66+20+4=90

1+4+8 = 13

hypoxia signature cancer microenvironment: 386

hypoxia signature cancer microenvironment autoencoder: 0

Purposive and sensitive search strategy and explain

Boolean search operator (vien)

(hypoxia) and (signature) and ((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and ((develop) or (autoencoders) or (AE) or (machine learning) or (deep learning)): 199/4

(hypoxia) and (signature) and (transcriptomic) and ((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and ((develop) or (autoencoders) or (AE) or (machine learning) or (deep learning)):66/1

(hypoxia) and (signature) and ((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and ((develop) or (autoencoders) or (AE) or (machine learning) or (deep learning)):20/4

(hypoxia) and (signature) and (transcriptomic) and ((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and ((autoencoders) or (machine learning) or (deep learning)):4/8

not AE or other machine learning method (Molecular profiling) or not cancer(DSS-induced colitis) or not hypoxia (immue-related/KCNK Gene Signature) or not gene signature (hypoxia-inducible factor (HIF)) not gene level(tumor biopsies sampled) not Retracted

Before machine learning:

<https://www.scopus.com/record/display.uri?eid=2-s2.0-79551542410&origin=inward&txGid=8d609ca3bfeb2cbd481fbfc38d7208cb>

We used the hypoxia marker EF5 coupled with laser-capture microdissection to isolate RNA from viable hypoxic and normoxic regions of 9L experimental gliomas. Through microarray analysis,

<https://www.scopus.com/record/display.uri?eid=2-s2.0-34250323878&origin=inward&txGid=6e4a89151f9d233fa372d066bb0aa5af>: meta analysis, microarray based gene signatures, univariate, and multivariate analysis

<https://www.scopus.com/record/display.uri?eid=2-s2.0-75649117850&origin=inward&txGid=cd9e43883c0db2007efaa995ef2848db>

