

From Basic Science to Clinical Application of Polygenic Risk Scores A Primer

Naomi R. Wray, PhD; Tian Lin, PhD; Jehannine Austin, PhD; John J. McGrath, MD, PhD; Ian B. Hickie, MD; Graham K. Murray, MD, PhD; Peter M. Visscher, PhD

 [Supplemental content](#)

IMPORTANCE Polygenic risk scores (PRS) are predictors of the genetic susceptibilities of individuals to diseases. All individuals have DNA risk variants for all common diseases, but genetic susceptibility differences between people reflect the cumulative burden of these. Polygenic risk scores for an individual are calculated as weighted counts of thousands of risk variants that they carry, where the risk variants and their weights have been identified in genome-wide association studies. Here, we review the underlying basic science of PRS, providing a foundation for understanding the potential clinical utility and limitations of PRS.

OBSERVATIONS Polygenic risk scores can be calculated for a wide range of diseases from a saliva or blood sample using genotyping technologies that are inexpensive. While genotyping only needs to be done once for each individual in their lifetime, the PRS can be recalculated as identification of risk variants improves. On their own, PRS will never be able to establish or definitively predict future diagnoses of common complex conditions because genetic factors only contribute part of the risk, and PRS will only ever capture part of the genetic contributions. Nonetheless, just as clinical medicine uses a multitude of other predictive measures, PRS either on their own or as part of multivariable predictive algorithms could play a role.

CONCLUSIONS AND RELEVANCE Utility of PRS in clinical medicine and ethical issues related to their use should be evaluated in the context of realistic expectations of what PRS can and cannot deliver. For different diseases, PRS could have utility in community settings (stratification to better triage people into established screening programs) or could contribute to clinical decision-making for those presenting with symptoms but where formal diagnosis is unclear. In principle, PRS could contribute to treatment choices, but more data are needed to allow development of PRS in this context.

JAMA Psychiatry. 2021;78(1):101-109. doi:10.1001/jamapsychiatry.2020.3049
Published online September 30, 2020.

Author Affiliations: Author affiliations are listed at the end of this article.

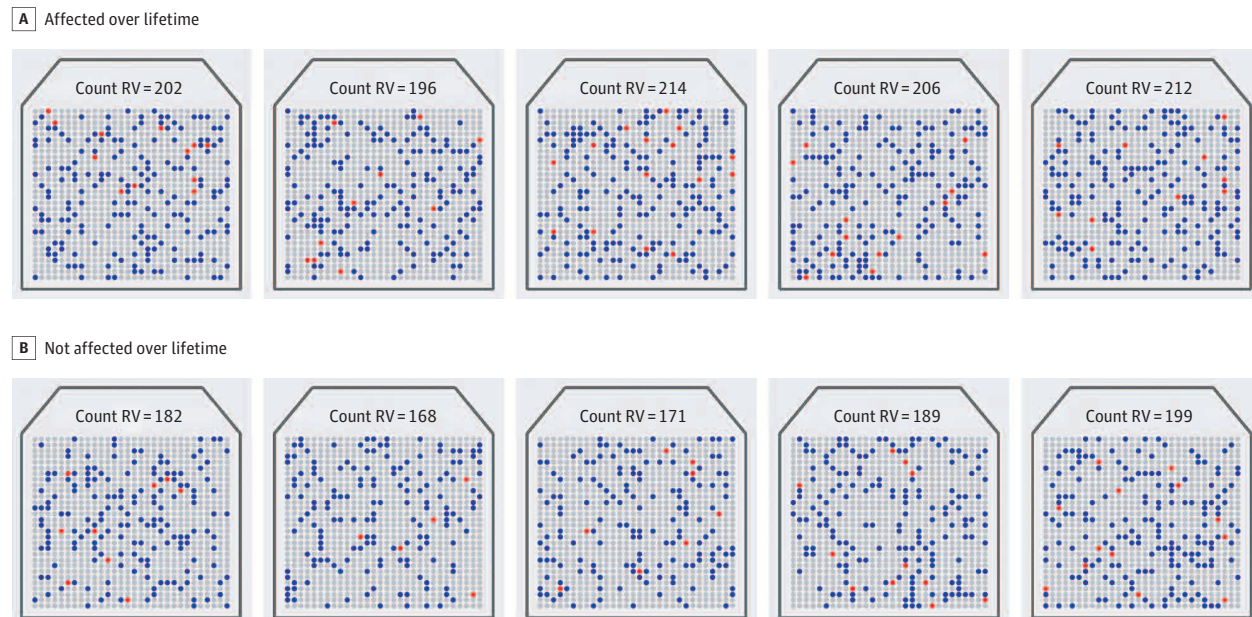
Corresponding Author: Naomi R. Wray, PhD, Institute for Molecular Bioscience, The University of Queensland, Brisbane, QLD 4067, Australia (naomi.wray@uq.edu.au).

In some medical disorders, a single genetic variant is sufficient to directly cause illness. However, common conditions are multifactorial in etiology, influenced by both genetic and nongenetic factors. Genome-wide association studies have shown that common diseases are polygenic, ie, thousands of DNA variants contribute to risk, and most of these have very small effect.¹⁻³ In spite of this complexity, it is now possible to estimate the degree to which an individual is at risk of common illnesses owing to their genetic makeup. The so-called polygenic risk scores^{4,5} (PRS) are generated from DNA taken from a saliva or blood sample with DNA variants measured using genotyping technologies that are inexpensive (< US \$100 per person). From these data, PRS can be calculated for a wide range of diseases (by multiplying count of DNA variants with trait-specific, predetermined effect sizes). The DNA collection is only needed once, but the PRS can be recalculated from the genetic data if new information to improve PRS for a given disease becomes available. As with many risk factors used in health care (eg, cholesterol levels⁶), these risk scores have limited predictive accuracy (ie, they cannot confidently predict the clinical outcome of interest with precision at the individual patient level). Even if the

risk DNA variants were identified with perfect accuracy, imperfect prediction by PRS is expected for 2 key reasons. First, genetic factors are not the only risk factors for common disorders. Second, the risk scores currently only provide data about part of the genetic contribution (that associated with common DNA variants, which typically each have small effect). Moreover, in real applications, other factors contribute to the accuracy with which risk variants and their weights are estimated (eAppendix in the [Supplement](#)).

