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Including multiracial individuals is crucial for race, ethnicity and ancestry frameworks in genetics and genomics

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Abstract

Current ontologies of race, ethnicity and genetic ancestry rely on categorization, but have limitations — as exemplified by multiracial individuals. We argue that including these individuals will foster inclusion by better capturing complex identities, with equity benefits for the full human population.

Recent conversations in genetics and genomics research around race, ethnicity and genetic ancestry have highlighted the misalignment between (1) how society defines, labels and groups individuals; (2) how populations are categorized for research; and (3) how findings are translated to benefit human health. Current ontologies largely rely on discrete and subjective grouping of participants, such as region- or continental-level categories, but the limitations of categorization are made apparent with multiracial individuals, who are often at the intersection of genomic and societal boundaries and therefore do not easily fit into such a framework. Including multiracial individuals in conversations about race, ethnicity and ancestry provides a means to create inclusive terminology and standards that better capture complex human identities.

Human genomics research is primarily built upon an over-representation of European-ancestry populations[1], concentrating potential benefits to a narrow subset of the global population and potentially exacerbating health disparities[2]. To address these issues, the genomics community has committed to enhancing diversity in genomics research by requiring the engagement and recruitment of diverse populations and individuals. A major complication in these efforts is a disconnect between how the genomics community defines populations and how society perceives and uses population descriptors. Populations and their definitions, or lack thereof, are constantly changing. Race, ethnicity and ancestry

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Competing interests

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(REA) are terms with interwoven histories and therefore are conflated by researchers and the public alike[3,4]. Although recent conversations in human genetics seek to improve the precision of population descriptors to prevent misunderstanding, this specificity prevents the scientific community from securing true inclusion by continuing to rely upon the separation of human genetic diversity into discrete groups. The borders around any given group are often drawn using race, ethnicity or estimated genetic similarity, often denoted as "genetic ancestry groups"[5]. These borders require the discretization of human diversity so that each individual is allowed to exist within only a single 'box'. Innovative approaches to characterizing REA that intentionally account for complex and continuous identities while being adaptive to a changing landscape are vital for advancing a socially and ethically responsible agenda of diversified genomic research. One diverse group relevant to this conversation is multiracial individuals.

People of multiracial backgrounds cannot be easily categorized and therefore have historically been treated as fringe cases, otherized, assumed to be a sum of parts and had their data excluded from health research. In this Comment, we reframe the challenge posed by the complexity of multiracial identity with respect to genetic ancestry and lived experiences as an opportunity for inclusive design of REA frameworks that address the limitations of discretization, particularly in genomic research. Our motivation is two-fold. First, multiracial individuals are a rapidly growing population[6,7], and their continued exclusion from biomedical research and subsequent downstream potential benefits[8] threatens equity and justice in research and clinical care. Second, principles of inclusive design or "design for all'[9] encourage designing for individuals on the 'extremes' as a means to build frameworks that work for everyone 'in between'. In this sense, multiracial individuals may be considered 'extreme' and are therefore disenfranchised from historically discrete REA frameworks. Although binning people into discrete categories may have been useful and straightforward during the early stages of research, it can be exclusionary and inherently limit the translational benefits of research to real populations. Until the field of human genetics adopts frameworks that are inclusive of everyone, efforts to achieve health equity in genomics research and medicine will remain hampered from the start.

We are a multidisciplinary team of multiracial researchers, with diverse professional expertise across the fields of bioethics, education, population genetics, genetic epidemiology, genetic counseling, translational research and family science (see positionality statements in Box 1). Here, we highlight how general shortcomings in REA frameworks have unique ramifications for multiracial individuals in genomic research and subsequent translation of results. We argue that any novel framework to establish standards around REA must deliberately and explicitly address multiracial individuals — a population at the intersection of both blended genetic ancestry and more flexible social identities[10]. Critically, we go beyond arguing that multiracial individuals are systematically neglected in genomic analyses; we point to specific restrictions and limitations in existing REA frameworks that multiracial peoples and their lived experiences make apparent in order to identify how human genetics can develop novel frameworks that move beyond discretization and toward 'design for all' practices.

We begin with a discussion of terminology surrounding multiracial identity. We then outline current practices in the scientific process and genomics research that fail multiracial individuals in both research and its translation Recommendations for agenda-setting and research conduct, translation and communication are intended to ensure that the benefits of genomic research and precision health are accessible to everyone.

