

Statistics Declaration

Title: Integrated analysis of single-cell and bulk RNA-seq establishes a novel signature for prediction in gastric cancer

KM-PLOTTER is a database that integrates gene expression and clinical data to analyze the prognostic value of particular genes. The database is manually curated, and gene expression data and survival information are downloaded from various sources. The statistical method used involves splitting patient samples into two groups based on various quantile expressions of the proposed biomarker, comparing the two cohorts using a Kaplan-Meier survival plot, and calculating the hazard ratio with 95% confidence intervals and logrank P value. The database is regularly supervised and extended. KM-plot recognizes 70,632 gene symbols, and multiple genes can be used simultaneously. To correct for multiple testing, a multiple testing calculator is available. The gene symbols are not unambiguous, and the system may include overlapping gene symbols. The database offers four options for obtaining better images of the results.

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