Amsterdam UMC
University Medical Centers

Introduction to the Basics and History of Genetics

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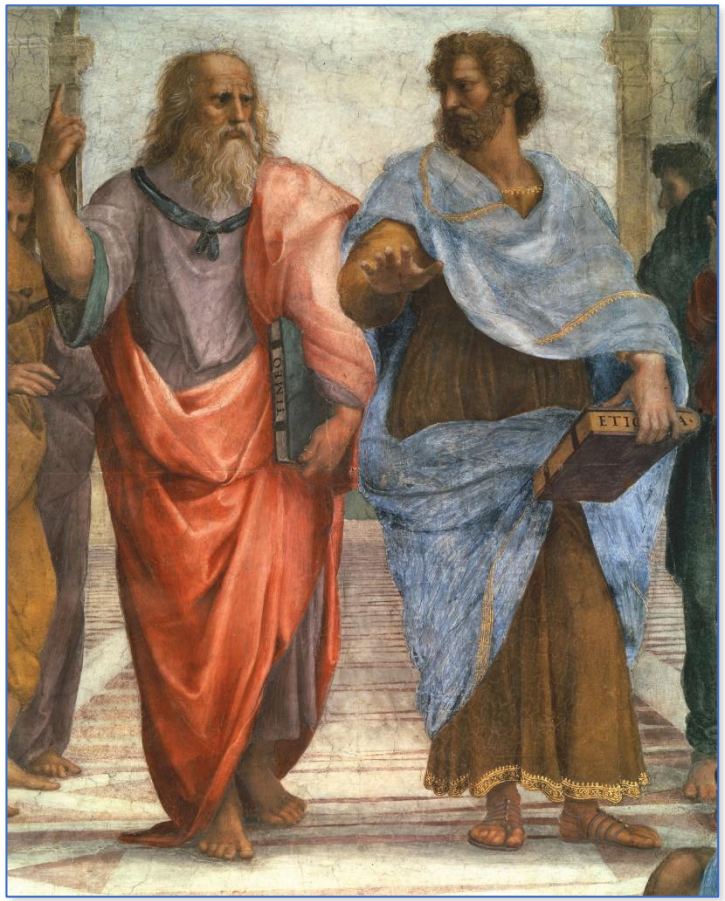
GENETICS NETWORK AMSTERDAM

Where do similarities and differences between living organisms come from?

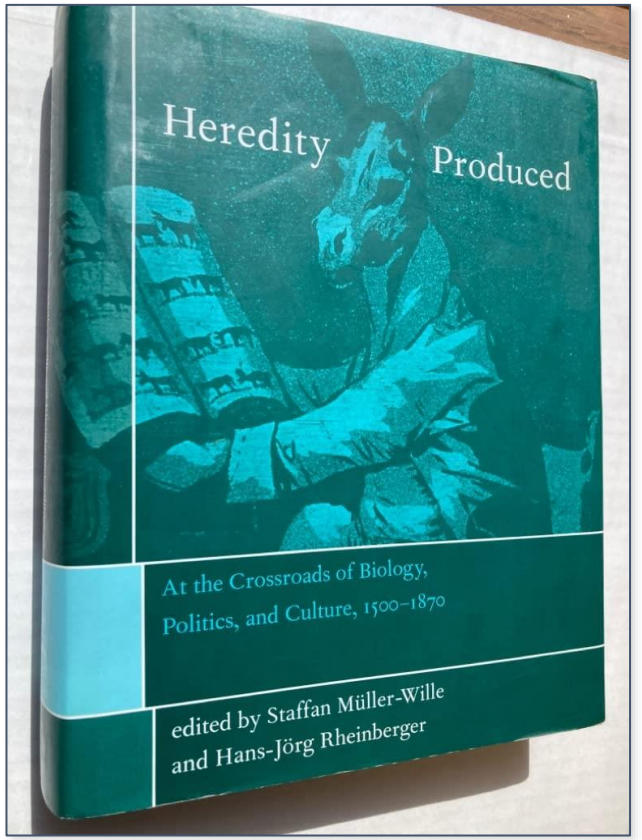
Pythagoras: father supplies essential characteristics ("**form**"), mother supplies material building blocks

Aristotle: children are made from purified blood (semen) and menstrual blood



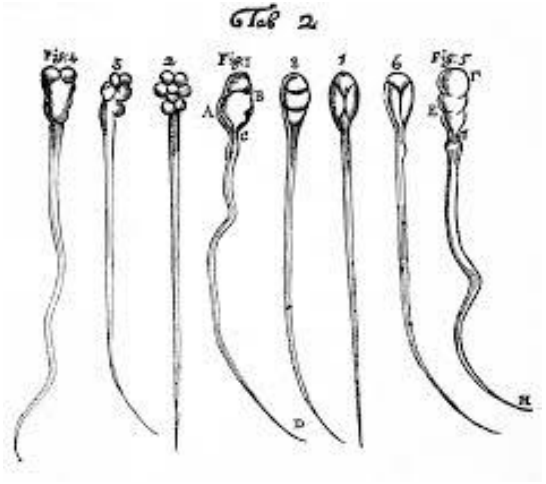
Heredity

The development of the concept of biological **heredity** in the 16th century was based on legal concepts of inheritance of **property** and **wealth**.



350 BC | 16th century | 17th century | 1859 | 1865 | 1875 | 1918 | 1920s | 1953 | 1980s | 90s/00s | 2005 | 2007–2023

- Scientists show in animals that “like breeds like” & that all female organisms produce eggs
- Two Dutch scientists see sperm cells and claim there were little human beings inside of sperm cells.



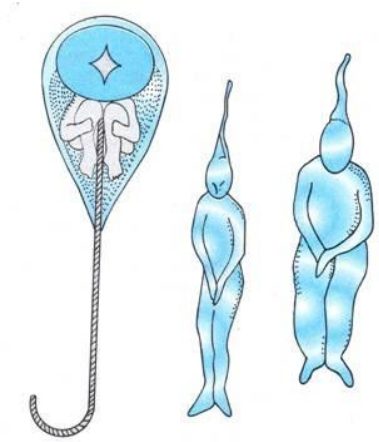
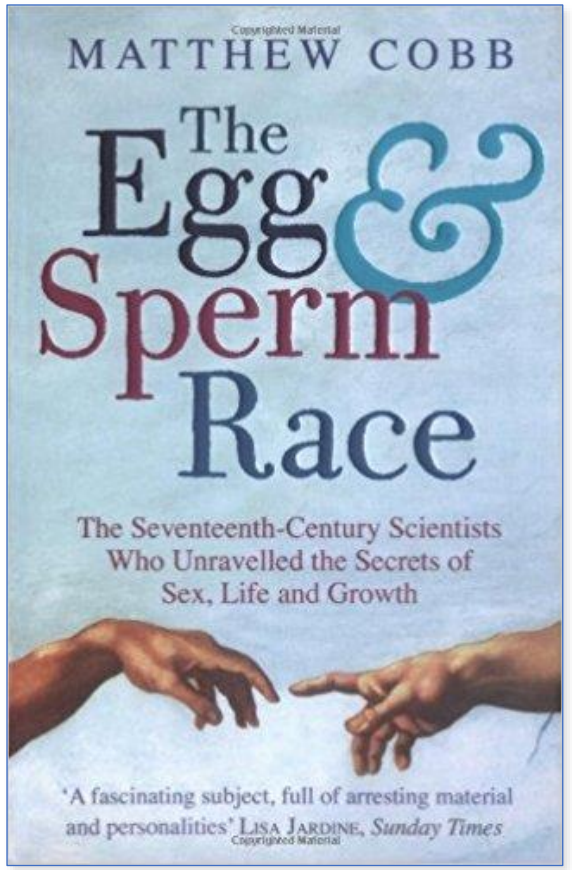


Fig. 5.2. ‘Homunculus’ “little man in a sperm cell” (From journal des Scavans, Feb. 7, 1695).



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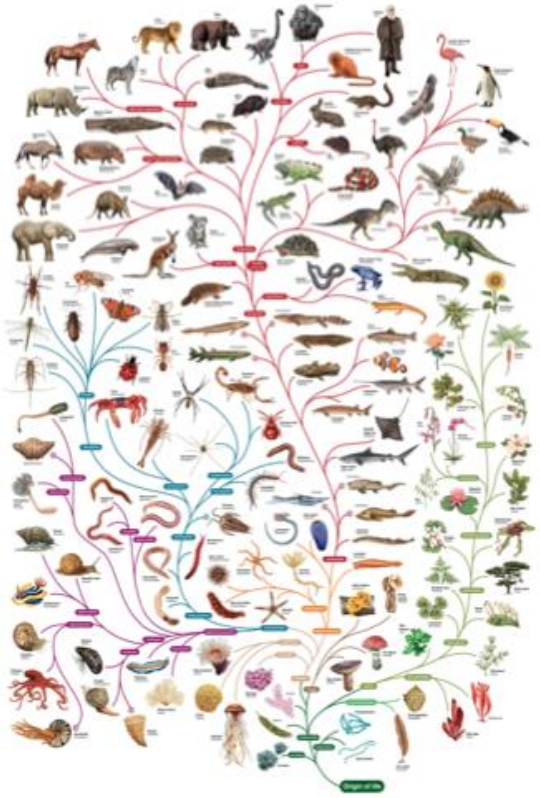
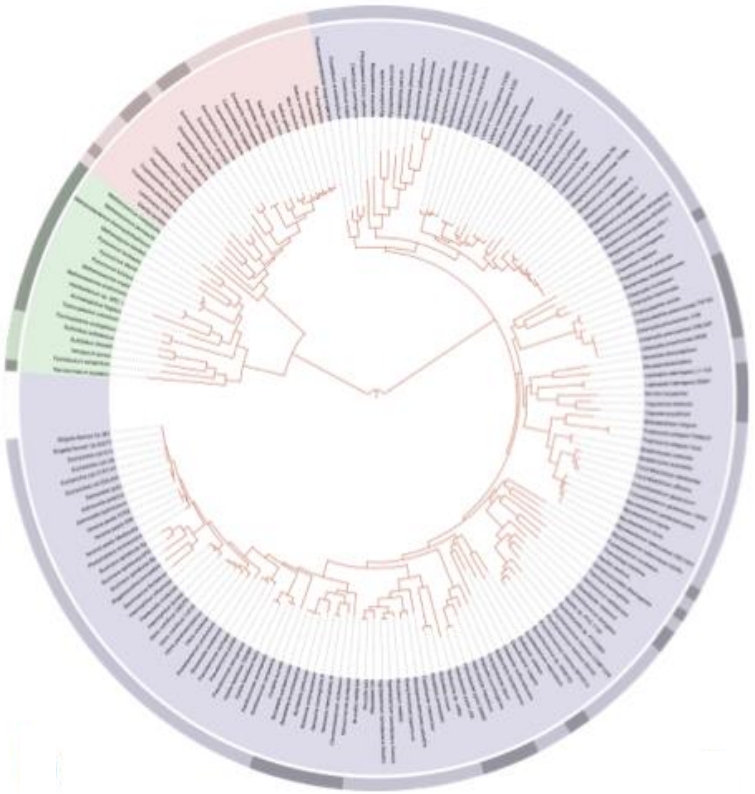
Theory of **Evolution**





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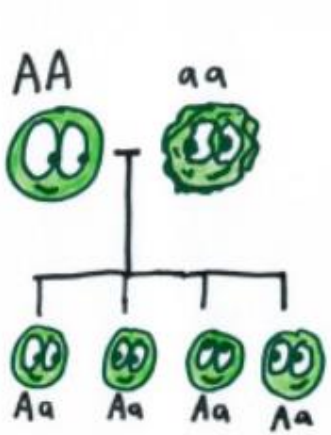
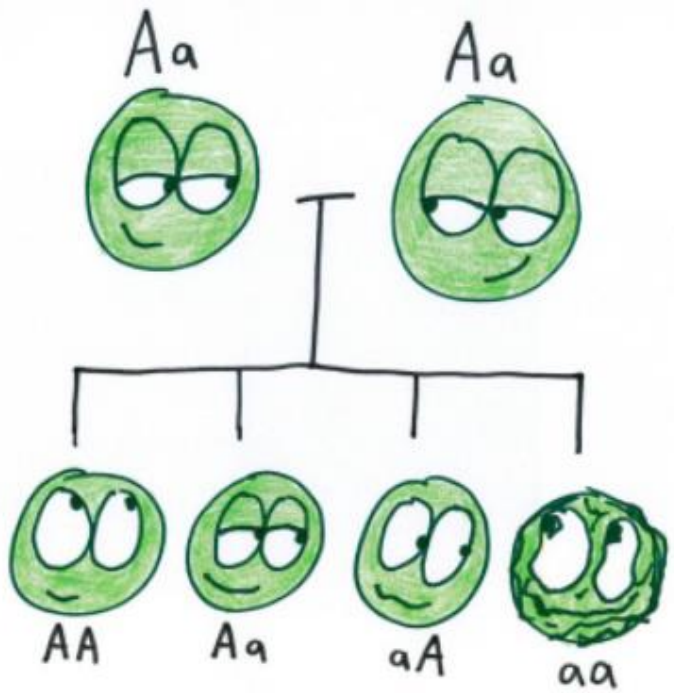
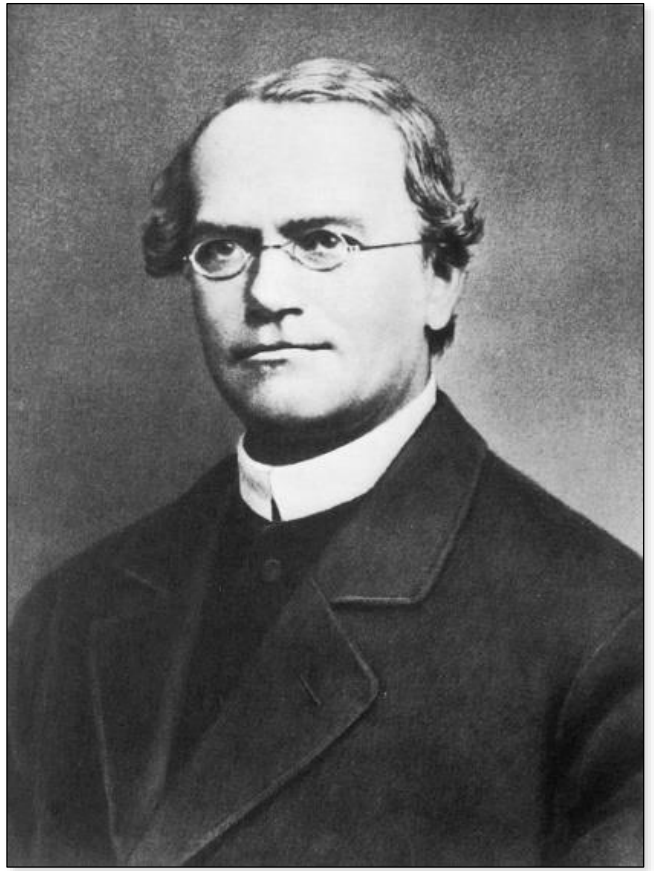
Laws of **Mendel**







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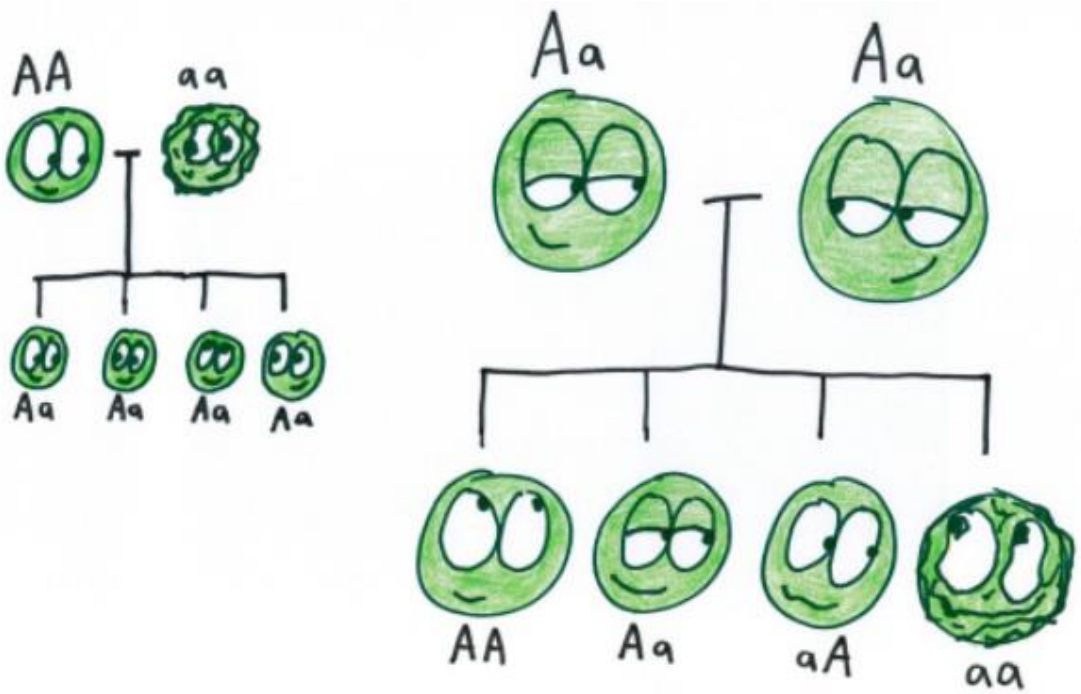

- Law of segregation:
  - One out of two alleles is passed down by each parent

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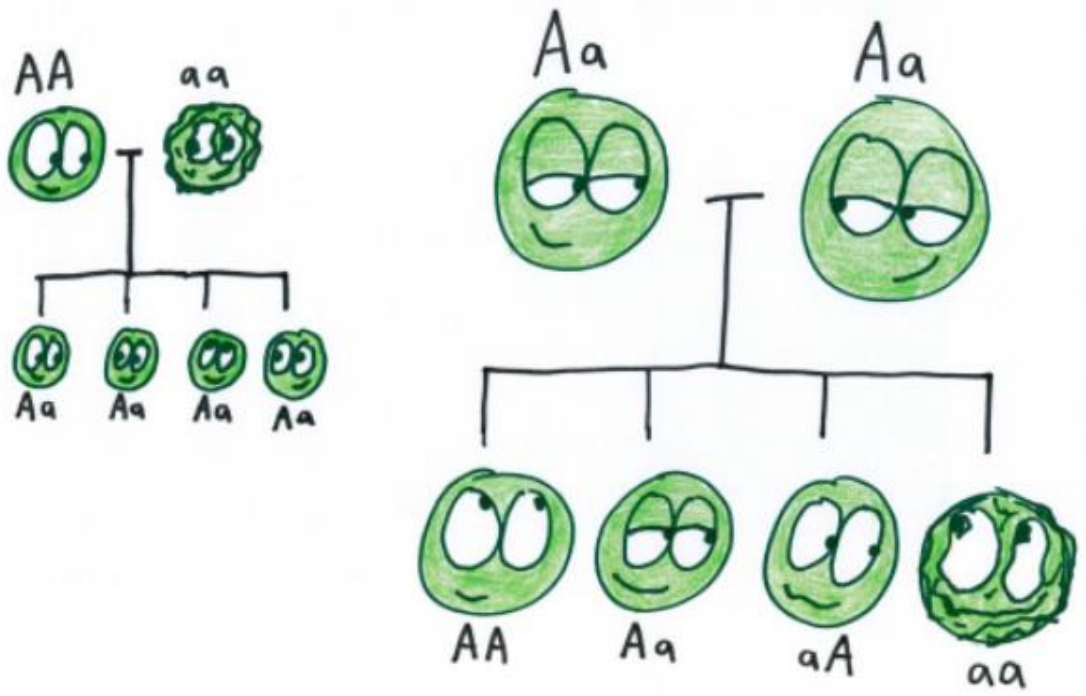

- Law of segregation:
  - One out of two alleles is passed down by each parent
- Law of dominance:
  - Some alleles are dominant or recessive. An organism with at least one dominant allele will display the effect of the dominant allele

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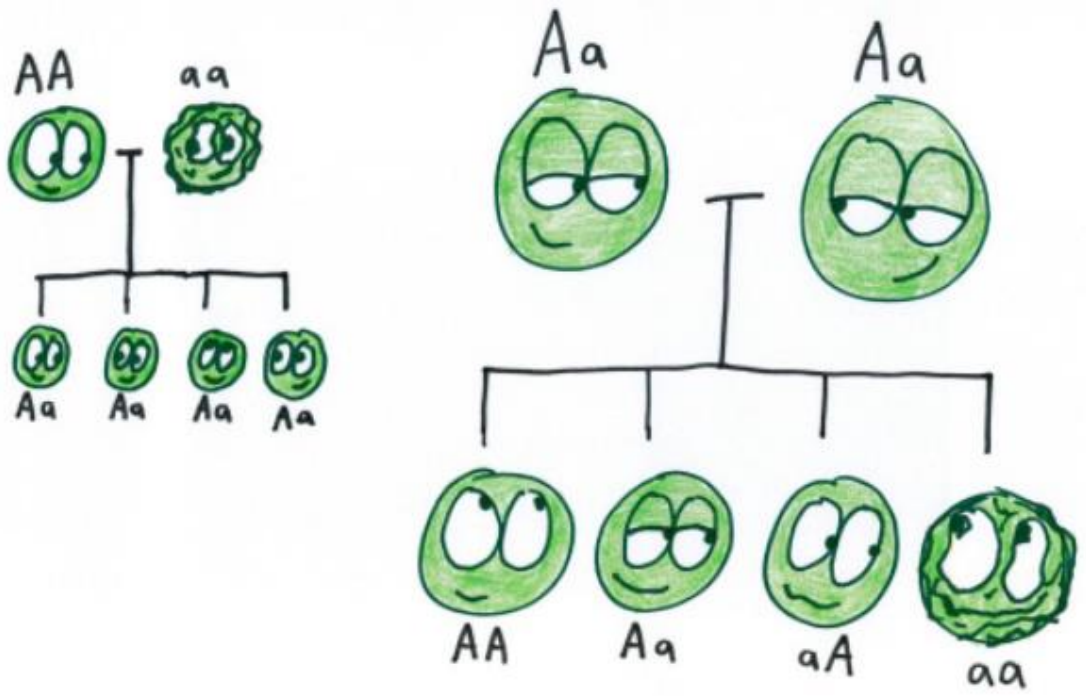


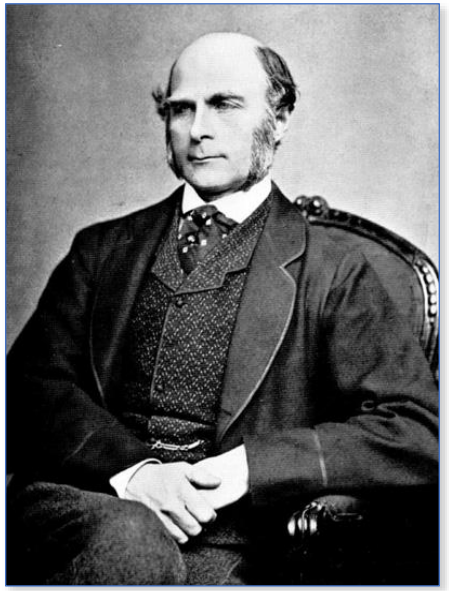
- Law of segregation:
  - One out of two alleles is passed down by each parent
- Law of dominance:
  - Some alleles are dominant or recessive. An organism with at least one dominant allele will display the effect of the dominant allele
- Law of independent assortment:
  - Genes for different traits are passed down independently from each other

Galton used twins to study the power of the environment to change twins.

He did not compare identical and fraternal twins to estimate heritability.

THE HISTORY OF TWINS, AS A CRITERION OF THE RELATIVE POWERS OF NATURE AND NURTURE.[1]

By Francis Galton, F.R.S.



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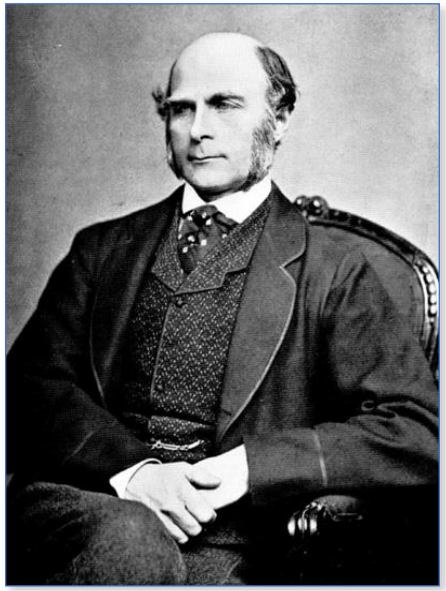
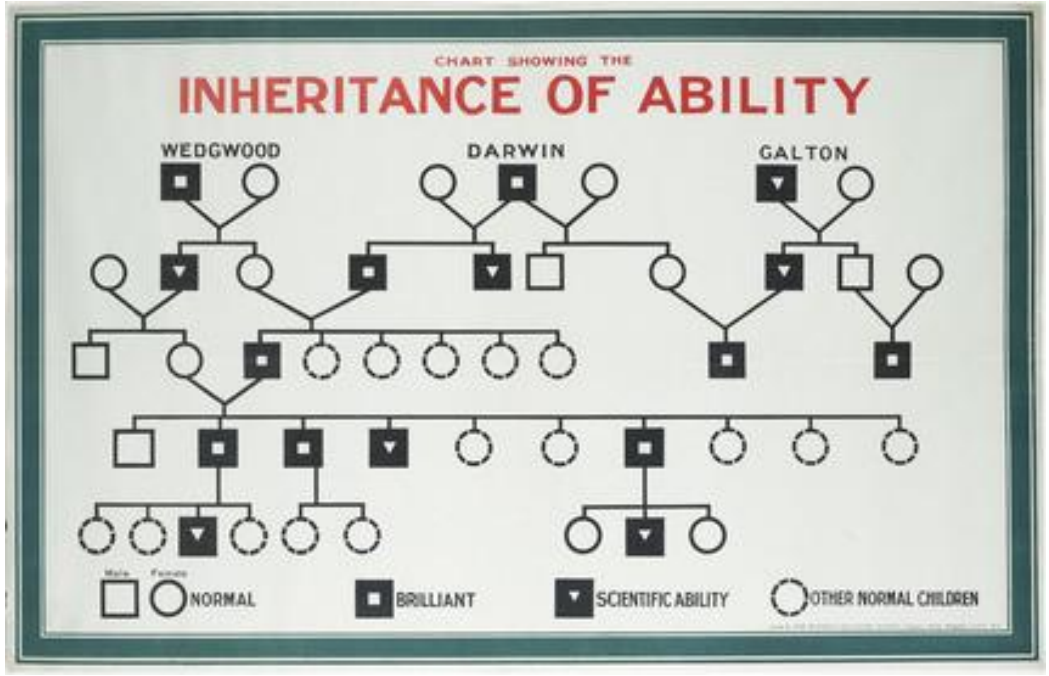
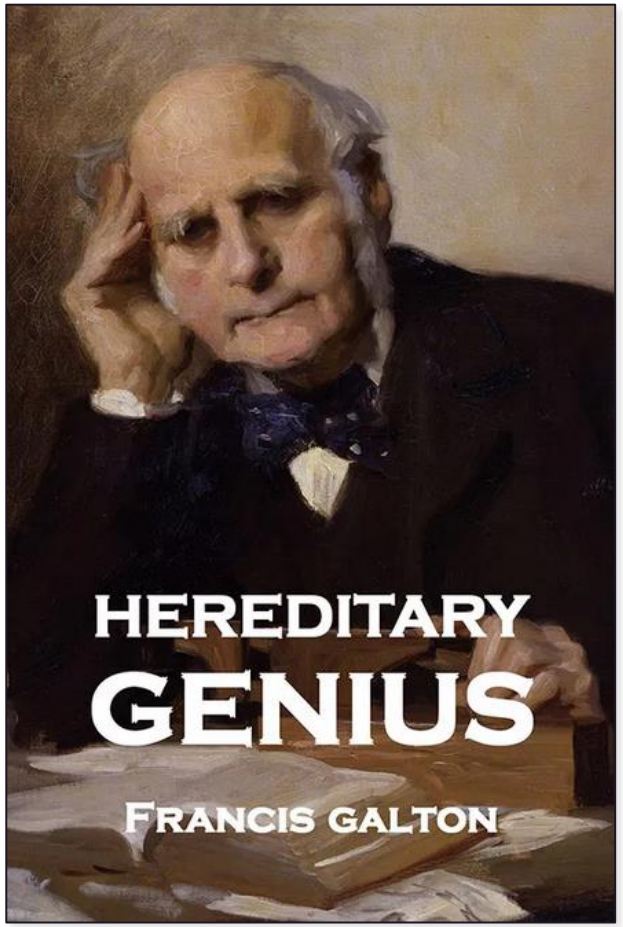


"There are twins of the same sex so alike in body and mind that not even their own mothers can distinguish them. Their features, voice, and expressions are similar; they see things in the same light, and their ideas follow the same laws of association."

In *Hereditary Genius* (1869), Francis Galton applied statistics to show that offspring of "eminent" figures were more likely to succeed in high-profile professions.





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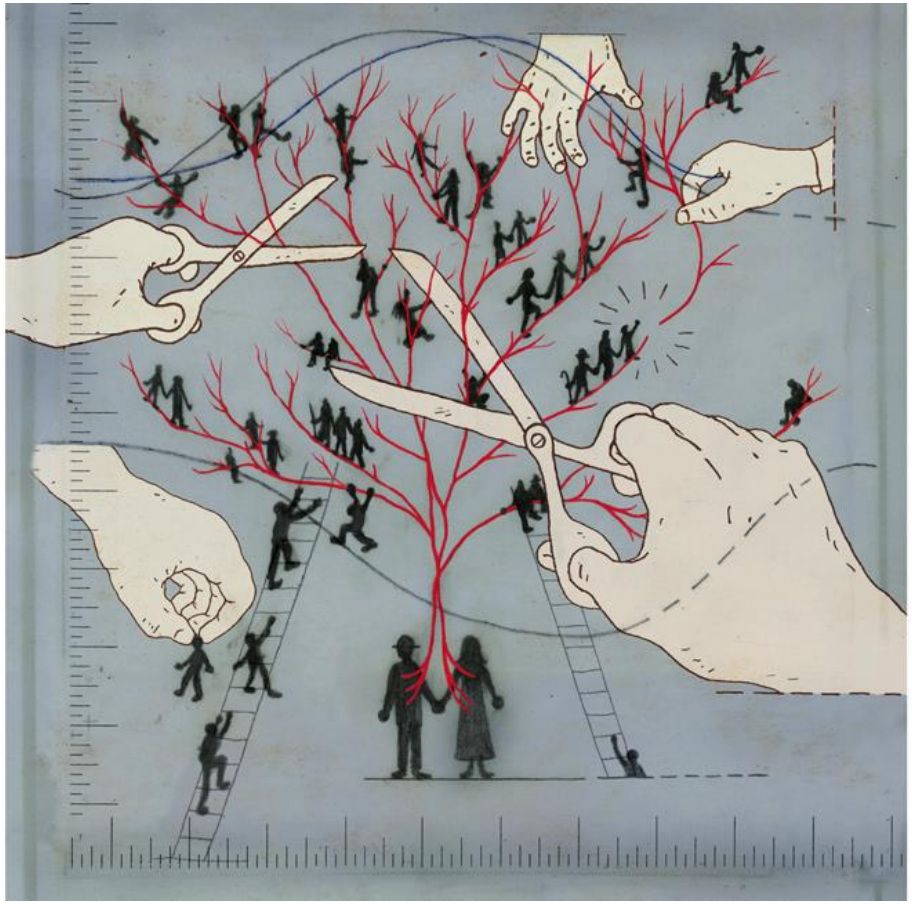
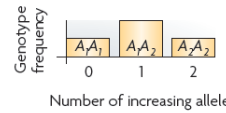
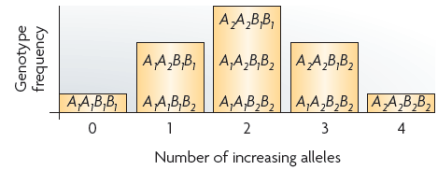
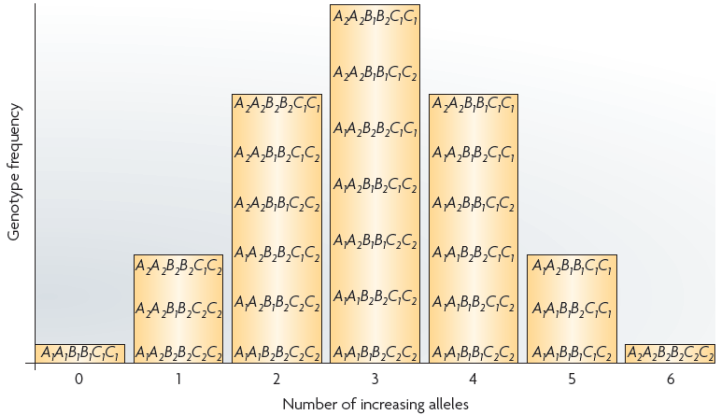
Galton also invented **Eugenics**:
Improving the “genetic quality” of the population through selective parenthood.