What is ‘multiracial’? a note on terminology

What it means to be multiracial is complex[11]. As Box 2 illustrates, researchers use many different terms to describe individuals who cannot be neatly classified into a single continental-level group (that is, European, African, etc.). For the purposes of this Comment, we use the term ‘multiracial’ to describe individuals with backgrounds from multiple socially constructed races, as this is the context in which individuals are likely to engage with genomic research as either participants or beneficiaries of genomic findings. However, we recognize that (1) there is a lack of consensus within the research community on how to define REA terminology[12], and (2) there are specific efforts underway to define and establish protocols for the use of these REA terms in human genetics[4,13].

Despite these caveats, being mindful of and transparent about how we define terms will help to clarify the relationship between definitions and how we (1) conduct research, including who we choose to include and not include in our studies, and (2) translate and communicate research findings to support the health of everyone. Decisions about how to classify people are rooted in a history informed by social, economic and political influences[14]. A failure to acknowledge these processes will perpetuate problematic uses of language and outdated frameworks for genomic research.

Additionally, users of the term ‘multiracial’ in genomics should be mindful of the dangerous slippage between race and genetic ancestry. ‘Multiracial’ should not be used as a proxy for genetic admixture, and vice versa. Therefore, this Comment does not refer to groups defined in part by their possible admixture, such as African American and Hispanic/Latino groups at large. Although there is often overlap between individuals who are admixed (have recent ancestry from two or more populations) and those who identify as multiracial, race is ascribed by oneself or others and is often based on societal norms and expectations along with physical characteristics such as skin color. As such, some individuals may not identify or be recognized as multiracial, instead identifying with a monoracial group (for example, ‘Asian,’ or ‘Black’).

Finally, ‘multiracial’ cannot be assumed as a distinct and non-overlapping group. Yet, the term indicates an ascribed category that represents yet another way to categorize people. Any use of the term ‘multiracial’ in this Comment is not intended to mask the diversity in cultural, ethnic and lived experiences among those who do not identify as one race, ethnicity or ancestry. For example, we authors each identify differently under the broad umbrella of ‘multiracial’, and we cannot and do not try to represent or speak for all multiracial individuals. In response to the journal’s call for commentaries on terminology, we use ‘multiracial’ as an inclusive term while acknowledging its strengths and limitations.

Agenda setting and justice

Ensuring that all members of society benefit equitably from scientific research is central to achieving justice, a context-dependent concept broadly entailing treating people fairly by giving each person their due. However, equitable benefit-sharing in genomic research is stymied by outdated governmental practices and policies that do not reflect current realities (e.g., census categories) and by disproportionate funding for individuals and conditions that affect a relatively small and privileged subset of the global population[15,16]. This includes a lack of both accounting for and funding for multiracial researchers and/or multiracial individuals' health[17]. Funding disparities such as these are problematic considering that much of the funding for research is allocated from public, taxpayer money[18]. In an attempt to share the benefits of genomic research with the full human population, genomics researchers and funding agencies are increasing efforts to diversify biobanks and include community stakeholders' views in setting research agendas and assessing community needs[19]. Building partnerships between researchers and community members builds trust, as researchers are then more likely to respect community values, anticipate potential risks and optimize potential benefits[20–22].

Although community engagement is central to achieving justice in genomics research, it is only successful if one can define and reach a community. Given their diversity of experiences and agendas, multiracial individuals will be difficult to engage under current models. The number of people who identify as multiracial is growing, numbering 33.8 million people in the USA in 2020 according to the US Census[6]. Additionally, the heterogeneous nature of multiracial identity means that multiracial individuals may not identify as a coherent group. A recent poll from the Pew Research Center demonstrated that the majority (61%) of Americans with a background that includes more than one race do not identify as multiracial[23]. Therefore, as multiracial individuals are engaged to discuss their needs or concerns, researchers should be prepared to adjust expectations around consensus and shared identity, given the heterogeneity of this community. Currently, there are no frameworks to guide researchers on how to define, recruit and engage a community of multiracial individuals.

