# Article information:

Graph pangenome captures missing heritability and empowers tomato breeding | Nature  
<https://www.nature.com/articles/s41586-022-04808-9>

# Article summary:

1. Missing heritability is a major obstacle to understanding biological questions and crop breeding.

2. A graph pangenome of tomato was constructed to capture missing heritability in GWAS and facilitate genomic breeding.

3. The graph pangenome was constructed using high-fidelity long reads and high-throughput chromosome conformation capture, resulting in an improved reference genome with fewer gaps than the previous build.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article provides a detailed description of the construction of a graph pangenome of tomato, which is intended to capture missing heritability in GWAS and facilitate genomic breeding. The authors provide evidence for the superiority of their approach over existing methods, such as mapping sequencing reads to a single linear reference genome, which can generate reference bias due to its inability to precisely map non-reference alleles. The authors also present data from simulations that demonstrate the accuracy of their method in identifying genetic variants.

The article appears to be well researched and reliable overall, however there are some potential biases that should be noted. For example, the authors do not discuss any potential risks associated with their approach or any possible limitations that could arise from using this method for capturing missing heritability or facilitating genomic breeding. Additionally, while the authors provide evidence for the superiority of their approach over existing methods, they do not explore any counterarguments or consider other approaches that could be used for this purpose. Furthermore, while the article does present both sides of the argument (i.e., why existing methods are inadequate and why their proposed method is superior), it does not present them equally; rather, it focuses more on promoting their own approach than exploring alternative solutions or discussing potential drawbacks or risks associated with it.

# Topics for further research:

* Potential risks of graph pangenome construction
* Alternative methods for capturing missing heritability
* Limitations of graph pangenome construction
* Accuracy of existing methods for GWAS
* Advantages of graph pangenome construction
* Genomic breeding applications of graph pangenome construction

# Report location:

<https://www.fullpicture.app/item/ec23fe51fe63088f9821306764eb79bb>