Accepting that PRS are never going to be able to definitively predict complex conditions, the natural question for a physician, the patient, or their family, is "can PRS be useful in clinical practice, now or ever?" While a single test can generate risk scores for many diseases simultaneously, the utility of those scores varies between conditions. Here, we highlight some aspects of the basic science underpinning PRS that are relevant to considerations of clinical applications.

While the costs of generating PRS are low, we do not consider downstream associated costs in a health system nor implications for health insurance. This is outside of our expertise, but evaluation of these topics needs to be informed by an understanding of what PRS

Figure 1. A Visualization of Genetic Profiles of Individuals for Polygenic Disease

A toy example to visualize the genetic profiles for 10 individuals for a polygenic disease. Each block represents the genetic profile of an individual for 900 common DNA locations that contribute to risk of disease. Each dot is the genotype of the individual at a risk variant. The dots are colored gray if the person carries nonrisk (or protective) variants on both chromosomes, blue if

they carry 1 risk and 1 nonrisk variant, and red if they carry 2 risk variants. The count at the top of the box is the sum of the total number of risk variants. For simplicity, each risk variant has frequency 0.1 and each contributes equal risk to disease. See the eAppendix in the [Supplement](#) for more detail. RV indicates DNA risk variants.

can and cannot deliver. In particular, it is important to dispel the dogma that equates a genetic test with high levels of accuracy of current/future diagnosis. We hope this article will contribute to this understanding. We also do not consider deeply the way in which risk should be communicated to the general public or to those presenting with current or past clinical symptoms, ie, genetic risk literacy. This is an important topic, and we recognize that the interrelationship between genetic test information and mental health may be complex^{7,8}; we refer readers to some thoughtful commentaries.⁹⁻¹¹ We do note that return of PRS to patients is already undergoing research trials in health systems around the world. Moreover, commercial genotyping is now available in the public domain from a number of private companies by mailing in a saliva sample. Some direct-to-consumer companies report PRS for a number of diseases and traits. Consumers can also download their genotype (genetic variant) data and upload them into online PRS calculators.¹² Clinicians may wish to consider the possibility of a patient (and/or family member or future spouse) attending their consultation in the near future armed with their own, commercially derived, individual disease-specific PRS in the expectation that the clinician will interpret them. Our goal is to present an understandable narrative about the utility of PRS for the general reader (there are many other useful review articles¹³⁻¹⁹), and we plan to provide a psychiatry-specific evaluation in a future article.

risk, where a variant is defined as a difference in DNA code at a particular location between people. Given we each carry 2 versions of each chromosome, at each DNA variant location, individuals can have 2 risk-associated variants (variants are often called alleles), 2 protective variants, or 1 of each (where risk and protective are relative terms). So when we say common diseases are polygenic, it means each of us have some risk variants in our DNA for all diseases, but those who carry a higher burden of risk variants for a particular disease have increased risk for that disease (Figure 1 provides a visualization of this) or are more vulnerable to developing a condition in the context of other risk factors, and chance. In fact, we expect manyfold more rare variants to contribute to disease risk than common variants. However, rare variants are difficult to identify with confidence. There are so many of them that testing for their association with disease massively increases the multiple testing burden; therefore, very large samples are needed to identify those associated with disease. When so many risk loci contribute to disease etiology, it is likely that each person has a unique combination of risk variants (Figure 1), which, together with an individual's unique combination of life experiences, generates the variable presentation and life course that characterize common disorders, such as heart disease, type 2 diabetes, cancers, immune disorders, and mental health disorders.

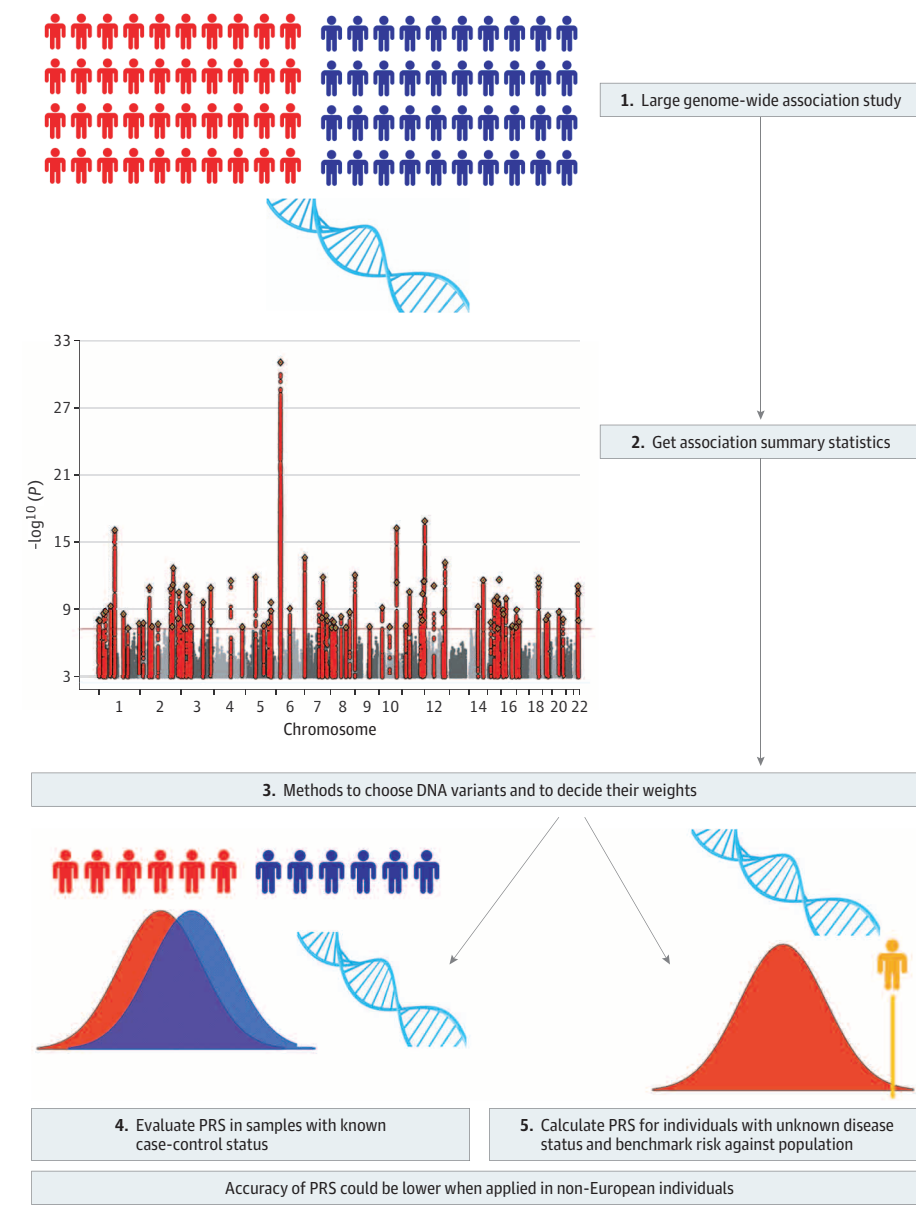
What Does "Polygenic" Mean for Individuals?