A novel framework is thus needed to both recruit and engage multiracial individuals and researchers to aid in study design for genomic research and help foster trust with participants. Therefore, both funders and researchers need to (1) cultivate an ethos of diversity in the workplace that appreciates the perspectives of multiracial researchers[24], and (2) prioritize building trust through dynamic, bidirectional communication between multiracial community members and researchers from the beginning of the research process. One step toward building trust with community members is to enhance transparency about who researchers are as individuals and what motivates them. Positionality statements are frequently utilized in ethnographic, qualitative research to clarify researchers' potential existing biases by outlining (for example, within an academic publication or at the beginning of a lecture) the position that a researcher has adopted within a given research study, as well as to provide space for discussing a researcher's complex identity and relationship to the research. Normalizing these statements, especially in quantitative genomics research where they are underutilized, would enable multiracial researchers to validate and explain

their positions outside of one racial ‘box’ and better contextualize research while engaging participants (see Box 1 for the authors’ positionality statements). Recognizing the role and relevance of researchers’ positionalities for agenda setting, research conduct and research translation might humanize the field of human genetics while instilling the cultural humility[25] and openness to diverse identities required for successful community engagement.

Federal agencies and funders can shape institutional culture by setting policies, priorities and funding calls that (1) consider the unique and multifaceted lived experiences of multiracial individuals in genomics, and (2) push the boundaries of traditional research that has relied so heavily on REA categories that lack relevance to this population. Revisiting funding priorities and governmental policies to account for multiracial individuals can encourage more inclusive and person-centered agenda setting and research designs that prioritize justice, trust and trustworthiness and maximize the benefits of genomics research for all.

Genetic and genomic research

Once research is funded, it is often expected to translate into meaningful goods for public knowledge, health or consumption — thus creating a cycle between public agenda setting, research, translation and public benefit. Every phase of the genomic research pipeline, including the recruitment of participants, the analysis of curated data and the interpretation of results, has been shaped by the assumed default of European ancestry populations. The expansion to other populations has followed the same model: data is often stratified by a combination of race, ethnicity and/or genetic similarity[26]. This framework often leads to the exclusion of multiracial individuals, who may not fit within these defined groupings and have unique genetic architectures in which entire chromosomes or large haplotype blocks are of disparate genetic ancestry, which may require additional considerations to account for linkage disequilibrium or allele frequency differences.

The recruitment and representation of multiracial individuals in genomic studies is limited and difficult to quantify in large-scale genomic studies, as detailed in Box 2[27]. Beyond participation, there remain steps along the data processing and analytical pipeline in which those who do not fit within a single ‘box”, whether delineated by race/ethnicity or by genetic similarity, are filtered out. Multiracial individuals are often removed during preliminary quality control steps that stratify based on race, ethnicity or a homogeneous genetic similarity grouping[4,28]. When race/ethnicity is missing, investigators often assign a label, such as by principal components using recent machine learning methods; if an individual’s determined genetic background does not fit cleanly within a cluster, they can end up being dropped from further analysis[29].

Past the filters of data processing and quality control, multiracial individuals also find themselves excluded from the discovery stage. It is common to stratify large-scale genomic studies, such as genome-wide association studies (GWAS), either by metrics of genetic similarity with often arbitrary cut-offs or by race/ethnicity, to prevent complications from population substructure[4]. However, this is often no longer necessary with the development of newer, underutilized methods that allow the pooling of individuals from multiple

genetic backgrounds. By directly modeling relatedness, for example through a genetic relatedness matrix, these statistical tools leverage shared ancestry across individuals who would otherwise be separated — thereby no longer necessitating the exclusion of multiracial individuals[30,31].

Another potential reason many researchers may stratify based on racial/ethnic categories is to capture unmeasured environmental confounders such as social determinants of health[32]. However, the use of these proxies is often imprecise and can lead to misinterpretation of results. Recent calls for the direct measurement of social determinants of health instead of an over-reliance on imprecise proxies[14] would not only result in more interpretable and robust findings, but minimize the need for stratification and enable the increased inclusion of multiracial individuals to better understand the role of genetics and environment in human health. However, in situations in which researchers may need to stratify, such as when examining population-specific alleles, they should provide justification for this practice as well as the decision-making process behind the definitions of the stratified study populations.

