

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 8, 2026

## sva package

RRID:SCR\_012836

Type: Tool

### Proper Citation

sva package (RRID:SCR\_012836)

### Resource Information

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

**Proper Citation:** sva package (RRID:SCR\_012836)

**Description:** Contains functions for removing batch effects and other unwanted variation in high-throughput experiment.

**Abbreviations:** sva package

**Synonyms:** Surrogate Variable Analysis

**Resource Type:** software resource

**Resource Name:** sva package

**Resource ID:** SCR\_012836

**Alternate IDs:** OMICS\_00861

**Record Creation Time:** 20220129T080312+0000

**Record Last Update:** 20260808T185947+0000

### Ratings and Alerts

No rating or validation information has been found for sva package.

No alerts have been found for sva package.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 100 mentions in open access literature.

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

Du JO, et al. (2026) Machine learning-driven transcriptomic and single-cell profiling of programmed cell death patterns in colon cancer. *Science progress*, 109(1), 368504261432995.

Kinget L, et al. (2026) Prognostic and Predictive Value of the Clearseq1-4 Tumor Microenvironment Classification in Localized and Metastatic Clear-Cell Renal Cell Carcinoma. *Cancer research communications*, 6(4), 884.

Yan X, et al. (2026) NDC80 kinetochore complex component is a potential molecular target of adenoid cystic carcinoma. *Oncology letters*, 31(3), 114.

Hu Z, et al. (2026) Multi-omics integration and machine learning reveal gut-immune signatures in idiopathic pulmonary fibrosis: insights from bulk RNA-seq, single-cell profiles, spatial transcriptomics, and experimental validation. *Frontiers in immunology*, 17, 1730289.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Thursby SJ, et al. (2026) Epigenetic Instability-Based Metrics in Cell-Free DNA for Early Cancer Detection. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1528.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtube Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Abdi K, et al. (2026) miR-132 overexpression is associated with modulation in miR-21 expression and glioblastoma cell behavior. *PloS one*, 21(7), e0352119.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. *Cell reports*, 45(1), 116835.

Ayabe H, et al. (2025) Cellular crosstalk mediated by TGF- $\beta$  drives epithelial-mesenchymal transition in patient-derived multi-compartment biliary organoids. *Nature communications*, 16(1), 6575.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. *EBioMedicine*, 113, 105569.

Xiong J, et al. (2025) Screening of PANoptosis regulator-associated long noncoding RNAs and construction of a survival prognostic model in cutaneous melanoma. *Translational*

cancer research, 14(9), 5979.

Rohan P, et al. (2025) High expression of THY1 is a prognostic marker for gastric Cancer: Deciphering its transcriptional regulation as a component of the Epithelial-mesenchymal transition. *Biochemistry and biophysics reports*, 42, 102050.

Tan C, et al. (2025) A Machine Learning-Based Diagnostic Nomogram for Moyamoya Disease: The Validation of Hypoxia-Immune Gene Signatures. *Bioengineering (Basel, Switzerland)*, 12(6).

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

Alfaro-García JP, et al. (2025) Characterization of the Temporal Dynamics of the Endothelial-Mesenchymal-like Transition Induced by Soluble Factors from Dengue Virus Infection in Microvascular Endothelial Cells. *International journal of molecular sciences*, 26(5).

Huang P, et al. (2025) Identification of aberrantly expressed genes during aging in the mouse heart via integrated bioinformatics analysis. *Medicine*, 104(13), e41972.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. *medRxiv : the preprint server for health sciences*.

Wang X, et al. (2025) Integrative machine learning and transcriptomic analysis identifies key molecular targets in MNPN-associated oral squamous cell carcinoma pathogenesis. *Frontiers in bioinformatics*, 5, 1664576.