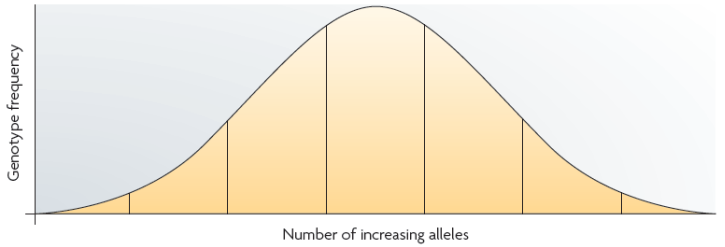


Ronald Fisher reconciles Mendel's laws & quantitative traits









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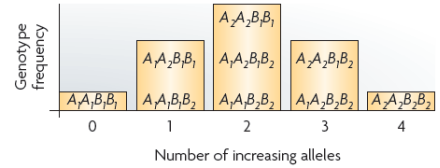
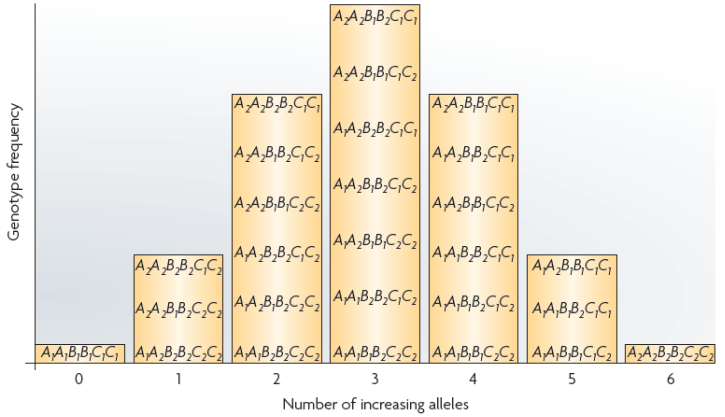
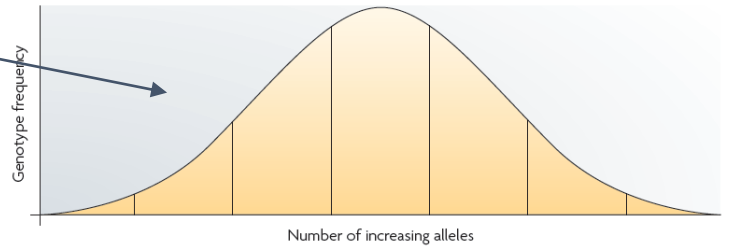


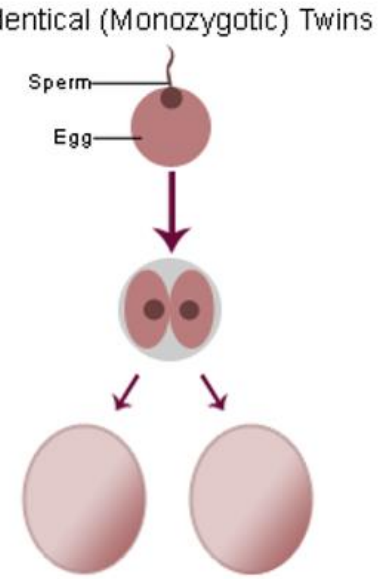


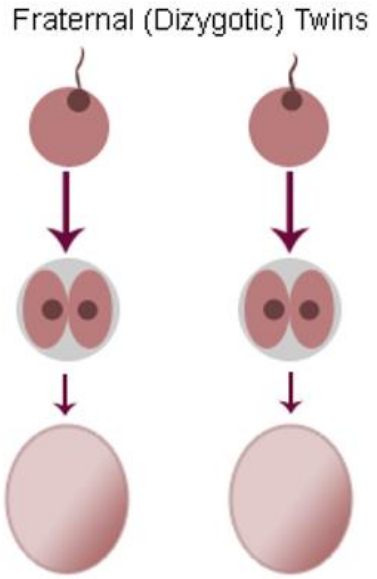
Complex trait =

many genes + environment



First classical twin studies (monozygotic [MZ] vs dizygotic [DZ] twins) were done in the late 1920s on intelligence.





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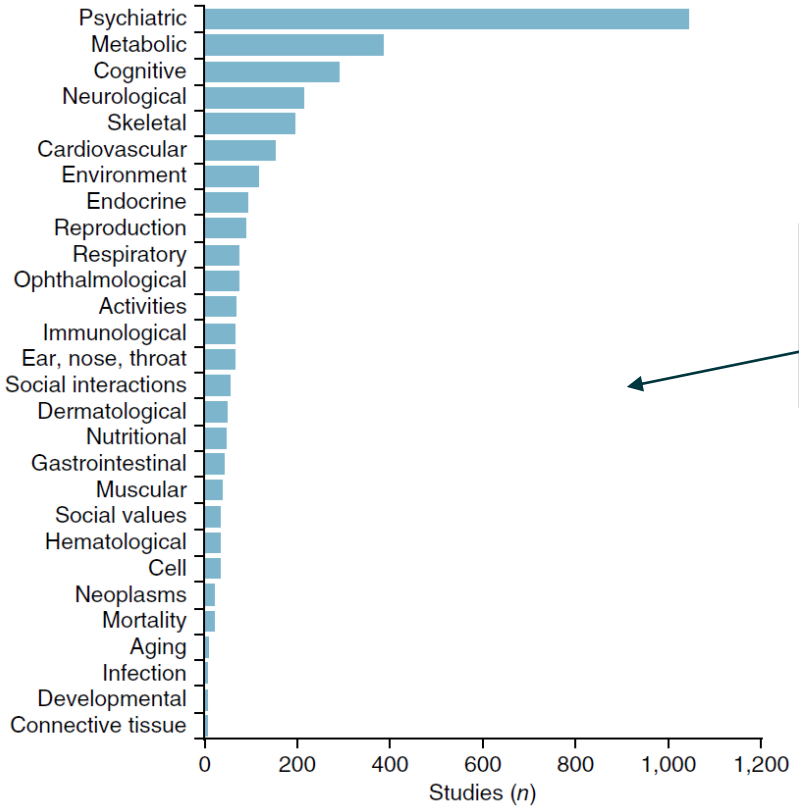
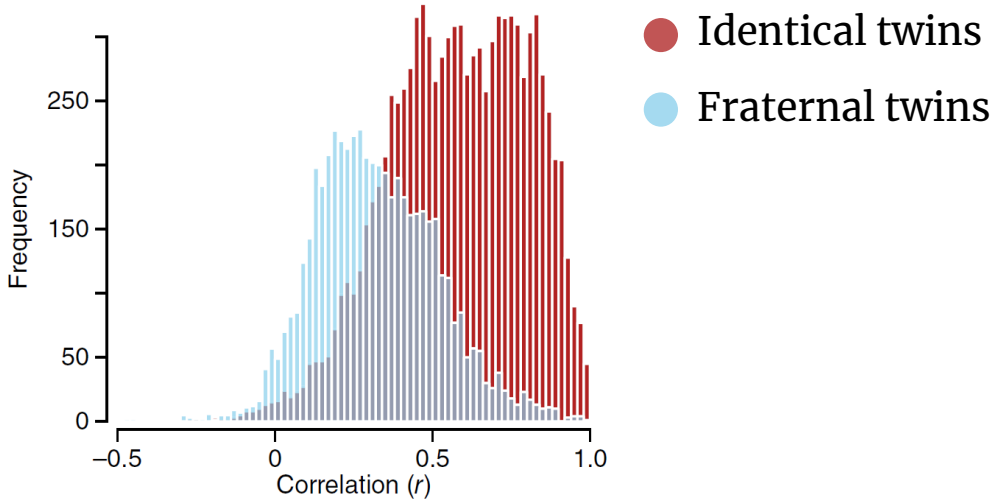


All twin studies between 1958 & 2012



nature genetics

Meta-analysis of the heritability of human traits based on fifty years of twin studies

Tinca J C Polderman[1,10], Beben Benyamin[2,10], Christiaan A de Leeuw[1,3], Patrick F Sullivan[4–6], Arjen van Bochoven[7], Peter M Visscher[2,8,11] & Danielle Posthuma[1,9,11]

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“First law of behavior genetics”: All human behavioral traits are heritable.

Genetic influences
Shared environmental influences
Unique environmental influences

NATURE REVIEWS | GENETICS

CLASSICAL TWIN STUDIES AND BEYOND

Dorret Boomsma, Andreas Busjahn‡ and Leena Peltonen§*

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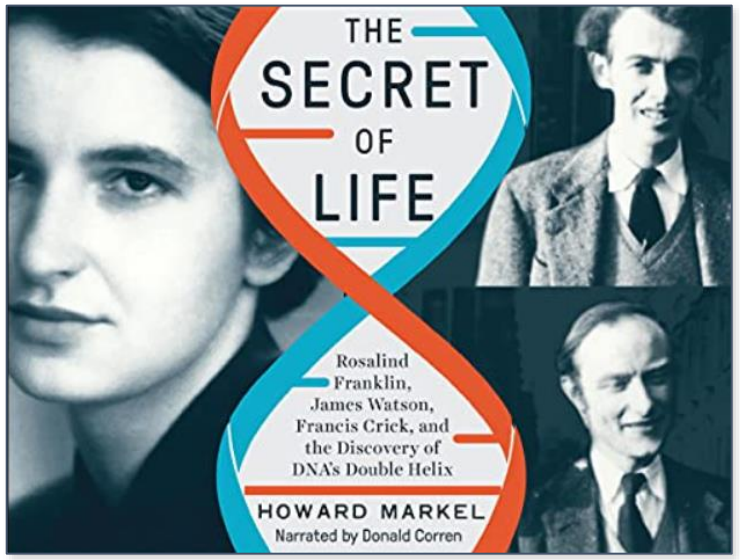
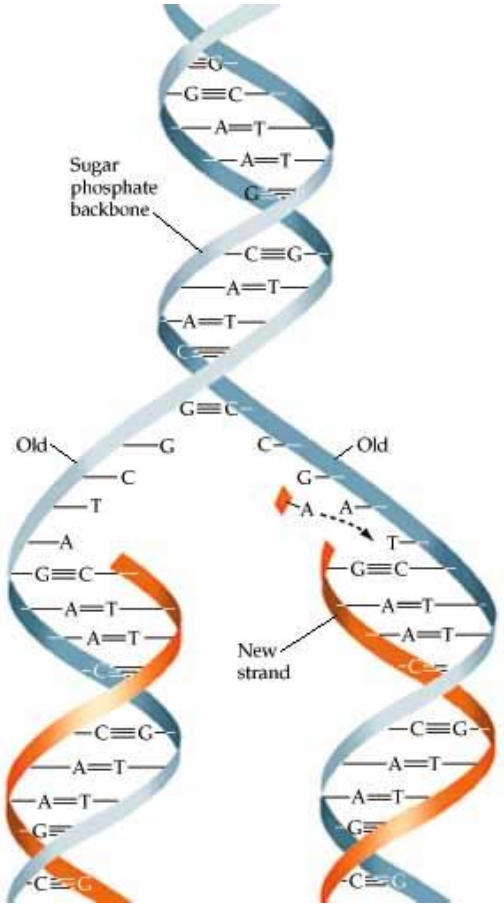
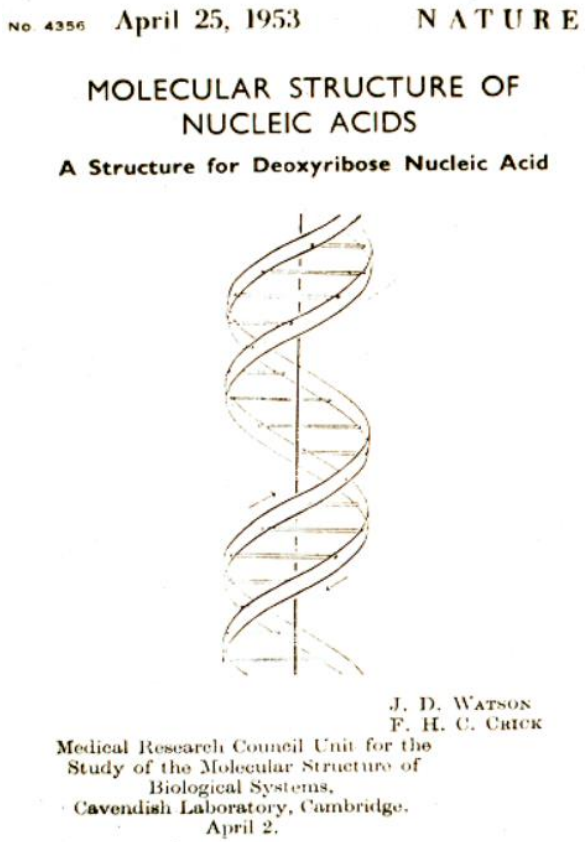
DNA = double helix!







No. 4356 April 25, 1953 NATURE

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

J. D. Watson
F. H. C. Crick

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge. April 2.

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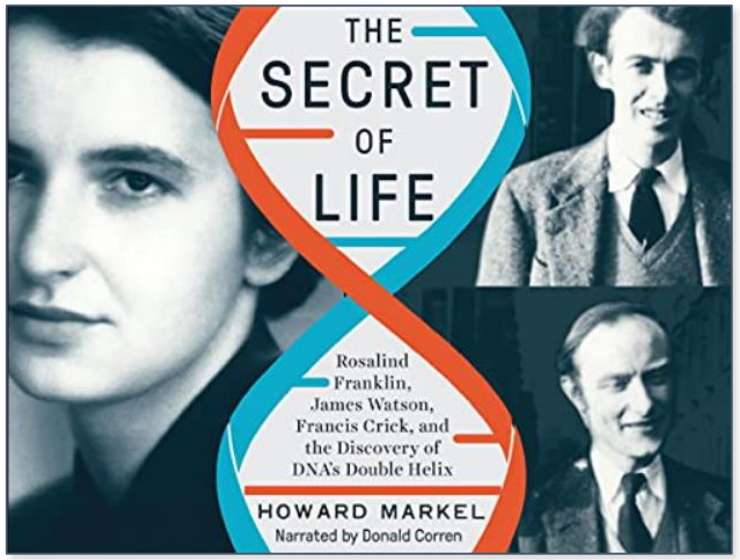

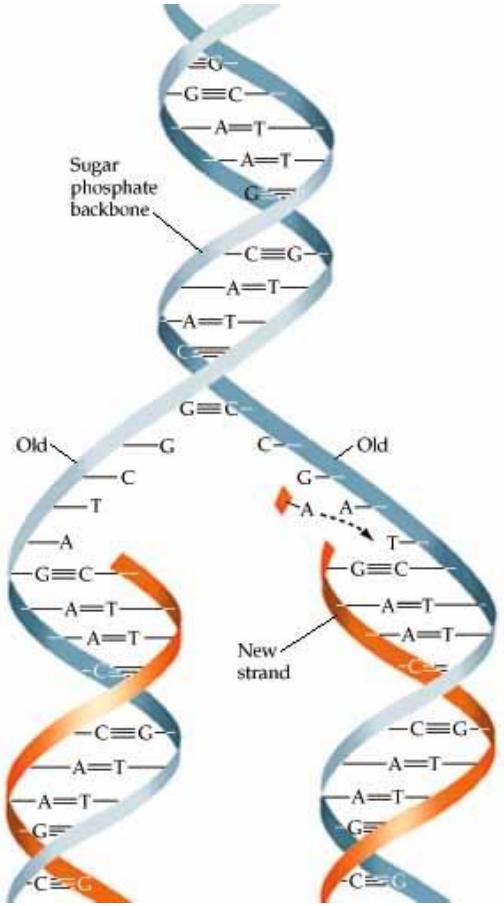

second base in codon

first base in codon	T	C	A	G	third base in codon
T	TTT Phe	TCT Ser	TAT Tyr	TGT Cys	T
	TTC Phe	TCC Ser	TAC Tyr	TGC Cys	C
	TTA Leu	TCA Ser	TAA stop	TGA stop	A
	TTG Leu	TCG Ser	TAG stop	TGG Trp	G
C	CTT Leu	CCT Pro	CAT His	CGT Arg	T
	CTC Leu	CCC Pro	CAC His	CGC Arg	C
	CTA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CTG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	ATT Ile	ACT Thr	AAT Asn	AGT Ser	T
	ATC Ile	ACC Thr	AAC Asn	AGC Ser	C
	ATA Ile	ACA Thr	AAA Lys	AGA Arg	A
	ATG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GTT Val	GCT Ala	GAT Asp	GGT Gly	T
	GTC Val	GCC Ala	GAC Asp	GGC Gly	C
	GTA Val	GCA Ala	GAA Glu	GGA Gly	A
	GTG Val	GCG Ala	GAG Glu	GGG Gly	G

There are 20 amino-acids coded for in three letter words called "codons"

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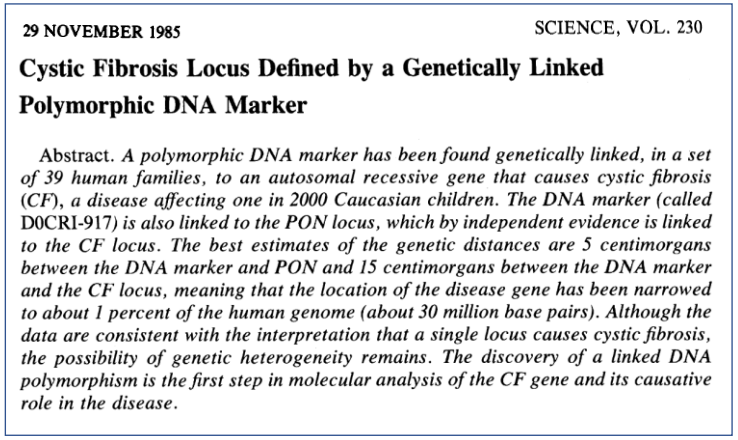
Linkage studies

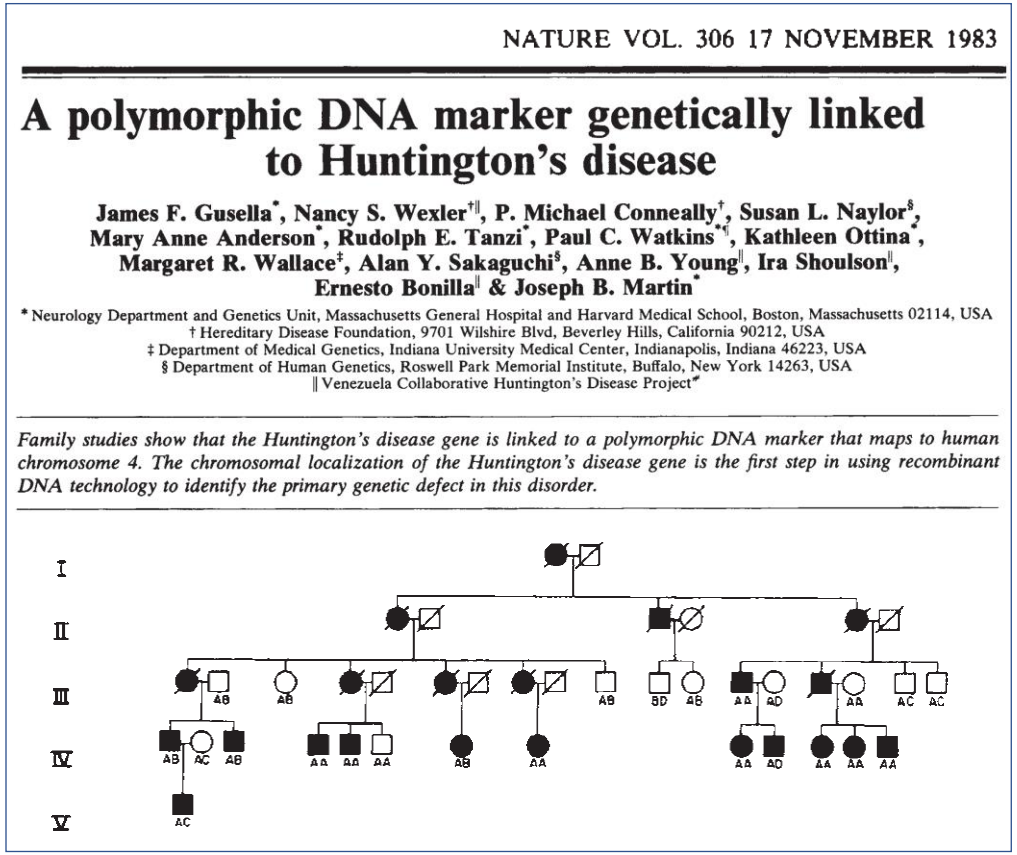
Only work for very big effects



29 NOVEMBER 1985 SCIENCE, VOL. 230

Cystic Fibrosis Locus Defined by a Genetically Linked Polymorphic DNA Marker

Abstract. *A polymorphic DNA marker has been found genetically linked, in a set of 39 human families, to an autosomal recessive gene that causes cystic fibrosis (CF), a disease affecting one in 2000 Caucasian children. The DNA marker (called* D0CRI-917*) is also linked to the PON locus, which by independent evidence is linked to the CF locus. The best estimates of the genetic distances are 5 centimorgans between the DNA marker and PON and 15 centimorgans between the DNA marker and the CF locus, meaning that the location of the disease gene has been narrowed to about 1 percent of the human genome (about 30 million base pairs). Although the data are consistent with the interpretation that a single locus causes cystic fibrosis, the possibility of genetic heterogeneity remains. The discovery of a linked DNA polymorphism is the first step in molecular analysis of the CF gene and its causative role in the disease.*



NATURE VOL. 306 17 NOVEMBER 1983

A polymorphic DNA marker genetically linked to Huntington's disease

James F. Gusella*, Nancy S. Wexler†‖, P. Michael Conneally†, Susan L. Naylor§, Mary Anne Anderson*, Rudolph E. Tanzi*, Paul C. Watkins*¶, Kathleen Ottina*, Margaret R. Wallace‡, Alan Y. Sakaguchi§, Anne B. Young‖, Ira Shoulson‖, Ernesto Bonilla‖ & Joseph B. Martin*

* Neurology Department and Genetics Unit, Massachusetts General Hospital and Harvard Medical School, Boston, Massachusetts 02114, USA
† Hereditary Disease Foundation, 9701 Wilshire Blvd, Beverley Hills, California 90212, USA
‡ Department of Medical Genetics, Indiana University Medical Center, Indianapolis, Indiana 46223, USA
§ Department of Human Genetics, Roswell Park Memorial Institute, Buffalo, New York 14263, USA
‖ Venezuela Collaborative Huntington's Disease Project#

Family studies show that the Huntington's disease gene is linked to a polymorphic DNA marker that maps to human chromosome 4. The chromosomal localization of the Huntington's disease gene is the first step in using recombinant DNA technology to identify the primary genetic defect in this disorder.

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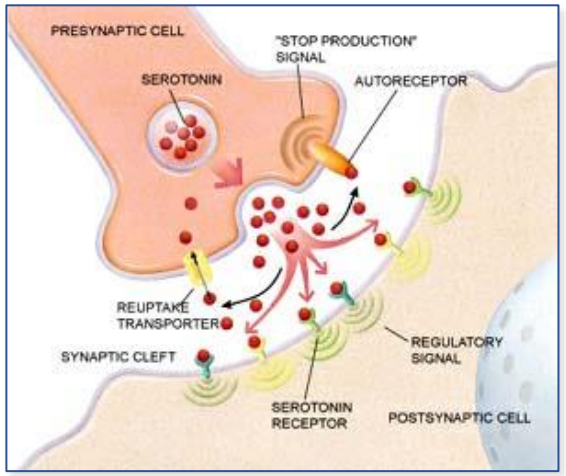
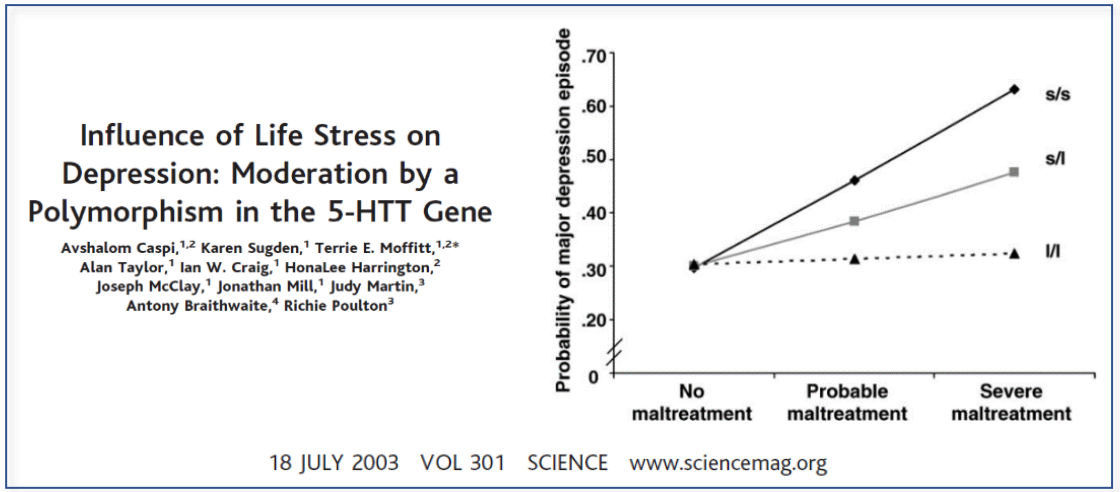
Candidate Gene Studies

- **Serotonin transporter** transports **serotonin** from synaptic cleft to presynaptic neuron
- Serotonin affects mood, sleep, appetite, memory, and more



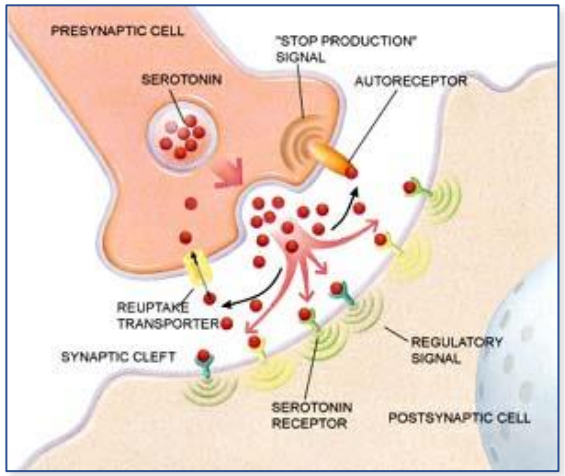
Candidate Gene Studies



Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene

Avshalom Caspi,[1,2] Karen Sugden,[1] Terrie E. Moffitt,[1,2*] Alan Taylor,[1] Ian W. Craig,[1] HonaLee Harrington,[2] Joseph McClay,[1] Jonathan Mill,[1] Judy Martin,[3] Antony Braithwaite,[4] Richie Poulton[3]

18 JULY 2003 VOL 301 SCIENCE www.sciencemag.org



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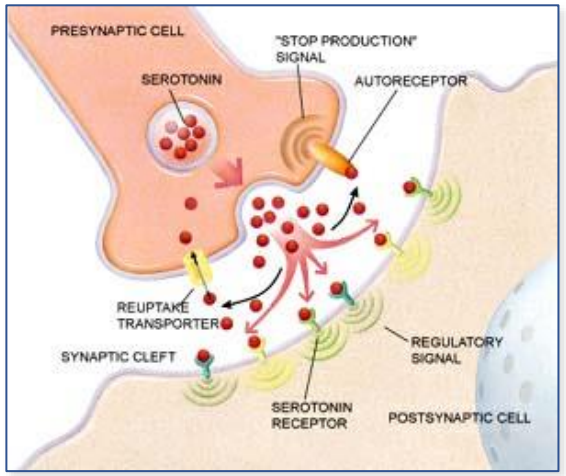
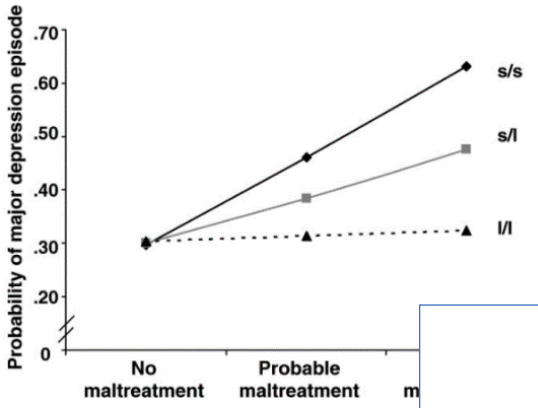


Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene

Avshalom Caspi,[1,2] Karen Sugden,[1] Terrie E. Moffitt,[1,2*] Alan Taylor,[1] Ian W. Craig,[1] HonaLee Harrington,[2] Joseph McClay,[1] Jonathan Mill,[1] Judy Martin,[3] Antony Braithwaite,[4] Richie Poulton[3]



18 JULY 2003 VOL 301 SCIENCE www.sciencemag.org

Molecular Psychiatry (2017) 00, 1–10

www.nature.com/mp

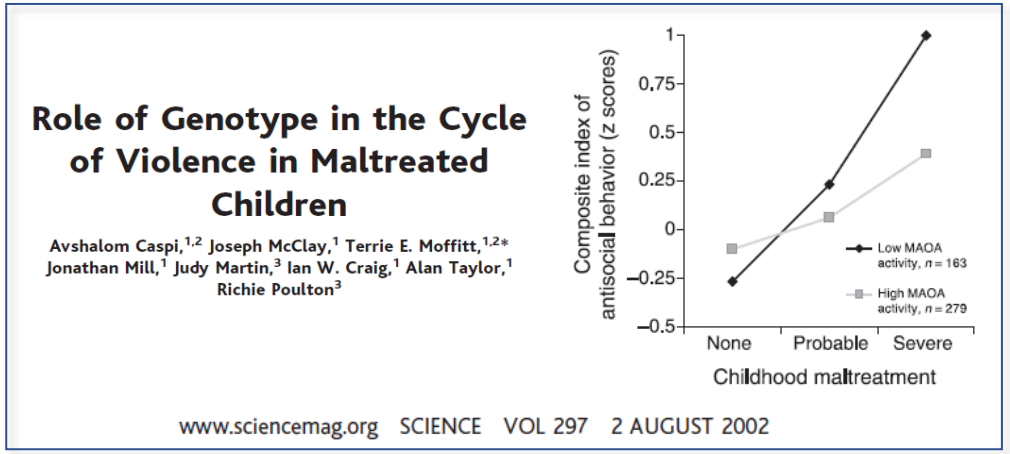
ORIGINAL ARTICLE

Collaborative meta-analysis finds no evidence of a strong interaction between stress and 5-HTTLPR genotype contributing to the development of depression

350 BC — 16th century — 17th century — 1859 — 1865 — 1875 — 1918 — 1920s — 1953 — 1980s — 90s/00s — 2005 — 2007–2023

Candidate Gene Studies

Mono-amine oxidase (MAO-A): an enzyme that degrades noradrenaline, adrenaline, serotonin, and dopamine.



Role of Genotype in the Cycle of Violence in Maltreated Children

Avshalom Caspi,[1,2] Joseph McClay,[1] Terrie E. Moffitt,[1,2]* Jonathan Mill,[1] Judy Martin,[3] Ian W. Craig,[1] Alan Taylor,[1] Richie Poulton[3]

www.sciencemag.org SCIENCE VOL 297 2 AUGUST 2002

Published online 30 October 2009 | Nature | doi:10.1038/news.2009.1050

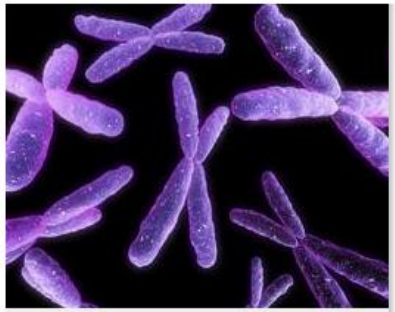
News

Lighter sentence for murderer with 'bad genes'

Italian court reduces jail term after tests identify genes linked to violent behaviour.

Emiliano Feresin

An Italian court has cut the sentence given to a convicted murderer by a year because he has genes linked to violent behaviour — the first time that behavioural genetics has affected a sentence passed by a European court. But researchers contacted by *Nature* have questioned whether the decision was based on sound science.



A court in Italy has cut a prisoner's jail term because he has genes associated with aggressive behaviour. *Ingram Publishing*

Human Genome Project

- Planning in 1984, launch in 1990, completion in 2003
- Goal: map all 3 billion nucleotides of the human genome
- Costs: **3 billion dollars**

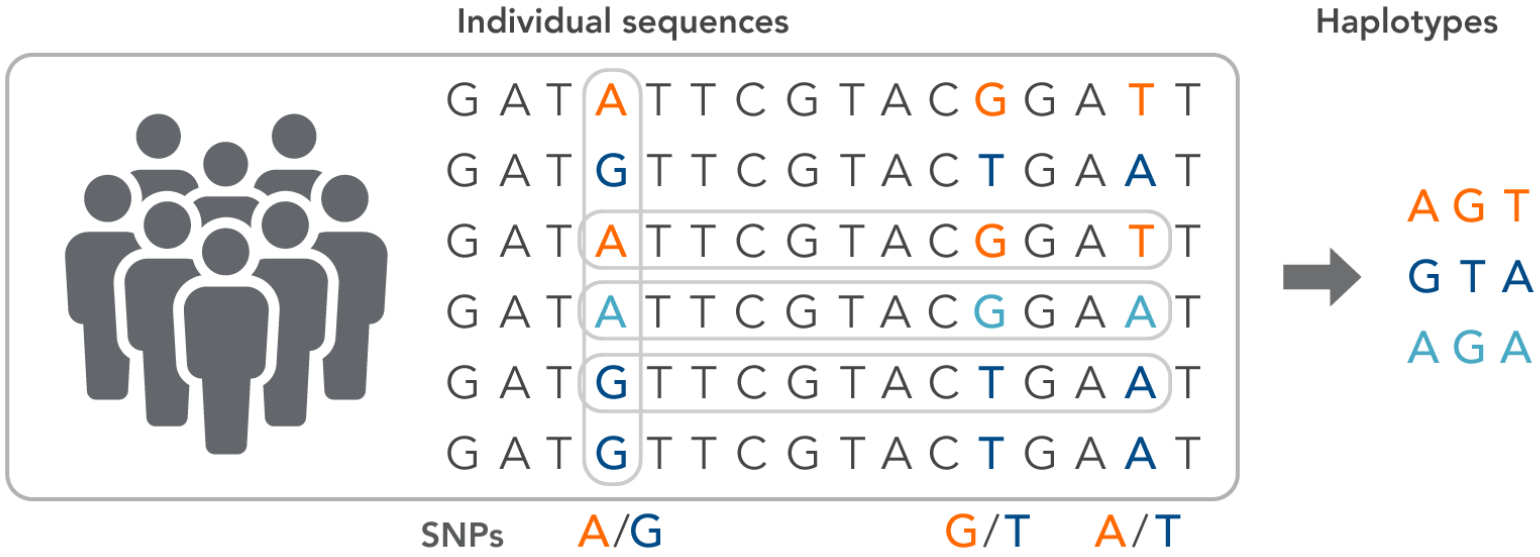
Human Genome Project

"We are here to celebrate the completion of the first survey of the entire human genome. Without a doubt, this is the most important, most wondrous map ever produced by humankind."

