

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

DSS

RRID:SCR_002754

Type: Tool

Proper Citation

DSS (RRID:SCR_002754)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/DSS.html>

Proper Citation: DSS (RRID:SCR_002754)

Description: Software R library performing differential analysis for count-based sequencing data. It detects differentially expressed genes (DEGs) from RNA-seq, and differentially methylated loci or regions (DML/DMRs) from bisulfite sequencing (BS-seq). The core of DSS is a new dispersion shrinkage method for estimating the dispersion parameter from Gamma-Poisson or Beta-Binomial distributions.

Synonyms: Dispersion Shrinkage for Sequencing data, DSS - Dispersion shrinkage for sequencing data

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:24561809](#)

Keywords: standalone software, unix/linux, mac os x, windows, r, differential expression, rna-seq, chip-seq, dna methylation, differential expression, sequencing

Availability: Free, Freely available, Available for download

Resource Name: DSS

Resource ID: SCR_002754

Alternate IDs: OMICS_03273

License: GNU General Public License

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260912T195546+0000

Ratings and Alerts

No rating or validation information has been found for DSS.

No alerts have been found for DSS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Zhang Q, et al. (2026) Integrated analysis of DNA methylation and transcriptome profiles in broiler heart and lung tissues reveals epigenetic regulatory mechanisms underlying ascites syndrome. Poultry science, 105(1), 106034.

Karwaciak I, et al. (2025) Staphylococcus aureus ??-hemolysin induces DNA methylation changes in human Th1 cells. Immunologic research, 73(1), 95.

Akbulut S, et al. (2024) Role of Epigenetic Factors in Determining the Biological Behavior and Prognosis of Hepatocellular Carcinoma. Diagnostics (Basel, Switzerland), 14(17).

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.

Graham MK, et al. (2024) The TERT Promoter is Polycomb-Repressed in Neuroblastoma Cells with Long Telomeres. Cancer research communications, 4(6), 1533.

Ewing AD, et al. (2020) Nanopore Sequencing Enables Comprehensive Transposable Element Epigenomic Profiling. Molecular cell, 80(5), 915.

Luo C, et al. (2019) Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. eLife, 8.

Ziller MJ, et al. (2018) Dissecting the Functional Consequences of De Novo DNA Methylation Dynamics in Human Motor Neuron Differentiation and Physiology. Cell stem cell, 22(4), 559.

Gaspar JM, et al. (2017) DMRfinder: efficiently identifying differentially methylated regions from MethylC-seq data. BMC bioinformatics, 18(1), 528.