

Resource Summary Report

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MBASED

RRID:SCR_002584

Type: Tool

Proper Citation

MBASED (RRID:SCR_002584)

Resource Information

URL: <http://www.bioconductor.org/packages/devel/bioc/html/MBASED.html>

Proper Citation: MBASED (RRID:SCR_002584)

Description: Software package containing functions for allele-specific gene expression (ASE) analysis using meta-analysis based allele-specific expression detection.

Synonyms: Meta-analysis Based Allele-Specific Expression Detection, MBASED - Package containing functions for ASE analysis using Meta-analysis Based Allele-Specific Expression Detection

Resource Type: software resource

Defining Citation: [PMID:25315065](#)

Keywords: software package, unix/linux, mac os x, windows, r, gene expression, sequencing, transcription

Availability: Free, Available for download, Freely available

Resource Name: MBASED

Resource ID: SCR_002584

Alternate IDs: OMICS_05502

Alternate URLs: <http://www.bioconductor.org/packages/release/bioc/html/MBASED.html>

License: Artistic License, v2

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260725T190526+0000

Ratings and Alerts

No rating or validation information has been found for MBASED.

No alerts have been found for MBASED.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Ramasamy R, et al. (2025) Genome-wide allele-specific expression in multi-tissue samples from healthy male baboons reveals the transcriptional complexity of mammals. *Cell genomics*, 5(5), 100823.

Zhang Y, et al. (2025) M6Allele: a toolkit for detection of allele-specific RNA N6-methyladenosine modifications. *GigaScience*, 14.

Andersson J, et al. (2024) Characterizing the allele-specific gene expression landscape in high hyperdiploid acute lymphoblastic leukemia with BASE. *Scientific reports*, 14(1), 23181.

O'Neill K, et al. (2024) Long-read sequencing of an advanced cancer cohort resolves rearrangements, unravels haplotypes, and reveals methylation landscapes. *Cell genomics*, 4(11), 100674.

Dyer NA, et al. (2023) Mechanisms of transcriptional regulation in *Anopheles gambiae* revealed by allele specific expression. *bioRxiv : the preprint server for biology*.

Villarroel CA, et al. (2021) Uncovering Divergence in Gene Expression Regulation in the Adaptation of Yeast to Nitrogen Scarcity. *mSystems*, 6(4), e0046621.

McGirr JA, et al. (2021) Few Fixed Variants between Trophic Specialist Pupfish Species Reveal Candidate Cis-Regulatory Alleles Underlying Rapid Craniofacial Divergence. *Molecular biology and evolution*, 38(2), 405.

Berardi AE, et al. (2021) Complex evolution of novel red floral color in *Petunia*. *The Plant cell*, 33(7), 2273.

Przytycki PF, et al. (2020) Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. *Cell systems*, 10(2), 193.

Yarahmadv T, et al. (2020) Identification of transcription factors controlling floral morphology in wild *Petunia* species with contrasting pollination syndromes. *The Plant journal : for cell and molecular biology*, 104(2), 289.

Fan J, et al. (2020) ASEP: Gene-based detection of allele-specific expression across individuals in a population by RNA sequencing. *PLoS genetics*, 16(5), e1008786.

Greenwald WW, et al. (2019) Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. *Nature communications*, 10(1), 1054.

McGirr JA, et al. (2019) Hybrid gene misregulation in multiple developing tissues within a recent adaptive radiation of *Cyprinodon* pupfishes. *PloS one*, 14(7), e0218899.

Banos G, et al. (2019) Genetic and genomic analyses underpin the feasibility of concomitant genetic improvement of milk yield and mastitis resistance in dairy sheep. *PloS one*, 14(11), e0214346.

York RA, et al. (2018) Behavior-dependent cis regulation reveals genes and pathways associated with bower building in cichlid fishes. *Proceedings of the National Academy of Sciences of the United States of America*, 115(47), E11081.

DeBoever C, et al. (2017) Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. *Cell stem cell*, 20(4), 533.

Nieminen TT, et al. (2016) Pseudoexons provide a mechanism for allele-specific expression of APC in familial adenomatous polyposis. *Oncotarget*, 7(43), 70685.