- President Bill Clinton, 26-06-2000, the White House

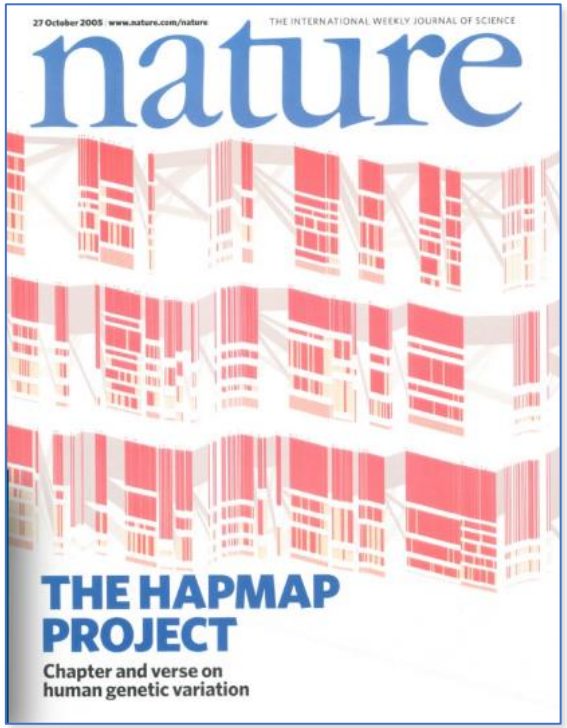
Next step:

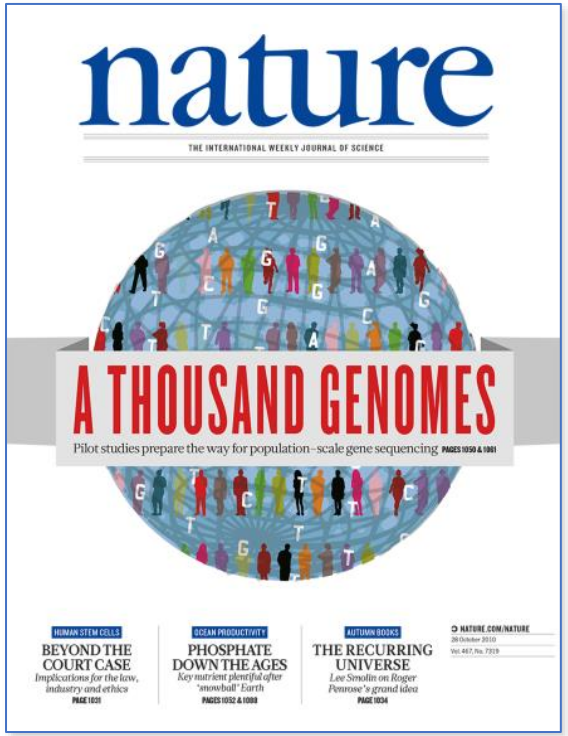
Make *haplotype* maps



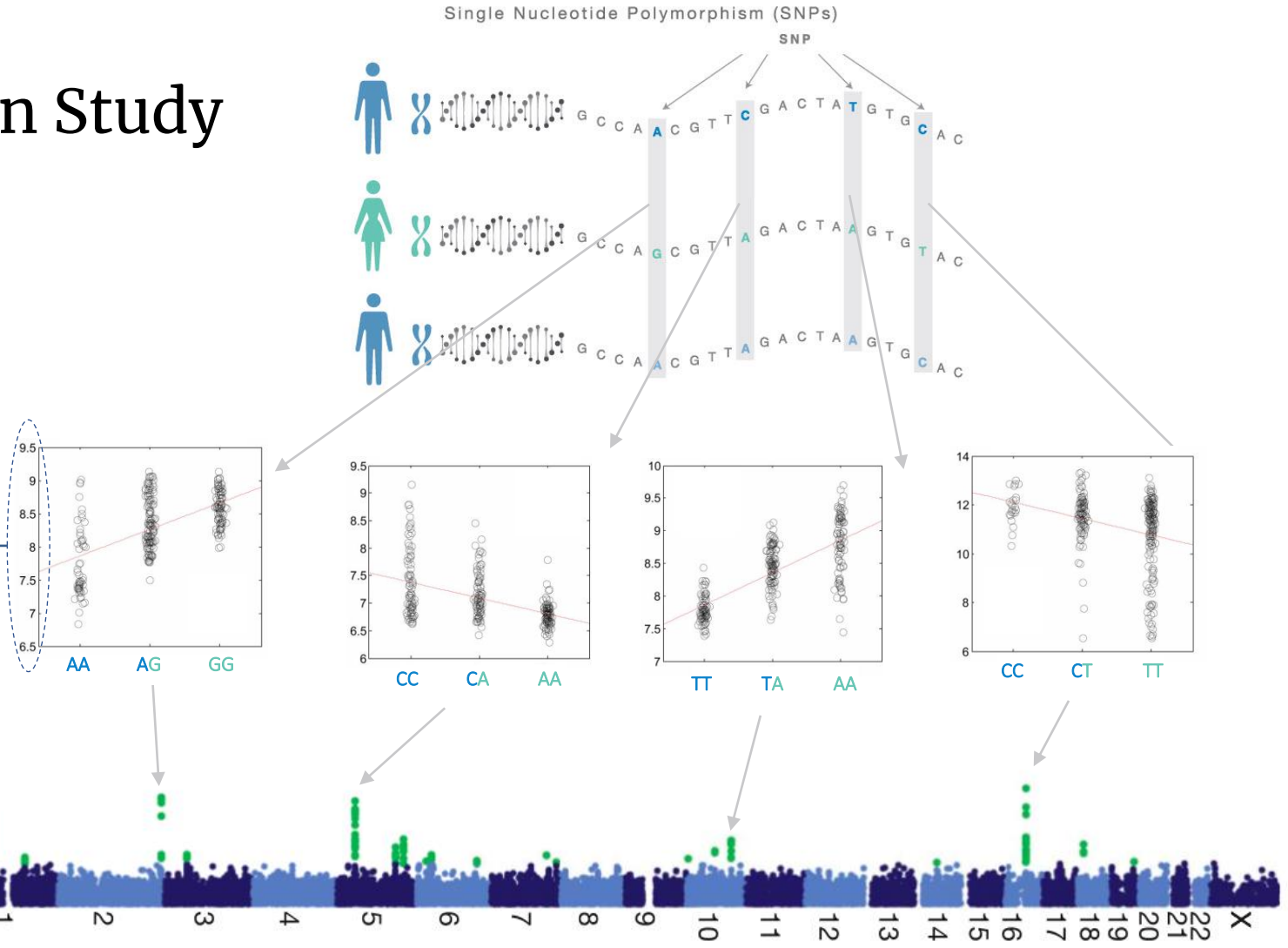
Next step:

Make *haplotype* maps

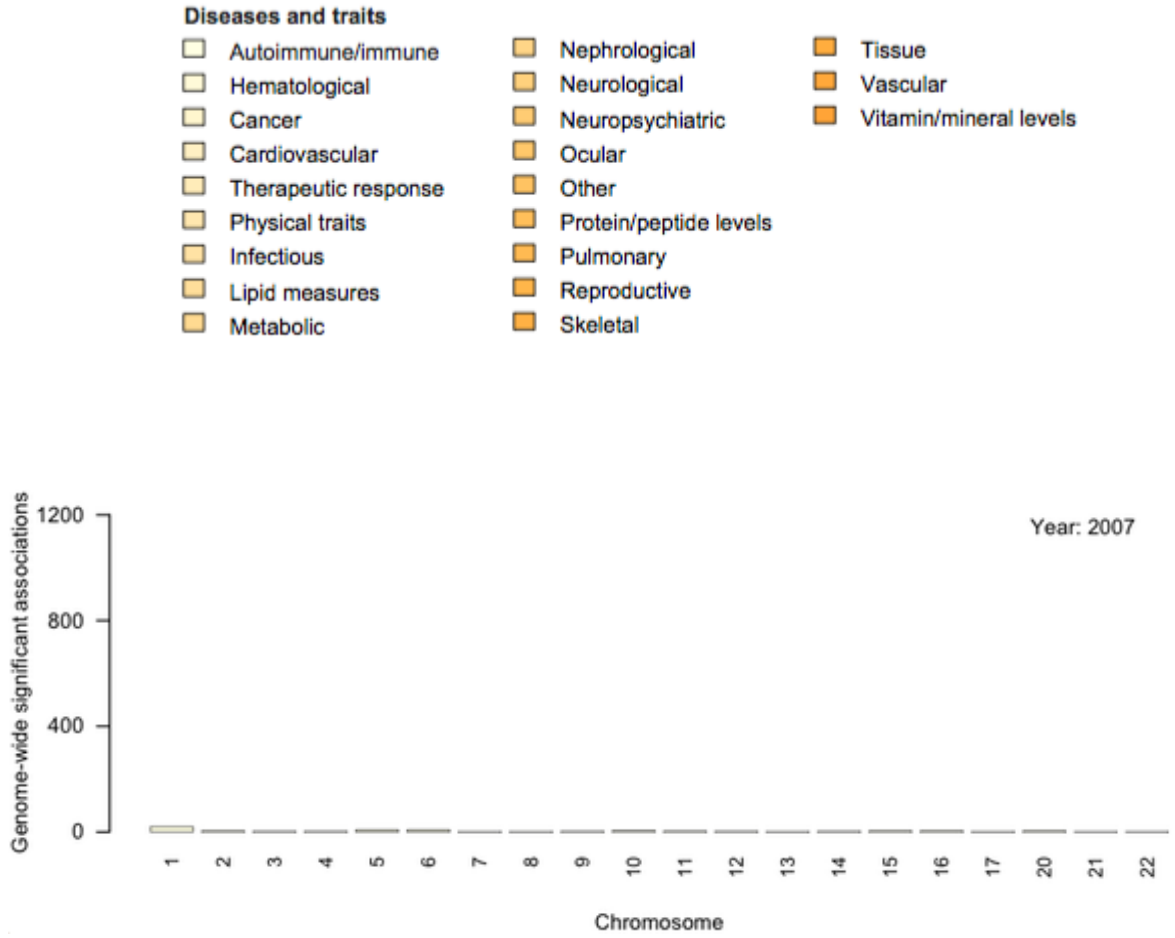




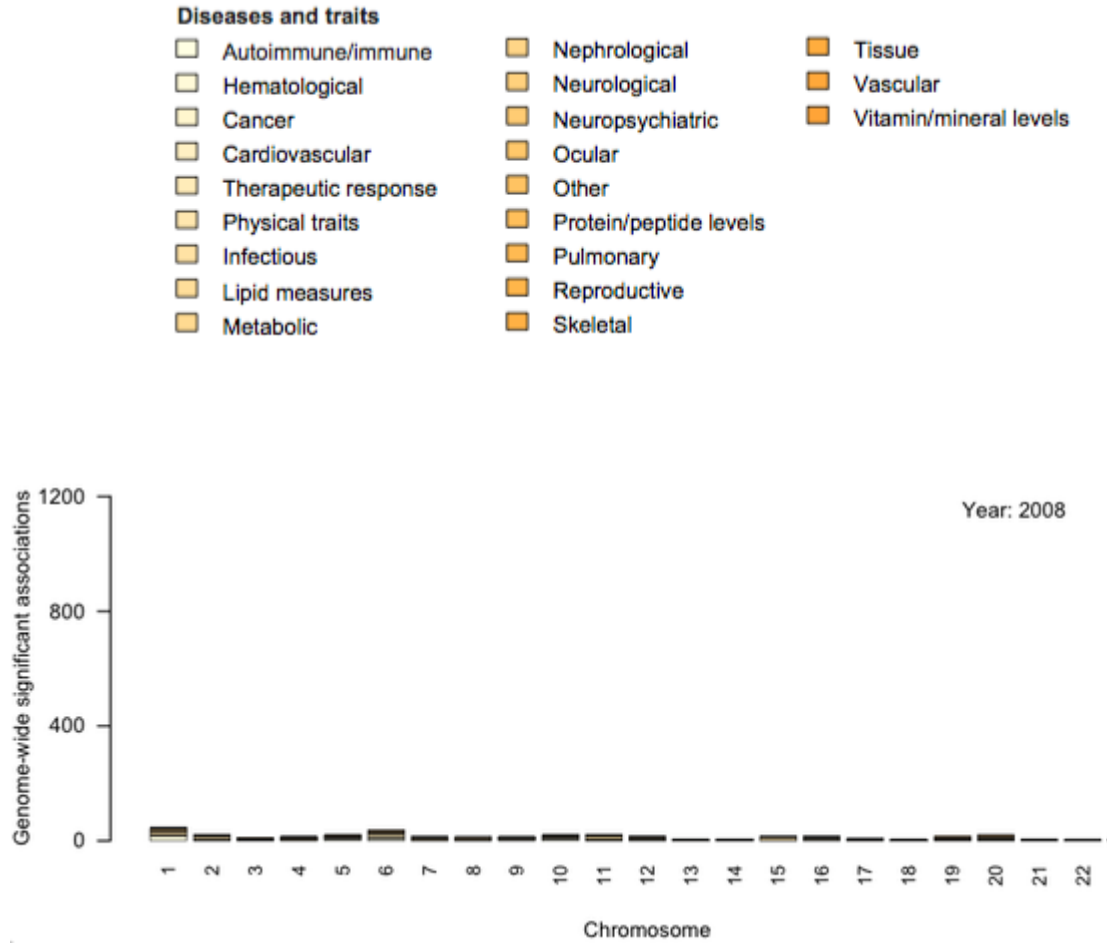
Genome-Wide Association Study (GWAS)



350 BC — 16th century — 17th century — 1859 — 1865 — 1875 — 1918 — 1920s — 1953 — 1980s — 90s/00s — 2005 — 2007–2023



350 BC | 16th century | 17th century | 1859 | 1865 | 1875 | 1918 | 1920s | 1953 | 1980s | 90s/00s | 2005 | 2007-2023



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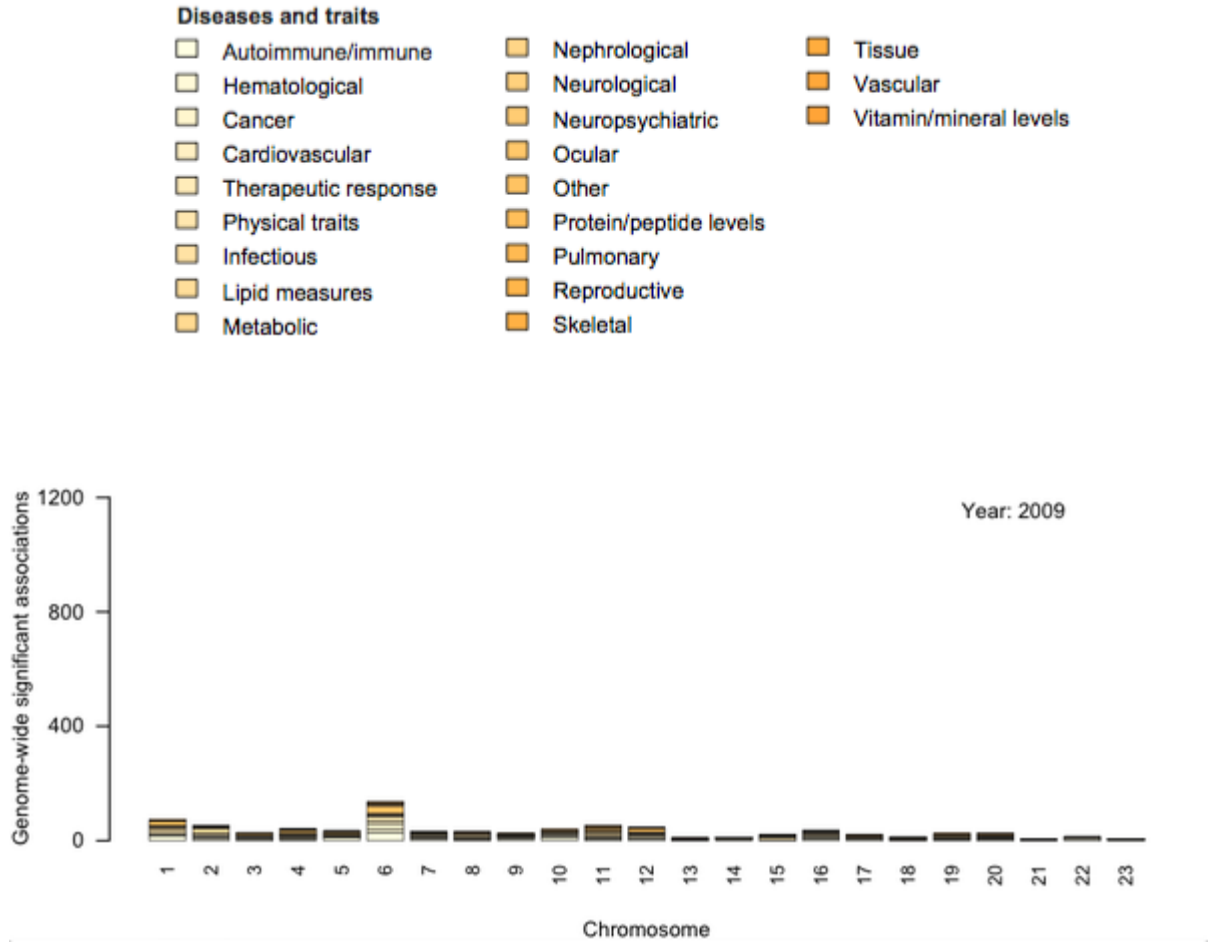

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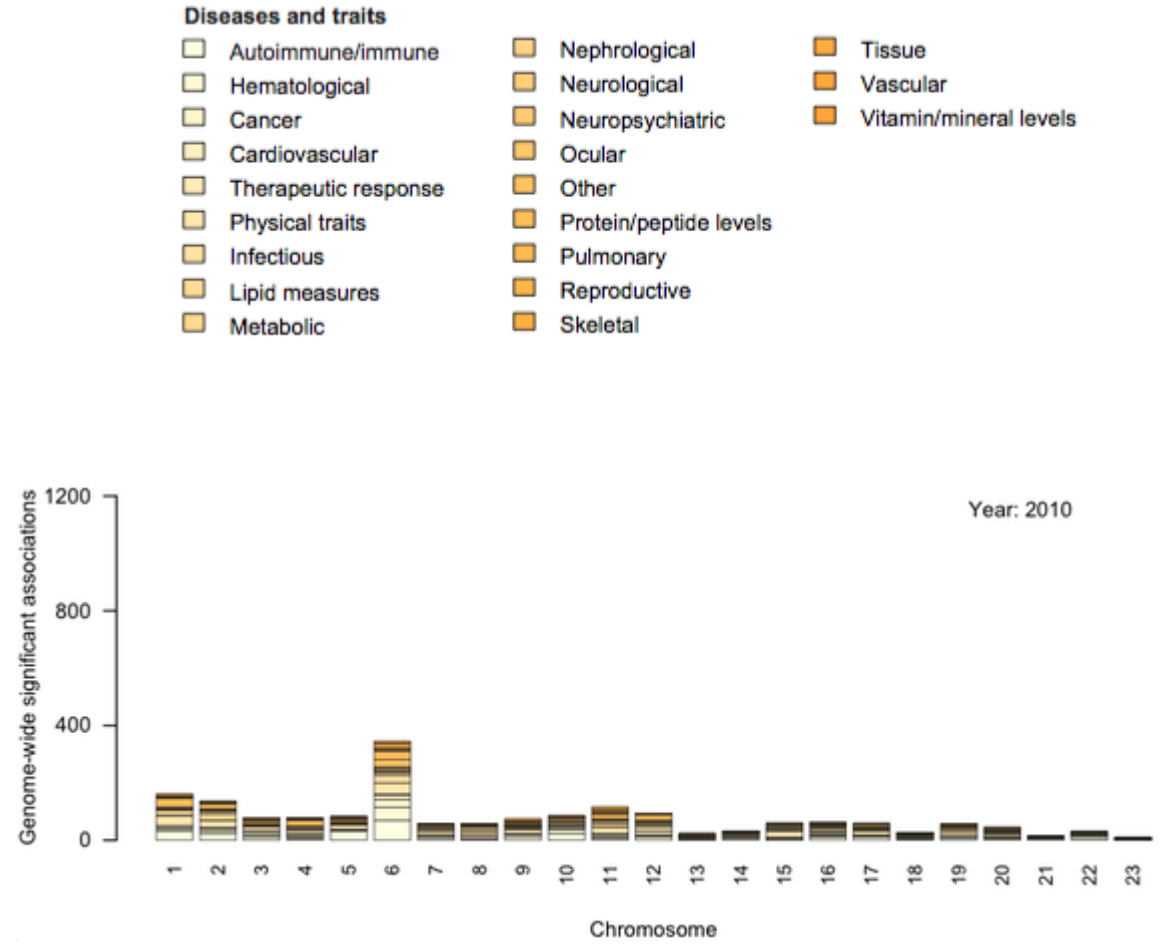
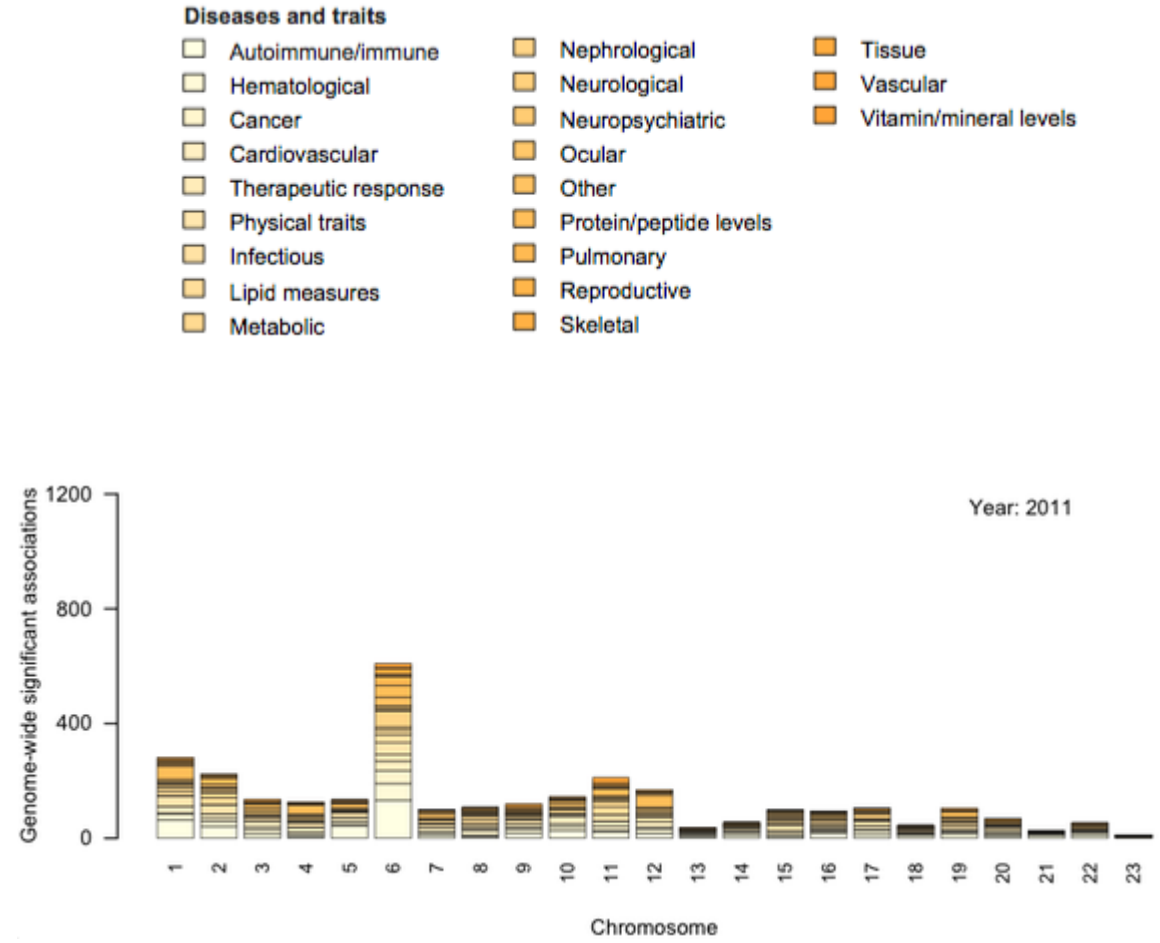


350 BC | 16th century | 17th century | 1859 | 1865 | 1875 | 1918 | 1920s | 1953 | 1980s | 90s/00s | 2005 | 2007-2023



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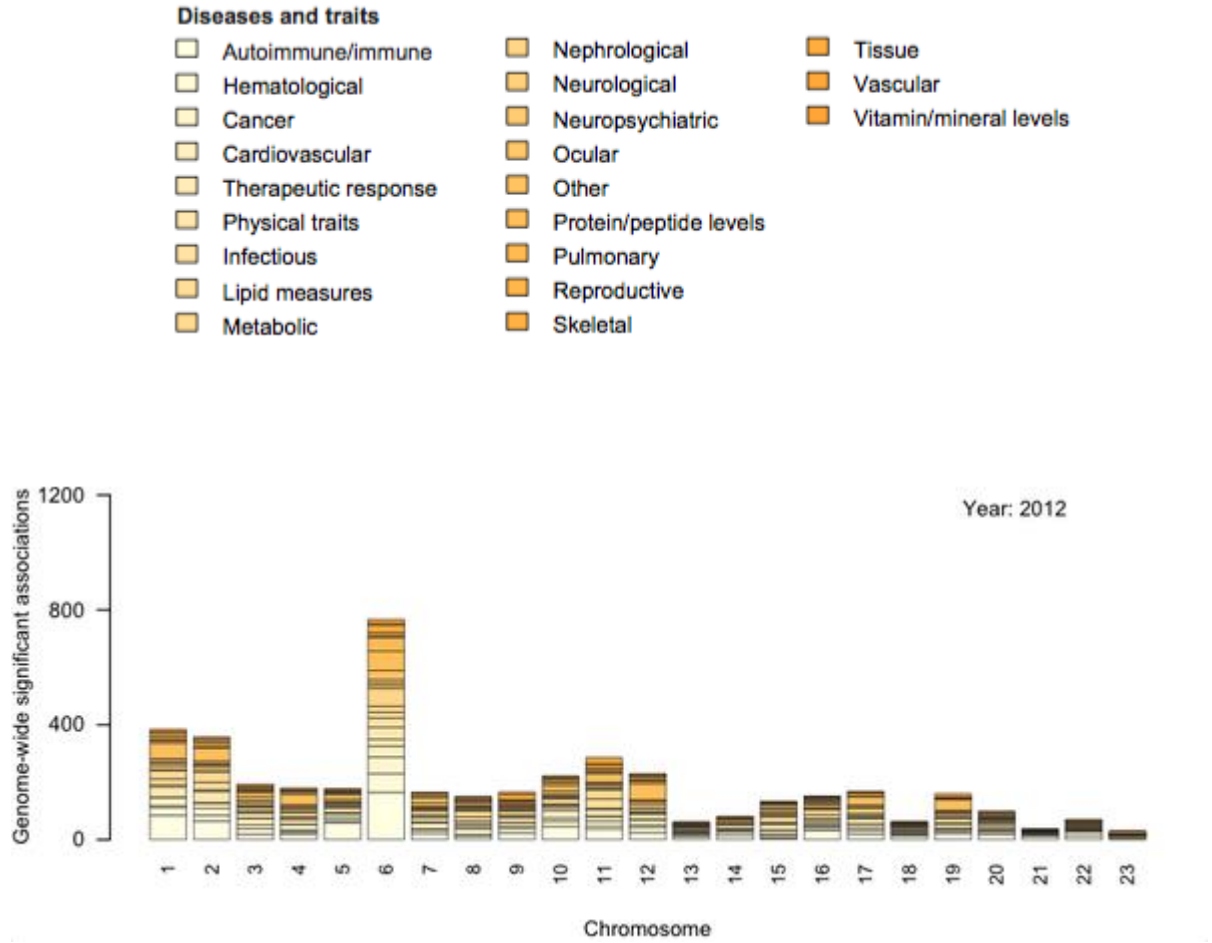

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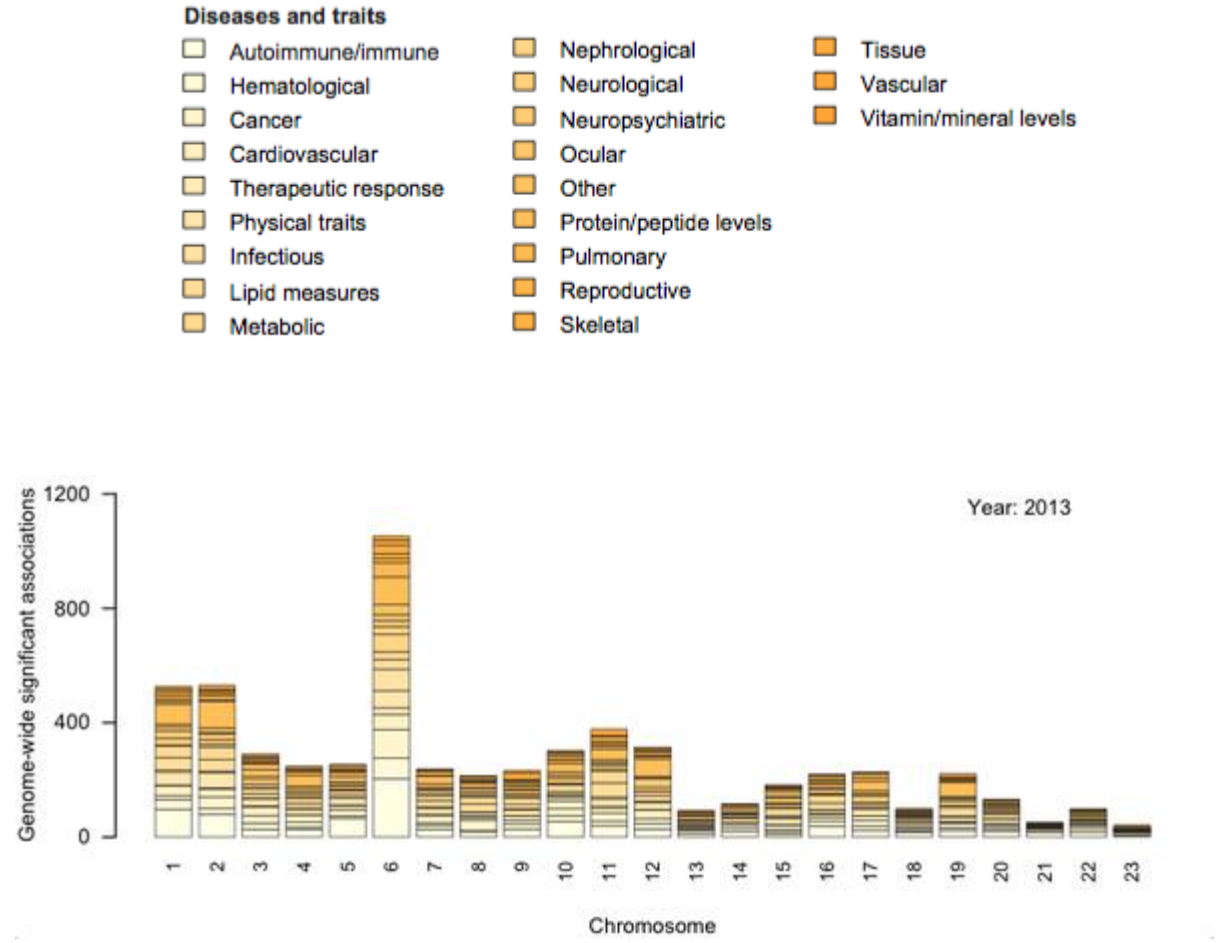
Diseases and traits
Autoimmune/immune
Hematological
Cancer
Cardiovascular
Therapeutic response
Physical traits
Infectious
Lipid measures
Metabolic
Nephrological
Neurological
Neuropsychiatric
Ocular
Other
Protein/peptide levels
Pulmonary
Reproductive
Skeletal
Tissue
Vascular
Vitamin/mineral levels
Year: 2013
Genome-wide significant associations
1200
800
400
0
1
2
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4
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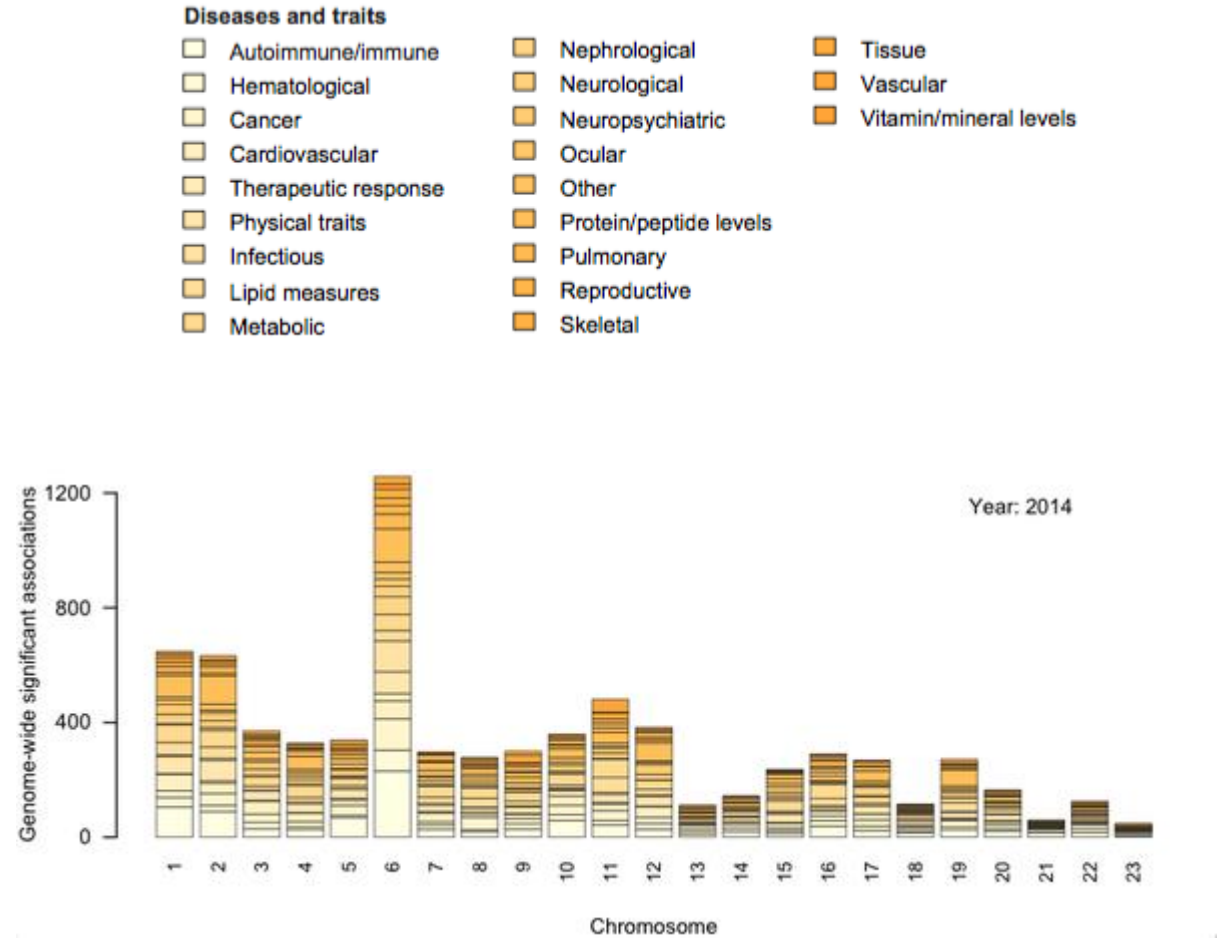
23
Chromosome


