

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

TIGAR

RRID:SCR_006650

Type: Tool

Proper Citation

TIGAR (RRID:SCR_006650)

Resource Information

URL: <https://github.com/nariai/tigar>

Proper Citation: TIGAR (RRID:SCR_006650)

Description: Software to estimate transcript isoform abundances from RNA-Seq data by variational Bayesian inference. The statistical method can handle gapped alignments of reads against reference sequences so that it allows insertion or deletion errors within reads.

Abbreviations: TIGAR

Synonyms: TIGAR: Transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference

Resource Type: software resource

Defining Citation: [PMID:23821651](#)

Resource Name: TIGAR

Resource ID: SCR_006650

Alternate IDs: OMICS_01294

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260829T182240+0000

Ratings and Alerts

No rating or validation information has been found for TIGAR.

No alerts have been found for TIGAR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Liu Q, et al. (2026) Cell-type-aware transcriptome-wide association studies identify 91 independent risk genes for Alzheimer's disease dementia. *Communications biology*, 9(1).

Chen Y, et al. (2026) The metabolic escape: how tumor metabolic reprogramming drives drug resistance. *PeerJ*, 14, e21400.

Tang Y, et al. (2026) TIGAR deficiency enhances cardiac resilience through epigenetic programming of Parkin expression. *JCI insight*, 11(8).

Cui J, et al. (2025) Blockade of TIGAR prevents CD8+ T cell dysfunction and elicits anti-AML immunity. *Cancer immunology, immunotherapy : CII*, 74(6), 183.

Liu Y, et al. (2025) TIGAR regulated by HPV E6 is correlated with disease stage, drug sensitivity, and immune microenvironment in cervical cancer. *Scientific reports*, 15(1), 20618.

Lee JS, et al. (2025) E. coli genetically modified for purine nucleobase release promotes butyrate generation and colonic wound healing during DSS insult. *Gut microbes*, 17(1), 2490211.

Song C, et al. (2025) E2F8-induced GRPEL2 promoted colorectal cancer progression via targeting TIGAR. *Journal of translational medicine*, 23(1), 466.

Feng Y, et al. (2025) TIGAR inhibits glucose-metabolism and cisplatin-chemosensitivity in human lung cancer cells. *Discover oncology*, 16(1), 1420.

Hu T, et al. (2025) Proteome-wide association studies using summary pQTL data of brain, CSF, and plasma identify 30 risk genes of Alzheimer's disease dementia. *Alzheimer's research & therapy*, 17(1), 135.

Nam HY, et al. (2024) TIGAR coordinates senescence-associated secretory phenotype via lysosome repositioning and α -tubulin deacetylation. *Experimental & molecular medicine*, 56(12), 2726.

Song S, et al. (2024) Partitioning and aggregating cross-tissue and tissue-specific genetic effects to identify gene-trait associations. *Nature communications*, 15(1), 5769.

Azimi M, et al. (2024) Spatial Effects of Infiltrating T cells on Neighbouring Cancer Cells and Prognosis in Stage III CRC patients. *bioRxiv : the preprint server for biology*.

Shao M, et al. (2024) Multiome-wide Association Studies: Novel Approaches for Understanding Diseases. *Genomics, proteomics & bioinformatics*, 22(5).

Parrish RL, et al. (2024) SR-TWAS: leveraging multiple reference panels to improve transcriptome-wide association study power by ensemble machine learning. *Nature communications*, 15(1), 6646.

Zhang P, et al. (2024) Glutamine promotes the proliferation of intestinal stem cells via inhibition of TP53-induced glycolysis and apoptosis regulator promoter methylation in burned mice. *Burns & trauma*, 12, tkae045.

Wang D, et al. (2024) Disruption of TIGAR-TAK1 alleviates immunopathology in a murine model of sepsis. *Nature communications*, 15(1), 4340.

Qiu L, et al. (2024) Immune landscape of hepatocellular carcinoma: The central role of TP53-inducible glycolysis and apoptosis regulator. *Open medicine (Warsaw, Poland)*, 19(1), 20240999.

Parrish RL, et al. (2023) SR-TWAS: Leveraging Multiple Reference Panels to Improve TWAS Power by Ensemble Machine Learning. *medRxiv : the preprint server for health sciences*.

Dai Q, et al. (2023) OTTERS: a powerful TWAS framework leveraging summary-level reference data. *Nature communications*, 14(1), 1271.

Hua X, et al. (2023) Gestational age and hospital admission costs from birth to childhood: a population-based record linkage study in England. *Archives of disease in childhood. Fetal and neonatal edition*, 108(5), 485.