Common diseases and disorders are recognized to be polygenic.³ This means that thousands of DNA variants contribute to genetic

What Are PRS?

Polygenic risk scores for a disorder are calculated as weighted sums of risk variants for that disorder (Figure 2). Polygenic risk

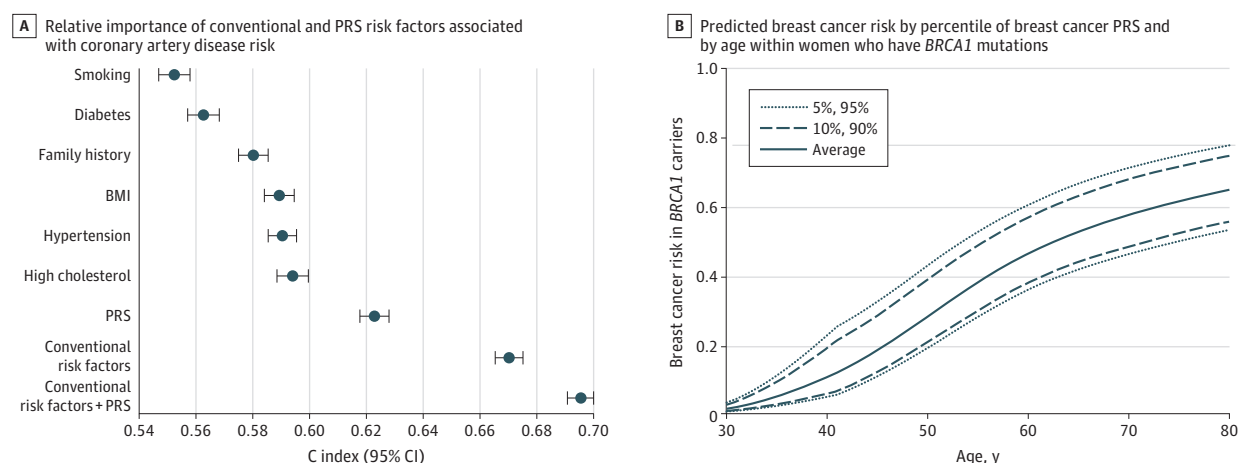
Figure 2. Schematic of the Steps Needed to Generate and Validate Polygenic Risk Scores (PRS)



scores can be calculated from an individual's DNA sample for all disorders for which risk variants have been identified and are essentially a count of the number of the risk variants present in the person's DNA, weighted so that the presence of some risk variants is considered more important than others. The identities of the specific risk variants, and the basic information about how to weigh them, comes from the allele frequency differences between cases and controls identified in genome-wide association studies (GWAS).⁵ The optimal selection of variants and the weights associated with them is an active area of research (eAppendix in the [Supplement](#)). Notably, risk prediction does not need knowledge of causal variants and can tolerate inclusion of some false-positive variants. Polygenic risk scores are validated by application in cohorts with already known case/control status. If the PRS are found to be predictive of the disease, then the PRS

can be applied to an individual with unknown disease status, with the score benchmarked against a large group of ancestry-matched individuals. Ideally, at this stage, the PRS should be further validated for utility through formal clinical trials. Although the acronym *PRS* is currently the most widely used nomenclature, other acronyms are used (eAppendix in the [Supplement](#)). There are many statistics to evaluate PRS and they are interrelated (eAppendix in the [Supplement](#)). Most GWAS to date have been conducted in those of European ancestry; therefore, while some predictive ability is expected for individuals from other ancestral populations, the prediction is expected to be attenuated particularly into those with African ancestry^{20,21} (eAppendix in the [Supplement](#)). There is considerable effort to increase GWAS sample collection across worldwide population groups to address this concern.^{20,21}

Figure 3. Examples of Polygenic Risk Scores (PRS) Applications in Heart Disease and Breast Cancer



A, Relative importance of conventional and PRS risk factors associated with coronary artery disease risk.²⁶ The y-axis can be interpreted as the probability that a person who went on to have coronary artery disease ranked higher on the risk predictor than someone who did not get the disease. Results from Cox regression of incident coronary artery disease in the UK Biobank for

conventional risk factors individually and in combination with the PRS, including covariates (sex-stratified age-as-timescale). B, Predicted breast cancer risk by percentile of breast cancer PRS and by age within women who have *BRCA1* mutations.²⁷ See the eAppendix in the Supplement for more detail.

Applications and Evaluations of PRS

To demonstrate why there is considerable discussion about implementation of PRS into health systems, we consider the application in cardiovascular medicine because it was highlighted²² that PRS provide a level of predictive information that can be considered similar to the risk of specific single rare variants that are currently clinically actionable. In standard practice, the detection of such rare variants (often investigated in families that have multiple affected individuals) can lead to changes in clinical management (eg, surveillance or prophylactic measures).²² In this retrospective study, it was shown that those in the top 1% of cardiovascular PRS had lifetime risk of greater than 10%, which is equivalent to the risk faced by those carrying single rare genetic variants that, when detected, can inform changes in clinical management. On the flip side, approximately 90% of people in this top 1% would not go on to have heart disease, but encouraging this subgroup of the population to consider prevention strategies could be worthwhile in reducing risk. Use of risk information in this way is sometimes referred to as precision prevention genomics, where the precision focus is a population stratum.