350 BC
16th century
17th century
1859
1865
1875
1918
1920s
1953
1980s
90s/00s
2005
2007-2023



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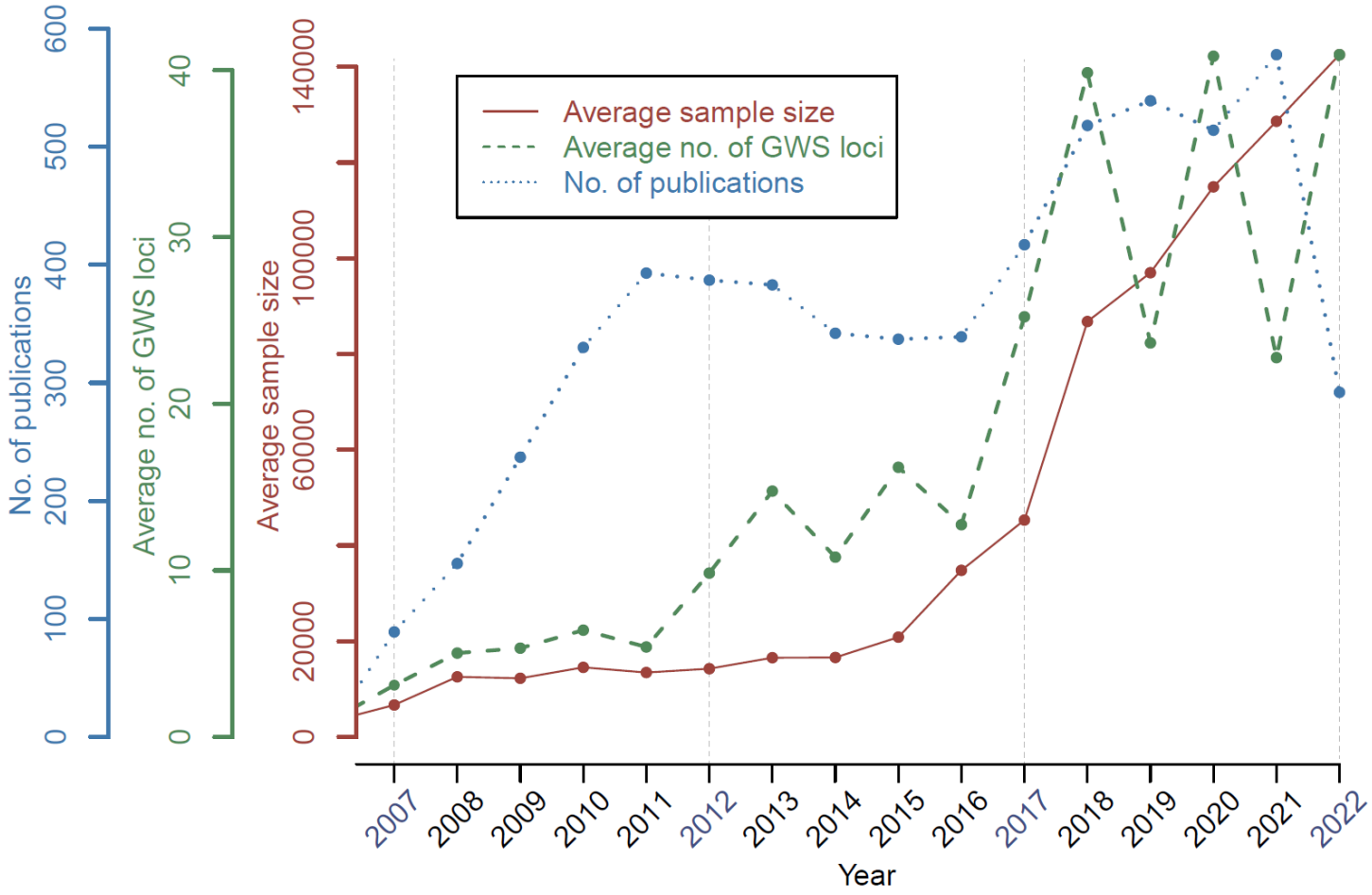


The American Journal of Human Genetics **REVIEW**

15 years of GWAS discovery: Realizing the promise

Abdel Abdellaoui,[1,*] Loic Yengo,[2] Karin J.H. Verweij,[1] and Peter M. Visscher[2]


PGC
Psychiatric Genomics Consortium

2016

PRESS RELEASES / 01.26.16

Genetic study provides first-ever insight into biological origin of schizophrenia

ARTICLE

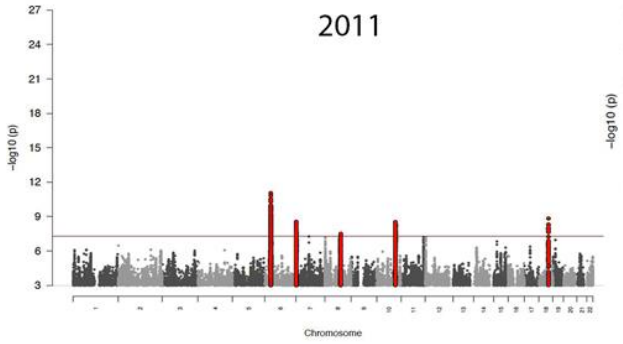
doi:10.1038/nature16549

Schizophrenia risk from complex variation of complement component 4

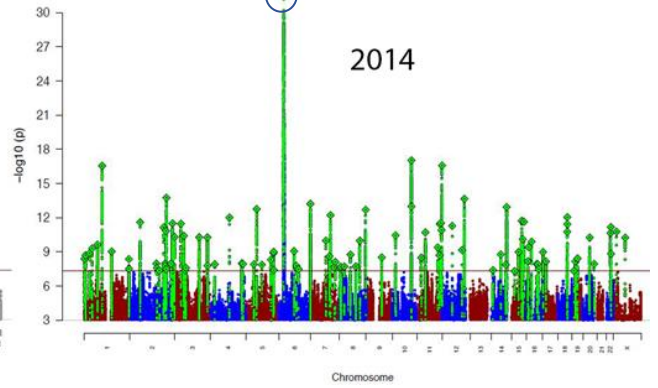
Aswin Sekar[1,2,3], Allison R. Bialas[4,5], Heather de Rivera[1,2], Avery Davis[1,2], Timothy R. Hammond[4], Nolan Kamitaki[1,2], Katherine Tooley[1,2], Jessy Presumey[5], Matthew Baum[1,2,3,4], Vanessa Van Doren[1], Giulio Genovese[1,2], Samuel A. Rose[2], Robert E. Handsaker[1,2], Schizophrenia Working Group of the Psychiatric Genomics Consortium*, Mark J. Daly[2,6], Michael C. Carroll[5], Beth Stevens[2,4] & Steven A. McCarroll[1,2]

Schizophrenia is a heritable brain illness with unknown pathogenic mechanisms. Schizophrenia's strongest genetic association at a population level involves variation in the major histocompatibility complex (MHC) locus, but the genes and molecular mechanisms accounting for this have been challenging to identify. Here we show that this association arises in part from many structurally diverse alleles of the complement component 4 (*C4*) genes. We found that these alleles generated widely varying levels of *C4A* and *C4B* expression in the brain, with each common *C4* allele associating with schizophrenia in proportion to its tendency to generate greater expression of *C4A*. Human C4 protein localized to neuronal synapses, dendrites, axons, and cell bodies. In mice, C4 mediated synapse elimination during postnatal development. These results implicate excessive complement activity in the development of schizophrenia and may help explain the reduced numbers of synapses in the brains of individuals with schizophrenia.

Influences "synaptic pruning" – the elimination of connections between neurons



N ~50,000



N ~150,000

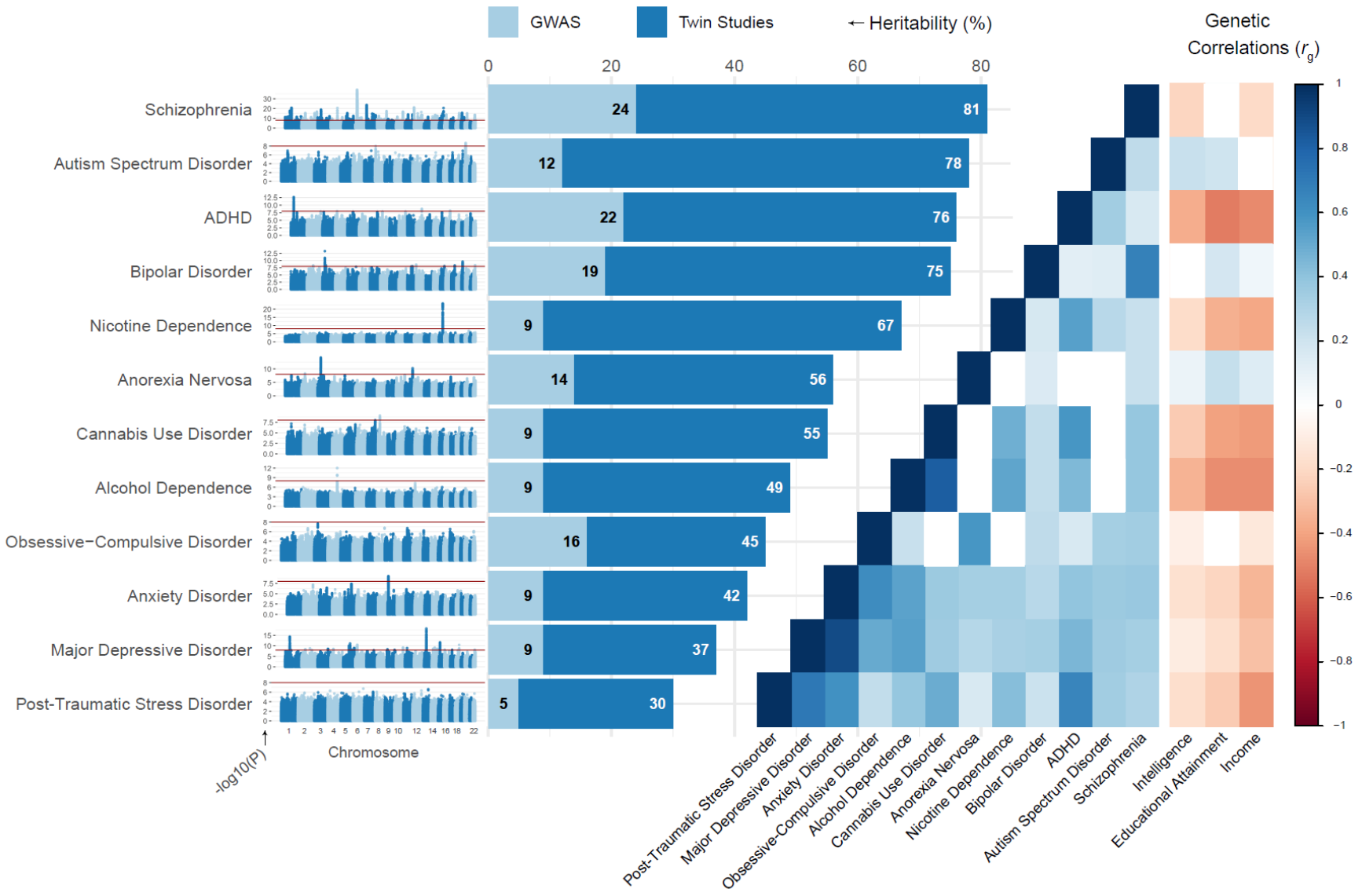
PGC
Psychiatric Genomics Consortium

TIJDSCHRIFT VOOR PSYCHIATRIE - JAARGANG 64 - MEI 2022

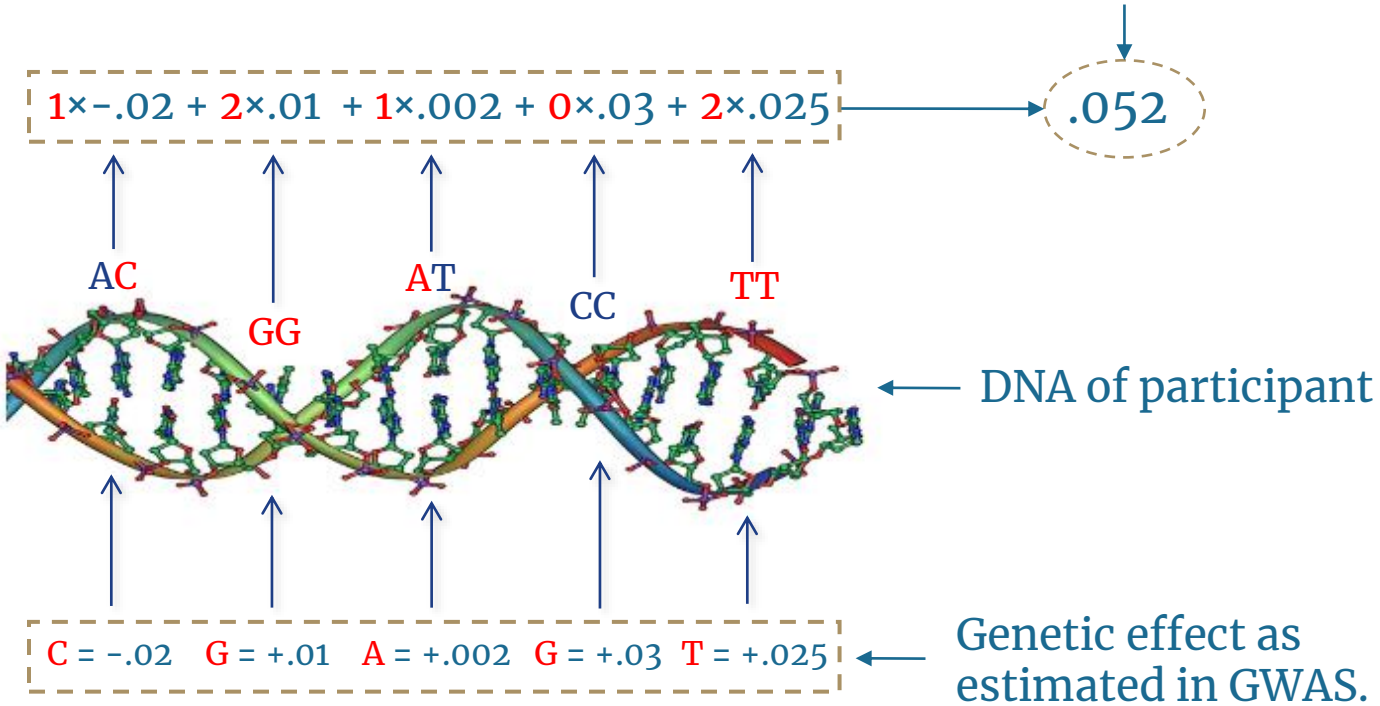
Genetica en psychiatrie

A. Abdellaoui, K.J.H. Verweij

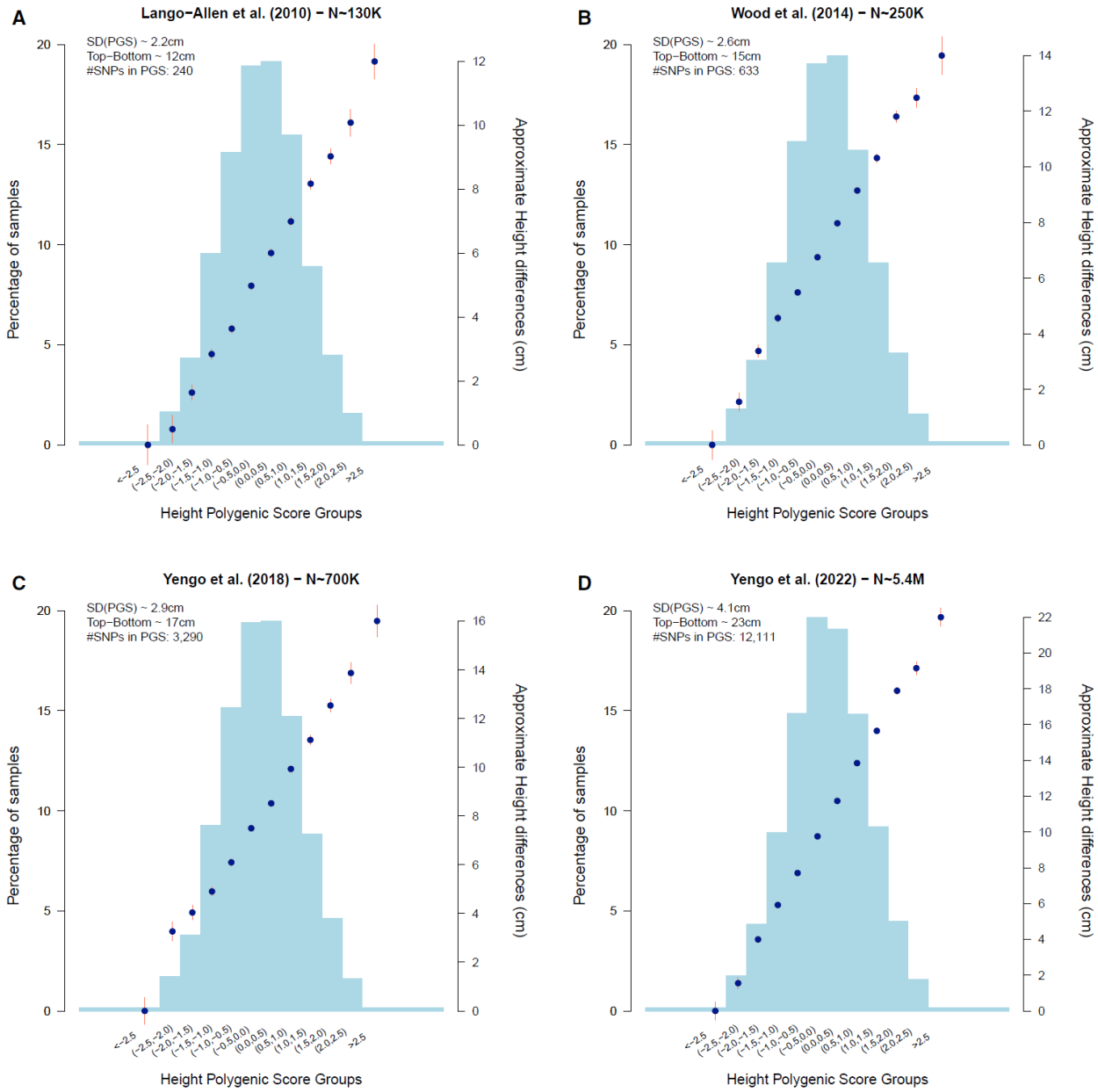
PGC
Psychiatric Genomics Consortium



Polygenic Score / Polygenic Index



Polygenic Score Prediction



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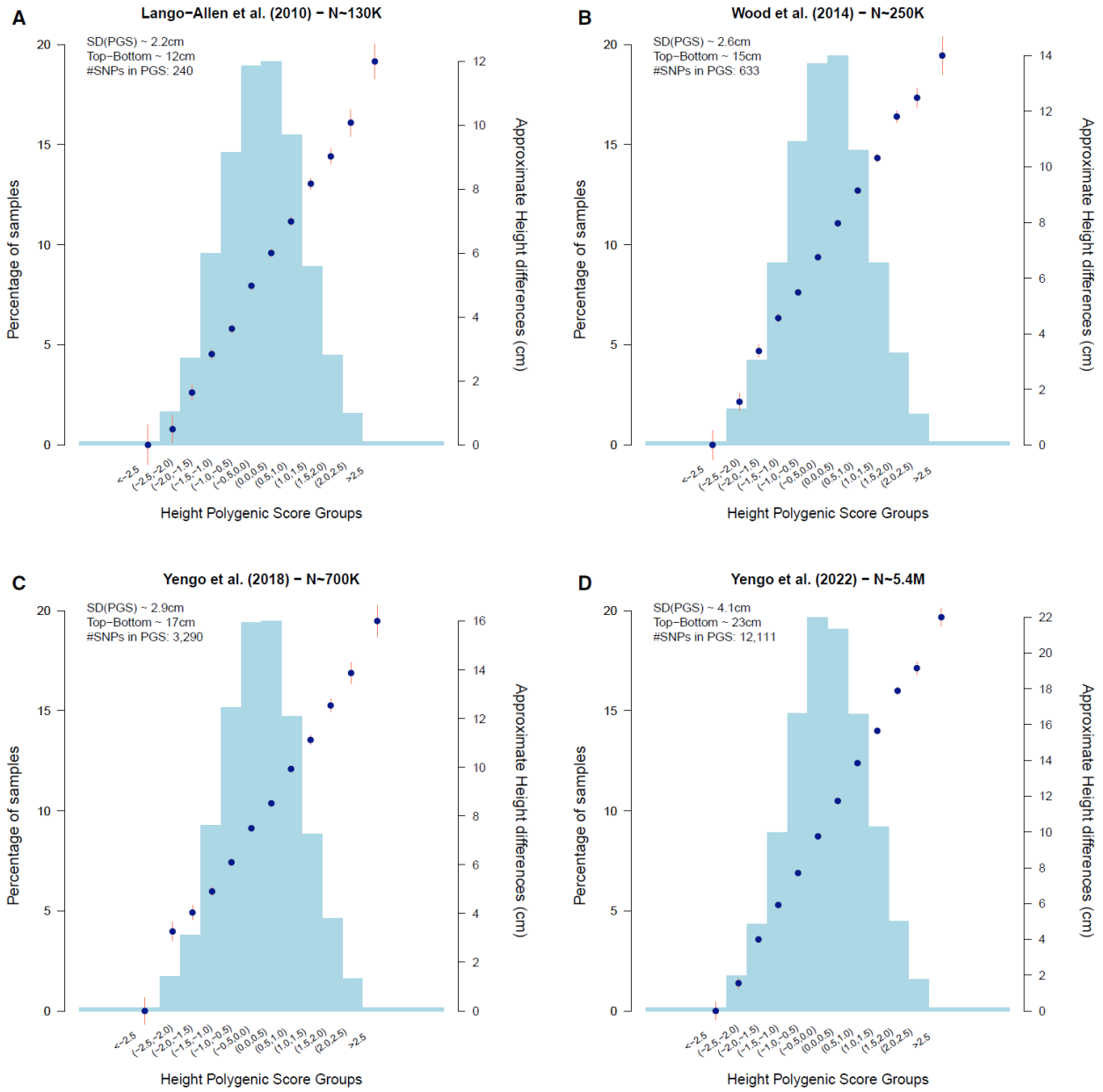
Polygenic Score Prediction

SD of outcome around the prediction:

$$\sigma_Y\sqrt{1-R^2}$$



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SD of outcome around the prediction:

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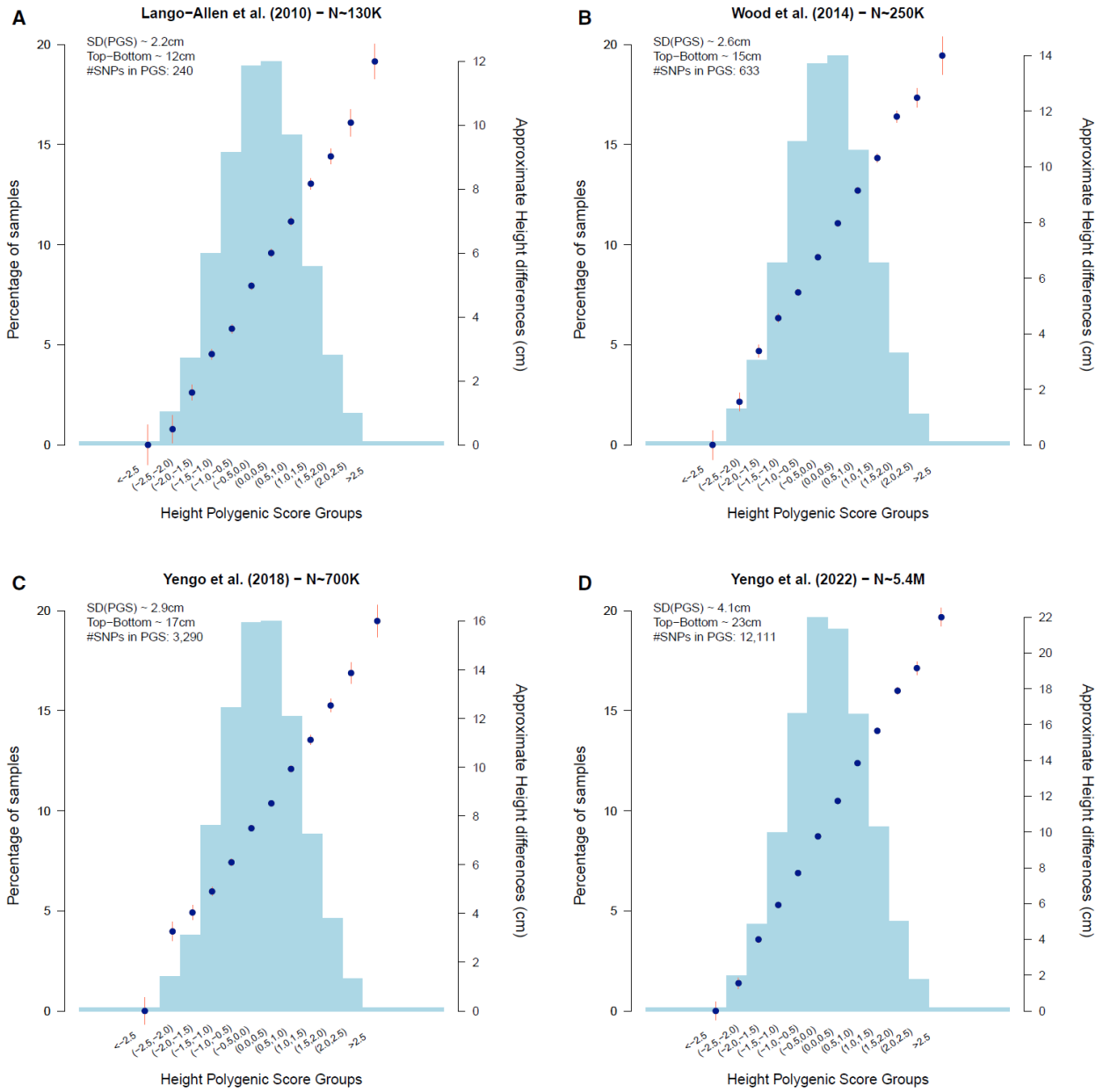
Upper bound (maximum predictive power):

$$\sigma_Y\sqrt{1-h^2}$$



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Polygenic Score Prediction

SD of outcome around the prediction:

$$\sigma_Y\sqrt{1-R^2}$$

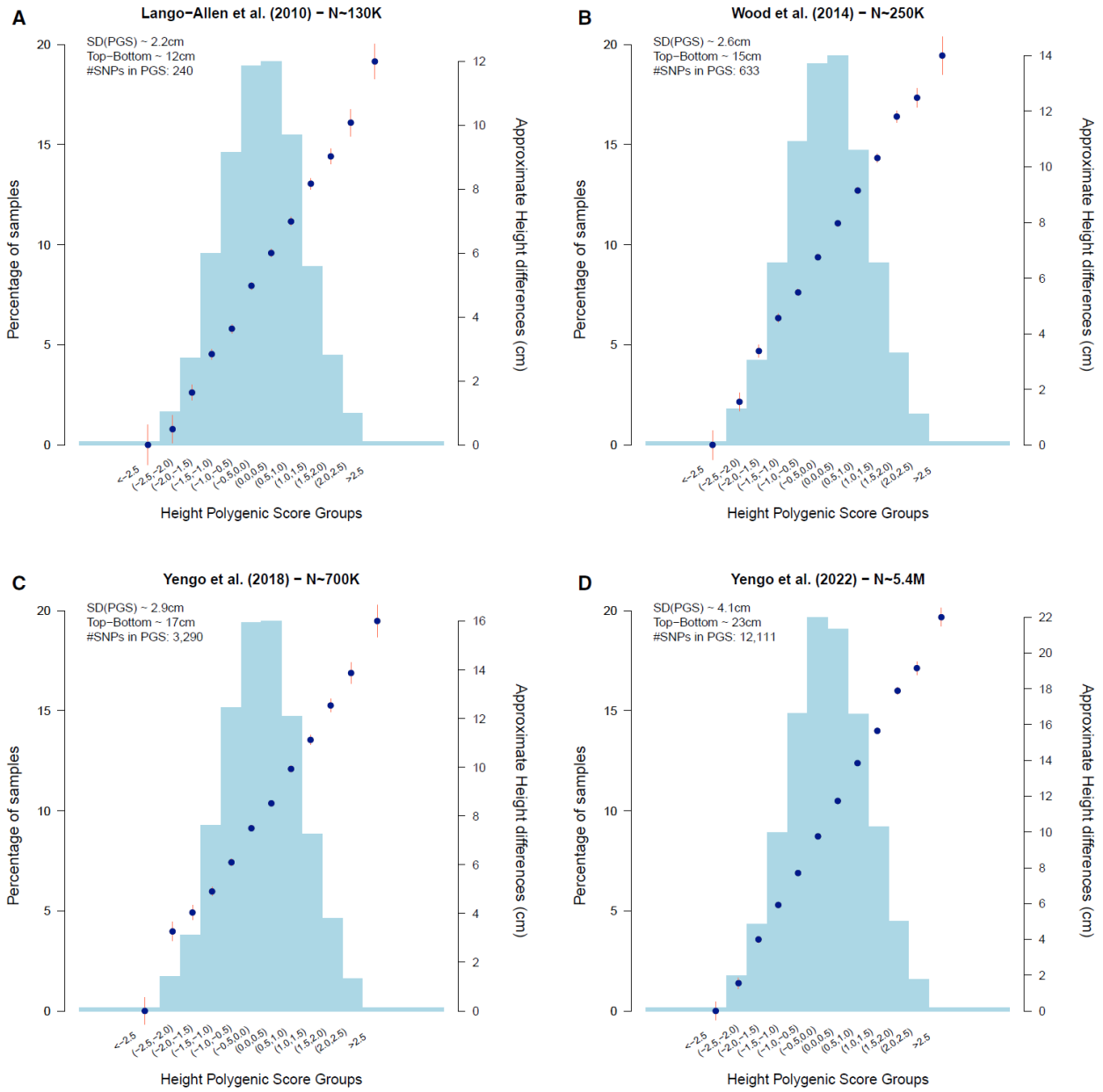
Upper bound (maximum predictive power):

