

Resource Summary Report

Generated by [NIF](#) on Sep 18, 2026

Cuffmerge

RRID:SCR_015688

Type: Tool

Proper Citation

Cuffmerge (RRID:SCR_015688)

Resource Information

URL:

<http://software.broadinstitute.org/cancer/software/genepattern/modules/docs/Cuffmerge/3>

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Description: The main purpose of Cufflinks.cuffmerge is to merge together several Cufflinks assemblies, making it easier to produce an assembly GTF file suitable for use with Cufflinks.cuffdiff. Cufflinks.cuffmerge also runs Cuffcompare in the background and automatically filters out transcribed fragments (transfrags) that are likely to be artifacts. Trapnell C, Hendrickson D, Sauvageau S, Goff L, Rinn JL, Pachter L. Differential analysis of gene regulation at transcript resolution with RNA-seq. Nature Biotechnology. 2013;31:46-53.

Resource Type: software tool

Resource Name: Cuffmerge

Resource ID: SCR_015688

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260912T195829+0000

Ratings and Alerts

No rating or validation information has been found for Cuffmerge.

No alerts have been found for Cuffmerge.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 951 mentions in open access literature.

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

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. *Science* (New York, N.Y.), 391(6784), eadw9154.

Wu L, et al. (2026) Genome-Wide Analysis of the lncRNAs and miRNAs Involved in Flower Development in Radish. *Plant direct*, 10(2), e70155.

Yingping W, et al. (2026) Expression and regulation of lncRNAs in the testes of Yili geese with high and low sperm motility. *BMC genomics*, 27(1).

OuYang F, et al. (2026) Response of DNA methylation and gene expression to light treatments in Norway spruce [*Picea abies* (L.) Karst.]. *BMC genomics*, 27(1).

Wu G, et al. (2026) Transcriptomic Analysis Reveals Molecular Mechanisms of Fleeing, Adhesion, and Thanatosis Patterns in Sea Cucumber *Apostichopus japonicus*. *Biology*, 15(12).

Mladenovi?? M, et al. (2026) Genetic Relatedness and Heterotic Grouping in MRIZP Elite Maize Inbred Lines Using SNP Markers from 25k SNP Array and RNA-seq Data. *Current issues in molecular biology*, 48(6).

Liu L, et al. (2026) Blast Resistance Gene Pish Derived Reprogramming of Noncoding RNAs in Rice. *Rice* (New York, N.Y.), 19(1).

Ghosh S, et al. (2026) Genebody specific epigenomic reprogramming of transcriptome promotes immune evasion in oropharyngeal cancer patients in North-Eastern India. *Clinical epigenetics*, 18(1).

Chimata P, et al. (2026) KCNA2 variants cause dilated cardiomyopathy, obesity and sleep apnea through RAC-ERK pathway. *EMBO molecular medicine*, 18(4), 1134.

Gu S, et al. (2026) Identification and expression characteristics of porcine embryonic circRNAs during the peri-implantation. *BMC genomics*, 27(1).

Muniz MMM, et al. (2026) Gestational Feed Restriction Induces Differential Expression of Novel Long Non-Coding RNAs in Offspring Skeletal Muscle. *Animal genetics*, 57(4), e70160.

Jan S, et al. (2026) Deciphering Cold Stress Resilience: Multiomics Insights in Contrasting Wheat Genotypes From the Western Himalayas. *Plant biotechnology journal*, 24(7), 4577.

Branscom GA, et al. (2026) Long non-coding RNA profiling of hypertrophic cardiomyopathy in mice. *Scientific data*, 13(1).

Liu C, et al. (2026) Integrative multi-omics analysis reveals microbiota alterations and clinical indicators predictive of pulmonary fibrosis progression following SARS-CoV-2 infection. *Briefings in bioinformatics*, 27(2).

Singh P, et al. (2025) Alternative mRNA splicing in anthracycline-induced cardiomyopathy - a COG-ALTE03N1 report. *Cardio-oncology* (London, England), 11(1), 47.

Cornelissen FMG, et al. (2025) The translome of glioblastoma. *Molecular oncology*, 19(3), 716.

Zhang J, et al. (2025) Engineered EVs from LncEEF1G - overexpressing MSCs promote fibrotic liver regeneration by upregulating HGF release from hepatic stellate cells. *Experimental & molecular medicine*, 57(3), 584.

Kim H, et al. (2025) Genome Evolution of Two Intertidal Sargassum Species (*S. fusiforme* and *S. thunbergii*) and Their Response to Abiotic Stressors. *Genome biology and evolution*, 17(5).

Yu Z, et al. (2025) Selectively Inhibition of MAPK pathway showed positive effects on Porcine embryo-derived stem cells pluripotency. *Scientific reports*, 15(1), 39974.

Liu J, et al. (2025) lncRNA-ZFAS1, an Emerging Gate-Keeper in DNA Damage-Dependent Transcriptional Regulation. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(31), e12385.