

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 toolkit, software resource

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

Record Last Update: 20260729T044455+0000

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 14 mentions in open access literature.

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

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.

Kim J, et al. (2024) Runs of homozygosity analysis for selection signatures in the Yellow Korean native chicken. *Animal bioscience*, 37(10), 1683.

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.

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.

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.

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.

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).

Braga LG, et al. (2023) Identification of copy number variations in the genome of Dairy Gir cattle. *PloS one*, 18(4), e0284085.

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.

Martin AAA, et al. (2022) Unravelling the genetics of non-random fertilization associated with gametic incompatibility. *Scientific reports*, 12(1), 22314.

Gozalo-Marcilla M, et al. (2021) Genetic architecture and major genes for backfat thickness in pig lines of diverse genetic backgrounds. *Genetics, selection, evolution : GSE*, 53(1), 76.

Fonseca PAS, et al. (2020) GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. *GigaScience*, 9(12).