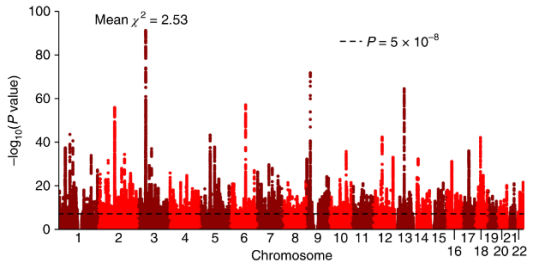
$$\sigma_Y\sqrt{1-h^2}$$

Height has heritability of ~0.8 and standard deviation of ~6.5 cm

$$6.5cm \times \sqrt{1-0.8} \approx 3cm$$

Equivalent to 95% confidence interval of ~**12cm**

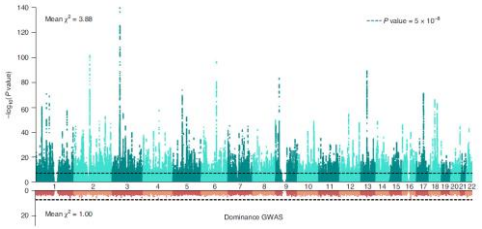




ARTICLES
https://doi.org/10.1038/s41588-018-0147-3
nature genetics

Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals

2018 – N = 1,131,881

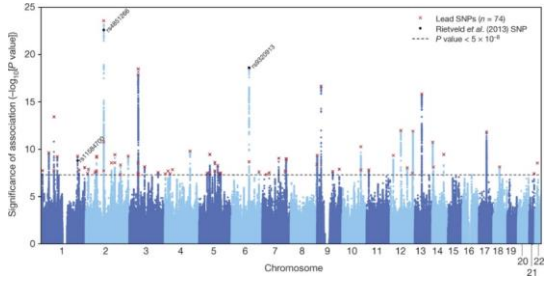


nature genetics
ARTICLES
https://doi.org/10.1038/s41588-022-01016-z
Check for updates

OPEN

Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals

2022 – N = 3,037,499

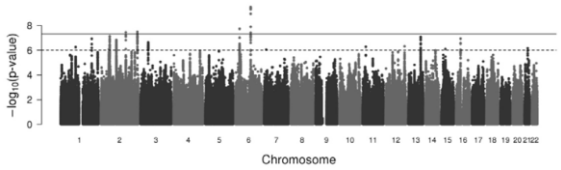


LETTER
doi:10.1038/nature17671

Genome-wide association study identifies 74 loci associated with educational attainment

26 MAY 2016 | VOL 533 | NATURE

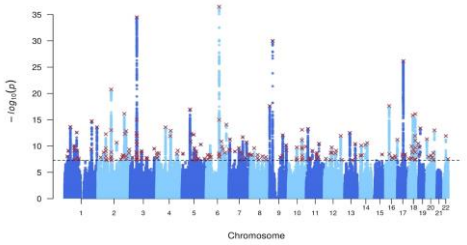
2016 – N = 293,723



SCIENCE VOL 340 21 JUNE 2013

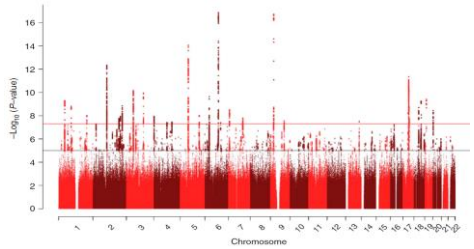
GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment

2013 – N = 126,559



2023 – N = 668,288

Manuscript in preparation…



2019 – N = 286,301

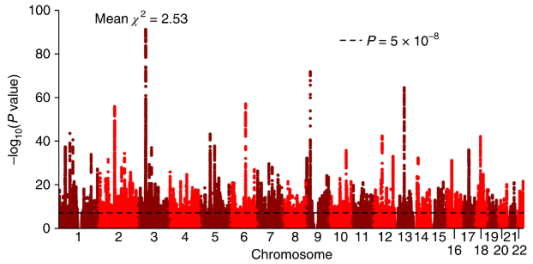
nature COMMUNICATIONS

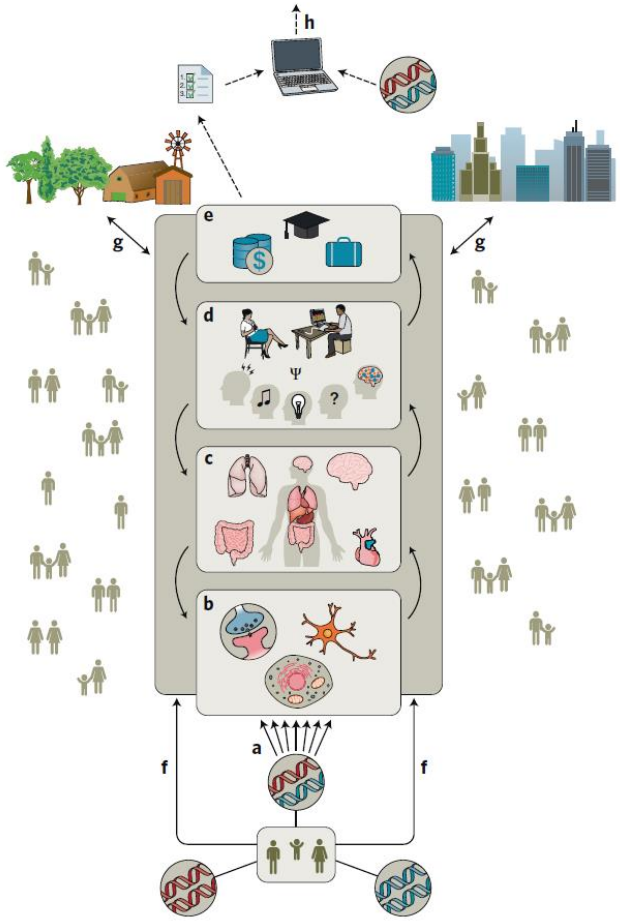
ARTICLE
https://doi.org/10.1038/s41467-019-13585-5 OPEN

Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income

Educational Attainment

Income



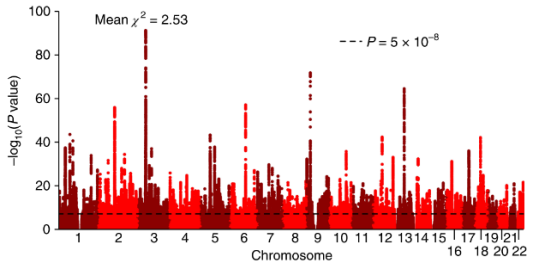


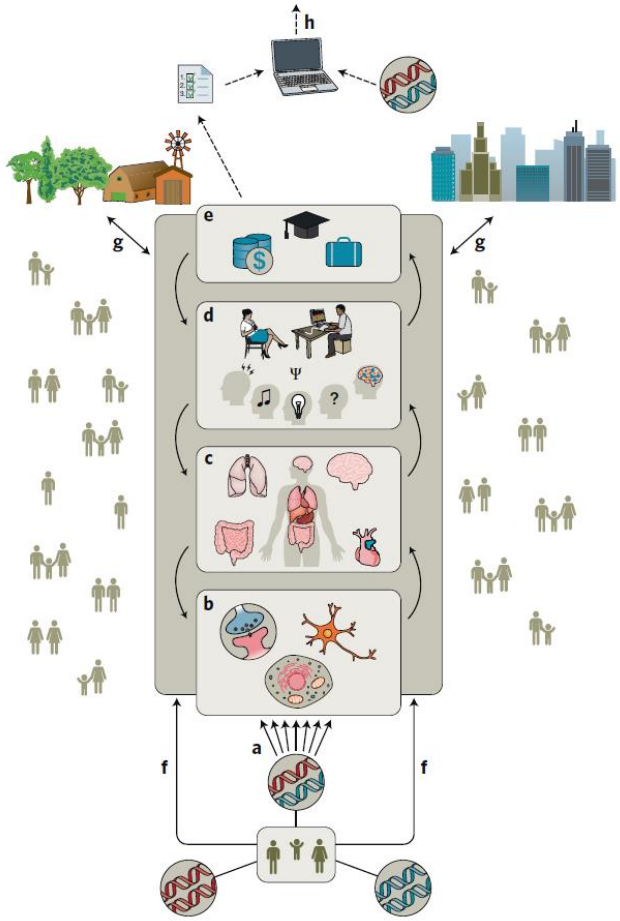
GWASs on behavioural traits contain signals from **correlated traits** and the **environment**

nature human behaviour
REVIEW ARTICLE
https://doi.org/10.1038/s41562-021-01110-y
Check for updates

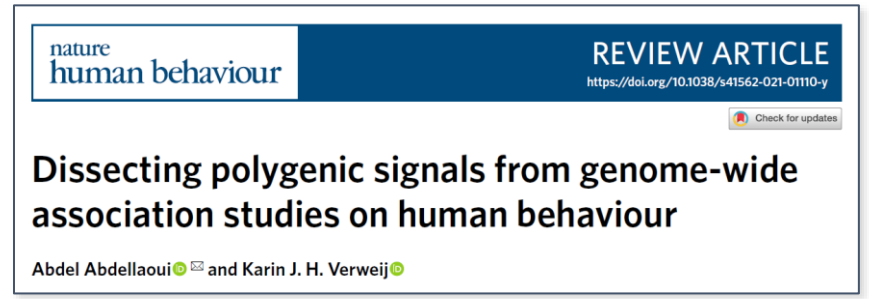
Dissecting polygenic signals from genome-wide association studies on human behaviour

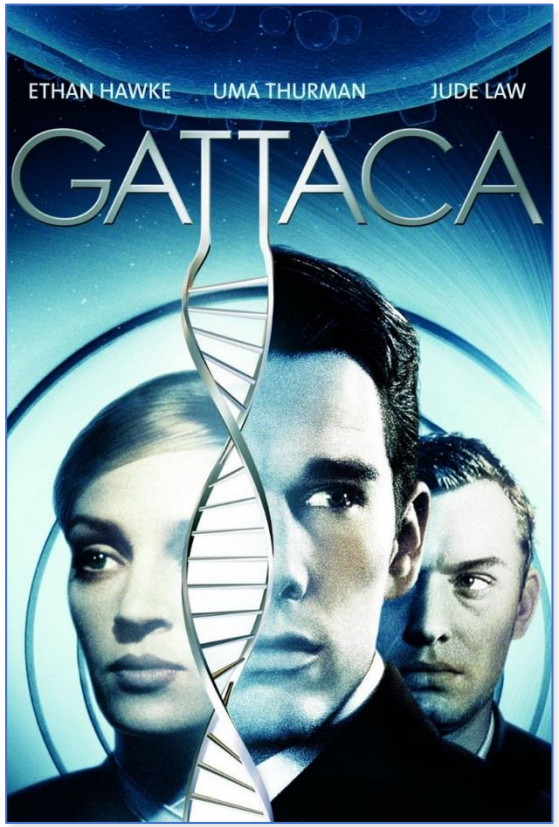
Abdel Abdellaoui and Karin J. H. Verweij

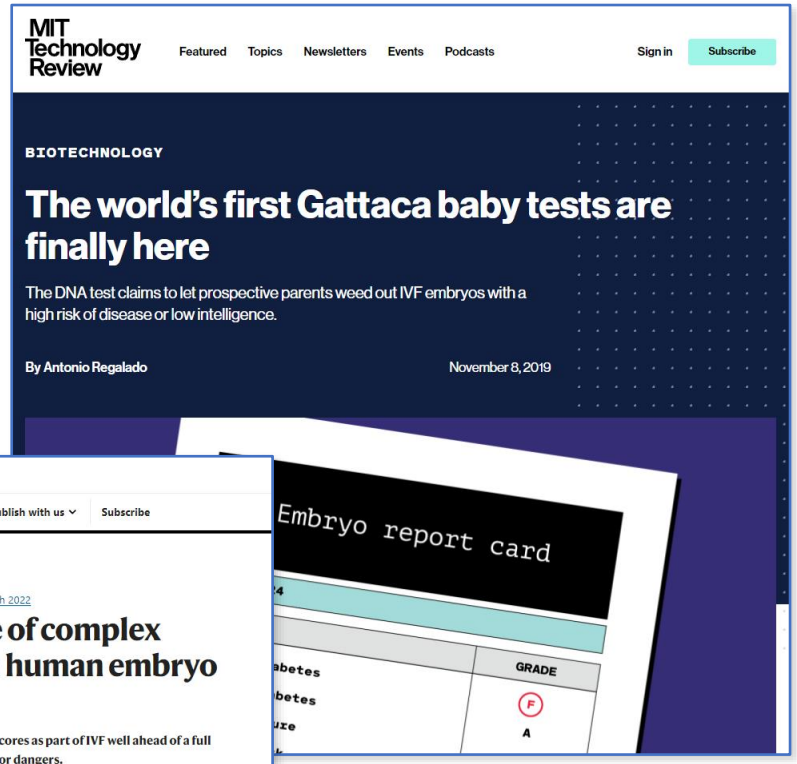




"When the nature of the predictive ability of polygenic scores for behavioural traits is not fully understood, applying them in either scientific research or the clinic can lead to incorrect interpretations and conclusions."




ETHAN HAWKE
UMA THURMAN
JUDE LAW
GATTACA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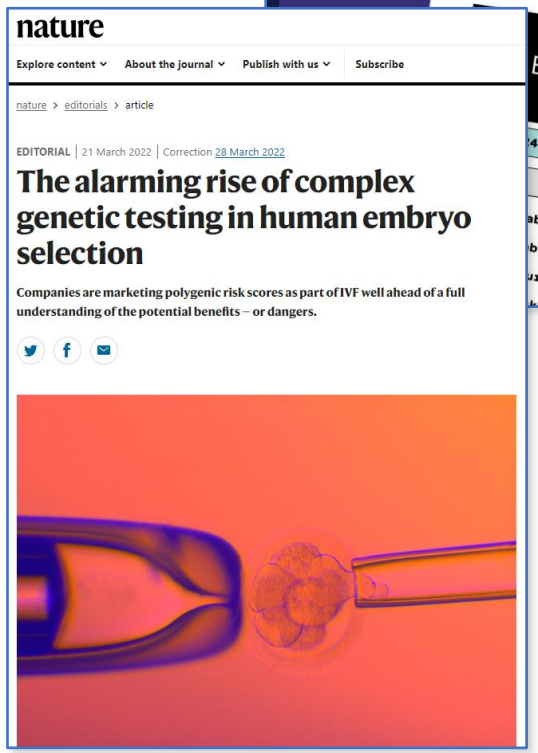
The world's first Gattaca baby tests are finally here
The DNA test claims to let prospective parents weed out IVF embryos with a high risk of disease or low intelligence.
By Antonio Regalado
November 8, 2019
Embryo report card
GRADE
F
A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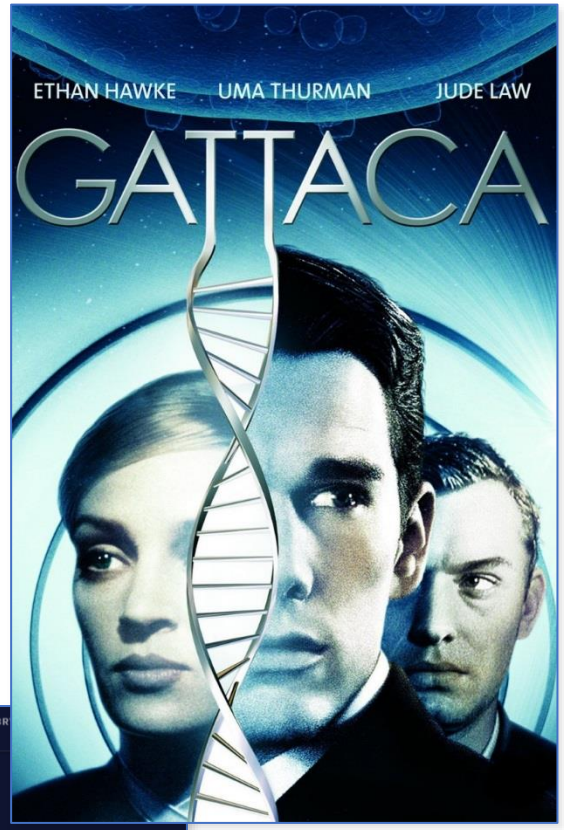
EDITORIAL | 21 March 2022 | Correction 28 March 2022
The alarming rise of complex genetic testing in human embryo selection
Companies are marketing polygenic risk scores as part of IVF well ahead of a full understanding of the potential benefits – or dangers.


ETHAN HAWKE
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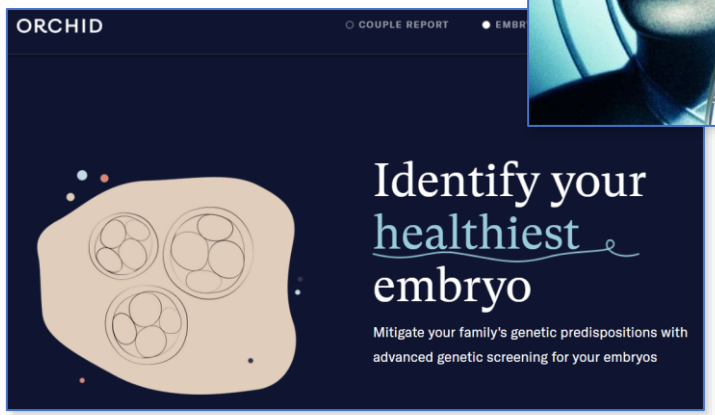
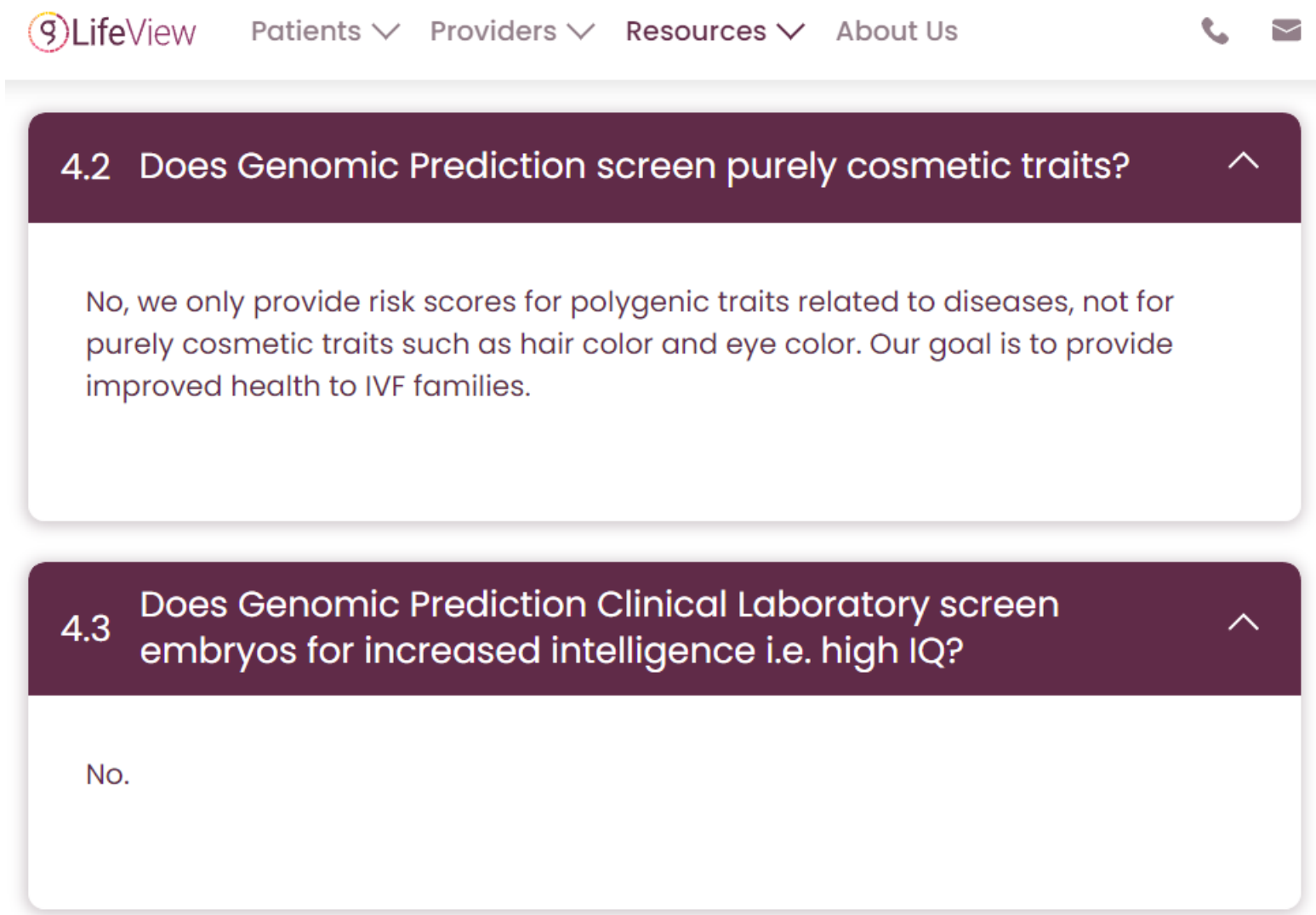
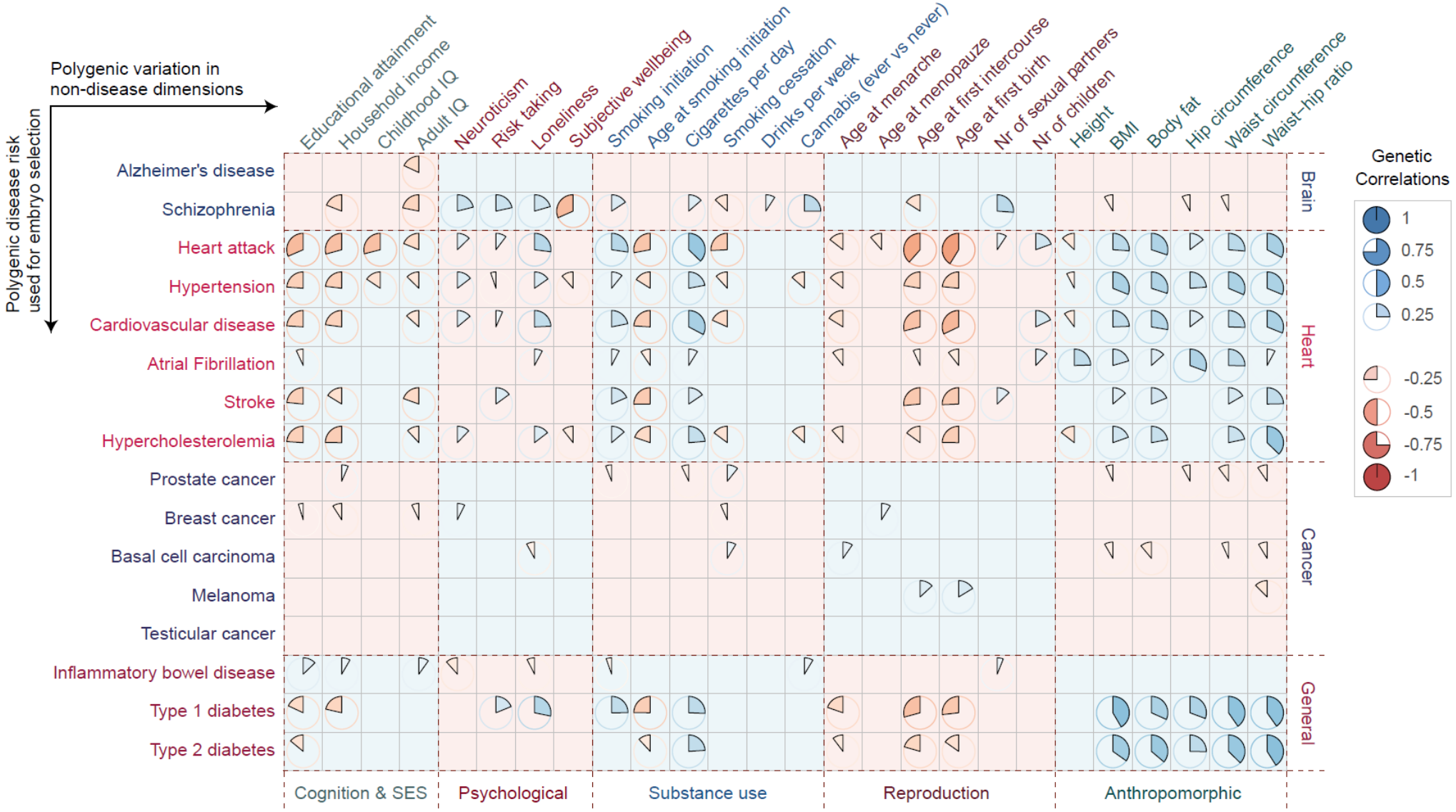
GATTACA


ORCHID
COUPLE REPORT
Identify your healthiest embryo
Mitigate your family's genetic predispositions with advanced genetic screening for your embryos

WIRED **Genetic Screening Now Lets Parents Pick the Healthiest Embryos**

AT 18 MONTHS old, Aurea Yenmai Smigrodzki is inquisitive like any other toddler. She likes peanut butter, the beach, and mobile phones—or any toys that look like phones. She likes to copy her mum and dad, Thuy and Rafal, when they are using theirs. Aurea doesn't know it yet, but her birth was very special: She is the world's first PGT-P baby, meaning she is statistically less likely than the rest of us to develop a genetic disease or disorder throughout her life.


LifeView
Patients
Providers
Resources
About Us
4.2 Does Genomic Prediction screen purely cosmetic traits?
No, we only provide risk scores for polygenic traits related to diseases, not for purely cosmetic traits such as hair color and eye color. Our goal is to provide improved health to IVF families.
4.3 Does Genomic Prediction Clinical Laboratory screen embryos for increased intelligence i.e. high IQ?
No.



Unpublished results

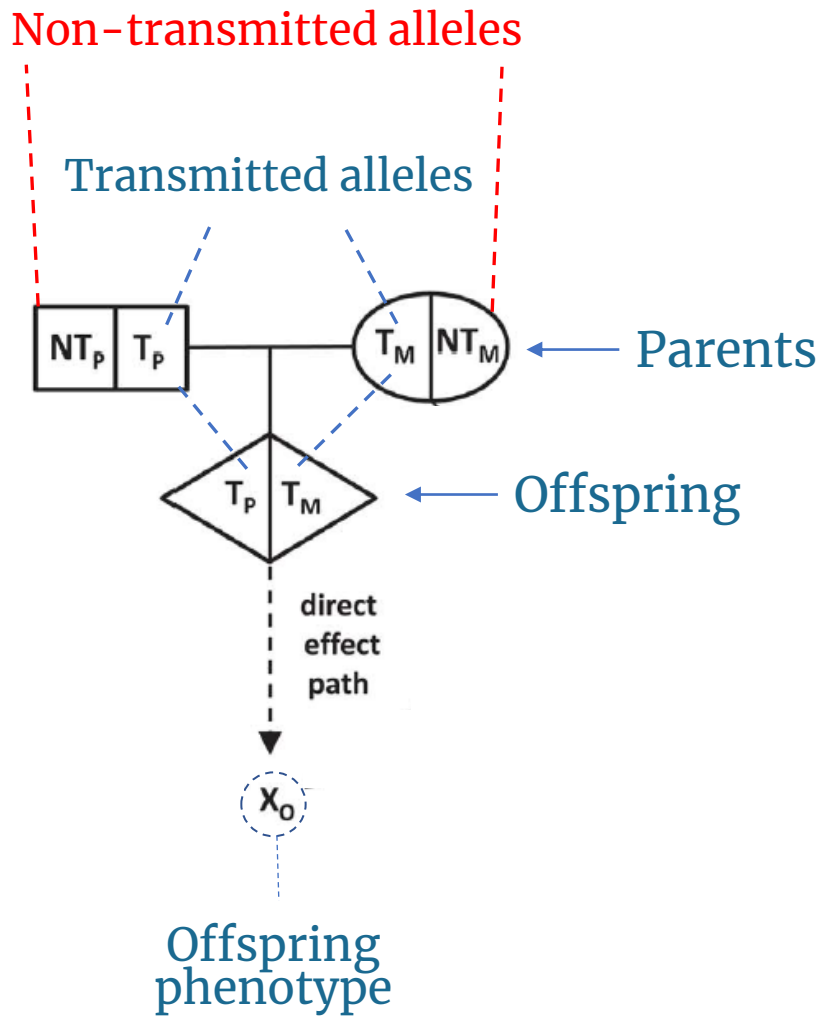
Gene-Environment Correlations - Families

Science **359**, 424–428 (2018)

HUMAN GENOMICS

The nature of nurture: Effects of parental genotypes

Augustine Kong,[1,2,3]* Gudmar Thorleifsson,[1] Michael L. Frigge,[1] Bjarni J. Vilhjalmsson,[4,5] Alexander I. Young,[1,2,6] Thorgeir E. Thorgeirsson,[1] Stefania Benonisdottir,[1] Asmundur Oddsson,[1] Bjarni V. Halldorsson,[1] Gisli Masson,[1] Daniel F. Gudbjartsson,[1,3] Agnar Helgason,[1,7] Gyda Bjornsdottir,[1] Unnur Thorsteinsdottir,[1,8] Kari Stefansson[1,8]*



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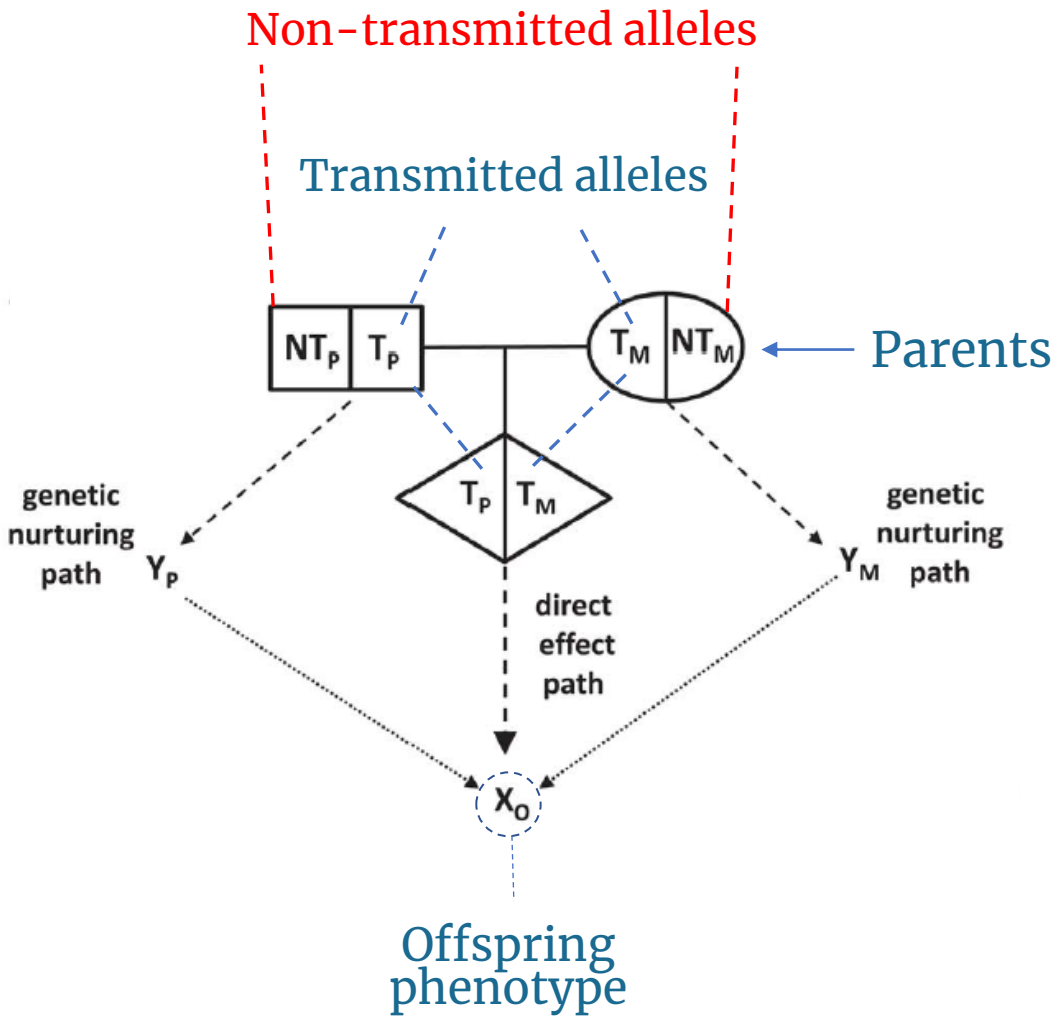

