

Peer Review

Review of: "Enhancing Cancer Treatment and Understanding Through Clustering of Gene Responses to Categorical Stressors"

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This research article explores clustering of cancer gene expression responses to antiglycolytic stressors and presents a novel integrative bioinformatics approach that combines GEO datasets, dimensionality reduction, and consensus clustering to identify molecular response subtypes potentially relevant for personalized oncology. The study is scientifically interesting and methodologically ambitious; however, several weaknesses limit its robustness and translational value. First, the work relies heavily on heterogeneous publicly available microarray datasets with substantial variability in experimental conditions (cell lines, drug doses, exposure times), which introduces confounding bias and reduces reproducibility. Second, the lack of independent validation datasets, external cohort confirmation, or experimental wet-lab validation weakens the reliability of the identified clusters and their clinical relevance. Third, the statistical justification for selecting clustering parameters and thresholds, although partially described, lacks sensitivity analyses and comparative machine learning validation. Fourth, the study remains largely descriptive and speculative in linking clusters to therapeutic recommendations without functional or survival outcome data. To improve the study, the authors should validate findings using independent transcriptomic datasets or RNA-seq cohorts, perform experimental validation (e.g., functional assays or drug response experiments), apply additional clustering or ML comparison methods, and integrate clinical or pharmacological outcome data to strengthen translational significance.

Declarations

Potential competing interests: No potential competing interests to declare.