The division of genomic data into supposed discrete groups can also hinder the potential benefits of precision health[26]. For example, polygenic scores (PGS) often rely on previously published GWAS, which have historically been stratified by some combination of race, ethnicity and/or estimates of genetic similarity. These sometimes arbitrary designations are then carried forward when forming a reference population for the estimation of relative genetic risk, which further prevents the inclusion of multiracial individuals in translational research[2]. Even newer PGS development methods that include more than one population still require the formation of separate groups to account for multiple linkage disequilibrium and allele frequency patterns between populations assumed to be distinct[33]. Methods that account for local ancestry, a more granular estimate of genetic similarity at the level of haplotype blocks instead of the average across an entire genome, may improve performance and inclusion of multiracial individuals both within discovery analyses and in downstream studies, given the recency of admixture and the scale of segments from an inferred genetic background[34]. However, more research is needed to incorporate disparate genomic architecture not only between individuals but within a single individual. Additionally, open questions remain regarding the formation of appropriate reference groups to estimate relative and absolute risk.

Throughout genomic research, there are outstanding questions regarding ‘lumping and splitting’ of individuals and the extent to which individuals need to be grouped for data to be meaningful[4]. Taken together, these practices within genomic research compound and result in a dearth of results applicable to multiracial individuals, restricting downstream benefits and inviting downstream harms. Although recently the field of genetics has renewed efforts to develop statistical methods inclusive of diverse populations, it is essential that these be applied, when possible, with consideration of these limitations. Moving forward, a critical goal of analytical frameworks in human genetics should be to acknowledge and account for the complexity of human diversity that is not adequately accounted for in discrete bins that necessitate the exclusion of multiracial individuals.

Genetics and genomics in clinical care and population health

Once genomics research has demonstrated benefit, it is expected to translate to clinical and public health practice for individual and population health benefit. Like other historically excluded groups, multiracial individuals suffer inequities in the availability of health benefits and clinical services downstream of basic genomics research. However, the causes and consequences can differ for multiracial individuals compared to other marginalized monoracial groups. Health inequities for multiracial individuals occur at two levels: genetic test availability and performance, and access to genetic services.

Some genetic tests (such as next-generation sequencing, polygenic scores or carrier testing) are inherently limited to the populations represented in the research, often white or European-genetic-ancestry populations; this results in a higher rate of 'uncertain' results in non-white and non-European-genetic-ancestry populations, including but not limited to multiracial individuals[35]. One call to action for mitigating this gap has been to diversify biobanks, with the rationale that greater representation will result in a wider reach of target clinical audiences by elucidating the performance of tests in groups external to the original training data, including recent efforts to develop and validate PGS across diverse groups (such as the PRIMED consortium; https://primedconsortium.org/). Improved capture of self-identified race and ethnicity will be vital to these efforts, especially for multiracial individuals who are often miscategorized or consolidated into a single group[36]. When applying a lens of multiracial inclusivity, these efforts are helpful but insufficient. External validity still relies upon the assumption that there are in fact circumscribed and discrete populations external to the training data in which to validate, which may still exclude multiracial individuals.

Using validity across populations as the sole solution is a missed opportunity to question the processes in place for interpreting the clinical significance of genetic variation, along with the dependency on binning people to make meaning of variation. For example, PGS methods adjusting for population substructure still require binning of the tested individual within a single genetic similarity grouping and/or racial/ethnic label. Considering this, multiracial individuals would remain excluded from such tests or inappropriately binned, even with increased representation in reference biobanks, because their care pathways for directing or interpreting testing may require that each individual can first be categorized.

Binning of individuals in direct testing and care is not new to medicine and has relevance to criticisms about race-based medicine. Clinicians and public health researchers often utilize race rather than genetic ancestry, or use race as a proxy for genetic ancestry. Additionally, inconsistency between self-identified racial or ethnic identity and perceived identity in the medical system adds another layer to this use of an imperfect proxy. Differential treatment by race occurs in clinical genetics for a variety of reasons, including implicit biases and racial profiling; it plays out in access to genetic testing, genetic counseling, and downstream services following genetic testing[37].

Because multiracial individuals are often not thought to belong to one specific population, they may not be perceived as at 'genetic risk' for a particular disease if there are stereotyped

non-genetic risk factors associated with a population. Additionally, misunderstandings about ancestry-based limitations of testing may result in differential test utilization for different individuals by providers. For example, one aspect of inequities in access is that carrier testing may only be ordered on certain subpopulations with well-publicized founder mutations; this could exclude multiracial individuals for whom there is no referent subpopulation if providers do not consider such an individual a member of that subpopulation. Recent recommendations from the American College of Medical Genetics and Genomics (ACMG) directly address this barrier and outline that "carrier screening paradigms should be ethnic and population neutral", which will move clinical care away from this framework and enable multiracial individuals to benefit[38].