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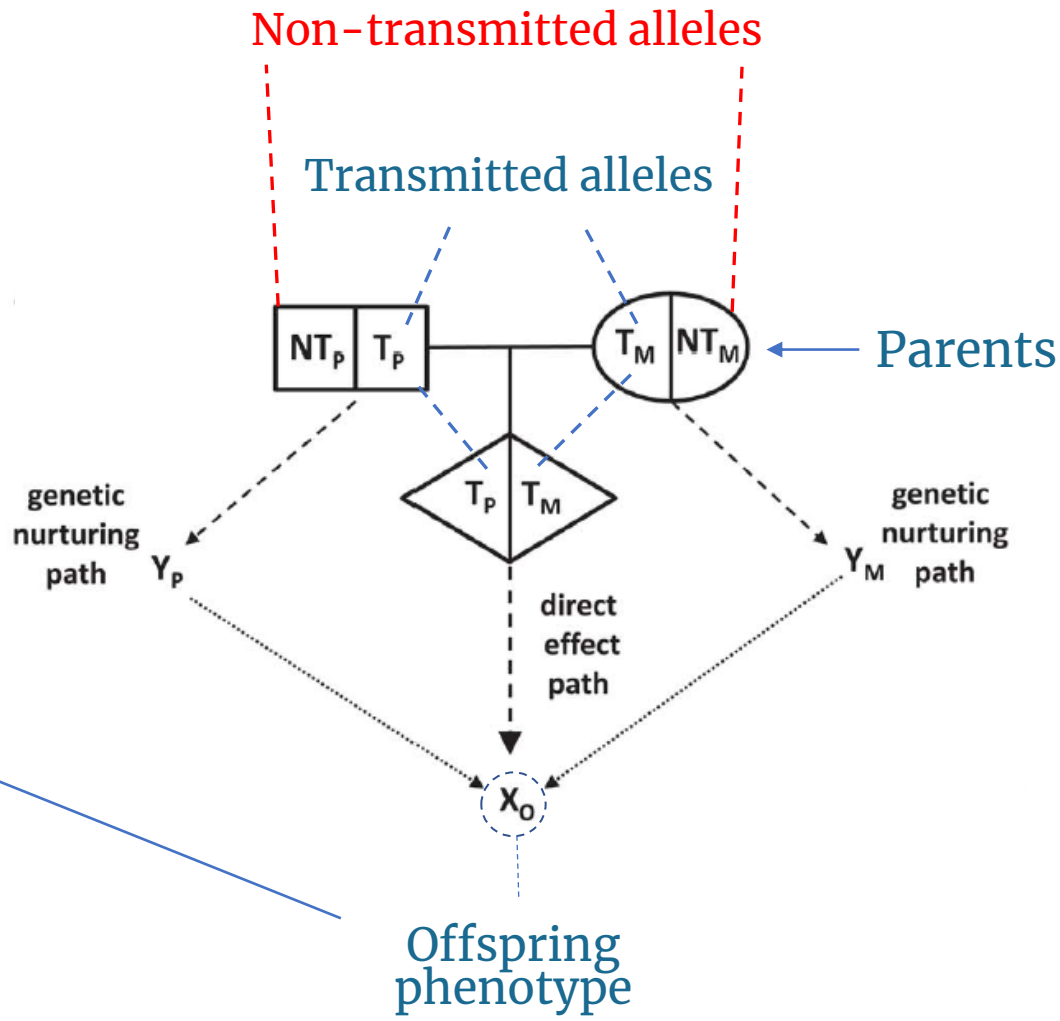
Non-transmitted educational attainment alleles are associated with:

- Educational attainment
- Age at first child
- High-density lipoprotein (HDL)
- BMI
- Fasting glucose level
- Height
- Cigarettes per day
- Overall health



Research Article

Comparison of Adopted and Nonadopted Individuals Reveals Gene–Environment Interplay for Education in the UK Biobank

Rosa Cheesman[1], Avina Hunjan[1,2], Jonathan R. I. Coleman[1,2], Yasmin Ahmadzadeh[1], Robert Plomin[1], Tom A. McAdams[1], Thalia C. Eley[1,2], and Gerome Breen[1,2]

Psychological Science
2020, Vol. 31(5) 582–591

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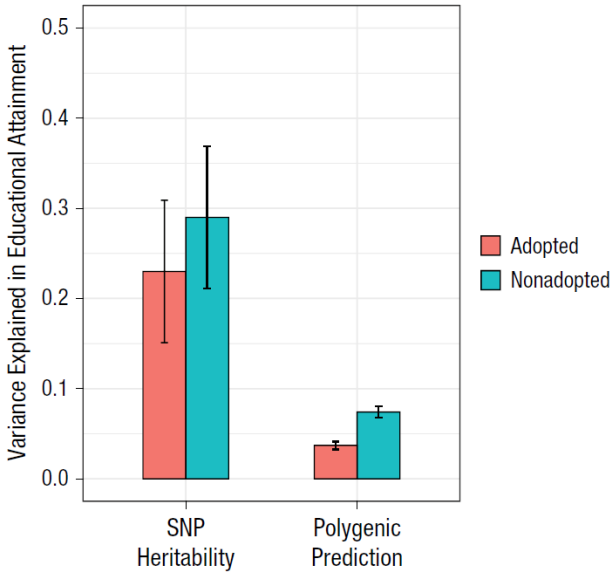
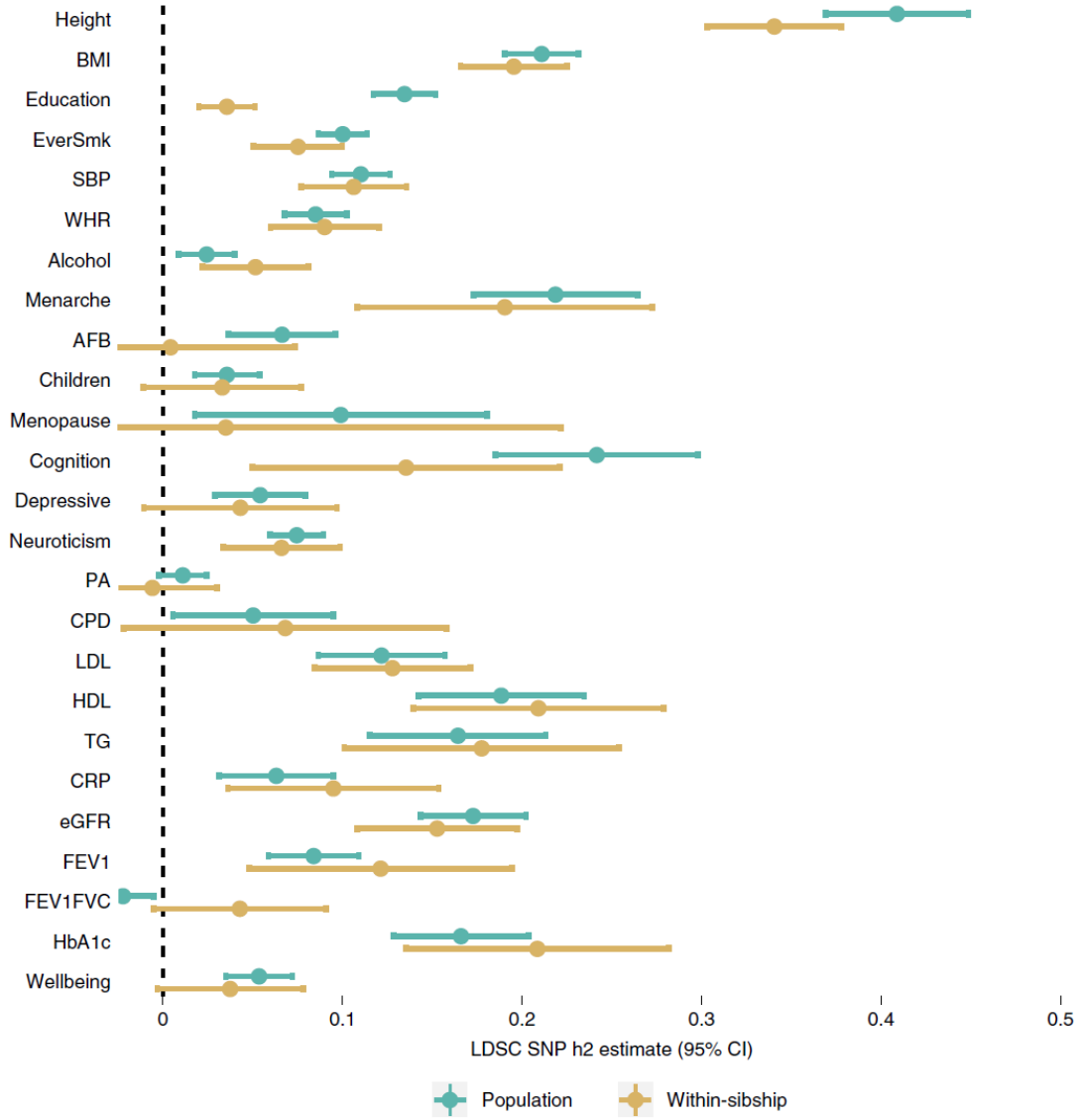
DOI: 10.1177/0956797620904450
www.psychologicalscience.org/PS



nature genetics
ARTICLES
https://doi.org/10.1038/s41588-022-01062-7
Check for updates

OPEN

Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects



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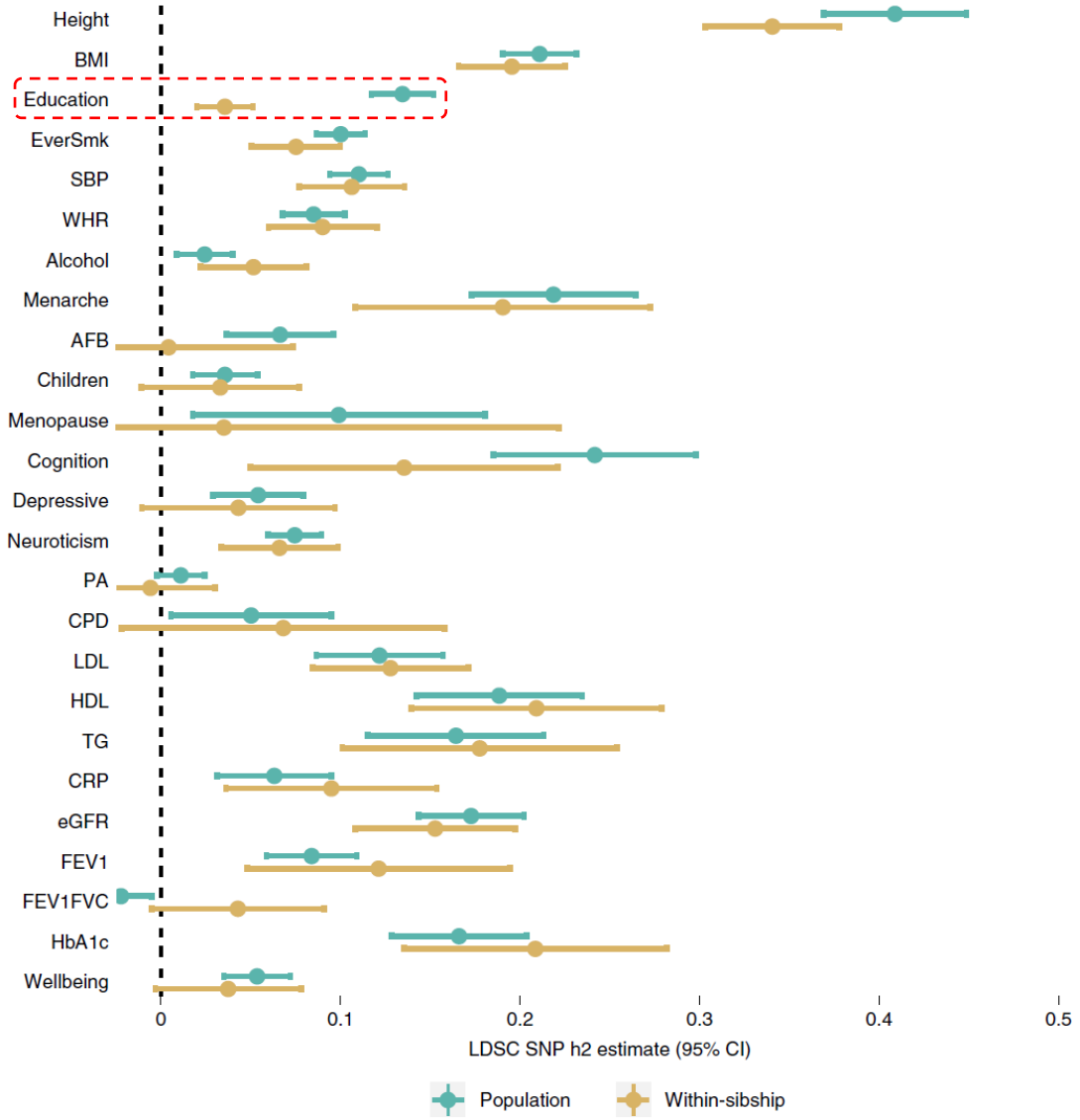

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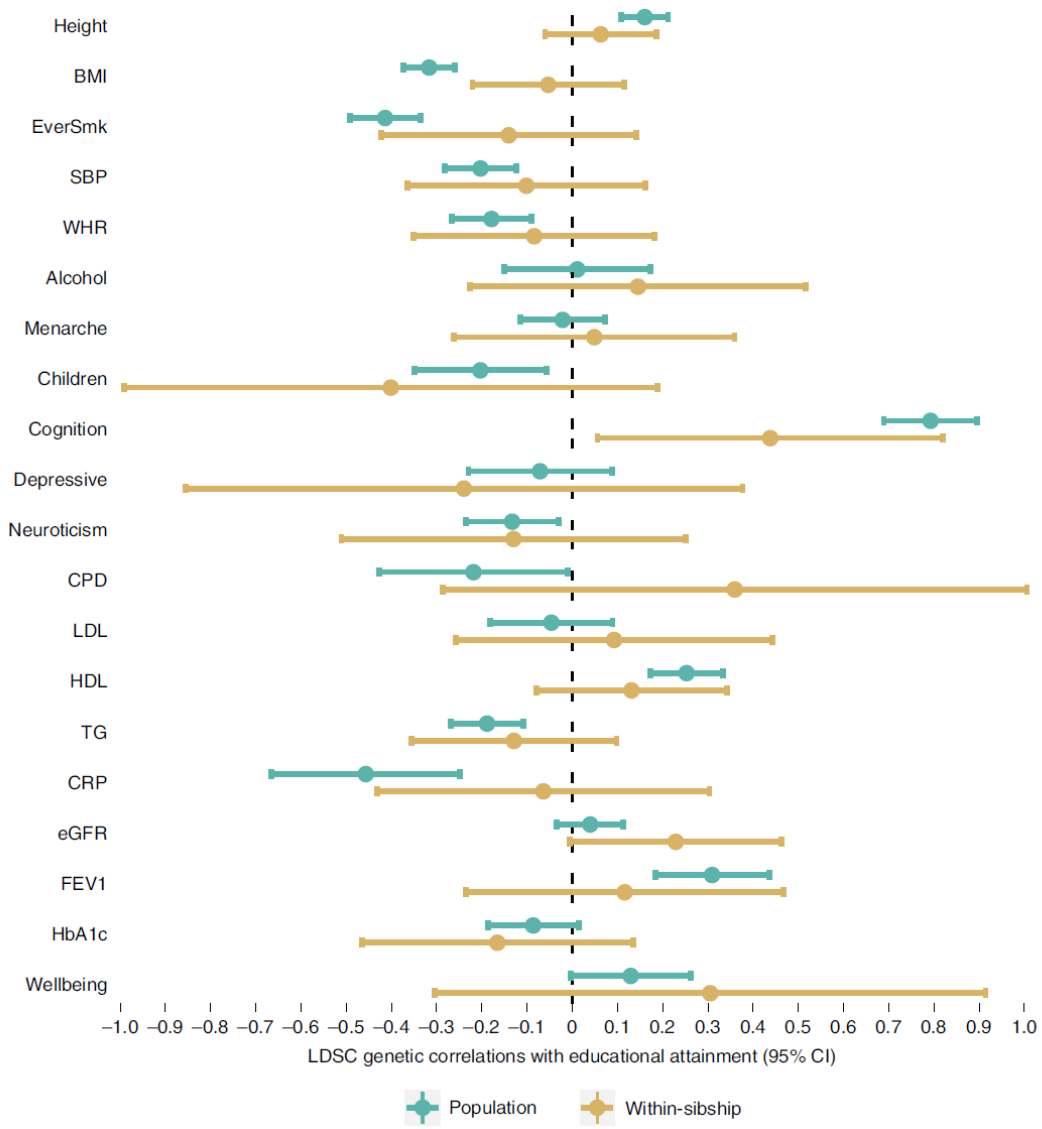

Gene-Environment Correlations - Geographic

Geography & Polygenic Scores

ARTICLES
https://doi.org/10.1038/s41562-019-0757-5
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Genetic correlates of social stratification in Great Britain

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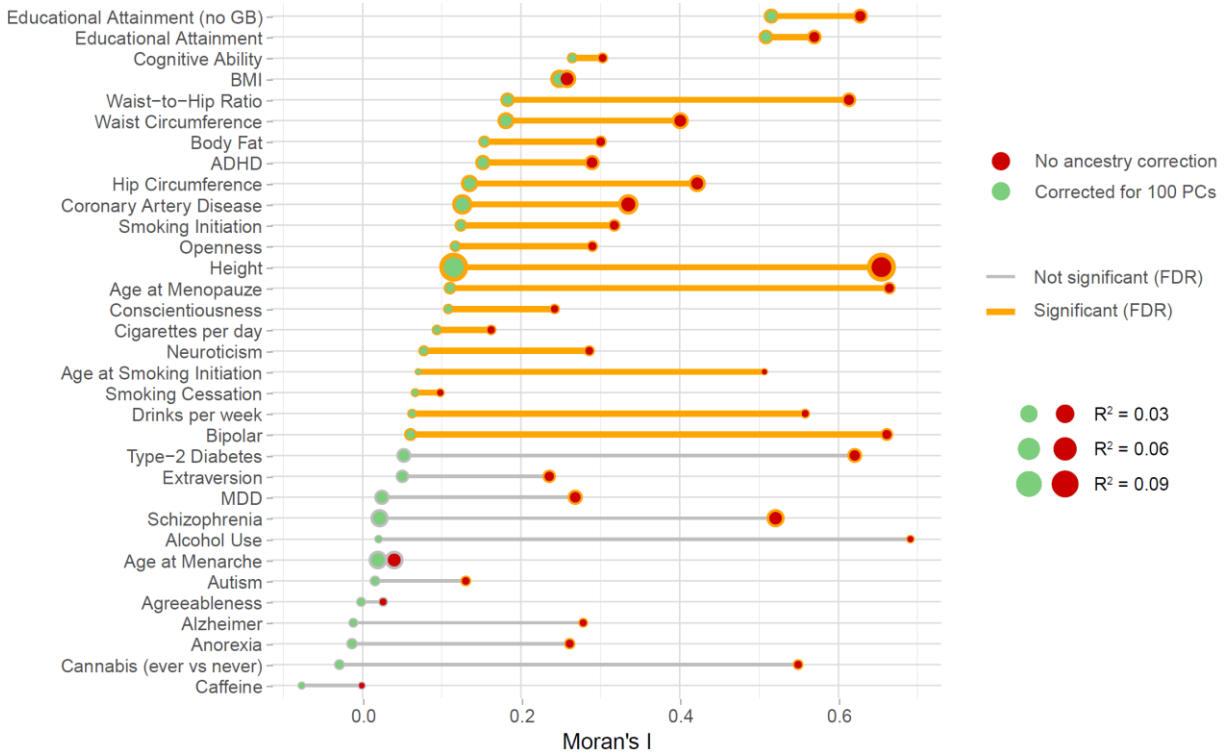

Moran's I = measure for geographic clustering

Geography & Polygenic Scores

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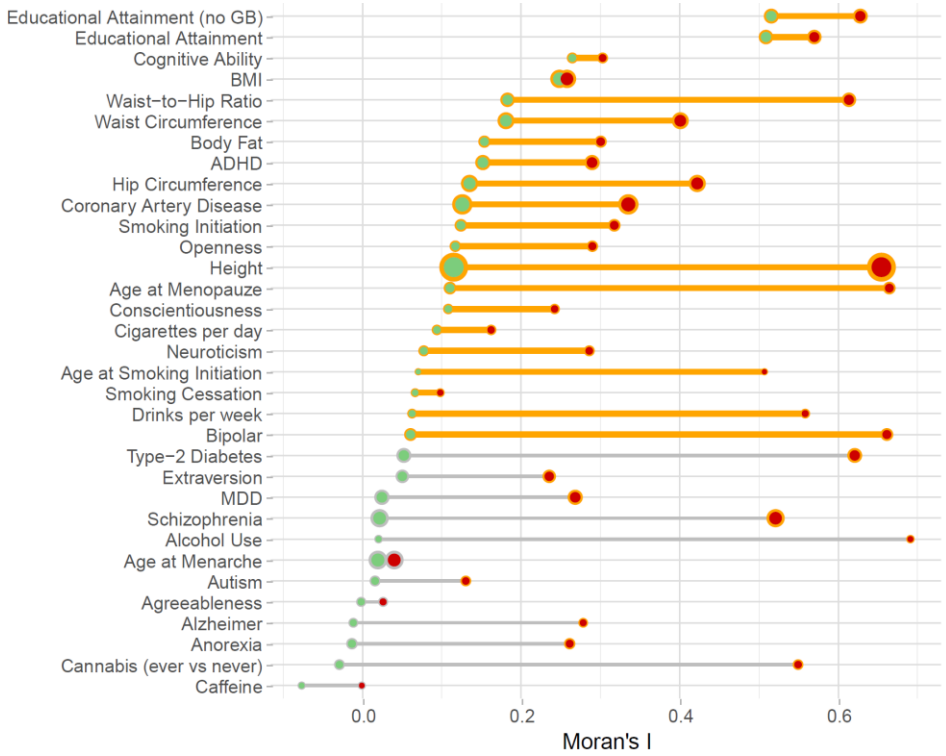

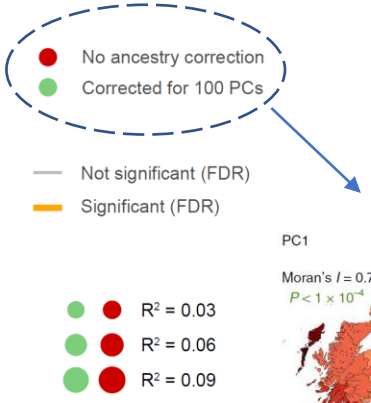

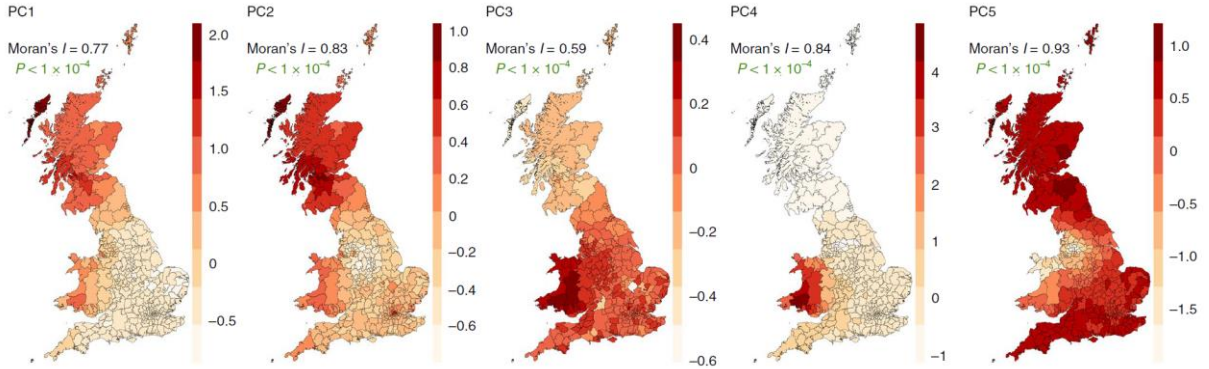

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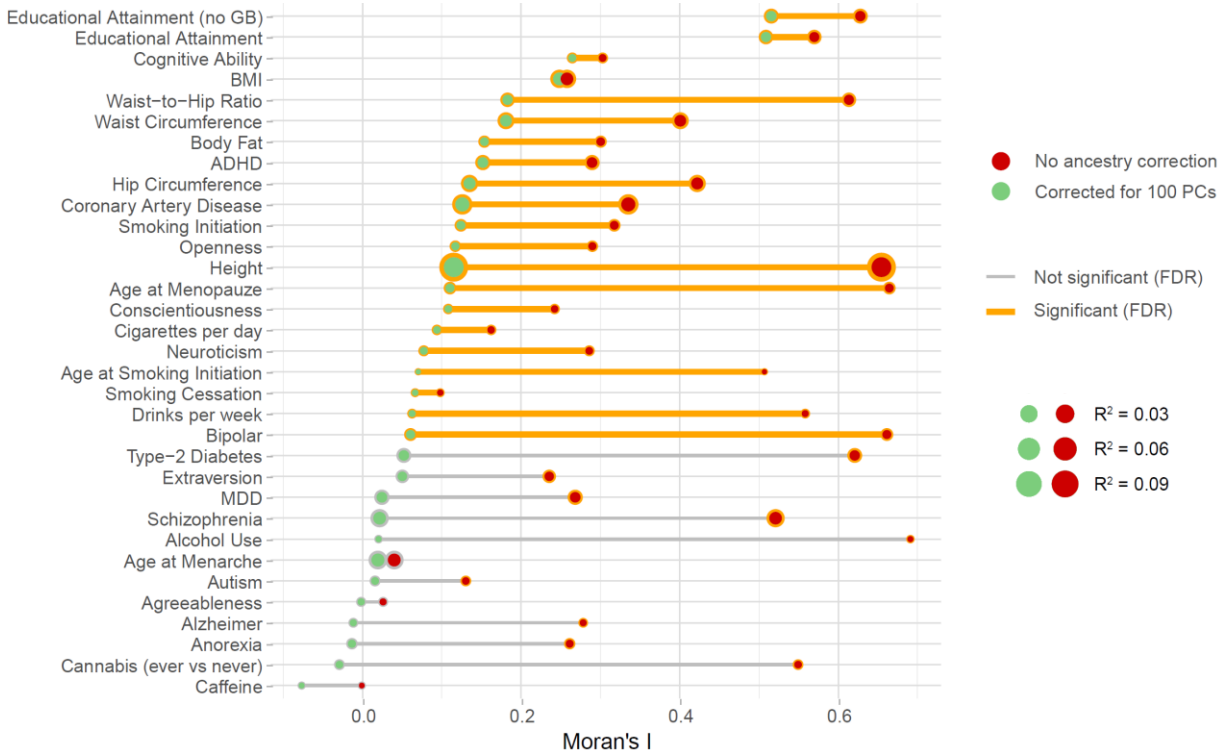

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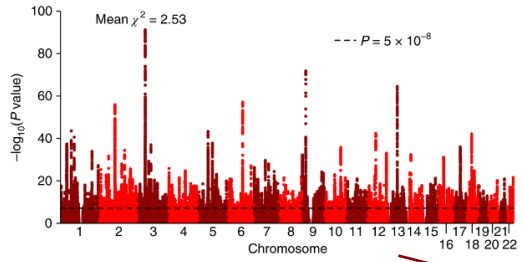
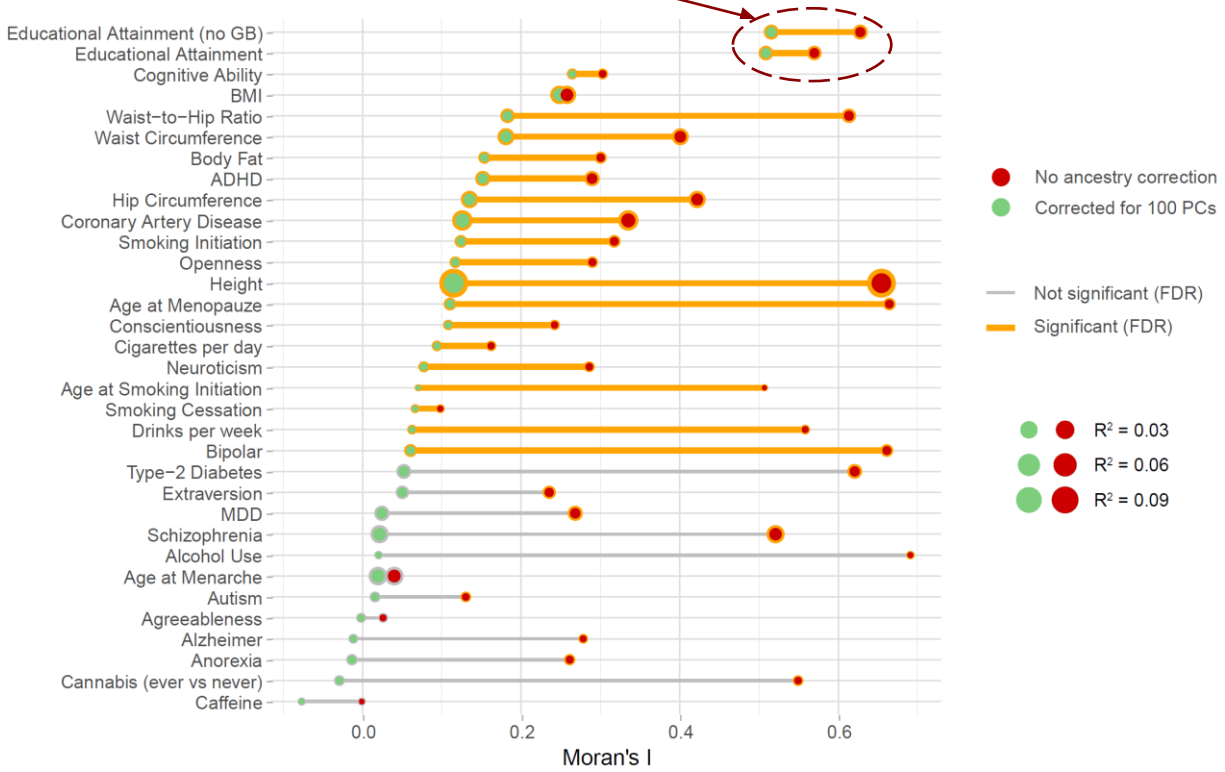
Geography & Polygenic Scores





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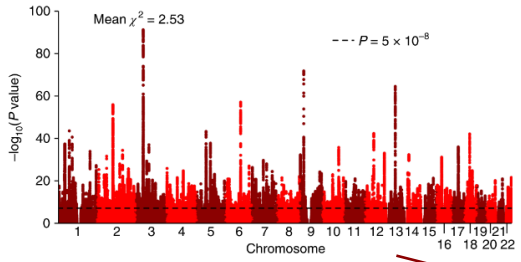

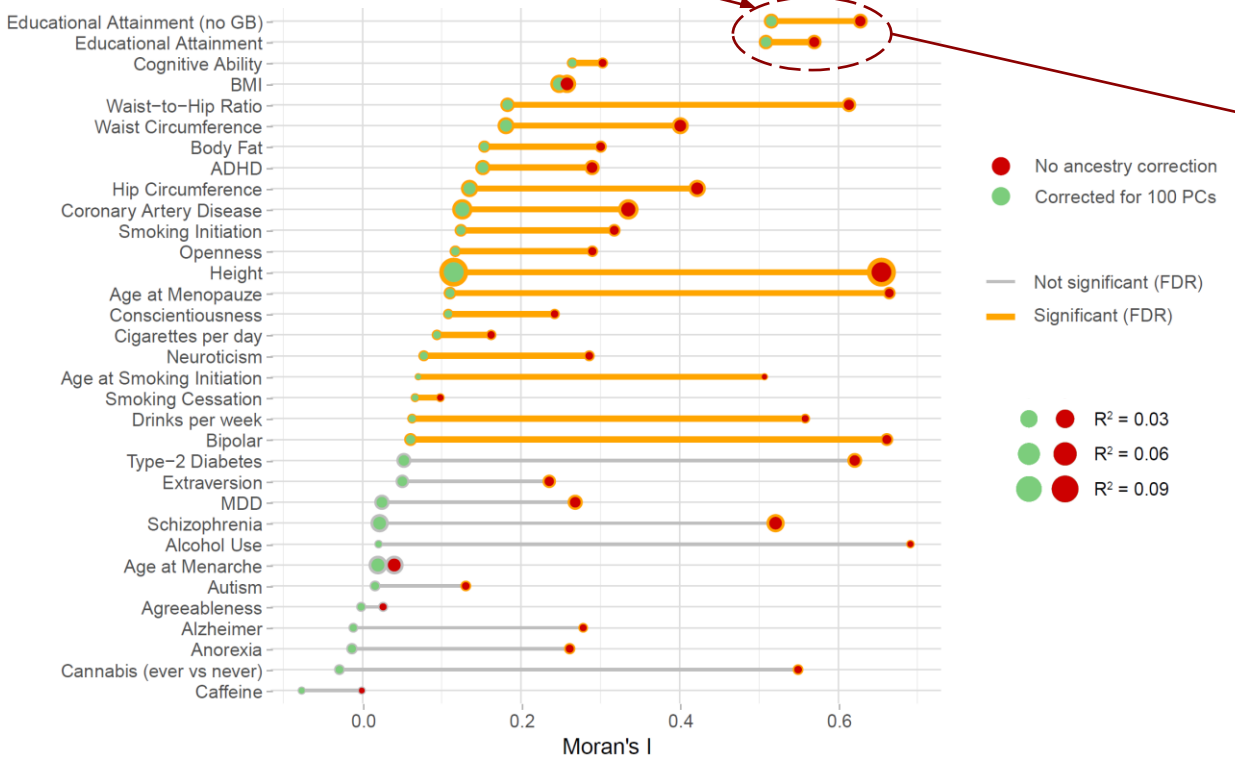

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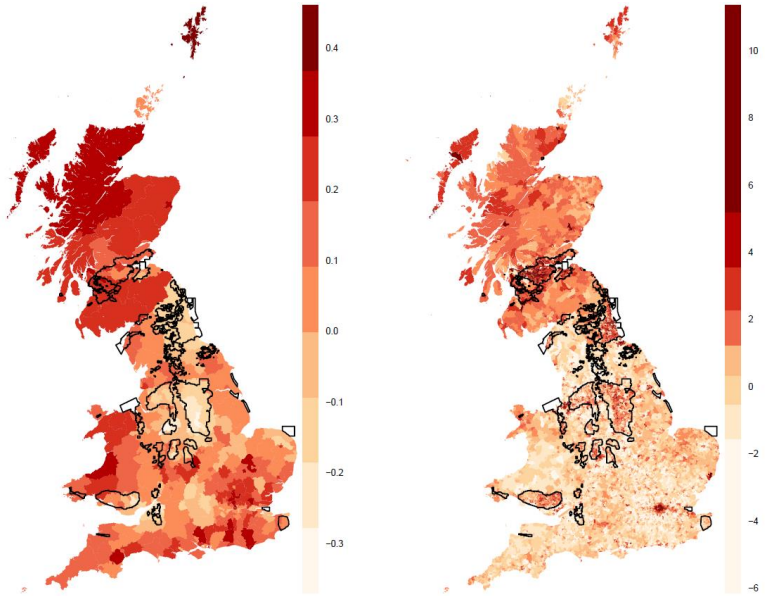
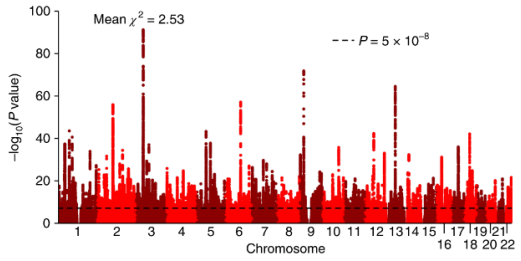