Risk prediction for heart disease is already well established around the world.²³⁻²⁵ These predictors can be found in online tools and combine information associated with clinical risk factors, such as sex, age, blood pressure, smoking status, family history of cardiovascular disease, total and high-density lipoprotein cholesterol, diabetes, and electrocardiogram measures, into a total risk score. None of the individual contributing factors is a useful risk predictor alone, but the combination of factors is used to inform prescription of statins and other lifestyle preventive interventions. Another study²⁶ using prospective, longitudinal data from the UK Biobank²⁶ showed that while coronary artery disease PRS were a less accurate predictor of a subsequent coronary artery disease event than the other clinical risk predictors when they were combined, it was

more accurate than any of the other individual clinical risk factors (Figure 3A).²⁷ Additionally, when PRS were added to the existing combination of clinical risk predictors, the accuracy increased. Extrapolating the UK Biobank results to 13 million UK residents aged 40 to 55 years, it is estimated that incorporating PRS into the QRISK algorithm²³ could lead to many hundreds of thousands of people changing risk category: more than 500 000 could move from less than the threshold for statin prescription to greater than the risk threshold, while more than 200 000 people could move from greater than the risk threshold for statin prescription to less than the threshold.²⁸ Although application of PRS in prediction of cardiovascular risk is an ongoing topic of discussion,^{29,30} incorporating genetic data into such risk algorithms used routinely in primary care could have significant public health implications.

Global interest in using PRS is most notable for diseases that already have population-based screening and prevention programs. Because screening programs carry both benefits and risks (eg, unnecessary invasive test and/or treatments), additional information with which to stratify risk could result in screening being focused on a more restricted group, which could potentially decrease risks associated with screening for the population overall, and lead to cost savings.³¹ Hence, PRS-based risk stratification could be of potential utility in other contexts such as colorectal cancer (where screening kits are posted biannually to those older than 50 years and where resources to encourage kit return could focus on those at highest PRS-based risk³²) or breast cancer (where PRS could personalize age at first breast screening³³). Another example is application to common eye disorders, such as glaucoma, where those with high-glaucoma PRS³⁴ could be particularly encouraged to take up the ophthalmological screening because intervention on early detection of increased intraocular pressure can prevent otherwise irreversible blindness.

For some common diseases, there are known rare variants of large effect. For example, about 2% of breast cancers in women

of European ancestry are associated with variants in the *BRCA1* gene. These variants are individually rare in the population but are associated with massively increased risk in the families in which they segregate. In women with these *BRCA1* variants, high PRS for breast cancer (derived from nonfamilial breast cancer GWAS) are associated with earlier age at breast cancer diagnosis²⁷ (Figure 3B). Similar results using disease-specific PRS have been reported for *BRCA2* breast cancer, *BRCA1/2* ovarian²⁷ and prostate cancer,³⁵ familial (MYOC p.Gln368Ter) glaucoma,³⁴ and familial (Lynch syndrome) colorectal cancer risk.³⁶

Together, these examples demonstrate that risk prediction from PRS will be combined with other risk information for an individual. While predicted risk from both PRS and rare genetic variants of large effect are available from birth, lifestyle risk factors used to generate predictors of absolute risk will change with age.

Will People With Known Family History Have High PRS?

People with known family history of a common disease are likely to have higher than average PRS, but may not. Why not? First, because family history encompasses both genetic and nongenetic risk factors shared by family members, although the genetic contribution is on average larger.³⁷ Second, the risk variants included in the PRS only capture part of the genetic contribution, and so those with family history are not guaranteed to have high PRS. Third, an individual may share fewer risk variants than expected with their affected family members because of the random segregation of risk variants from parents to offspring. In fact, PRS have the potential to differentiate risk between family members who have the same family history information. In the clinical context, if people present with relevant family history of a disorder but low PRS, then the clinician should make any clinical decisions in a manner guided by the family history. Such patients could be prioritized for testing of other genetic risk factors not included in the PRS, such as chromosomal rearrangements or structural variants.³⁸

Could People Have High PRS But No Family History?

It is fully expected that many of those with high PRS for a specific disease will have no family history of that disease. From polygenic theory, the only way to reconcile both the polygenic nature of common disease and the frequency of a disease in the population is that most people presenting with common disease have no known affected family members.³⁹ This is consistent with the risk of disease being highly nonlinear with the genetic contribution to liability of disease (or “true” PRS).⁴⁰ For example, for a disease of lifetime risk of 1% and heritability 70% (approximately representative of a range of common diseases/disorders such as rheumatoid arthritis, schizophrenia, bipolar disorder, and colon cancer), just based on idealized families without the additional vagaries associated with real-life knowledge of family history, about 75% of those affected are expected to have no first-degree, second-degree, or third-degree relatives with the condition.^{39,40} These perhaps non-

intuitive but observationally endorsed results reflect that important genetic differences occur between family members as a result of the segregation of variants from parents to children at meiosis. While each child receives half their DNA complement from their mother and half from their father, there are more than 8 million ways that the chromosomes of each parent can be split. For polygenic disorders, the genetic variance between siblings in a family is expected to be half of the genetic variance in liability between all individuals in the population⁴¹ (Figure 1). For this reason, although the PRS of 2 family members will be more similar than the PRS of 2 people selected randomly, the PRS will vary between family members. As PRS become more accurate, the variation in PRS between full siblings will increase and will differentiate the risk between them despite having the same family history. Hence, a high polygenic risk for a condition is simply a consequence of the genetic lottery of life.

