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Title:

Corrigendum: Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues (Front. Genet., (2021), 12, (664379), 10.3389/fgene.2021.664379)

Date:

2021-09-21

Citation:

Prowse-Wilkins, C. P., Wang, J., Xiang, R., Garner, J. B., Goddard, M. E. & Chamberlain, A. J. (2021). Corrigendum: Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues (Front. Genet., (2021), 12, (664379), 10.3389/fgene.2021.664379). Frontiers in Genetics, 12, <https://doi.org/10.3389/fgene.2021.757331>.

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# Corrigendum: Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues

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**Keywords:** bovine, ChIP-seq, Histone modifications, function, causal variants, differential binding, annotation, chromHMM

## OPEN ACCESS

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### Specialty section:

This article was submitted to  
Livestock Genomics,  
a section of the journal  
Frontiers in Genetics

**Received:** 12 August 2021

**Accepted:** 07 September 2021

**Published:** 21 September 2021

### Citation:

Prowse-Wilkins CP, Wang J, Xiang R,  
Garner JB, Goddard ME and  
Chamberlain AJ (2021) Corrigendum:  
Putative Causal Variants Are Enriched  
in Annotated Functional Regions From  
Six Bovine Tissues.  
Front. Genet. 12:757331.  
doi: 10.3389/fgene.2021.757331

## A Corrigendum on:

### Putative Causal Variants Are Enriched in Annotated Functional Regions From Six BovineTissues

by Prowse-Wilkins C. P., Wang J., Xiang R., Garner J. B., Goddard M. E., and Chamberlain A. J. (2021).  
Front. Genet. 12:664379. doi:10.3389/fgene.2021.664379

In the original article, there was an error in the formula described for calculation of enrichment. This was a mistake in the text only and was not the method used to calculate enrichment.

A correction has been made to **Materials and Methods, Enrichment of Putative Causal SNPs in Functional Regions, Paragraph 2:**

“Enrichment = (C/A)/(B/D) where: A is the number of positions under peaks, B is the number of positions that were putative causal SNPs, C is the number of positions under peaks and also a putative causal SNP and D is the number of positions in the genome”

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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