Regrettably, European and European-descent ancestries continue to dominate human genetic databases. With the emergence of heavily funded public and private initiatives to increase diversity in human genomics, it is of utmost relevance to take the necessary time to discuss the ethical considerations of including Indigenous and other historically marginalized populations — which are greatly underrepresented in genomics — in these studies. It is crucial to consider their perspectives and needs throughout to avoid further scientific exploitation and harm, as has shamefully happened in the past. Otherwise, we run the risk of using ‘diversity tokens’ to attract funding and prestigious journals without a real benefit for the participants.

The results obtained in the study by Acuña-Alonzo et al. were disruptive and were only possible thanks to the inclusion of a large cohort of Indigenous participants. However, the work does not address several ethical considerations that would be expected from a similar study today, such as specifying whether Indigenous participants were involved in the study design and had a say in the future use of their samples and data. Such considerations are now explicitly recommended in the Global Code of Conduct for Research in Resource-Poor Settings (https://www.globalcodeofconduct.org).

My hope is that human genomics reaches a balanced representation across ancestries, and that it does so ethically and centred on the needs of historically underserved populations in the study design.

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Competing interests
The author declares no competing interests.

IN BRIEF

DNA methylation and cell fate in mouse embryos
Regulated DNA methylation (by DNA methyltransferases (DNMTs)) and demethylation (by ten-eleven translocation (TET) methylcytosine dioxygenases) is critical for mouse embryonic development, but mechanistic details are not well understood. Here, Clark et al. used single-cell RNA sequencing to create a transcriptomic atlas of E8.5 mouse embryos mutant for either Dnmt or Tet genes. Although all major cell types were present in Dnmt-mutant embryos, the presence of pluripotency markers and overexpression of extra-embryonic genes indicated that DNMT activity is required to suppress previous (pluripotency) and alternative (trophoblast) cell fates. By contrast, Tet-mutant embryos had marked lineage biases. In particular, multi-omic analysis showed that the lack of primitive erythrocytes was due to the absence of TET-dependent demethylation of distal regulatory elements in these embryos. In addition to the novel insights provided by the atlas, it also represents a useful resource to the research community.

ORIGINAL ARTICLE Clark, S. J. et al. Single-cell multi-omics profiling links dynamic DNA methylation to cell fate decisions during mouse early organogenesis. Genome Biol. 23, 202 (2022)

PLAN GENOMICS
Towards gut-friendly grains
There is growing interest in developing foods that predictably modulate the human gut microbiome to promote health. To this end, Yang et al. developed a system to genetically analyse seed traits in Sorghum bicolor that are associated with changes in the abundance of microbial taxa and/or metabolites in the human gut microbiome. Of the 10 genomic loci identified, two were close to genes involved in condensed tannin biosynthesis. Indeed, subsequent analyses showed that condensed tannins regulate the abundance of taxa associated with these loci and, in particular, supported and promoted growth of Faecalibacterium prausnitzii, a beneficial bacterium that is typically depleted in the gut of individuals with inflammatory bowel disease. This study provides a framework for identifying seed traits in food crops that have health-promoting effects on the gut microbiome and that can be incorporated into crop improvement schemes.

ORIGINAL ARTICLE Yang, Q. et al. Genetic analysis of seed traits in Sorghum bicolor that affect the human gut microbiome. Nat. Commun. 13, 5641 (2022)

RNA
Target-directed microRNA degradation in Drosophila
Target-directed microRNA (miRNA) degradation (TDMD) is the process by which binding of a miRNA to its cognate RNA triggers degradation of the miRNA, rather than the RNA as typically occurs. Until now, only four established examples of endogenous TDMD, all involving mammalian transcripts, were known. Now, Kingston et al. report a further six transcripts — five miRNAs and the long non-coding RNA Margr — that trigger TDMD of one or more miRNAs in Drosophila melanogaster embryos. TDMD was essential for embryonic development: mutations that disrupt TDMD de-repressed members of the miR-3 and miR-310 families and caused embryonic lethality; and genetic perturbation of Margr affected miR-310 family members and cuticle development. The authors posit that more triggers and roles for TDMD remain to be discovered.

ORIGINAL ARTICLE Kingston, E. R. et al. Endogenous transcripts direct microRNA degradation in Drosophila, and this targeted degradation is required for proper embryonic development. Mol. Cell 81, 2022.08.029 (2022)