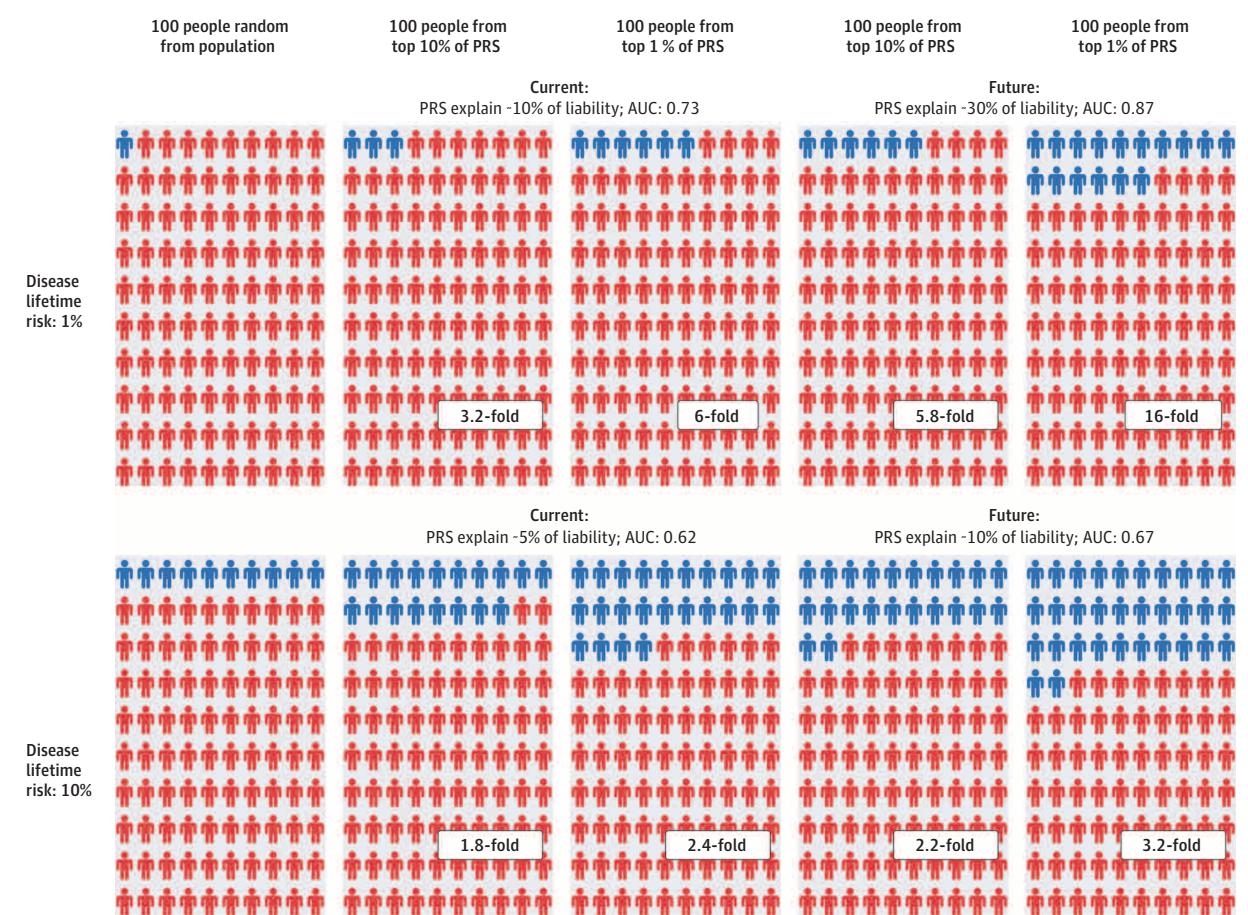
What Is the Maximum Expected Future Accuracy of PRS?

Polygenic risk scores can only explain part of the genetic aspect of a condition. Because nongenetic factors also contribute to risk, the maximum accuracy of genetic predictor is limited by the heritability of the disorder, where heritability is the proportion of the variance between people in their liability to a disease that is attributed to genetic factors.⁴² However, construction of PRS is, to date, limited to DNA risk variants that have frequency of at least 1% in the population (and in some applications, variants are only included if they have a frequency of more than 10%^{43,44} owing to greater instability in PRS using low frequency variants [currently]). Hence, PRS are not designed to capture all genetic variation only tagged by common single nucleotide variants (SNVs). Therefore, the so-called SNV-based heritability gives the upper limit of the variance between people in their liability to a disease that can be explained by PRS and represents the variance explained by common DNA variants. As GWAS sample sizes increase, the variance explained by PRS will also increase and approach the SNV-based heritability. The SNV-based heritability estimates vary across diseases, but an approximate upper limit is approximately 30%. Although in principle, use of whole-genome sequence data could increase the variance explained by PRS (because more variance would be tagged by measured markers, ie, the SNV-based heritability approaches the heritability), it is unlikely (at least in the short term) to improve PRS (eAppendix in the Supplement). Risk stratification based on current and future PRS is illustrated in Figure 4.

Conclusions

Polygenic risk scores are not and never will be stand-alone predictors of common diseases. The expected role for PRS across medical applications is partly predicated on the fact that the genotyping needed for calculation of PRS is cheap, that a one-off generation of genome-wide genotypes can provide PRS for multiple conditions, and that even small changes in health outcomes can have a large effect on health economics because polygenic diseases are common

Figure 4. Using Polygenic Risk Score (PRS) for Population Stratification



Rates of disease in the general population and those in the top 10% or top 1% of the PRS distribution. Top row: a disease with lifetime risk of 1%, where PRS explain 10% of liability variance now and 30% in the future. Bottom row: a disease with lifetime risk of 10% where PRS explain 5% of the variance in liability now and 10% in the future. These examples are selected to approximate

results from real data for diseases of these frequencies. AUC indicates area under the receiver operating characteristic curve, which can be interpreted as the probability that a person with disease ranks higher on PRS than a person without disease. See the eAppendix in the Supplement for more detail.

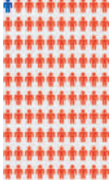
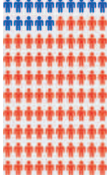
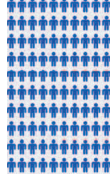
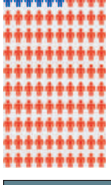
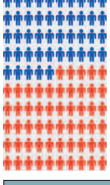
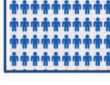
diseases of society. Polygenic risk scores are already available to those who have undertaken direct-to-consumer testing or through the up-load of genome-wide genotypes received through ancestry testing into PRS calculating online tools.¹² Therefore, it seems likely that PRS will become available; the question then becomes, if we have PRS, do we use them?

Polygenic risk scores could be used at 3 key stages (Figure 5). First, PRS could be applied in healthy populations. In principle, PRS could be available for an individual for all common diseases from birth. The genetic data would be held as part of the health record, with the latest score accessed for a specific disease at a point relevant to that disease. As described previously, PRS could easily be integrated into health systems for diseases where population screening programs and preventive health management strategies are already available. It is notable that if PRS were available for 20 different (and uncorrelated) diseases/disorders, while only 1% of the population is at high risk (defined as in top 1%) for any one of them, up to 20% of the population is expected to be in the high-risk category for one of them. It is the ability of the same genetic data to

provide multidisease results that are important for health economic evaluations.

