



OPEN

Author Correction: Population structure and identification of genomic regions associated with productive traits in five Italian beef cattle breeds

Daniele Colombi, Giacomo Rovelli, Maria Gracia Luigi-Sierra, Simone Ceccobelli, Dailu Guan, Francesco Perini, Fiorella Sbarra, Andrea Quaglia, Francesca Maria Sarti, Marina Pasquini, Marcel Amills & Emiliano Lasagna

Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-024-59269-z>, published online 12 April 2024

The original version of this Article contained errors. In the Results and discussion section, under the subheading ‘Genome-wide association study for productive traits’,

“The muscular hypertrophy phenotype segregates in the MAR breed due to a mutation at nucleotide 874 in exon 3 (g.874G > T) in the *MSTN* gene²⁷. This point mutation has a remarkable effect on the myostatin protein changing, a codon for glutamic acid into a stop codon (E291X variant), that blocks the translation of 254 bases of the third exon. The variant rs3423130174 (*P*-value 3.640819e−23) is indeed such causative mutation and confirms the implication of the third exon in the proper functioning of myostatin because it encodes the C-terminal region that is fundamental for the protein tridimensional folding²⁷.”

now reads:

“The muscular hypertrophy phenotype segregates in the MAR breed due to a mutation at nucleotide 871 in exon 3 (ENSBTAT00000015674.6:c.871G>T, represented by Ensembl sequence ENSBTAT00000015674.6) in the *MSTN* gene²⁷. This point mutation has a remarkable effect on the myostatin protein, changing a codon for glutamic acid into a stop codon (E291X variant) that blocks the translation of 257 bases of the third exon. The variant *MSTN*_SNP (*P*-value 3.640819e−23) is indeed such causative mutation and confirms the implication of the third exon in the proper functioning of myostatin because it encodes the C-terminal region that is fundamental for the protein tridimensional folding²⁷.”

Additionally, in Table 3, the position for Marchigiana breed in the top row was incorrect,

“rs3423130174 / 2 / 6283726 / T / 0.132 / 0.9037 / 0.0887 / 3.64E−23 / *MSTN*”

now reads:

“*MSTN*_SNP / 2 / 6283727 / T / 0.132 / 0.9037 / 0.0887 / 3.64E−23 / *MSTN*”.

As a result of this error, Figure 3 was incorrect. The original Figure 3 and accompanying legend appear below.

This correction does not affect the results and conclusions of this article.

The original Article has been corrected.

Published online: 16 April 2025

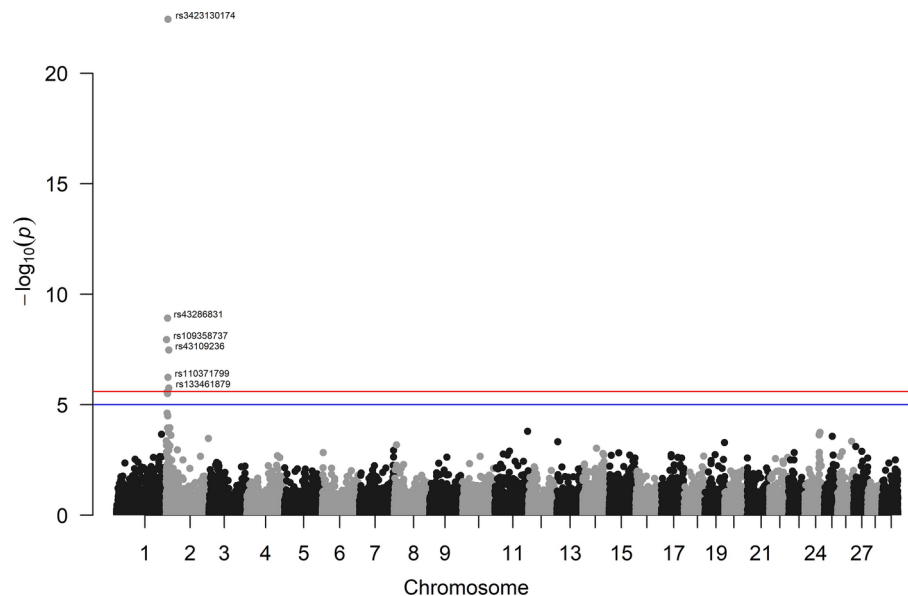


Fig. 3. Genome wide significant associations between SNPs and muscularity in Marchigiana breed. Negative $\log_{10}P$ -values (Y-axis) of the association between SNPs and the muscularity are plotted against the genomic location of each SNP marker (X-axis). The red line represents the Bonferroni-corrected threshold of significance, while the blue line represents the suggestive threshold of significance (P -value of 0.05).

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2025