Educational Attainment Polygenic Score

Townsend Index (measure of economic deprivation)

black lines = coal regions

Migration & SES



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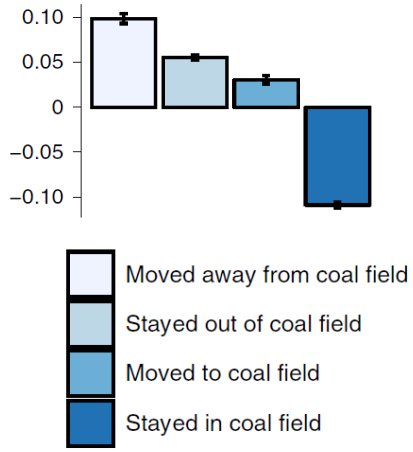

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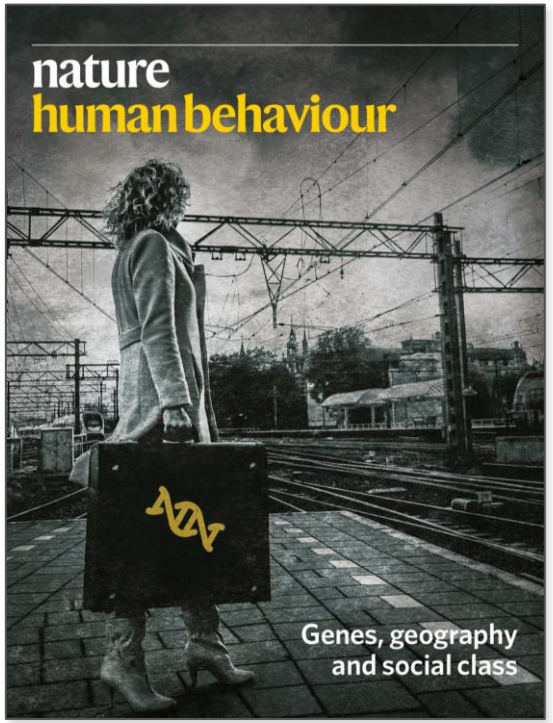
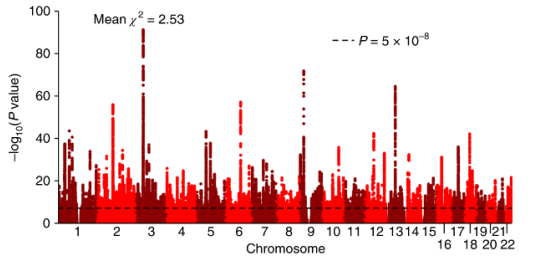
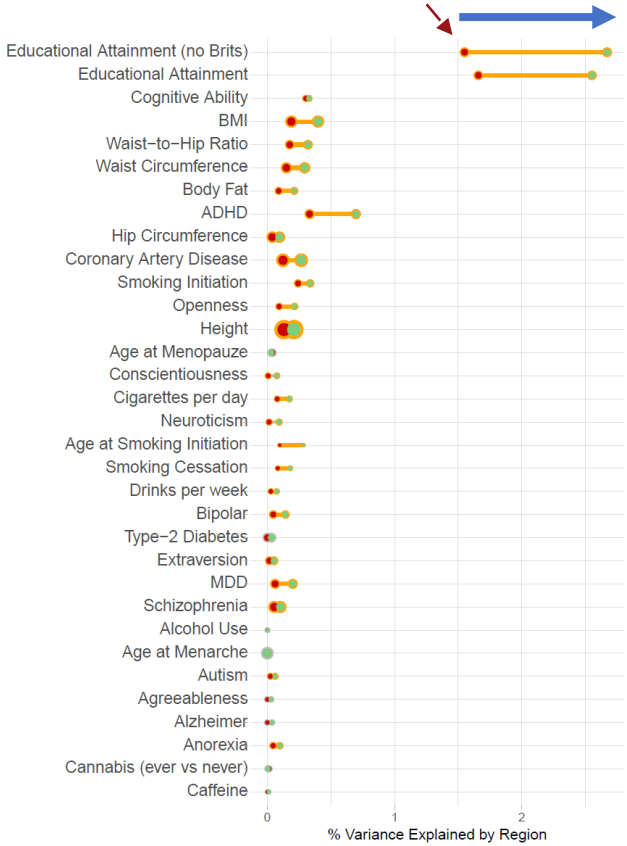


Migration & SES





← Polygenic Scores

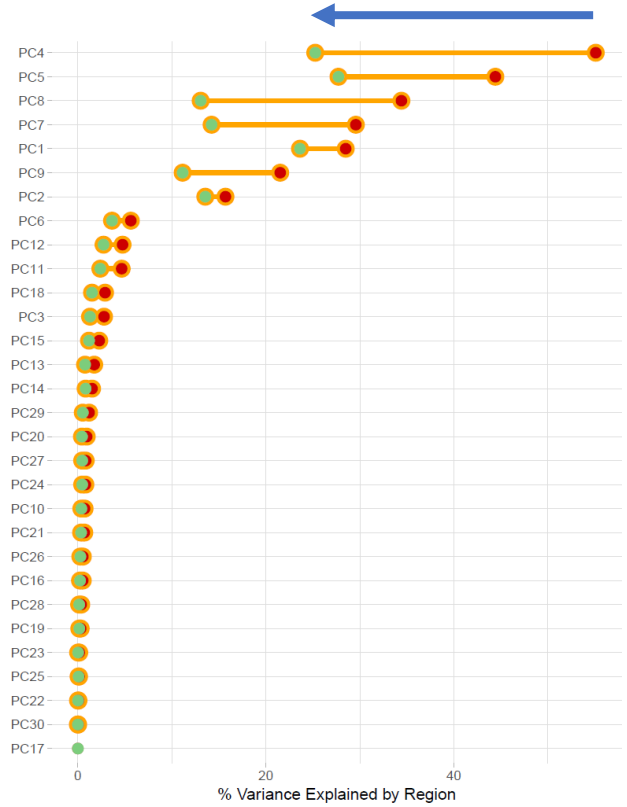
Birthplace

Current Address

Not significant (FDR)

Significant (FDR)

PCs →



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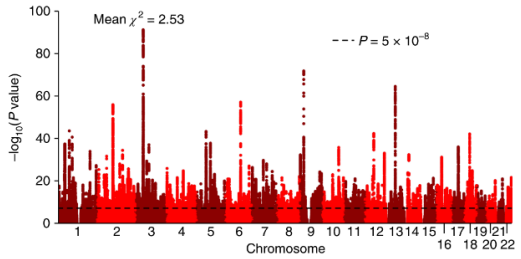

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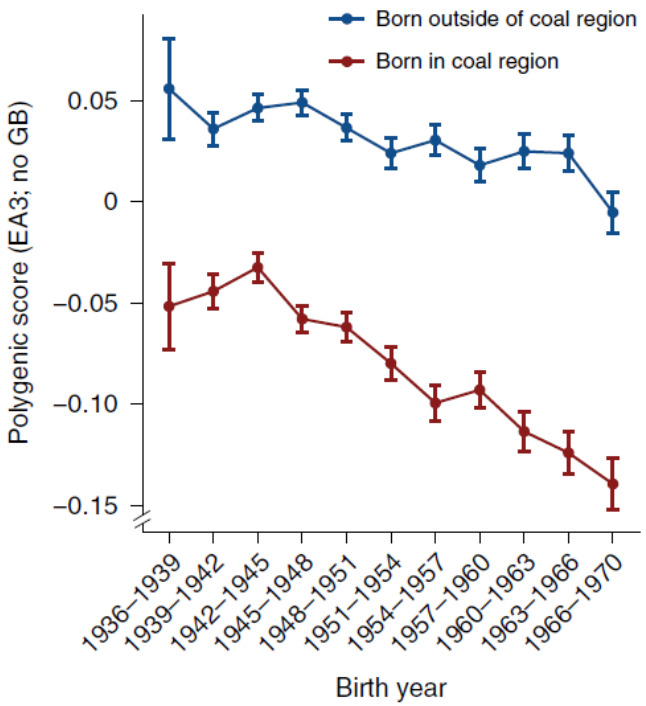

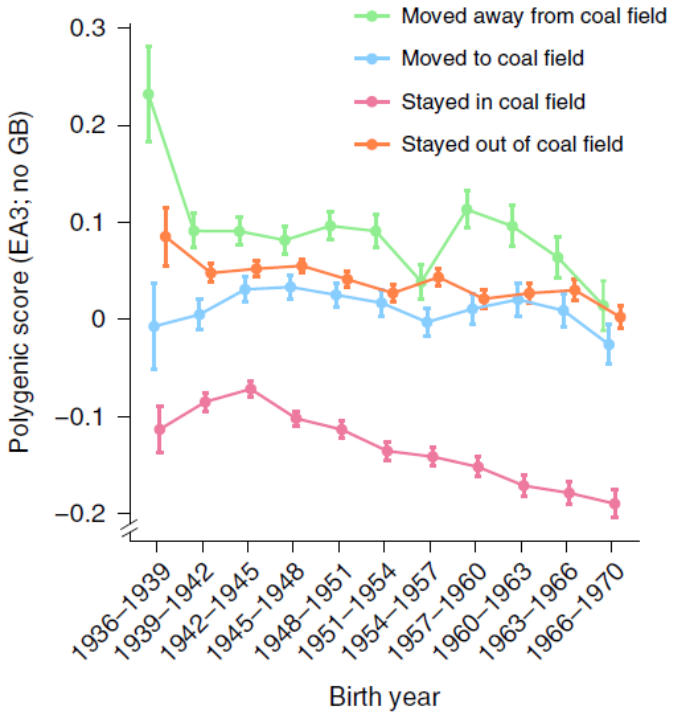

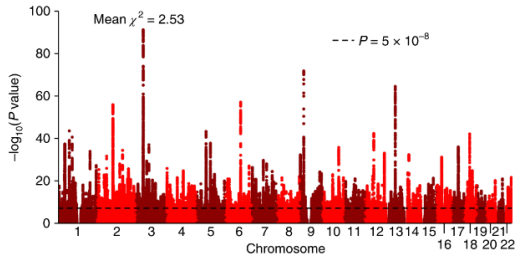

Sharing more genetic effects with EA = stronger geographic clustering

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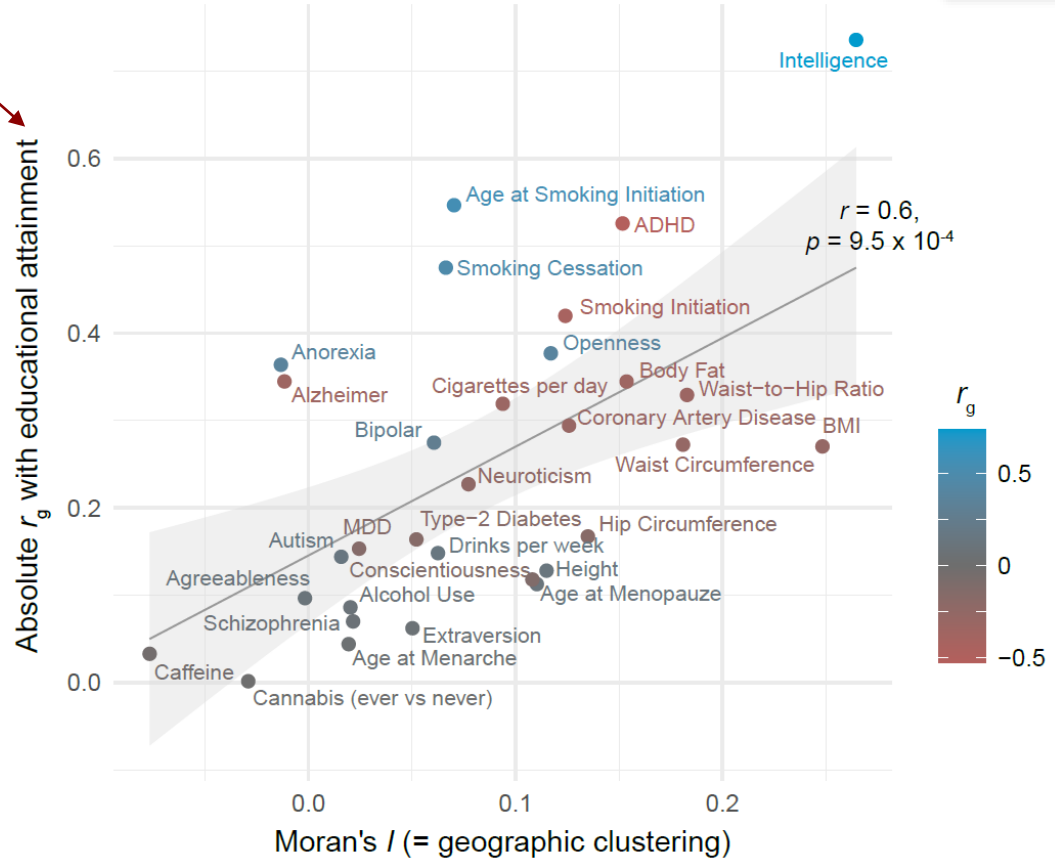
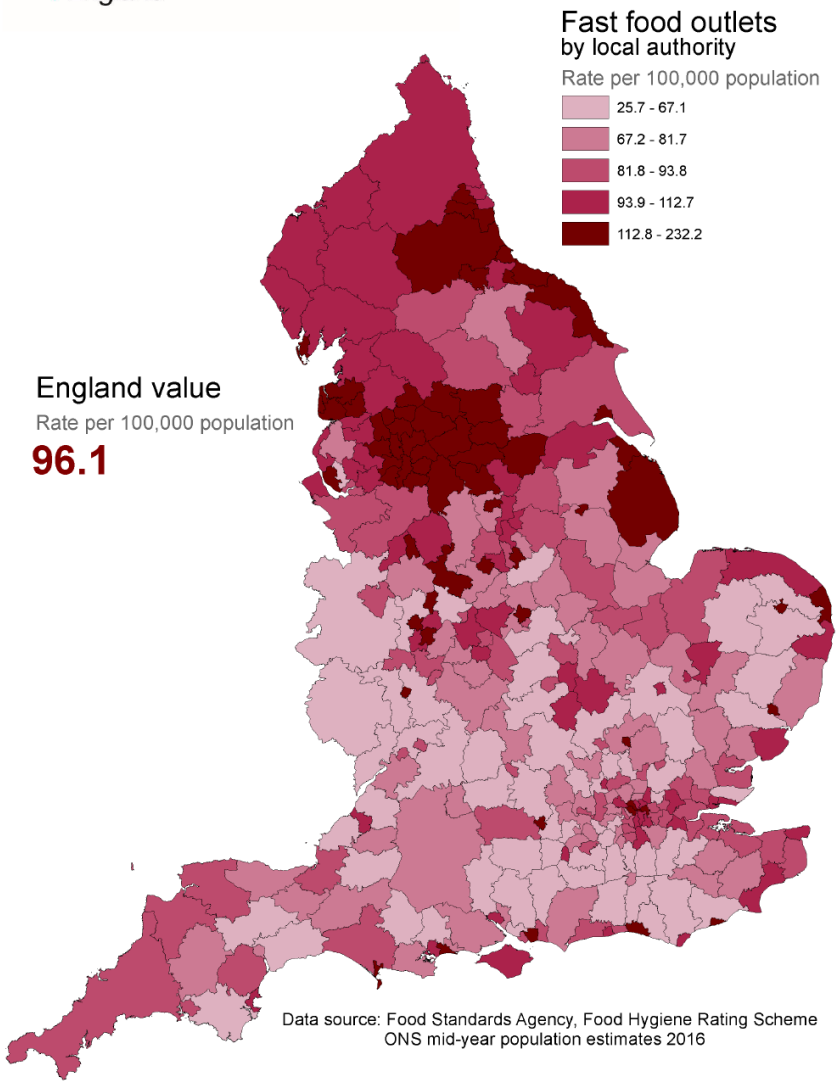


Public Health England

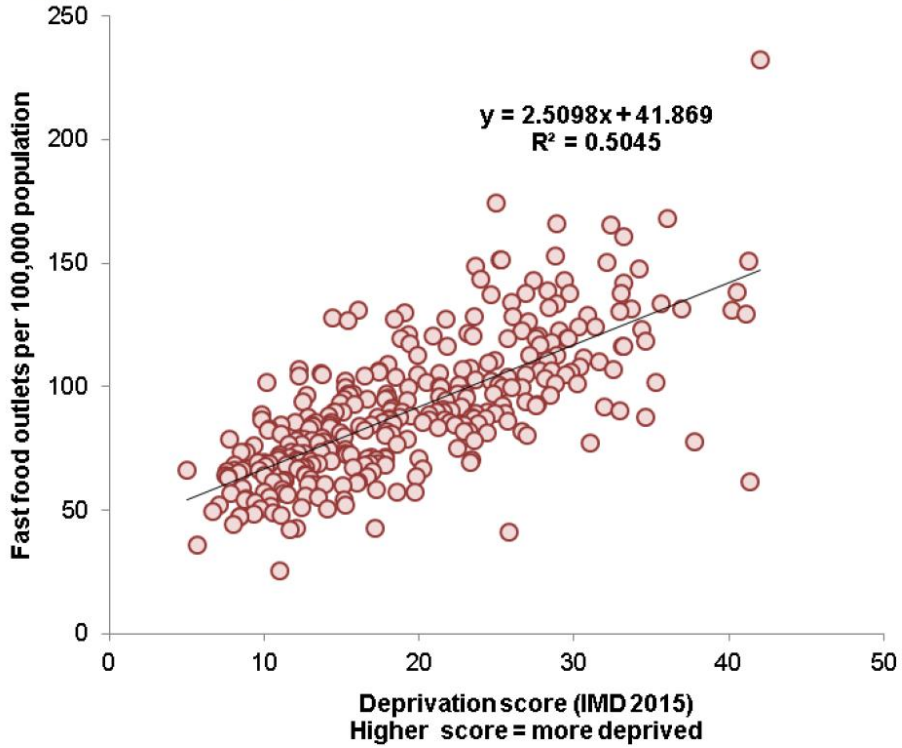
Obesity and the environment

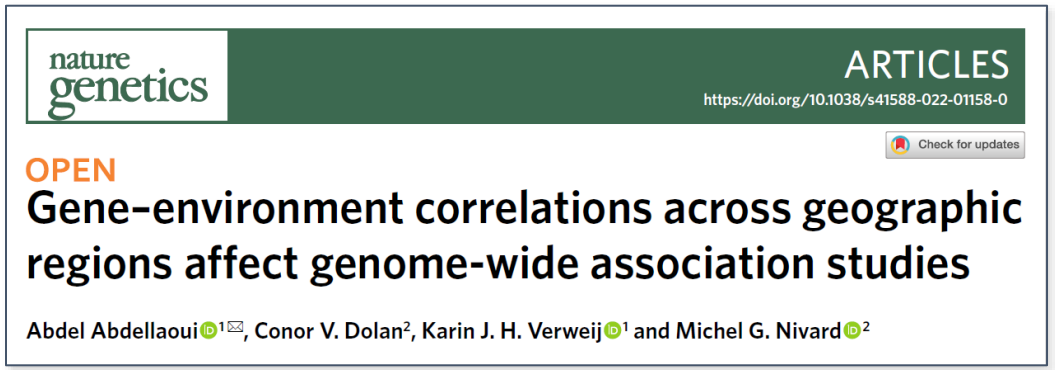
Density of fast food outlets at 31/12/2017



Public Health England

Relationship between density of fast food outlets and deprivation by local authority*



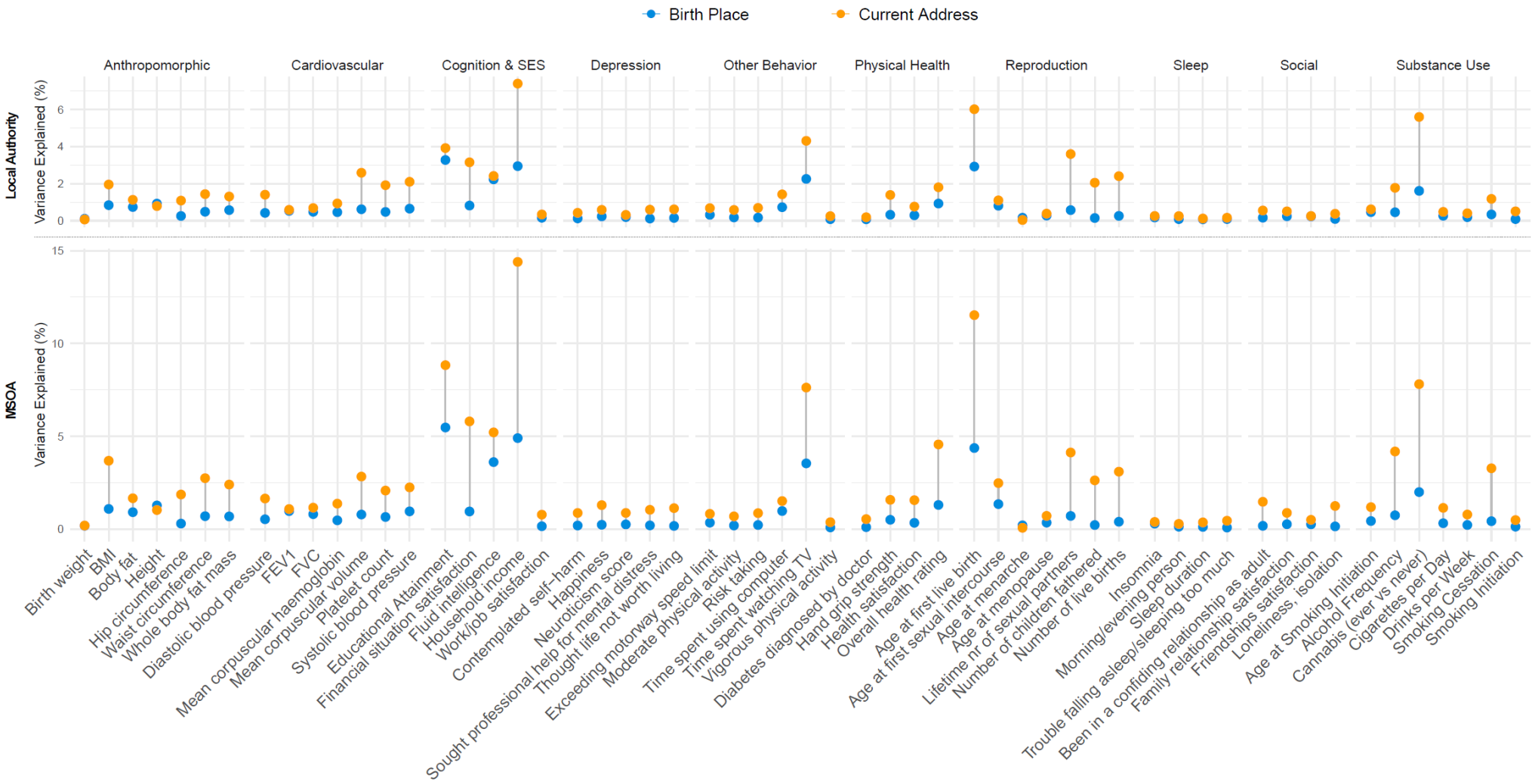


The paper consists of two parts:

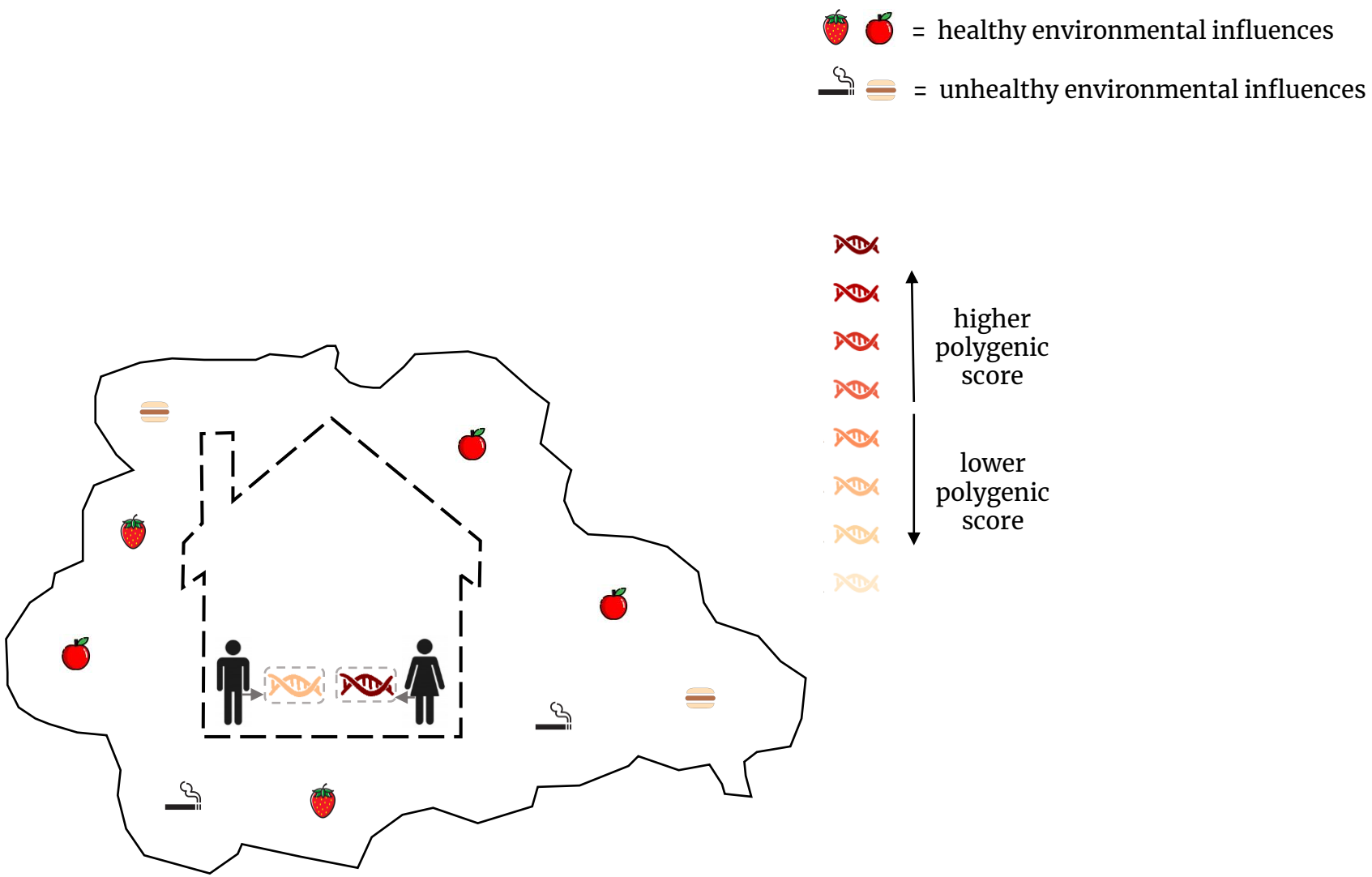
- **Part 1**: detecting gene-environment correlations using polygenic scores in up to 43,516 siblings

- **Part 2**: controlling for gene-environment correlations in GWASs in up to 254,387 participants

Variance explained by region:



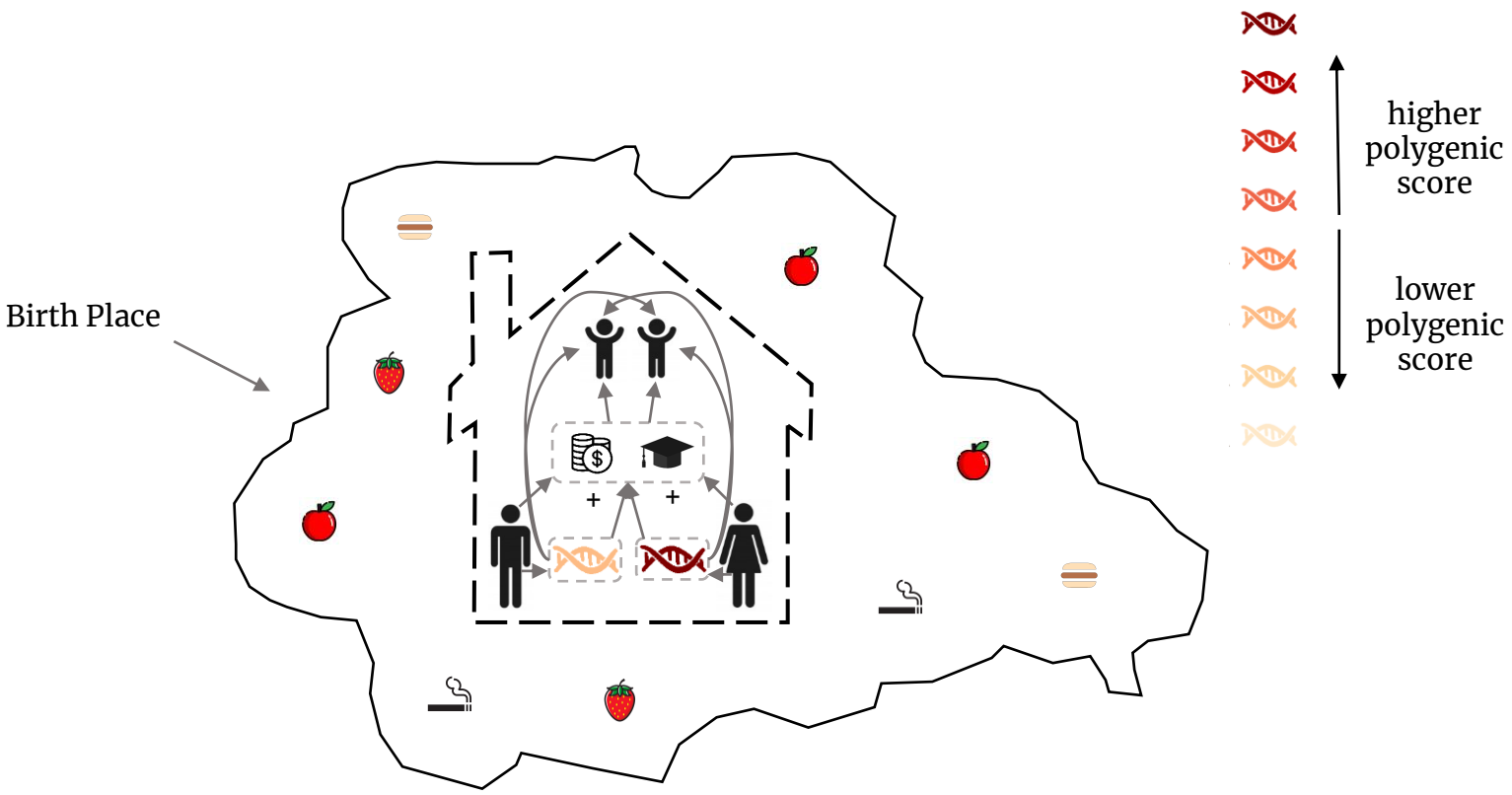
Polygenic Scores in Siblings

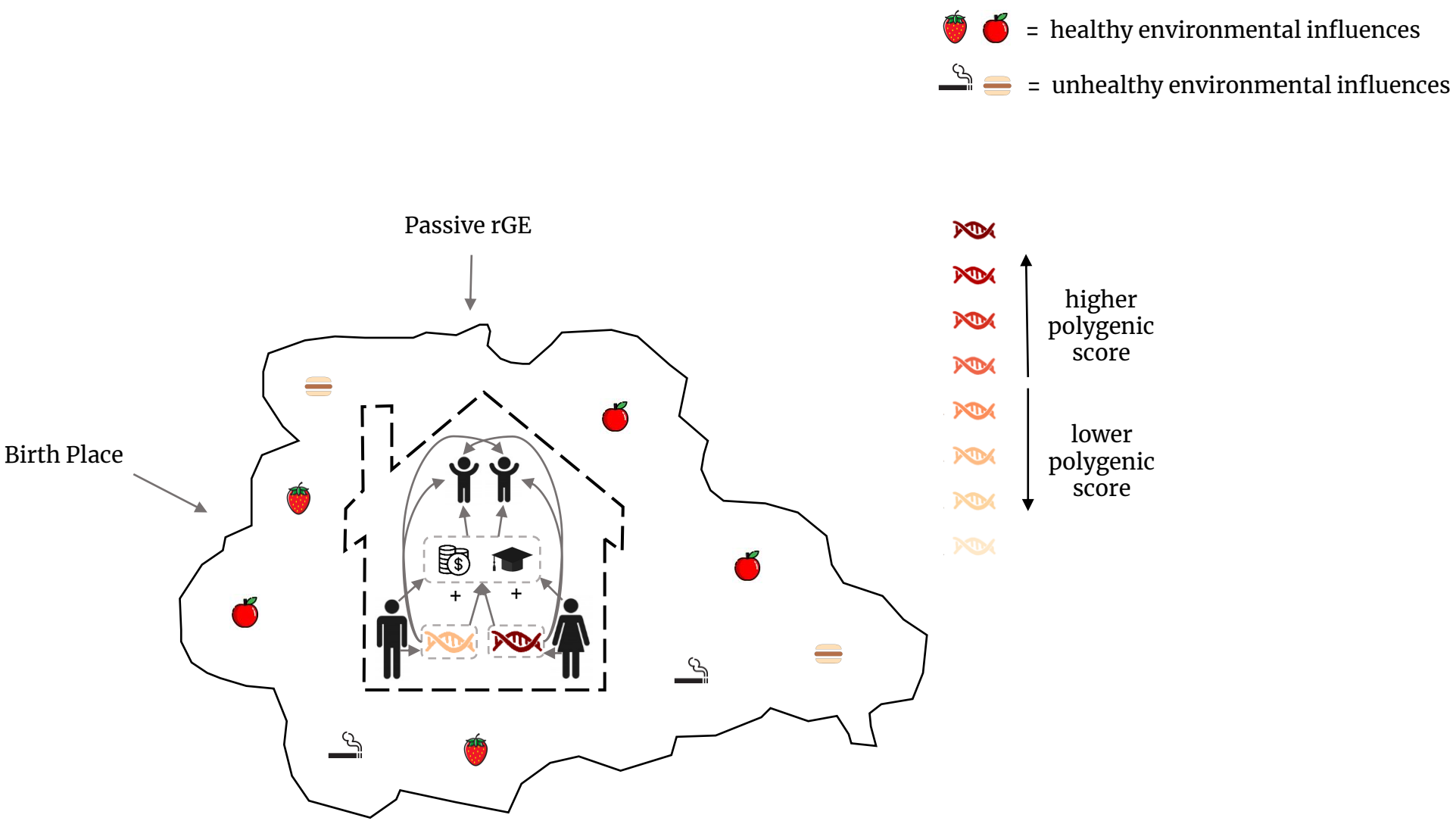

= healthy environmental influences
= unhealthy environmental influences
higher polygenic score
lower polygenic score

