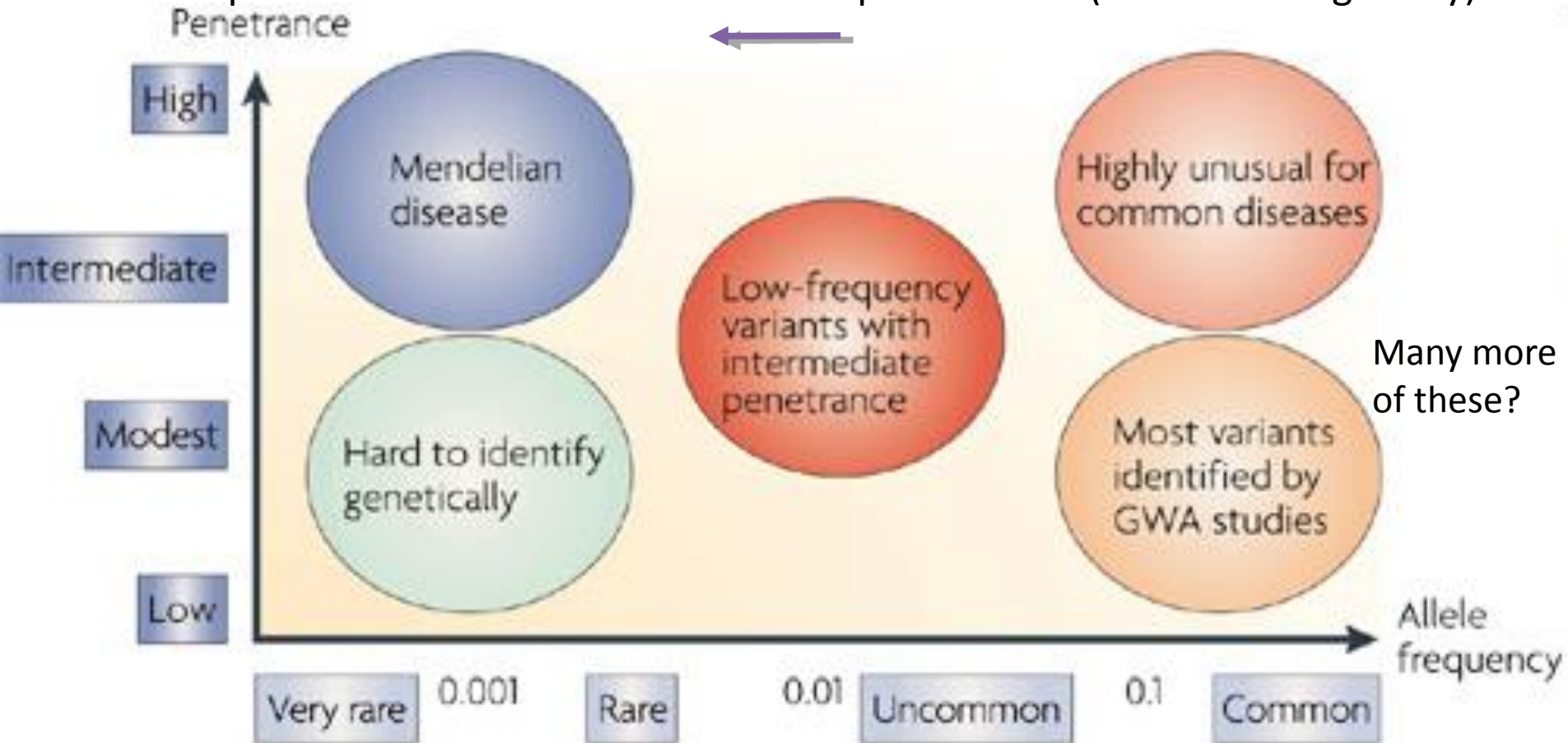


The case of the missing heritability

When scientists opened up the human genome, they expected to find the genetic components of common traits and diseases. But they were nowhere to be seen. **Brendan Maher** shines a light on six places where the missing loot could be stashed away.

Where's the heritability?

Common disease rare variant (CDRV) hypothesis: diseases due to multiple rare variants with intermediate penetrances (allelic heterogeneity)



See: NEJM, April 30, 2009

Will GWAS results explain more heritability?

Possibly, if...

1. Causal SNPs not yet detected due to power issues – weak effects
 - Previous GWAS designed/powered for $MAF > 0.05/0.10$; lower MAFs for newer arrays and larger reference panels
2. More complicated modeling necessary, e.g. gene-gene interaction (epistasis), gene-environment interaction, etc.

How much is left to discover?