A multiracial lens offers an opportunity for inclusive design in providing person-centered care. Little is known about how multiracial individuals are subjected to structural barriers. For example, when one parent belongs to a more privileged racial group (typically white), it should not be assumed that their experiences will be a 'sum of parts' of their various backgrounds. Multiracial individuals are likely to have varied experiences in the perception of care or access to services based on their specific backgrounds due to heterogeneity in socially assigned race and self-identity[39]. The existence of multiracial individuals challenges the intent and utility of using race in healthcare, especially regarding genomic considerations; understanding their experiences may inform what person-centered care can look like. Genomic research that accounts for health disparities, social determinants of health, the availability and accessibility of health services, and health inequities could benefit from challenging the practice of REA categorization and discussion of a new REA framework that is more inclusive of multiracial individuals.

Moving forward to close the gap

Any conceptual or empirical framework that is unable to accommodate the 'fringe' cases that multiracial individuals represent will perpetuate our over-reliance on discrete categories and prevent equitable benefit-sharing in genetics. If we are going to reimagine the field of human genetics, it must be done in an inclusive manner. Our main argument remains that including multiracial individuals' experiences and relationships with REA provide an opportunity to utilize inclusive design practices[9]. This call to action is responsive to changing world demographics and includes multiracial individuals in efforts to promote health equity and representation for all populations. Table 1 draws upon the prior sections of this Comment to summarize our recommendations for achieving these objectives during each step of the research process.

Multiracial individuals bring into question the purpose and utility of continental groupings in genomics by illustrating the complexity of human history in a field that has long sought to reduce such complexity. Therefore, as we reimagine standards for the reporting and treatment of race, ethnicity and genetic ancestry, it is imperative to develop a framework that is flexible with respect to multiracial individuals. Such flexibility is crucial as we develop novel genomic tests (such as PGS) to aid in clinical care. We must move away from the possible reification of race-based medicine and toward a full accounting of the intricacies of genetic ancestry and environmental contributors (such as socioeconomic status

and residential segregation) to health when integrating genomics into clinical research and care.

Being inclusive of multiracial individuals when we develop REA frameworks will support ontologies that better align with contextual realities. Nevertheless, focusing solely on terminology runs the risk of overlooking other foundational issues that are preventing genomics from celebrating the constellation that is human diversity. The genomics' community's understanding of approaches that support inclusive REA uses are likely to be enhanced via the act of engaging in activities outlined in Table 1, with opportunities at all stages of translation to include real-world populations. Multiracial individuals present an opportunity for the research community and society to end their reliance on discrete categorization not only in word choice, but in our governmental policies, funding calls, research priorities, methods of analysis and clinical care delivery. These changes, we argue, will enhance access, inclusivity and benefit-sharing in genomics and produce better, more just health outcomes for us all.

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Box 1

Author positionality statements

Daphne O. Martschenko *(she/her)*:

I self-identify as a biracial African American and I am most often identified by others as Black. My parents both immigrated to the USA — my father as a child from the Ukraine and my mother as an adult from Nigeria. I was born in England and spent portions of my childhood living in various Eastern European countries, ever aware of the curiosity my biracial family sparked in passersby. My multicultural upbringing and challenges with my racial identity motivate my work investigating the social and ethical implications of genetic/genomics and the fraught and violent relationship between race, genetics and human behavior.

Hannah Wand *(she/her)*:

I identify as a biracial Asian American. My mother grew up as an orphan in Korea and immigrated to the USA as an adult. My father's family immigrated from Poland. They met in college and built a family of choice with other immigrants. Both of my parents had mixed feelings toward their national/cultural origins: my mother holds a lot of resentment for how Korea treated orphans as a social class, and my father is an atheist from a Polish Catholic community. This led to their having a scattered sense of cultural identity, and where they lapsed, I adopted values and traditions from my other 'family' members. This blended upbringing made me interested in the complexity of intersecting genetics with self-identity, family, generational health and culture. It's driven my clinical work as a genetic counselor, and research in public health genetics where societal interactions with genetics create complex challenges.

Genevieve L. Wojcik *(she/her)*:

I am unsure as to how I identify, as my experience as a biracial individual in the USA has largely been defined by what I am not, instead of what I am. My mother immigrated here from Taiwan and my father's parents from France and Poland. My research interests in genetic epidemiology for diverse, and specifically admixed, populations have been partially motivated by my background to ensure that discoveries will also benefit my loved ones, whether family or friends, with increased urgency for my multiracial children.