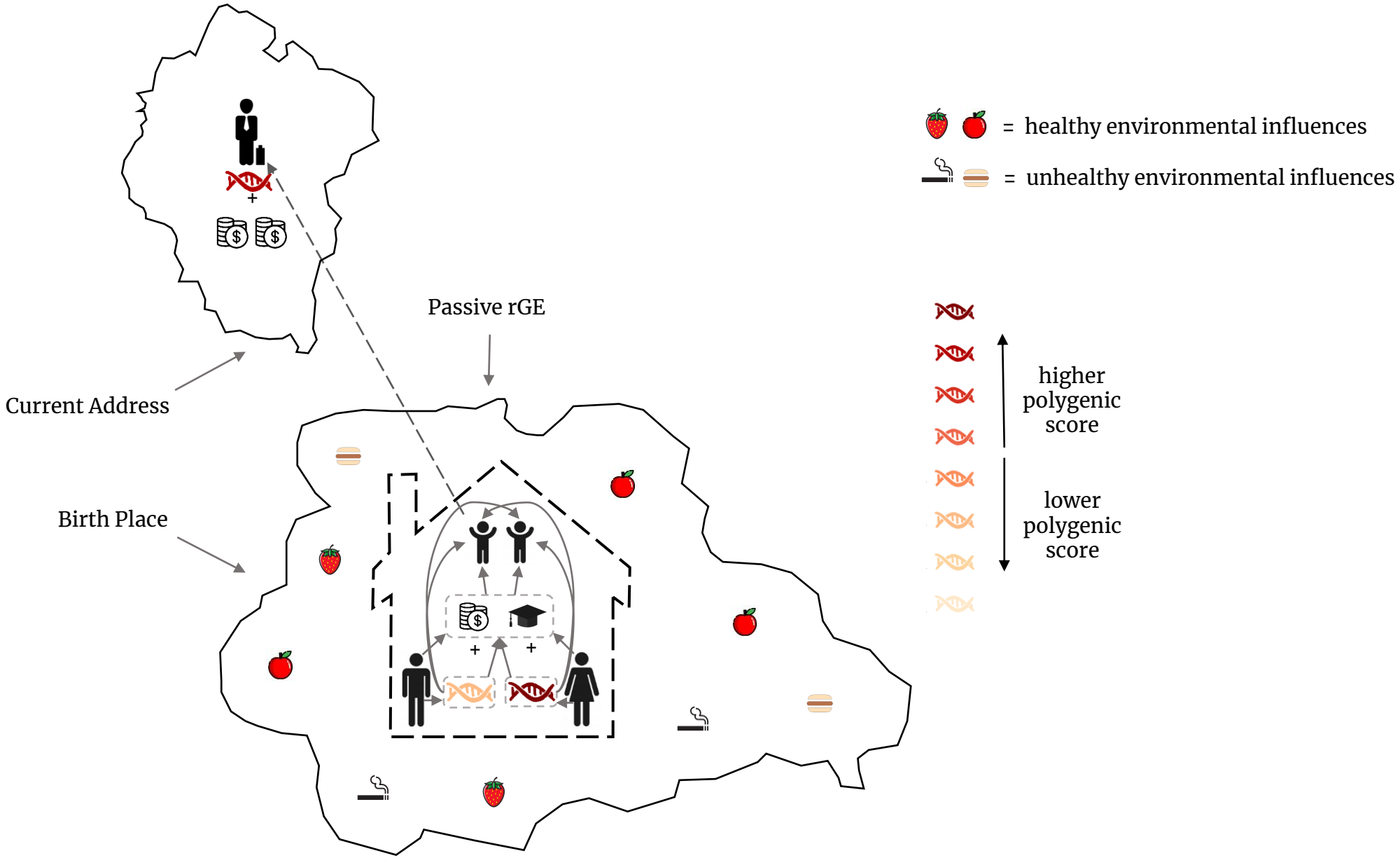

= healthy environmental influences
= unhealthy environmental influences
Birth Place
higher polygenic score
lower polygenic score

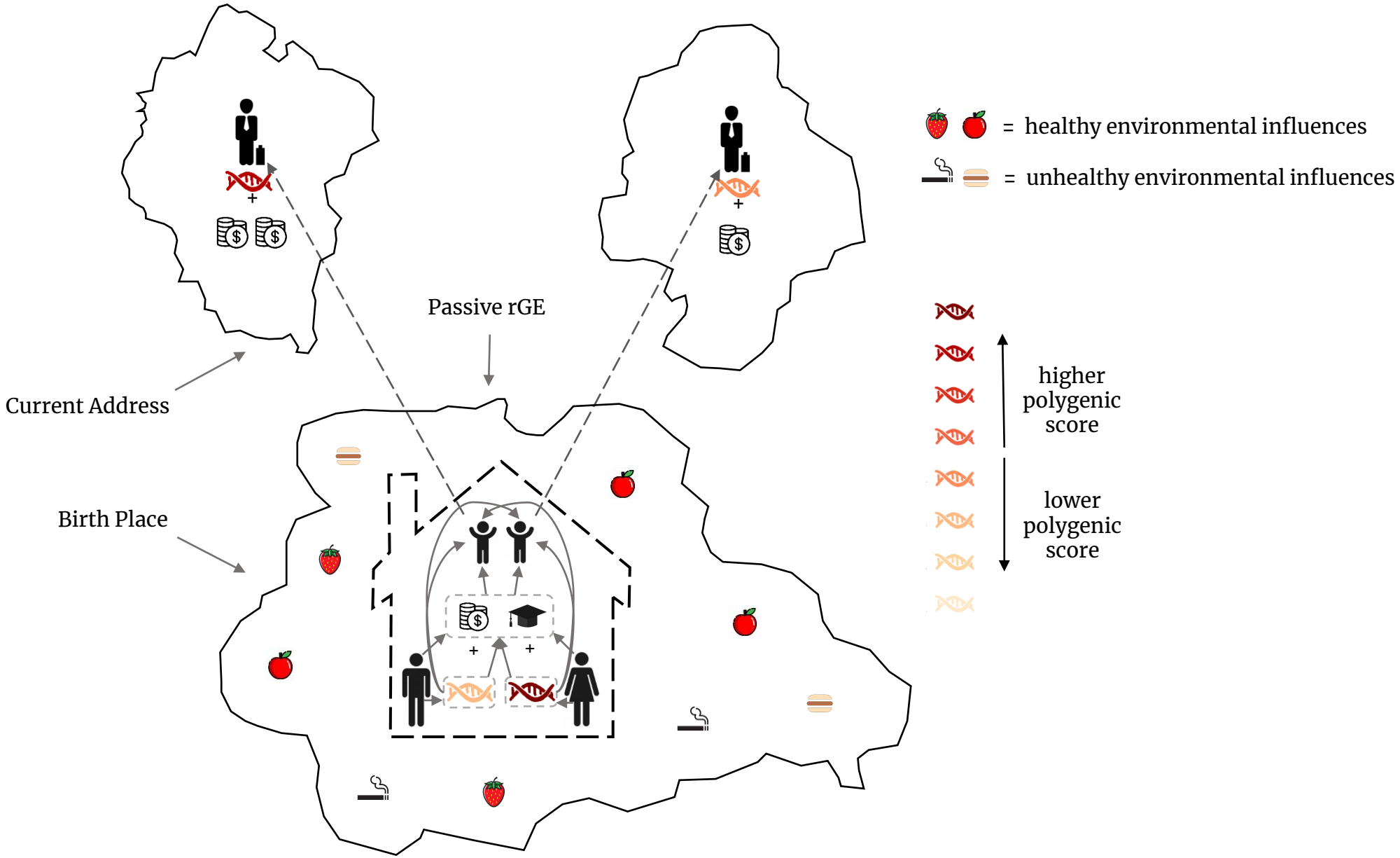
= healthy environmental influences

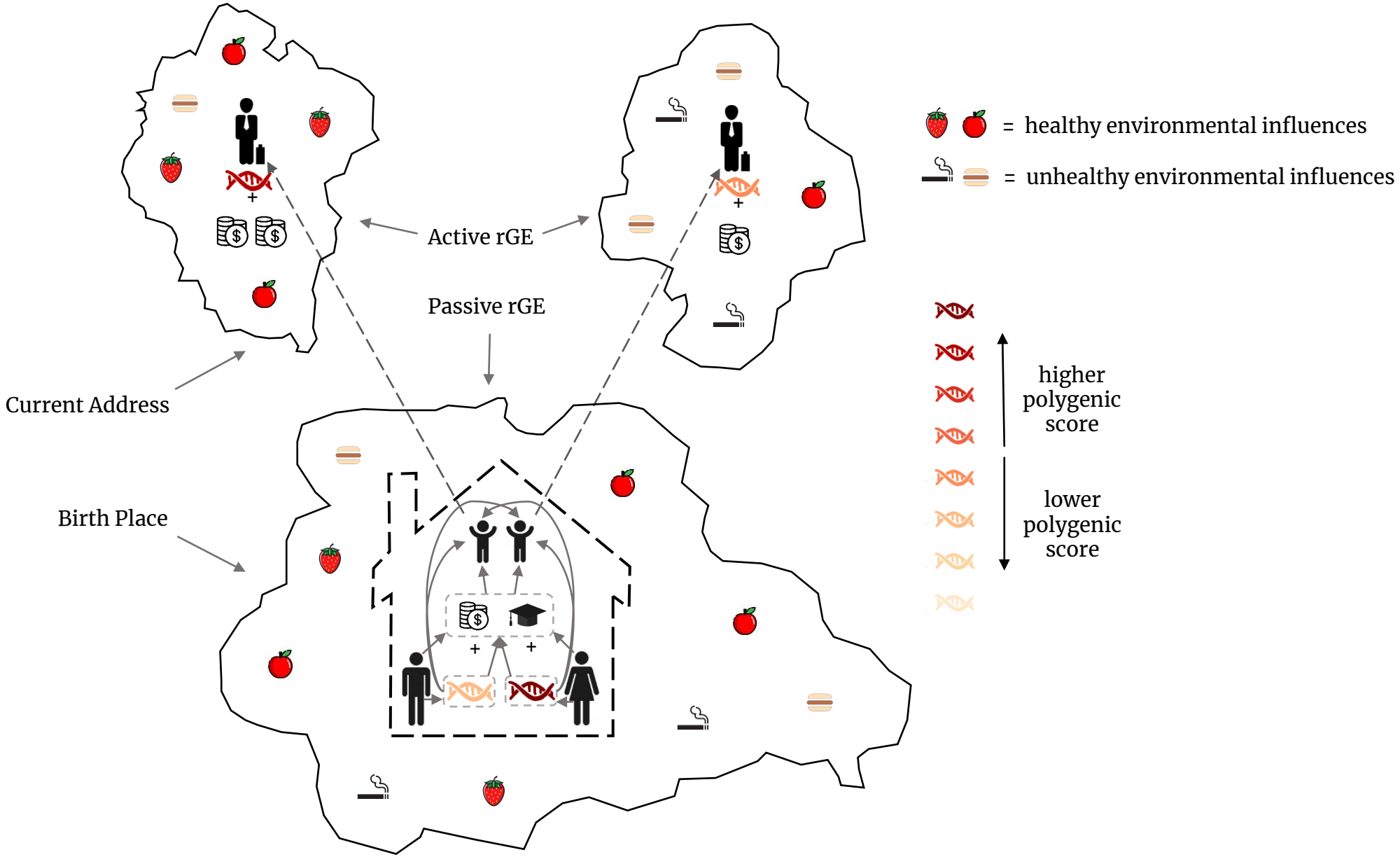
= unhealthy environmental influences




= healthy environmental influences
= unhealthy environmental influences
Passive rGE
Birth Place
higher polygenic score
lower polygenic score


= healthy environmental influences
= unhealthy environmental influences
Passive rGE
Current Address
Birth Place
higher polygenic score
lower polygenic score

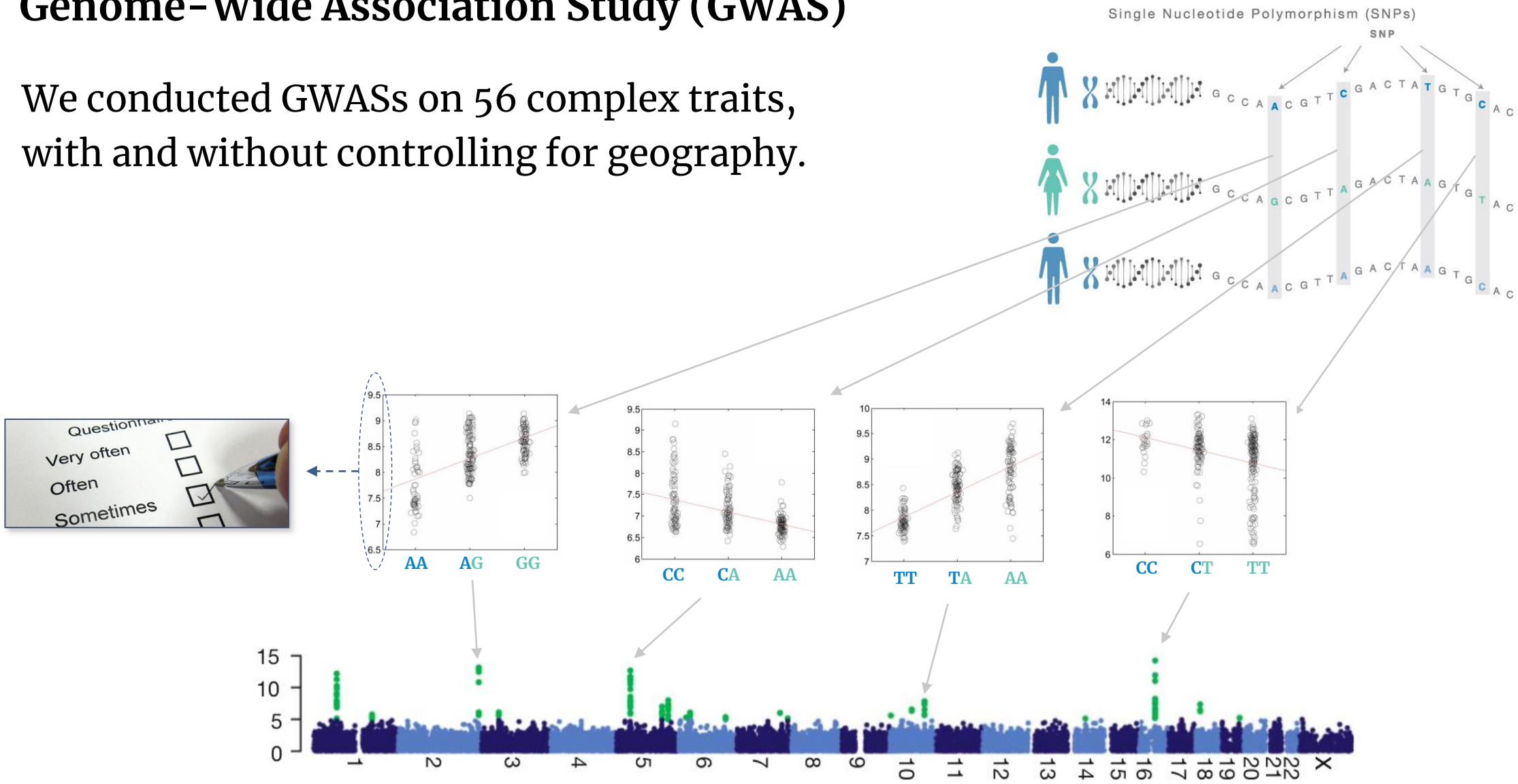

= healthy environmental influences
= unhealthy environmental influences
Passive rGE
Current Address
Birth Place
higher polygenic score
lower polygenic score


= healthy environmental influences
= unhealthy environmental influences
Active rGE
Passive rGE
Current Address
Birth Place
higher polygenic score
lower polygenic score

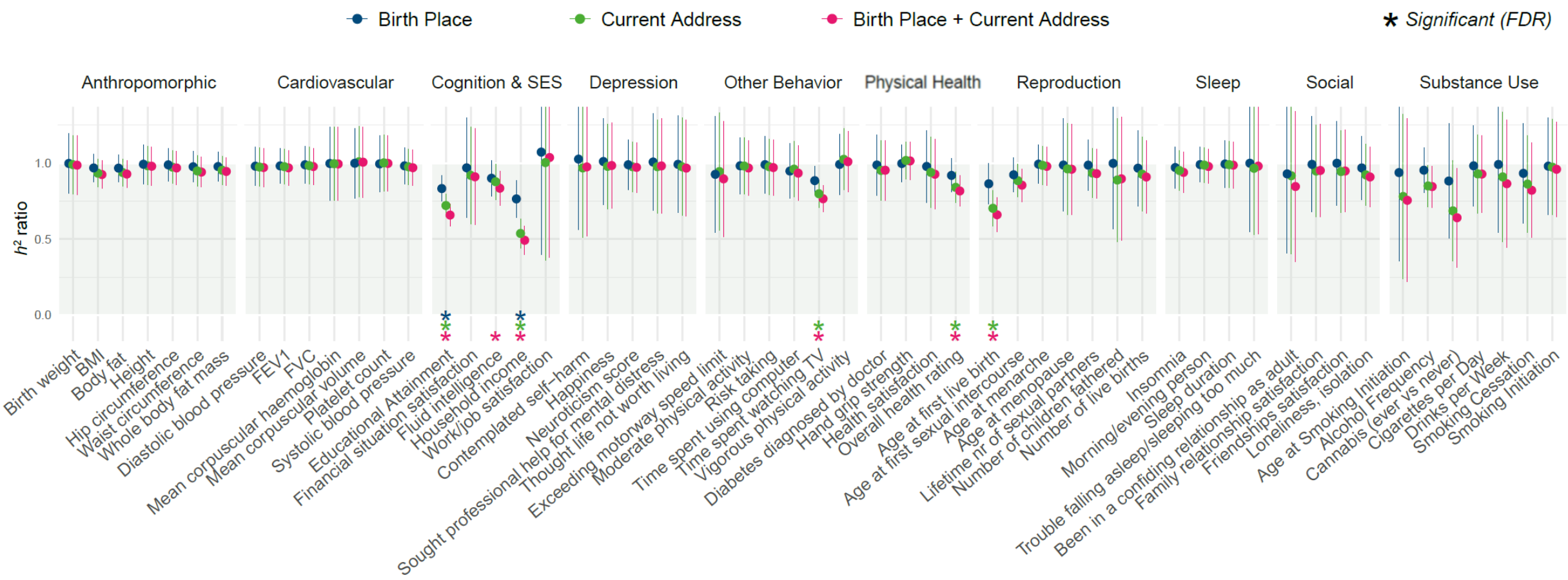
GWASs Controlled for Geography

Genome-Wide Association Study (GWAS)

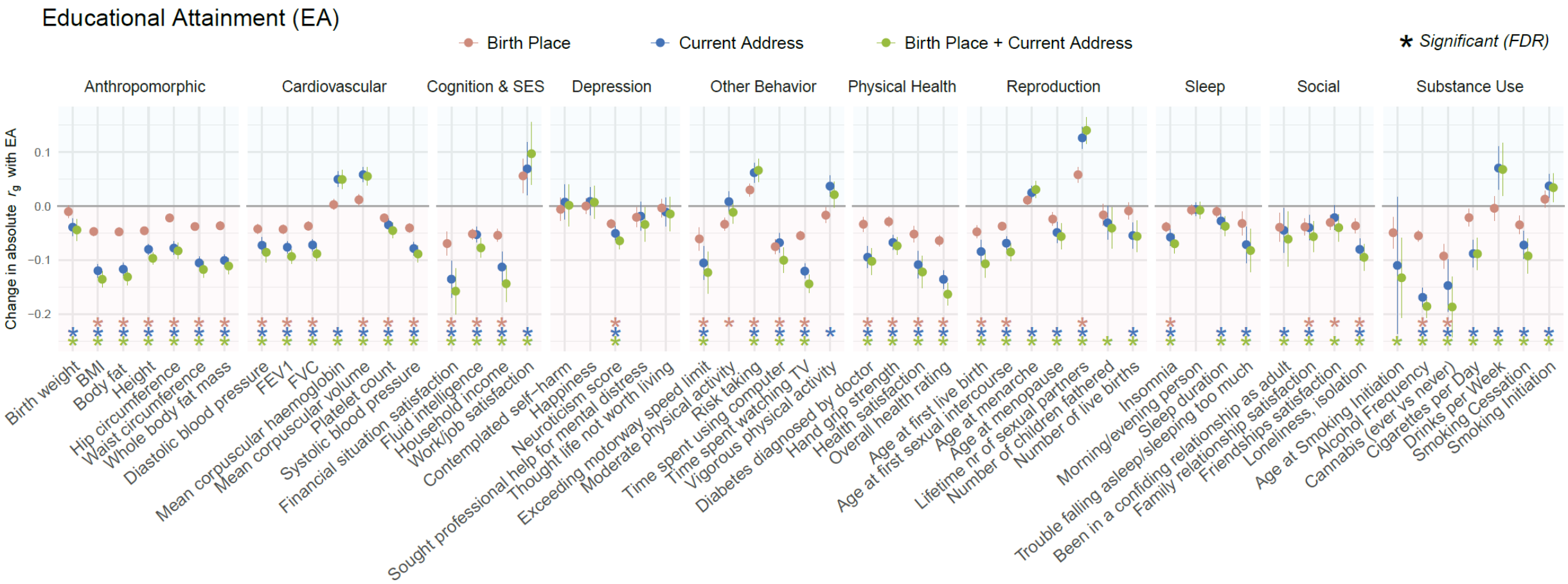
- We conducted GWASs on 56 complex traits, with and without controlling for geography.



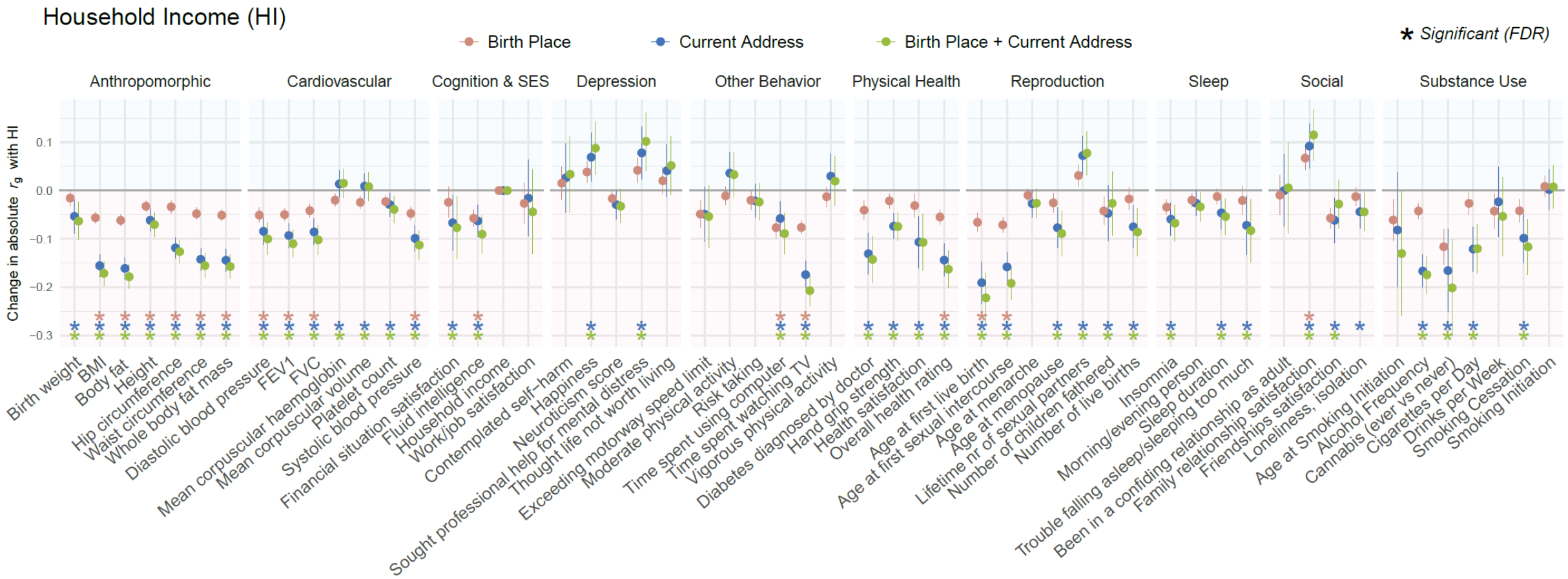
Changes in SNP-based heritability



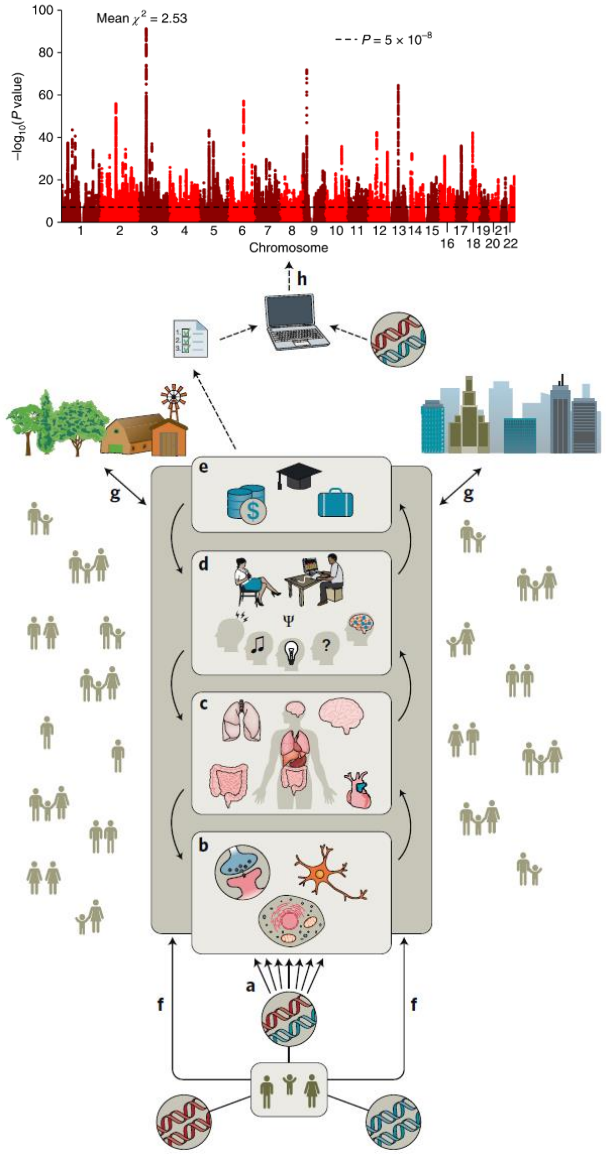
Changes in genetic correlation with SES - Educational Attainment



Changes in genetic correlation with SES - Household Income

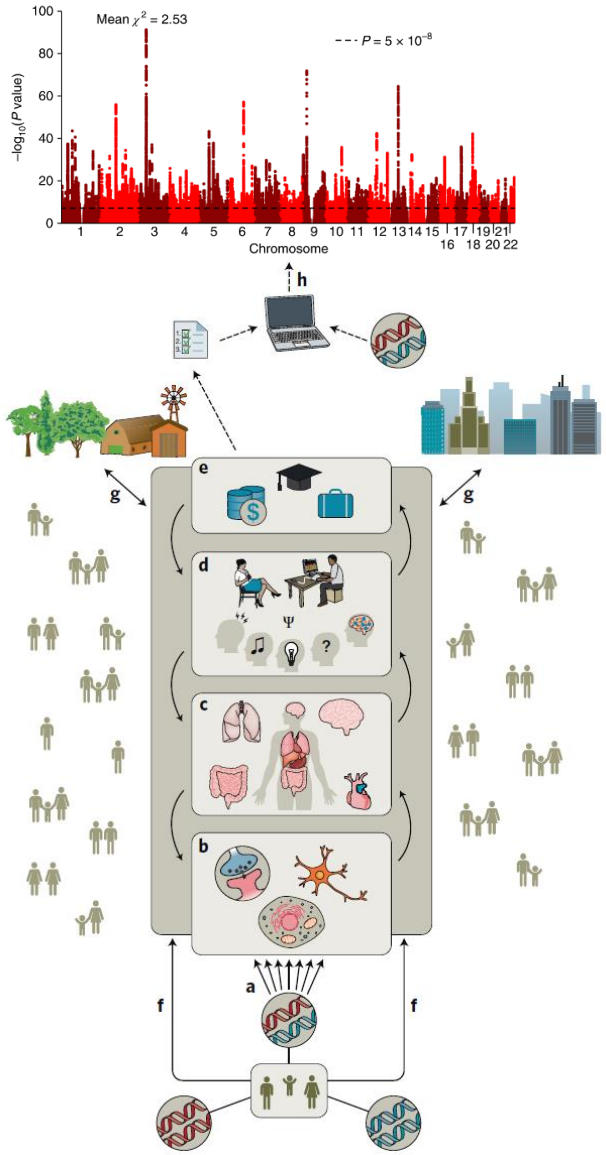


Society makes genetic effects stronger.



Society makes genetic effects stronger.

We reward certain genetic propensities with a better environment, and “punish” the lack of those propensities with a worse environment.

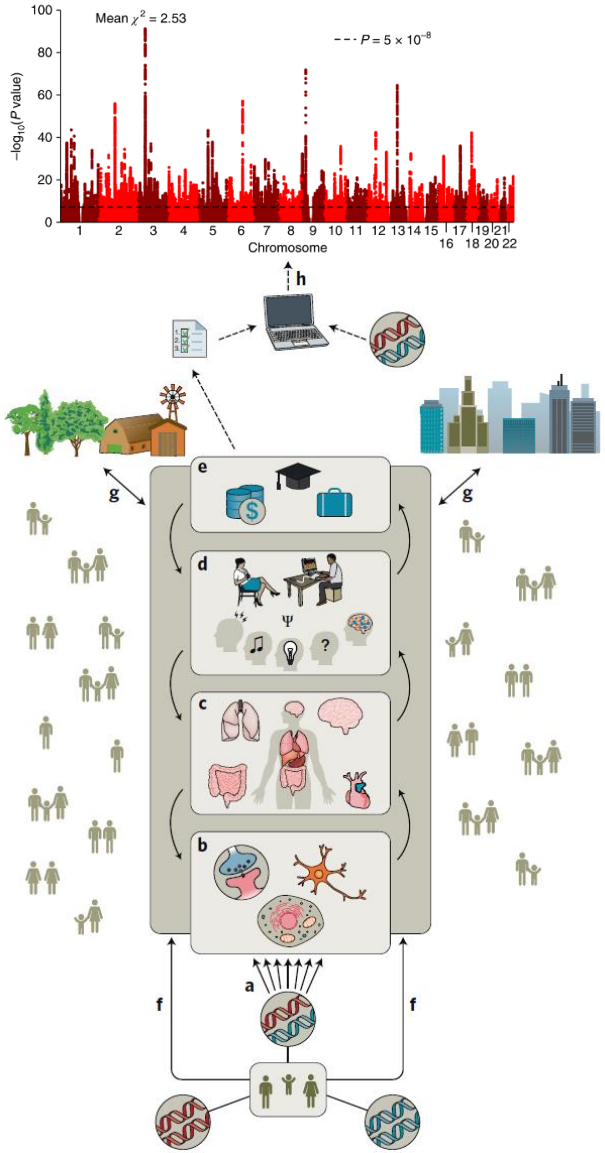


Society makes genetic effects stronger.

We reward certain genetic propensities with a better environment, and “punish” the lack of those propensities with a worse environment.

This makes society more unequal.

This makes studying genetics more difficult.



Thank you!