# Article information:

Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize | Genome Biology | Full Text  
<https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1273-4>

# Article summary:

1. This article presents a method for predicting transcriptional enhancers in the crop plant maize (Zea mays L. ssp. mays) by integrating available genome-wide DNA methylation data with newly generated maps for chromatin accessibility and histone 3 lysine 9 acetylation (H3K9ac) enrichment in young seedling and husk tissue.

2. Approximately 1500 intergenic regions, displaying low DNA methylation, high chromatin accessibility and H3K9ac enrichment, were classified as enhancer candidates.

3. The method identified three previously identified distal enhancers in maize, validating the new set of enhancer candidates and enlarging the toolbox for the functional characterization of gene regulation in the highly repetitive maize genome.

# 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 is generally reliable and trustworthy as it provides evidence to support its claims through references to other studies that have been conducted on similar topics. It also provides detailed information about the methods used to identify transcriptional enhancers in maize, which adds credibility to its findings. Furthermore, it includes a discussion section that highlights potential limitations of the study and suggests further research directions that could be taken to improve upon its results.

However, there are some potential biases present in the article that should be noted. For example, it does not provide any information about how many false positives may have been included among the 1500 intergenic regions classified as enhancer candidates or how this number was determined. Additionally, while it mentions potential limitations of the study such as incomplete coverage of epigenetic features due to technical constraints, it does not explore these issues further or discuss possible solutions for overcoming them. Finally, while it does mention potential risks associated with using transgenic plants for research purposes, it does not provide any details about these risks or discuss ways to mitigate them.

# Topics for further research:

* False positives in transcriptional enhancer identification
* Epigenetic features in maize
* Technical constraints in epigenetic research
* Risks associated with transgenic plants
* Mitigation strategies for transgenic plant risks
* Enhancer identification in other plant species

# Report location:

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