“Array” heritability

- Compute heritability using **all** SNPs
 - Be careful with QC, esp. case-control
- If you adjust for the known hits, how much remains yet to be found?
- Restricted to narrow sense heritability
- E.g.,

Lecture 2:

“Broad sense”: $H^2 = \sigma_G^2 / \sigma_P^2 = (\sigma_A^2 + \sigma_D^2) / \sigma_P^2$

“Narrow sense”: $h^2 = \sigma_A^2 / \sigma_P^2$

GCTA: <http://www.complextaitgenomics.com/software/gcta/>

LD Score (*can use summary statistics!*): <https://github.com/bulik/ldsc>

Common SNPs explain a large proportion of the heritability for human height

Jian Yang¹, Beben Benyamin¹, Brian P McEvoy¹, Scott Gordon¹, Anjali K Henders¹, Dale R Nyholt¹, Pamela A Madden², Andrew C Heath², Nicholas G Martin¹, Grant W Montgomery¹, Michael E Goddard³ & Peter M Visscher¹

SNPs discovered by genome-wide association studies (GWASs) account for only a small fraction of the genetic variation of complex traits in human populations. Where is the remaining heritability? We estimated the proportion of variance for human height explained by 294,831 SNPs genotyped on 3,925 unrelated individuals using a linear model analysis, and validated the estimation method with simulations based on the observed genotype data. We show that **45%** of variance can be explained by considering all SNPs simultaneously. Thus, most of the heritability is not missing but has not previously been detected because the individual effects are too small to pass stringent significance tests. We provide evidence that the remaining heritability is due to incomplete linkage disequilibrium between causal variants and genotyped SNPs, exacerbated by causal variants having lower minor allele frequency than the SNPs explored to date.

GWASs in human populations have discovered hundreds of SNPs significantly associated with complex traits^{1,2}, yet for any one

of variation that their effects do not reach stringent significance thresholds and/or the causal variants are not in complete linkage disequilibrium (LD) with the SNPs that have been genotyped. Lack of complete LD might, for instance, occur if causal variants have lower minor allele frequency (MAF) than genotyped SNPs. Here we test these two hypotheses and estimate the contribution of each to the heritability of height in humans as a model complex trait.

Height in humans is a classical quantitative trait, easy to measure and studied for well over a century as a model for investigating the genetic basis of complex traits^{9,10}. The heritability of height has been estimated to be ~0.8 (refs. 9,11–13). Rare mutations that cause extreme short or tall stature have been found^{14,15}, but these do not explain much of the variation in the general population. Recent GWASs on tens of thousands of individuals have detected ~50 variants that are associated with height in the population, but these in total account for only ~5% of phenotypic variance^{16–19}.

Data from a GWAS that are collected to detect statistical associations between SNPs and complex traits are usually analyzed by testing each SNP individually for an association with the trait. To account for the

UK Biobank h^2 for height

- https://nealelab.github.io/UKBB_Idsc/

UKBB Heritability

BROWSER

PLOTS ▼

TECHNICAL DETAILS

GITHUB REPO

NEALE LAB UK

UKBB SNP-Heritability Browser

Last updated 2017-09-20

Show 10 entries

Search: height

ID	↕	Phenotype	↕	N	↕	Prev.	↕	Int.	↕	Int. p	↕	h2	↕	h2 p	↕
20015		Sitting height		336,172				1.204		4.27e-13		0.322		3.96e-93	
50		Standing height		336,474				1.307		2.13e-11		<u>0.462</u>		7.50e-109	
1697		Comparative height size at age 10		332,021				1.137		7.23e-7		0.249		4.14e-92	

But, what about more complicated modeling? Epistasis

Epistasis – snp x snp, or gene x gene interactions

Very difficult to do genome-wide

Much less power to detect an interaction than a main effect in general

Multiple testing burden: Correct for 10^6 tests before? Now 10^{12} tests!!!

Some argue not worth testing for an interaction unless a main effect...

Epistasis in serum lipids

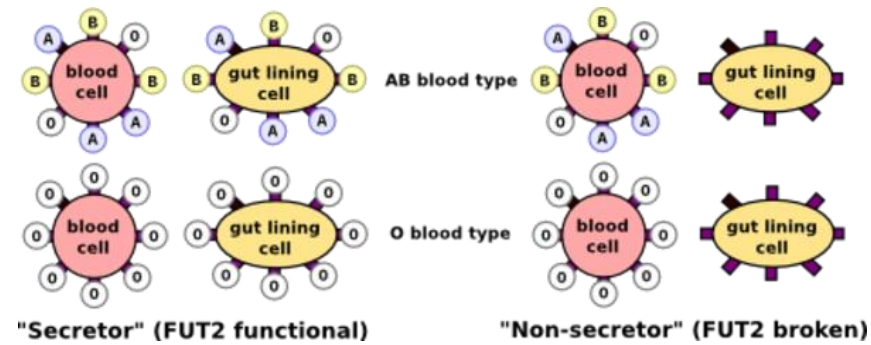
Serum lipids example

Tested all pairs of known GWAS hit variants

Rs2519093 (*ABO*) x rs492602 (*FUT2*): Interaction

$$P_{LDL} = 8.1 \times 10^{-10}$$

Rs492602 has $r^2 = 0.992$ with rs601338, a nonsense dominant variant determining *FUT2* non-secretor status