Second, PRS could be used in the early phase of illness, when patients present with very general and nonspecific symptoms that do not fit a specific diagnosis. For many diseases/disorders, presentation with clinical symptoms is sufficient together with biomarker testing (such as electrocardiogram for heart arrhythmia⁴⁵) to confirm diagnosis. For diabetes, although a blood glucose test confirms diagnosis, 15% of adults presenting with type 1 diabetes are misdiagnosed as the more common type 2 diabetes, an impactful misdiagnosis given differences in treatment and care.⁴⁶ Within those with type 1 diabetes, high PRS for type 1 diabetes could be used to trigger more frequent monitoring of insulin levels because type 1 diabetes PRS were found to predict progression to the critical phenotype of insulin deficiency.^{15,46} In some circumstances, PRS could be used to predict time to event.⁴⁷ For example, prediction of age at onset of breast cancer for those carrying causal variants in *BRCA1* could contribute to advice on timing of mastectomy.²⁷ We also propose that PRS could help with the triage and clinical staging of young

Figure 5. An Overview of the Population Cohorts Where Polygenic Risk Scores (PRS) Could Be Applied

Cohort where PRS applied:	Community	Symptoms: help-seeking	Established diagnosis
	 <p>Of 100 people in the population, 1 will get "the disease" in lifetime, assuming a disease of lifetime risk of 1%</p>	 <p>Of 100 people presenting at clinic with symptoms but without a clear diagnosis, a higher proportion than in a population sample will go on to get "the disease" in their lifetime</p>	 <p>100 people with diagnosis of "the disease"</p>
Utility of PRS:	PRS contribute to risk stratification	PRS contribute to clinical decisions	PRS contribute to treatment choices
	 <p>Of 100 people in the top PRS stratum, a higher proportion will get "the disease" in their lifetime and hence are particularly encouraged to enter established disease screening</p>	 <p>Of 100 people presenting with symptoms AND in the top PRS stratum, a higher proportion than in the clinic-presenting cohort will go on to get diagnosis of "the disease" in their lifetime</p>	 <p>Genetic information may contribute to more effective choice of treatment, with reduced adverse events</p>
Likely applications:	Common diseases/ disorders for which there is already population screening	When there is no clear diagnosis based on presenting symptoms, guide monitoring of emergent symptoms	Potentially all common diseases/disorders but little data available to date
Likely first applications:	Cancers: breast and colorectal; common eye disorders: glaucoma, macular degeneration; heart disease	Differentiating between type 1 and type 2 diabetes	Inflammatory bowel disease is a flagship in the genetics of common disease; perhaps we will see first applications here?

The cohort in which PRS are applied will be disease/disorder dependent.

adults when they first present to services with very general and non-specific symptoms (eg, anxiety, depression, or suicidal thoughts or behaviors), contributing to clinical decision-making.

Third, it is possible that in the future, PRS could contribute to treatment choices, because responses to treatment, including development of adverse health outcomes (such as weight gain), are likely complex genetic traits. However, investigating the utility of PRS in the context of choice of drug treatments requires larger data sets than are currently available. Compared with a decade ago, we now have the tools to develop models to predict treatment response, but are limited by data to develop and validate predictors. Large cohorts of patients treated with different medications must be followed up and responders contrasted with nonresponders to

generate genetic predictors of response or recovery. To date, the inflammatory bowel diseases research has been the flagship for translation of genetic associations into new treatments, and identification of treatment responding subtypes is an active area of research.⁴⁸

We conclude that the PRS available currently may have clinical utility for some diseases for which investigation in clinical settings is already justified. The breadth of applications will increase as genetic data become increasingly available as part of routine health records. Key to making this happen is to extinguish the dogma that equates a genetic test with a result of very high predictive value for current or future diagnosis and accept PRS to have an inherently limited accuracy, as do to many other tests routinely used in health care.^{6,49}

ARTICLE INFORMATION

Accepted for Publication: July 14, 2020.

Published Online: September 30, 2020.
doi:10.1001/jamapsychiatry.2020.3049

Author Affiliations: Institute for Molecular Bioscience, The University of Queensland, Brisbane, Queensland, Australia (Wray, Lin, Murray, Visscher); Queensland Brain Institute, The University of Queensland, Brisbane, Queensland, Australia (Wray, McGrath); Departments of Psychiatry and Medical Genetics, The University of British Columbia, Vancouver, British Columbia, Canada (Austin); BC Mental Health and Substance Use Services Research Institute, Vancouver, British Columbia, Canada (Austin); Queensland Centre for Mental Health Research, The Park Centre for Mental Health, Wacol, Queensland, Australia (McGrath); National Centre for Register-Based Research, Aarhus University, Aarhus, Denmark (McGrath); Brain and

Mind Centre, Faculty of Medicine and Health, University of Sydney, Sydney, New South Wales, Australia (Hickie); Cambridgeshire and Peterborough NHS Foundation Trust, Cambridge, England (Hickie, Murray); Department of Psychiatry, University of Cambridge, Cambridge, England (Murray).

Author Contributions: Drs Wray and Hickie had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Concept and design: Wray, Austin, McGrath, Hickie, Murray, Visscher.

Acquisition, analysis, or interpretation of data: Wray, Lin.

Drafting of the manuscript: Wray, McGrath, Hickie, Murray.

Critical revision of the manuscript for important intellectual content: Wray, Lin, Austin, Visscher.

Statistical analysis: Wray, Lin, Hickie, Visscher.

Obtained funding: Wray, Visscher.

Administrative, technical, or material support: Wray, Visscher.

Supervision: Wray.

Conflict of Interest Disclosures: Drs Wray and Visscher received funding from Illumina to attend a polygenic risk score think tank meeting in 2019. Dr Austin reported grants from Canada Research Chairs Program and BC Mental Health and Substance Use Services during the conduct of the study and from Pfizer outside the submitted work and has informally provided input to and engaged in research with impute.me, a nonprofit open source website that allows users to upload DTC genetic testing data to generate PRS, for which he have received no financial or other compensation. Dr Hickie reported being an inaugural Commissioner on Australia's National Mental Health Commission (2012-2018). He is the Co-Director, Health and Policy at the Brain and Mind Centre (BMC) University of Sydney, Australia. The BMC operates an early-intervention youth services at

Camperdown under contract to headspace. Dr Hickie had previously led community-based and pharmaceutical industry-supported (Wyeth, Eli Lilly, Servier, Pfizer, and AstraZeneca) projects focused on the identification and better management of anxiety and depression. He was a member of the Medical Advisory Panel for Medibank Private until October 2017, a Board Member of Psychosis Australia Trust and a member of Veterans Mental Health Clinical Reference group. He is the Chief Scientific Advisor to and a 5% equity shareholder in InnoWell Pty Ltd. InnoWell was formed by the University of Sydney (45% equity) and PwC (Australia; 45% equity) to deliver the \$30 million Australian Government-funded Project Synergy (2017-2020; a 3-year program for the transformation of mental health services) and to lead transformation of mental health services internationally through the use of innovative technologies. No other disclosures were reported.

