Resource Summary Report

Generated by RRID on Aug 12, 2026

MetaVolcanoR

RRID:SCR_018549
Type: Tool

Proper Citation

MetaVolcanoR (RRID:SCR_018549)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/MetaVolcanoR.html

Proper Citation: MetaVolcanoR (RRID:SCR_018549)

Description: Software R package to combine differential gene expression results. Differential expression meta analysis tool. Gene expression meta analysis visualization tool. Used to identify genes whose expression is consistently perturbed across several studies., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: software toolkit, software resource

Keywords: Differential gene expression, meta analysis, visualization tool, identify gene, gene expression result

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MetaVolcanoR

Resource ID: SCR_018549

Alternate URLs: https://github.com/csbl-usp/MetaVolcanoR

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260810T040715+0000

Ratings and Alerts

No rating or validation information has been found for MetaVolcanoR.

No alerts have been found for MetaVolcanoR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Navas A, et al. (2025) Plasma Proteomic Signature as a Predictor of Age Advancement in People Living With HIV. Aging cell, 24(5), e14468.

Burankova Y, et al. (2025) Privacy-preserving multicenter differential protein abundance analysis with FedProt. Nature computational science, 5(8), 675.

Bari SM, et al. (2025) A meta-analysis of public RNA-Seq data identifies conserved stress responses in rainbow trout. BMC genomics, 26(1), 999.

Stone E, et al. (2025) Transcriptional meta-analysis and immune cell profiles reveal altered neutrophil dynamics in chronic atrial fibrillation. Royal Society open science, 12(3), 241102.

Wang Y, et al. (2025) Meta-analysis of muscle transcriptome data identifies key genes influencing intramuscular fat content in pigs. Animal bioscience, 38(8), 1622.

Nagarajan G, et al. (2024) Distinct expression profile reveals glia involvement in the trigeminal system attributing to post-traumatic headache. The journal of headache and pain, 25(1), 203.

Garrido-Torres N, et al. (2024) miRNAs as biomarkers of autism spectrum disorder: a systematic review and meta-analysis. European child & adolescent psychiatry, 33(9), 2957.

Du H, et al. (2024) Substrate Stiffness Dictates Unique Doxorubicin-induced Senescence-associated Secretory Phenotypes and Transcriptomic Signatures in Human Pulmonary Fibroblasts. bioRxiv : the preprint server for biology.

Soueidan A, et al. (2024) Pooled analysis of oral microbiome profiles defines robust signatures associated with periodontitis. mSystems, 9(11), e0093024.

Wang CZ, et al. (2023) Comprehensive characterization of TGFB1 across hematological malignancies. Scientific reports, 13(1), 19107.

Alotaibi A, et al. (2023) Global comparative transcriptomes uncover novel and population-specific gene expression in esophageal squamous cell carcinoma. Infectious agents and cancer, 18(1), 47.

Handle F, et al. (2023) The Oncogenic Protein Kinase/ATPase RIOK1 Is Up-Regulated via the c-myc/E2F Transcription Factor Axis in Prostate Cancer. The American journal of pathology, 193(9), 1284.

Barton A, et al. (2023) Early transcriptional responses to human enteric fever challenge. Infection and immunity, 91(10), e0010823.

Taylor J, et al. (2023) Transcriptomic Comparison of Human Peripartum and Dilated Cardiomyopathy Identifies Differences in Key Disease Pathways. Journal of cardiovascular development and disease, 10(5).

Brown MR, et al. (2022) The nuclear receptor REV-ERB? is implicated in the alteration of ?-cell autophagy and survival under diabetogenic conditions. Cell death & disease, 13(4), 353.

Yi J, et al. (2022) Integrative Transcriptomic Analysis Identify Potential m6A Pathway-Related Drugs That Inhibit Cancer Cell Proliferation. Genes, 13(11).

Lee KA, et al. (2022) Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature medicine, 28(3), 535.

Jimenez L, et al. (2021) Acid pH Increases SARS-CoV-2 Infection and the Risk of Death by COVID-19. Frontiers in medicine, 8, 637885.

Basic V, et al. (2021) Integrative meta-analysis of gene expression profiles identifies FEN1 and ENDOU as potential diagnostic biomarkers for cervical squamous cell carcinoma. Oncology letters, 22(6), 840.

Pinto BGG, et al. (2020) ACE2 Expression is Increased in the Lungs of Patients with Comorbidities Associated with Severe COVID-19. medRxiv : the preprint server for health sciences.