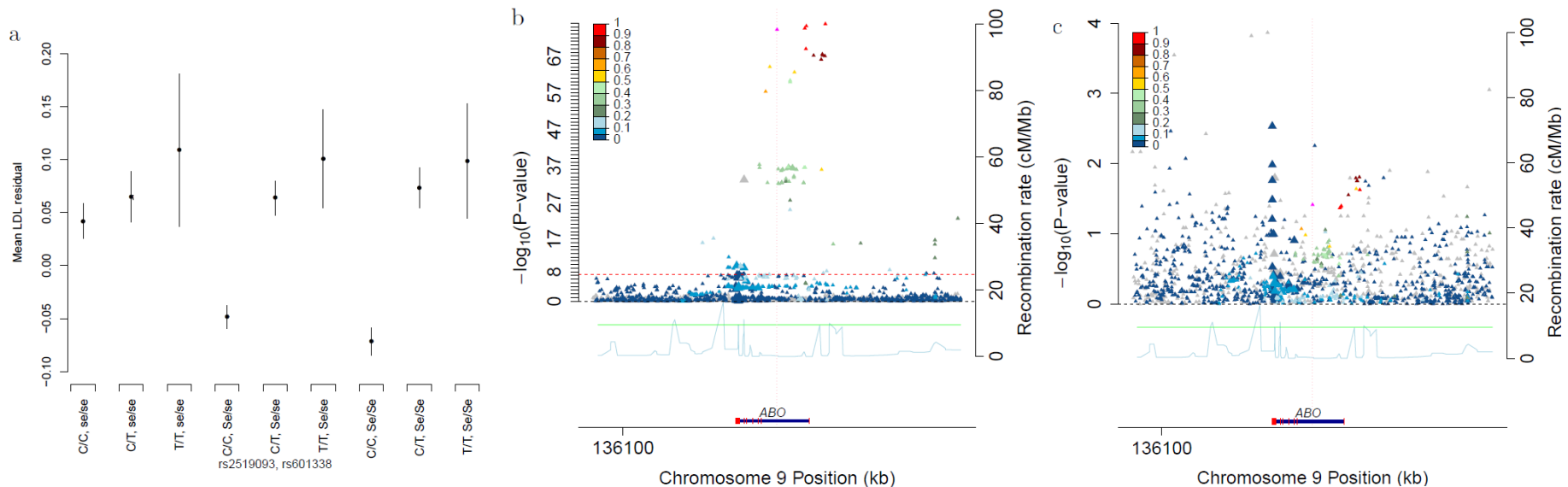


<http://genos.hr/en/laboratories/analytical-dna-laboratory-1/human-dna-analysis-1/secretor-status-dna-test-1/>

Residual LDL by genotype

ABO locus for secretors (Se/Se or Se/se)

ABO locus plot for non-secretors



Other things than SNPs

- Copy number variants (CNVs)
- Epigenetics, e.g., methylation, histone modification
- Gene expression (RNA levels) [eQTLs! we covered these]
- Proteomics (measures of proteins in cells)
- ...

Outline for GWAS

- Following up on hits
- eQTLs & Transcriptome-wide association studies (TWAS)
- Limitations, heritability, and “missing heritability”, Genetic risk scores
- Enriching weak signals?:
Gene/pathways/polygenic models

Ways to enrich weak signals?:

Gene/pathway-based tests

- Various ways of collapsing the genotype information in multiple genes
 - Less multiple comparison adjustment
- $\text{logit}(\text{Prob}(y=1 | \mathbf{x}, \mathbf{c})) = \alpha + \beta\mathbf{x} + \gamma\mathbf{c}$
e.g. $= \alpha + \beta_1 x_1 + \dots + \beta_{12} x_{12} + \{\text{PC's, other covariates}\}$
 - y : disease status)
 - $\mathbf{x}$ is a vector of genotypes (e.g., a gene, or a pathway)
 - $\mathbf{c}$ is a vector of covariates
- $H_0: \beta=0$
- Rare variant “burden” tests are along these lines
 - Make a lot of assumptions

Pathways - how to define?