Funding/Support: We acknowledge funding from the National Health and Medical Research Council (1173790, 1078901, 108788 [Dr Wray], and 1113400 [Drs Wray and Visscher]) and the Australian Research Council (FL180100072 [Dr Visscher]). Dr McGrath is supported by the Danish National Research Foundation (Niels Bohr Professorship and is employed by The Queensland Centre for Mental Health Research, which receives core funding from the Queensland Health).

Role of the Funder/Sponsor: The funding sources had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to submit the manuscript for publication.

REFERENCES

- Visscher PM, Wray NR, Zhang Q, et al. 10 Years of GWAS discovery: biology, function, and translation. *Am J Hum Genet*. 2017;101(1):5-22. doi:10.1016/j.ajhg.2017.06.005
- Gandal MJ, Leppa V, Won H, Parikshak NN, Geschwind DH. The road to precision psychiatry: translating genetics into disease mechanisms. *Nat Neurosci*. 2016;19(11):1397-1407. doi:10.1038/nn.4409
- Sullivan PF, Geschwind DH. Defining the genetic, genomic, cellular, and diagnostic architectures of psychiatric disorders. *Cell*. 2019;177(1):162-183. doi:10.1016/j.cell.2019.01.015
- Wray NR, Goddard ME, Visscher PM. Prediction of individual genetic risk to disease from genome-wide association studies. *Genome Res*. 2007;17(10):1520-1528. doi:10.1016/j.gr.6665407
- Purcell SM, Wray NR, Stone JL, et al; International Schizophrenia Consortium. Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature*. 2009;460(7256):748-752. doi:10.1038/nature08185
- Johnston N, Jernberg T, Lagerqvist B, Siegbahn A, Wallentin L. Improved identification of patients with coronary artery disease by the use of new lipid and lipoprotein biomarkers. *Am J Cardiol*. 2006;97(5):640-645. doi:10.1016/j.amjcard.2005.09.123
- McConkie-Rosell A, Hooper SR, Pena LDM, et al; Undiagnosed Diseases Network. Psychosocial profiles of parents of children with undiagnosed diseases: managing well or just managing? *J Genet Couns*. 2018;27(4):935-946. doi:10.1007/s10897-017-0193-5
- Caleshu C, Kasparian NA, Edwards KS, et al. Interdisciplinary psychosocial care for families with inherited cardiovascular diseases. *Trends Cardiovasc Med*. 2016;26(7):647-653. doi:10.1016/j.tcm.2016.04.010
- Ryan J, Virani A, Austin JC. Ethical issues associated with genetic counseling in the context of adolescent psychiatry. *Appl Transl Genom*. 2015;5:23-29. doi:10.1016/j.atg.2015.06.001
- Palk AC, Dalvie S, de Vries J, Martin AR, Stein DJ. Potential use of clinical polygenic risk scores in psychiatry: ethical implications and communicating high polygenic risk. *Philos Ethics Humanit Med*. 2019;14(1):4. doi:10.1186/s13010-019-0073-8
- Austin JC. Evidence-based genetic counseling for psychiatric disorders: a road map. *Cold Spring Harb Perspect Med*. 2020;10(6):a036608. doi:10.1101/cshperspect.a036608
- Folkersen L, Pain O, Ingasson A, Werge T, Lewis CM, Austin J. Impute.me: an open source, non-profit tool for using data from DTC genetic testing to calculate and interpret polygenic risk scores. *bioRxiv*. Published online December 2, 2019. doi:10.1101/861831
- Torkamani A, Wineinger NE, Topol EJ. The personal and clinical utility of polygenic risk scores. *Nat Rev Genet*. 2018;19(9):581-590. doi:10.1038/s41576-018-0018-x
- Chatterjee N, Shi J, García-Closas M. Developing and evaluating polygenic risk prediction models for stratified disease prevention. *Nat Rev Genet*. 2016;17(7):392-406. doi:10.1038/nrg.2016.27
- Udler MS, McCarthy MI, Florez JC, Mahajan A. Genetic risk scores for diabetes diagnosis and precision medicine. *Endocr Rev*. 2019;40(6):1500-1520. doi:10.1210/er.2019-00088
- Lewis CM, Vassos E. Polygenic risk scores: from research tools to clinical instruments. *Genome Med*. 2020;12(1):44. doi:10.1186/s13073-020-00742-5
- Martens FK, Tonk ECM, Janssens ACJW. Evaluation of polygenic risk models using multiple performance measures: a critical assessment of discordant results. *Genet Med*. 2019;21(2):391-397. doi:10.1038/s41436-018-0058-9
- Lambert SA, Abraham G, Inouye M. Towards clinical utility of polygenic risk scores. *Hum Mol Genet*. 2019;28(R2):R133-R142. doi:10.1093/hmg/ddz187
- Choi SW, Mak TS, O'Reilly PF. Tutorial: a guide to performing polygenic risk score analyses. *Nat Protoc*. 2020. doi:10.1038/s41596-020-0353-1
- Martin AR, Kanai M, Kamatani Y, Okada Y, Neale BM, Daly MJ. Clinical use of current polygenic risk scores may exacerbate health disparities. *Nat Genet*. 2019;51(4):584-591. doi:10.1038/s41588-019-0379-x
- Peterson RE, Kuchenbaecker K, Walters RK, et al. Genome-wide association studies in ancestrally diverse populations: opportunities, methods, pitfalls, and recommendations. *Cell*. 2019;179(3):589-603. doi:10.1016/j.cell.2019.08.051
- Khera AV, Chaffin M, Aragam KG, et al. Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. *Nat Genet*. 2018;50(9):1219-1224. doi:10.1038/s41588-018-0183-z
- Hippisley-Cox J, Coupland C, Brindle P. Development and validation of QRISK3 risk prediction algorithms to estimate future risk of cardiovascular disease: prospective cohort study. *BMJ*. 2017;357:j2099. doi:10.1136/bmj.j2099
- Alliance NVDP. Australian absolute cardiovascular disease calculator. Published 2020. Accessed August 24, 2020. <http://www.cvdcheck.org.au/calculator/>
- Lloyd-Jones DM, Wilson PW, Larson MG, et al. Framingham risk score and prediction of lifetime risk for coronary heart disease. *Am J Cardiol*. 2004;94(1):20-24. doi:10.1016/j.amjcard.2004.03.023
- Inouye M, Abraham G, Nelson CP, et al; UK Biobank CardioMetabolic Consortium CHD Working Group. Genomic risk prediction of coronary artery disease in 480,000 adults: implications for primary prevention. *J Am Coll Cardiol*. 2018;72(16):1883-1893. doi:10.1016/j.jacc.2018.07.079
- Kuchenbaecker KB, McGuffog L, Barrowdale D, et al. Evaluation of polygenic risk scores for breast and ovarian cancer risk prediction in BRCA1 and BRCA2 mutation carriers. *J Natl Cancer Inst*. 2017;109(7). doi:10.1093/jnci/djw302
- Donnelly P. Using Genomics to Understand an Individual's Risk for Common Diseases. Accessed August 24, 2020. <https://www.ukbiobank.ac.uk/wp-content/uploads/2019/06/P-Donnelly.pdf>
- Mosley JD, Gupta DK, Tan J, et al. Predictive accuracy of a polygenic risk score compared with a clinical risk score for incident coronary heart disease. *JAMA*. 2020;323(7):627-635. doi:10.1001/jama.2019.21782
- Elliott J, Bodinier B, Bond TA, et al. Predictive accuracy of a polygenic risk score-enhanced prediction model vs a clinical risk score for coronary artery disease. *JAMA*. 2020;323(7):636-645. doi:10.1001/jama.2019.22241
- Autier P, Boniol M. Mammography screening: a major issue in medicine. *Eur J Cancer*. 2018;90:34-62. doi:10.1016/j.ejca.2017.11.002
- Jenkins MA, Win AK, Dowty JG, et al. Ability of known susceptibility SNPs to predict colorectal cancer risk for persons with and without a family history. *Fam Cancer*. 2019;18(4):389-397. doi:10.1007/s10689-019-00136-6
- Lee A, Mavaddat N, Wilcox AN, et al. BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. *Genet Med*. 2019;21(8):1708-1718. doi:10.1038/s41436-018-0406-9
- Han X, Qassim A, An J, et al. Genome-wide association analysis of 95 549 individuals identifies novel loci and genes influencing optic disc morphology. *Hum Mol Genet*. 2019;28(21):3680-3690. doi:10.1093/hmg/ddz193
- Lecarpentier J, Silvestri V, Kuchenbaecker KB, et al; EMBACE; GEMO Study Collaborators; HEBON; KConFab Investigators. Prediction of breast and prostate cancer risks in male BRCA1 and BRCA2 mutation carriers using polygenic risk scores. *J Clin Oncol*. 2017;35(20):2240-2250. doi:10.1200/JCO.2016.69.4935

