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Genomics, Transcriptomics, and Computational Biology for Biodiversity Studies and Quality-Related Traits Selection in Livestock

Collection Editor:

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Message from the Collection Editor

Dear Colleagues,

Research efforts in livestock include the identification of the chromosomal regions and candidate genes related to novel complex and economically important traits, together with biodiversity and local breeds preservation.

Taking advantage of modern multi-omic approaches for complex traits like high-throughput genotyping, whole-genome sequencing, expression analysis (e.g., GWA studies and RNA sequencing analysis) and so on, it is useful to understand the degree of activation of the metabolic and physiological mechanisms involved with the traits of interest.

We invite original research papers on animal breeding, population genetics, genetic association studies, transcriptomics, and quantitative genomics in livestock, which address the biological mechanisms underlying the expression of complex (quantitative) traits, to give insight into the origin and impact of genetic variation and population stratification at the genome scale, so as to explore genomics opportunities for long-term selection strategies.

mdpi.com/si/34385

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Message from the Editor-in-Chief

Animals is an on-line open access journal that was first published in 2011. *Animals* adheres to rigorous peerreview and editorial processes and publishes only high quality manuscripts that address important issues in the many varied disciplines that involve animals, with a focus on animal science, animal welfare and animal ethics. *Animals* is covered in the Science Citation Index Expanded (SCIE) in Web of Science, with the latest Impact Factor: 3.0 (2022, ranks 12 /62 (Q1) in ‘Agriculture, Dairy & Animal Science’; 13/143 (Q1) in ‘Veterinary Sciences’), 5-Year Impact Factor: 3.2.

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Journal Rank: JCR - Q1 (Veterinary Sciences) / CiteScore - Q1 (General Veterinary)

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