

Resource Summary Report

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Genomic Annotation in Livestock for positional candidate LOci

RRID:SCR_019212

Type: Tool

Proper Citation

Genomic Annotation in Livestock for positional candidate LOci (RRID:SCR_019212)

Resource Information

URL: <https://cran.r-project.org/web/packages/GALLO/vignettes/GALLO.html>

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Description: Software R package developed for accurate annotation of genes and quantitative trait loci located in regions identified in common genomic analyses performed in livestock, such as Genome Wide Association Studies and transcriptomics using RNA-Sequencing. Allows graphical visualization of gene and QTL annotation results, data comparison among different grouping factors like methods, breeds, tissues, statistical models, studies and QTL enrichment in different livestock species including cattle, pigs, sheep, and chickens.

Abbreviations: GALLO

Resource Type: software resource, software toolkit

Keywords: QTLs, multi-omics integration, qtl annotation, gene annotation, datamining, qtl enrichment analysis, livestock, bio.tools

Availability: Free, Freely available

Resource Name: Genomic Annotation in Livestock for positional candidate LOci

Resource ID: SCR_019212

Alternate IDs:

biotools:genomic_annotation_in_livestock_for_positional_candidate_loci_gallo

Alternate URLs:

https://bio.tools/genomic_annotation_in_livestock_for_positional_candidate_loci_gallo

Record Creation Time: 20220129T080344+0000

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Ratings and Alerts

No rating or validation information has been found for Genomic Annotation in Livestock for positional candidate LOci.

No alerts have been found for Genomic Annotation in Livestock for positional candidate LOci.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Goli RC, et al. (2026) Adaptive introgression shaping genomic adaptation and ancestral mosaicism of Changthangi sheep for high-altitude survival and pashmina excellence. BMC genomics, 27(1).

Blaschikoff L, et al. (2026) Genomic Variation and Population Structure of Portuguese Native Dog Breeds. Animal genetics, 57(3), e70144.

da Silva Oliveira E, et al. (2026) Integrating reaction norm models and genome-wide association analyses to reveal the genetic architecture and environmental sensitivity of sexual precocity in Nellore cattle. BMC genomics, 27(1), 200.

Campos G, et al. (2026) A comprehensive genomic characterization of Nellore cattle. BMC genomics, 27(1).

Ojo AO, et al. (2026) Genome-wide association study of mature cow size traits in American Angus cattle. Mammalian genome : official journal of the International Mammalian Genome Society, 37(1).

Shirak A, et al. (2026) Gene variants in the pheromone vomeronasal receptors and QTLs around behavioral and fat metabolism genes associated with altered feed efficiency in cattle. Scientific reports, 16(1).

Neto JBS, et al. (2026) Modeling genotype-by-environment interactions across climatic conditions reveals environment-specific genomic regions and candidate genes underlying feed efficiency traits in tropical beef cattle. Scientific reports, 16(1), 643.

Arikawa LM, et al. (2025) Whole-genome sequencing GWAS reveals bovine genomic effects on enteric methane emissions in beef cattle. Scientific reports, 16(1), 2961.

- Wang Z, et al. (2025) Genomic insights into the demographic history and local adaptation of wild boars across Eurasia. *Cell genomics*, 5(9), 100954.
- Lai D, et al. (2025) Integrative Genomic, Transcriptomic and Epigenomic Analysis Reveals cis-regulatory Contributions to High-altitude Adaptation in Tibetan Pigs. *Molecular biology and evolution*, 42(7).
- Olasege BS, et al. (2024) Genomic regions and biological pathways associated with sex-limited reproductive traits in bovine species. *Journal of animal science*, 102.
- Mulim HA, et al. (2024) Genetic background of juniper (*Juniperus* spp.) consumption predicted by fecal near-infrared spectroscopy in divergently selected goats raised in harsh rangeland environments. *BMC genomics*, 25(1), 107.
- Kim J, et al. (2024) Runs of homozygosity analysis for selection signatures in the Yellow Korean native chicken. *Animal bioscience*, 37(10), 1683.
- de Oliveira LF, et al. (2024) Genomic regions, candidate genes, and pleiotropic variants associated with physiological and anatomical indicators of heat stress response in lactating sows. *BMC genomics*, 25(1), 467.
- Benfica LF, et al. (2024) Genome-wide association study between copy number variation and feeding behavior, feed efficiency, and growth traits in Nellore cattle. *BMC genomics*, 25(1), 54.
- Wang Z, et al. (2024) Whole-genome analysis reveals distinct adaptation signatures to diverse environments in Chinese domestic pigs. *Journal of animal science and biotechnology*, 15(1), 97.
- Gouveia GC, et al. (2023) Unravelling the genetic variability of host resilience to endo- and ectoparasites in Nellore commercial herds. *Genetics, selection, evolution : GSE*, 55(1), 81.
- Braga LG, et al. (2023) Identification of copy number variations in the genome of Dairy Gir cattle. *PloS one*, 18(4), e0284085.
- Badia-Bringu?? G, et al. (2023) Association between High Interferon-Gamma Production in Avian Tuberculin-Stimulated Blood from *Mycobacterium avium* subsp. *paratuberculosis*-Infected Cattle and Candidate Genes Implicated in Necroptosis. *Microorganisms*, 11(7).
- Martin AAA, et al. (2022) Unravelling the genetics of non-random fertilization associated with gametic incompatibility. *Scientific reports*, 12(1), 22314.