36. Fahed AC, Wang M, Homburger JR, et al. Polygenic background modifies penetrance of monogenic variants conferring risk for coronary artery disease, breast cancer, or colorectal cancer. *medRxiv*. Published online November 29, 2019. doi:10.1101/19013086
37. Polderman TJ, Benyamin B, de Leeuw CA, et al. Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nat Genet*. 2015;47(7):702-709. doi:10.1038/ng.3285
38. Sullivan PF, Owen MJ. Increasing the clinical psychiatric knowledge base about pathogenic copy number variants. *American Journal of Psychiatry*. Published online March 1, 2020. doi:10.1176/appi.ajp.2019.19040335
39. Yang J, Visscher PM, Wray NR. Sporadic cases are the norm for complex disease. *Eur J Hum Genet*. 2010;18(9):1039-1043. doi:10.1038/ejhg.2009.177
40. Baselmans BML, Yengo L, van Rheenen W, Wray NR. Risk in relatives, heritability, snp-based heritability, and genetic correlations in psychiatric disorders: a review. *Biol Psychiatry*. Published online June 10, 2020. S0006-3223(20)31669-3.
41. Lynch M, Walsh B. *Genetics and Analysis of Quantitative Traits*. Vol 1. Oxford: Oxford University Press; 1998.
42. Visscher PM, Hill WG, Wray NR. Heritability in the genomics era: concepts and misconceptions. *Nat Rev Genet*. 2008;9(4):255-266. doi:10.1038/nrg2322
43. Schizophrenia Working Group of the Psychiatric Genomics Consortium. Biological insights from 108 schizophrenia-associated genetic loci. *Nature*. 2014;511(7510):421-427. doi:10.1038/nature13595
44. Wray NR, Ripke S, Mattheisen M, et al; eQTLGen; 23andMe; Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nat Genet*. 2018;50(5):668-681. doi:10.1038/s41588-018-0090-3
45. Kapur S, Phillips AG, Insel TR. Why has it taken so long for biological psychiatry to develop clinical tests and what to do about it? *Mol Psychiatry*. 2012; 17(12):1174-1179. doi:10.1038/mp.2012.105
46. Oram RA, Patel K, Hill A, et al. A type 1 diabetes genetic risk score can aid discrimination between type 1 and type 2 diabetes in young adults. *Diabetes Care*. 2016;39(3):337-344. doi:10.2337/dc15-1111
47. Desikan RS, Fan CC, Wang Y, et al. Genetic assessment of age-associated Alzheimer disease risk: development and validation of a polygenic hazard score. *PLoS Med*. 2017;14(3):e1002258. doi:10.1371/journal.pmed.1002258
48. Graham DB, Xavier RJ. Pathway paradigms revealed from the genetics of inflammatory bowel disease. *Nature*. 2020;578(7796):527-539. doi:10.1038/s41586-020-2025-2
49. Watson J, Jones HE, Banks J, Whiting P, Salisbury C, Hamilton W. Use of multiple inflammatory marker tests in primary care: using Clinical Practice Research Datalink to evaluate accuracy. *Br J Gen Pract*. 2019;69(684):e462-e469. doi:10.3399/bjgp19X704309