- Many websites / companies provide 'dynamic' graphic models of molecular and biochemical pathways.
- Examples: GO (Gene Ontology), KEGG, BioCarta, Reactome
- May be interested in potential joint and/or interaction effects of multiple genes in one pathway.

Other Extreme: Polygenic Models

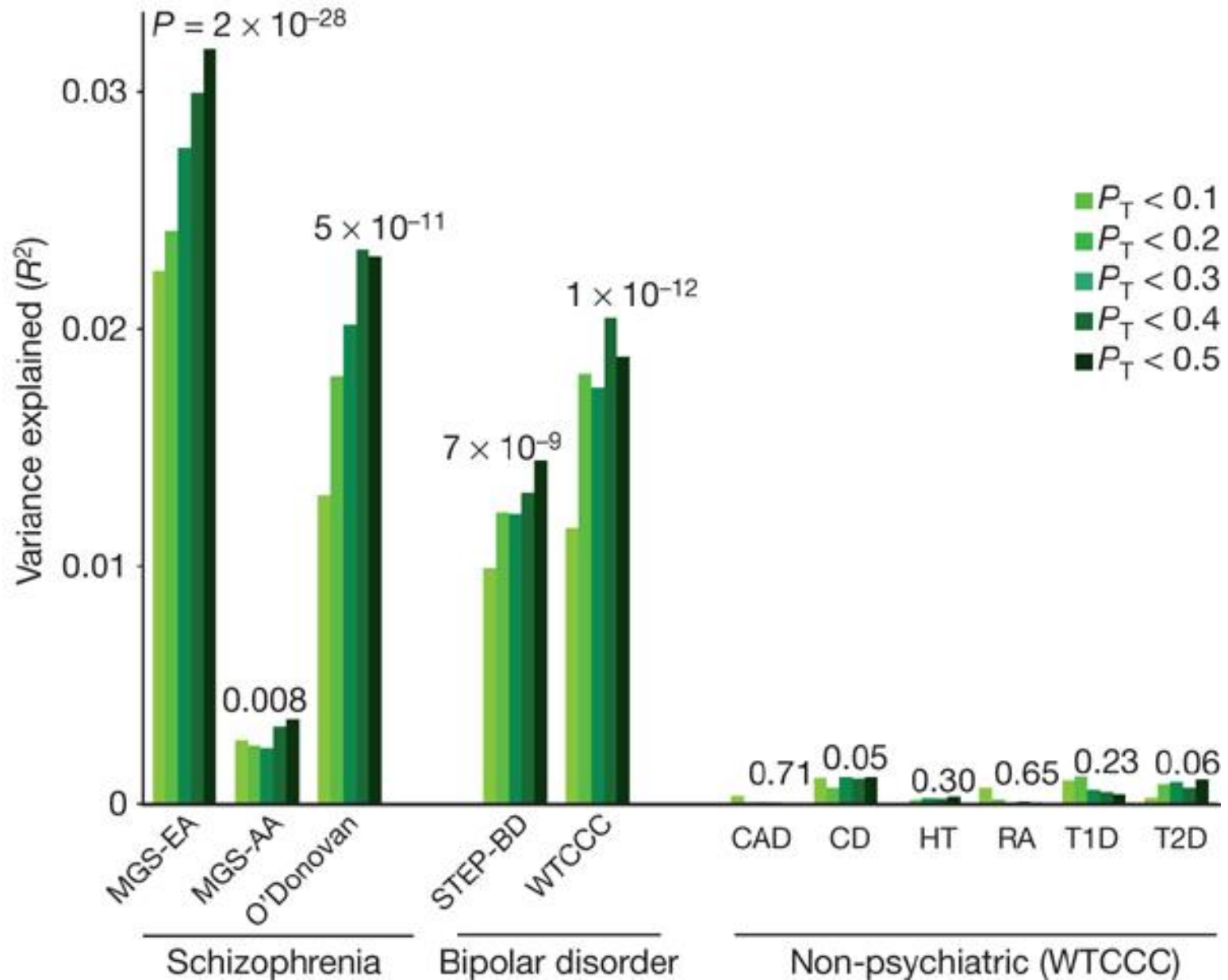
- Many weak associations combine to risk?
- Score model (use all GWAS SNPs):

$$x_j = \frac{\sum_{i=1}^m \ln(OR_i) \times SNP_{ij}}{m}$$

where

- $\ln(OR_i)$ = 'score' for SNP_i from 'discovery' sample
- SNP_{ij} = # of alleles (0,1,2) for SNP_i , person j in 'validation' sample.
- Large number of SNPs (m)
- x_j associated with disease?
- **ASIDE: Genetic risk score same idea, but only on *known hits***

Application of Model



Thanks!



Before the Genomic Era



Genomic Era

