

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[forestplot](#)

RRID:SCR_023633

Type: Tool

Proper Citation

forestplot (RRID:SCR_023633)

Resource Information

URL: <https://CRAN.R-project.org/package=forestplot>

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Description: Software R package that allows for multiple confidence intervals per row, custom fonts for each text element, custom confidence intervals, text mixed with expressions, and more. Advanced Forest Plot using 'grid' graphics. Used to extend the use of forest plots beyond meta analyses.

Resource Type: software resource, software toolkit

Keywords: multiple confidence intervals per row, custom fonts for each text element, custom confidence intervals, text mixed with expressions,

Availability: Free, Available for download, Freely available

Resource Name: forestplot

Resource ID: SCR_023633

License: GPL v2

Record Creation Time: 20230601T050210+0000

Record Last Update: 20260905T133315+0000

Ratings and Alerts

No rating or validation information has been found for forestplot.

No alerts have been found for forestplot.

Data and Source Information

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Xie H, et al. (2026) B2M regulates ELANE in pyroptosis to affect pancreatic cancer progression. *Translational oncology*, 63, 102613.

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. *Scientific reports*, 16(1).

Li X, et al. (2026) A P4HA2 hypoxia signature derived from single cell atlas stratifies conserved subtypes with prognostic significance in cervical squamous cell carcinoma. *BMC cancer*, 26(1), 257.

Li P, et al. (2026) A novel immune-related gene signature stratifies prognosis and characterizes the tumor immune microenvironment in head and neck squamous cell carcinoma. *Frontiers in cell and developmental biology*, 14, 1756922.

Xun Y, et al. (2026) Integrative analysis of a novel snoRNA-based prognostic signature in patients with breast cancer. *Frontiers in oncology*, 16, 1779697.

Wei H, et al. (2026) Integrative multi-omics analysis identifies key ubiquitination regulators in prostate cancer. *Translational oncology*, 68, 102788.

He J, et al. (2026) Regulatory B cell-related gene signature predicts prognosis and immune landscape in head and neck squamous cell carcinoma. *Frontiers in immunology*, 17, 1739076.

Li X, et al. (2026) STXBP1 inhibits glioma progression by modulating ferroptosis and epithelial-mesenchymal transition. *Archives of medical science : AMS*, 22(2), 1097.

Zhang J, et al. (2026) Prognostic risk model based on cholesterol metabolism-Associated gene module for idiopathic pulmonary fibrosis. *PloS one*, 21(4), e0345310.

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. *Cancer immunology research*, 14(5), 771.

Liu J, et al. (2025) Identification and validation of T cell senescence-related prognostic genes in gastric carcinoma and investigation of their potential regulatory mechanisms. *Discover oncology*, 16(1), 986.

Pang KL, et al. (2025) Deciphering a proliferation-essential gene signature based on CRISPR-Cas9 screening to predict prognosis and characterize the immune microenvironment in HNSCC. *BMC cancer*, 25(1), 756.

Yao XR, et al. (2025) C16orf74 is a novel prognostic biomarker and associates with immune infiltration in head and neck squamous cell carcinoma. *PloS one*, 20(5), e0322701.

You P, et al. (2025) Knockdown of RFC4 inhibits cell proliferation of oral squamous cell carcinoma in vitro and in vivo. *FEBS open bio*, 15(2), 346.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. *Clinical and translational medicine*, 15(1), e70094.

Xiao W, et al. (2025) Prognostic implications of a programmed cell death-related long non-coding RNA signature and its relevance to immune features in esophageal carcinoma. *Translational cancer research*, 14(12), 8705.

Wang D, et al. (2024) Race as a prognostic factor of breast mucinous carcinoma. *Journal of cancer research and clinical oncology*, 151(1), 25.

Lu Z, et al. (2024) High expression of CCNB2 is an independent predictive poor prognostic biomarker and correlates with immune infiltrates in breast carcinoma. *Heliyon*, 10(10), e31586.

Liu W, et al. (2024) SnapHiC-G: identifying long-range enhancer-promoter interactions from single-cell Hi-C data via a global background model. *Briefings in bioinformatics*, 25(5).

Zhen L, et al. (2024) Activated hedgehog gene pattern correlates with dismal clinical outcome and tumor microenvironment heterogeneity in hepatocellular carcinoma. *Heliyon*, 10(5), e26989.