Jennifer L. Young *(she/her)*:

I identify as a biracial Asian American. My parents both immigrated to the USA, one from China and one from England. I grew up in a very international neighborhood in the midwestern USA, which exposed me to a range of different cultures, but people who identified as multiracial were still a significant minority in my hometown. Issues of racial identity and cross-cultural families have been at the center of my family systems research as well as my clinical work as a family therapist.

Box 2

The challenge of defining multiracial individuals

Describing multiracial individuals with both precision and inclusivity is a challenge. The EBI-NHGRI GWAS Catalog currently collapses genetic ancestry, geography, nationality and race when determining the 'ancestry' of GWAS participants. Participants can only be assigned to a single category, such as "Other admixed ancestry" or the more specific "African American or Afro-Caribbean" or "Hispanic or Latin American"[27]. However, individuals may also fall into "Other" or "Not Reported" depending on a specific study's definitions. The All of Us research program lists "More than one race/ethnicity" as a category with 6.6% of their participants. However, the collapsing of race and ethnicity within a single question makes this number uninterpretable on its own[40].

Although we have chosen to use "multiracial" throughout this Comment to ensure inclusivity grounded in social contexts, not genetics, other terms are used in the literature. This is an illustrative list intended to demonstrate heterogeneity and complexity among individuals who may not identify as monoracial. It is neither comprehensive nor weighted in importance or usage.

Further, we recognize that individuals' racial identities are shifting with the advent of molecular genetic data. In particular, the tendency to conflate genetic ancestry with race, coupled with direct-to-consumer genetic ancestry testing, is influencing how people racially identify[41].

Many of the terms that are often used for multiracial individuals are broad and nonspecific. Additionally, they may refer to concepts that are unrelated to the construct relevant to a specific genomic study.

- **Admixed:** refers to *genetic ancestry* independent of racial or ethnic identity. Some racial/ethnic groups are characterized in part by recent ancestry from more than one lineage (e.g., African American, Hispanic/Latino groups). Therefore, an individual who is admixed may identify as multiracial or choose to identify with a single racial/ethnic group.
- **Multiracial, biracial, mixed race:** referring to *race*, with biracial being limited to only two racial categories and mixed race being derogatory in certain contexts.
- **Multicultural:** referring only to *culture* and not necessarily to race, ethnicity or genetic ancestry.
- **Other:** a catch-all term that lacks precision and promotes 'otherization' of individuals.

Many terms that are too specific to refer to multiracial individuals at large originate from specific violent histories (for example, mulatto, hapa) or a particular cultural context[42]. In general, these terms are neither broadly accepted nor well understood among the individuals who may be referred to as such.

Additionally, the societal contexts in which we have defined the above terms often differ globally, compounding the complexity of defining and enumerating multiracial individuals[43,44]. These may include small, nation-specific communities or individuals who form a transnational community whose members share only the socially meaningful — however it is defined locally — experience of being considered racially mixed[45].

In short, terminology used in genomic studies, or any study in general, should be responsive to both the cultural contexts and the scope of ancestries included, genetic or non-genetic. A lack of precision and inclusiveness in terminology can hinder the characterization and translation of genomic findings, limiting downstream benefits and inducing downstream harms.

Table 1 |

Closing the gap in service of public health

Stage of scientific process	Suggestions to close the gap	
Agenda setting	Engage multiracial individuals in decision making and health equity initiatives across all stages	• Engage diverse array of multiracial stakeholders, including both participants and researchers—governmental policies and funding calls can encourage this • Require clear definitions of diversity or health disparity, inclusive to multiracial individuals, in funding calls, governmental policies and academic journal submission guidelines
Research conduct		• Recruit more multiracial participants • Avoid placing participants into discrete racial/ethnic/ancestral categories • If possible, pool individuals from multiple genetic backgrounds and leverage shared ancestry across groups
Research translation		• Include multiracial individuals in health equity efforts • Expand research frameworks to explicitly include the experiences of multiracial individuals in healthcare systems • Prioritize person-centered clinical genetics practice over previous race-based medicine approaches
Research communication		• Establish and follow standard guidelines on reporting race/ethnicity/ancestry, inclusive to multiracial individuals • Avoid grouping multiracial individuals into single monolithic categories • Disclose authors' positionality and biases