

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 13, 2026

Cufflinks

RRID:SCR_014597

Type: Tool

Proper Citation

Cufflinks (RRID:SCR_014597)

Resource Information

URL: <http://cole-trapnell-lab.github.io/cufflinks/cuffmerge/>

Proper Citation: Cufflinks (RRID:SCR_014597)

Description: Software tool for transcriptome assembly and differential expression analysis for RNA-Seq. Includes script called cuffmerge that can be used to merge together several Cufflinks assemblies. It also handles running Cuffcompare as well as automatically filtering a number of transfrags that are likely to be artifacts. If the researcher has a reference GTF file, the researcher can provide it to the script to more effectively merge novel isoforms and maximize overall assembly quality.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [DOI:10.1038/nbt.1621](https://doi.org/10.1038/nbt.1621)

Keywords: transcriptome, rna-seq, rna seq, cuffmerge, cufflink, cuffcompare, transfrags, artifacts, gtf file, transcriptome assembly, expression analysis, bio.tools, bio.tools

Availability: Acknowledgement requested, Source code available on GitHub

Resource Name: Cufflinks

Resource ID: SCR_014597

Alternate IDs: biotools:cufflinks, OMICS_01304, SCR_013307

Alternate URLs: <https://github.com/cole-trapnell-lab/cufflinks>, <https://bio.tools/cufflinks>, <https://sources.debian.org/src/cufflinks/>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260912T195819+0000

Ratings and Alerts

No rating or validation information has been found for Cufflinks.

No alerts have been found for Cufflinks.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9083 mentions in open access literature.

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

Xue Y, et al. (2026) Mucosal-associated invariant T cells recognize a tumor-derived metabolite in the DNA synthesis pathway. *Frontiers in immunology*, 17, 1797918.

Kuo HH, et al. (2026) Patient-derived organoids across cancers reveal conserved tumor heterogeneity and actionable therapeutic vulnerabilities. *Science advances*, 12(26), eadz3351.

Kim DH, et al. (2026) Tumor Exosomal L1 Cell Adhesion Molecule Promotes Brain Metastasis of Lung Cancer. *Research (Washington, D.C.)*, 9, 1126.

Boudjadi S, et al. (2026) Involvement of the FGF8/FGF Receptor Signaling Pathway in the Maintenance and Progression of Fusion-Positive Rhabdomyosarcoma. *Molecular cancer therapeutics*, 25(3), 493.

Komura S, et al. (2026) Expression of Glycoprotein B (gB) Correlates With Poor Prognosis in Nasopharyngeal Carcinoma. *Cancer science*, 117(5), 1481.

Nakajo S, et al. (2026) Hypoxic CAF studies unveil PTHrP?vitamin D?RAS axis as pivotal in the CAF. *Oncology reports*, 55(6).

Gautier M, et al. (2026) A regulatory circuitry driving a noradrenergic to mesenchymal transition highlights YAP/TAZ as critical players in neuroblastoma plasticity. *Cell reports*, 45(5), 117351.

Yu YH, et al. (2026) Transcriptome and microbiota analysis reveal differences in the cecum of weaning pigs in response to different dietary crude protein levels. *Animal bioscience*, 39(1), 250135.

Zeng H, et al. (2026) The ZmFKF1b-ZmDi19-5 Regulatory Module Coordinates Drought Tolerance and Flowering Time in Maize. *Plant biotechnology journal*, 24(3), 1044.

Li N, et al. (2026) A Trypsin-Like Serine Protease ZmNAL1a Fine-Tunes Maize Floral Transition and Flowering Time. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(10), e14635.

Cai Y, et al. (2026) EIF5A Couples Translational Control With Transcriptional Reprogramming Through Chromocenter Reorganization During Spermiogenesis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(9), e17423.

Zhao ZY, et al. (2026) Sodium butyrate regulates proliferation of skeletal muscle satellite cells in Arbas cashmere goats: molecular mechanisms from an in vitro study. *BMC veterinary research*, 22(1), 93.

Jiao H, et al. (2026) HUWE1 in Skeletal Muscle Prevents Muscle Fatigue via Maintaining Iron and Calcium Homeostasis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e16719.

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. *Nature*, 649(8095), 216.

Torland LA, et al. (2026) Multi-platform analysis of the tumor immune microenvironment associated with breast cancer subtypes. *Oncoimmunology*, 15(1), 2610535.

Zhou H, et al. (2026) Hyperandrogenemia Induces Trophoblast Ferroptosis and Early Pregnancy Loss in Patients With PCOS via CMA-Dependent FTH1 Degradation. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(12), e06091.

Lei FL, et al. (2026) Chromosome-level genome assembly of *Nemipterus japonicus* based on PacBio sequencing and Hi-C technology. *Scientific data*, 13(1), 218.

Foote AG, et al. (2026) A non-canonical role of Myc in programming basal cells as sentinels of upper airway immunity during influenza infection. *bioRxiv : the preprint server for biology*.

Feng Z, et al. (2026) Essential role of NONO-HOXA1-Wnt axis in cardiomyocyte differentiation. *Nature communications*, 17(1).

Ito H, et al. (2026) Gene expression changes in lymphocytes and monocytes from patients with traumatic brain injury. *Scientific reports*, 16(1).