An approach for deriving signatures that combine knowledge of gene function and analysis of in vivo co-expression patterns was used to define a common hypoxia signature from three head and neck and five breast cancer studies.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Title | Type/Topic | Data/ Data Availability | Method/ Performance Metrics/ | Result |
| [Development and Validation of a Combined](https://aacrjournals.org/clincancerres/article/25/17/5315/81611/Development-and-Validation-of-a-Combined-Hypoxia)  [Hypoxia and Immune Prognostic Classifier for](https://aacrjournals.org/clincancerres/article/25/17/5315/81611/Development-and-Validation-of-a-Combined-Hypoxia)  [Head and Neck Cancer](https://aacrjournals.org/clincancerres/article/25/17/5315/81611/Development-and-Validation-of-a-Combined-Hypoxia) | Primary  Head and Neck Cancer | A 54-gene hypoxia-immune signature was constructed based on a literature review and analyzed using gene expression data from the Cancer Genome Atlas (TCGA) HNC dataset. | unsupervised hierarchical clustering, to classify patients based on gene expression patterns. | demonstrated the potential of the hypoxia-immune prognostic classifier to predict clinical outcomes in HNC patients. The findings suggest that considering both hypoxia and immune response signatures may provide valuable prognostic information for personalized treatment strategies in HNC. |
| [Performance Comparison of Deep Learning Autoencoders for](https://www.mdpi.com/2072-6694/13/9/2013)  [Cancer Subtype Detection Using Multi-Omics Data](https://www.mdpi.com/2072-6694/13/9/2013) | Primary  Cancer Subtype Detection: Glioblastoma multiforme, Colon Adenocarcinoma, Kidney renal clear cell carcinoma, and Breast invasive carcinoma | gene expression, DNA methylation, and miRNA expression | vanilla, denoising, sparse, and variational autoencoders | autoencoders were able to detect distinct subtypes of cancer based on the multi-omics data, and the identified subtypes exhibited significant differences in survival profiles. |
| [A new thinking: extended application of genomic selection to screen multiomics data for development of novel hypoxia-immune biomarkers and target therapy of clear cell renal cell carcinoma](https://pubmed.ncbi.nlm.nih.gov/34237133/) |  |  | First, t-SNE and ssGSEA analysis were used to establish tumor subtypes related to hypoxia-immune, and we investigated the hypoxia-immune-related differences in three types of genetic or epigenetic characteristics (gene expression profiles, somatic mutation, and DNA methylation) by analyzing the multiomics data from The Cancer Genome Atlas (TCGA) portal. Additionally, a four-step strategy based on lasso regression and Cox regression |  |
| [Identification and Development of Subtypes with Poor Prognosis in Gastric Cancer Based on Both Hypoxia and Immune Cell Infiltration](https://pubmed.ncbi.nlm.nih.gov/34908867/) |  |  | Based on the results, unsupervised clustering was performed to obtain different gastric cancer subtypes. |  |
| [A Novel Hypoxia-Related Gene Signature with Strong Predicting Ability in Non-Small-Cell Lung Cancer Identified by Comprehensive Profiling](https://pubmed.ncbi.nlm.nih.gov/35634481/) |  |  | Cox |  |
| [Construction of a 3-mRNA hypoxia prognostic model to evaluate immune microenvironment in hepatocellular carcinoma](https://pubmed.ncbi.nlm.nih.gov/36181125/) |  |  | nivariate Cox regression analysis. Then, the hypoxia prognosis model was established via multivariate Cox regression analysis, |  |
| [Development of a prediction model for radiotherapy response among patients with head and neck squamous cell carcinoma based on the tumor immune microenvironment and hypoxia signature](https://pubmed.ncbi.nlm.nih.gov/35505641/) |  |  | We first evaluated the hypoxia status and tumor immune microenvironment in the Cancer Genome Atlas (TCGA) cohort by using transcriptomic data. Differentially expressed genes (DEGs) were identified between the "high immunity and low hypoxia" and "low immunity and high hypoxia" groups and those DEGs significantly associated with disease-specific survival in the univariate Cox regression analysis were selected as the prognostic DEGs. We selected the immune hypoxia-related genes (IHRGs) by intersecting prognostic DEGs with immune and hypoxia gene sets. We used the IHRGs to train a multivariate Cox regression model in the TCGA cohort, based on which we calculated the IHRG prognostic index (IHRGPI) for each patient and validated its efficacy in predicting radiotherapy response in the Gene Expression Omnibus cohorts. Furthermore, we explored potential mechanisms and effective combinational treatment strategies for different IHRGPI groups. |  |
| [Development and validation](https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-020-02366-0)  [of a hypoxia-immune-based microenvironment](https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-020-02366-0)  [gene signature for risk stratification in gastric](https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-020-02366-0)  [cancer](https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-020-02366-0) | Primary  gastric  cancer | the GEO database, which included 357 gastric cancer patients | LASSO Cox regression was used to select the most prognostic gene signature from the identified hypoxia-immune-related DEGs and to derive the individual-level risk scores for developing the prognosis classifier. | a hypoxia-immune-based prognosis classifier that could stratify patients into different risk groups and predict survival outcomes. |
| [A Hypoxia-Related Signature for Predicting Prognosis, Cellular Processes, Immune Microenvironment and Targeted Compounds in Lung Squamous Cell Carcinoma](https://www.dovepress.com/getfile.php?fileID=79860) | Primary  Lung Squamous Cell Cancer | Transcriptome data and clinical information for LUSC were obtained from The Cancer Genome Atlas (TCGA) database. | GSVA algorithm for calculating hypoxia scores, weighted gene co-expression network analysis (WGCNA), differential expression analysis, and various enrichment analyses like Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) | Prognostic Signature Development: A 3-gene prognostic signature for LUSC, including HELLS, GPRIN1, and FAM83A, was developed and validated.  Risk Score as an Independent Factor: The risk score was found to be an independent prognostic factor for LUSC.  Immune Microenvironment Influence: Functional enrichment and immune landscape analyses suggested that the risk scoring system might alter the immune microenvironment of LUSC patients, influencing patient outcomes. |
| [Hypoxic Characteristic Genes Predict Response to Immunotherapy for Urothelial Carcinoma](https://pubmed.ncbi.nlm.nih.gov/34901008/) |  |  |  |  |
| [Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study](https://www.thelancet.com/journals/lanonc/article/PIIS1470-2045(14)71021-6/fulltext) | Primary  prostate cancer | Copy-Number Profiles: Taken from 126 pre-image-guided radiotherapy diagnostic biopsies, these profiles were analyzed using machine learning techniques to develop prognostic signatures. | unsupervised and supervised machine learning techniques to the copy-number profiles of 126 pre-image-guided radiotherapy diagnostic biopsies to develop prognostic signatures | A novel 100-loci DNA signature was developed, which accurately classified treatment outcomes in the MSKCC low-risk to intermediate-risk cohort and was more effective in predicting biochemical relapse than 23 previously published RNA signatures. |
| [A novel hypoxia- and lactate metabolism-related signature to predict prognosis and immunotherapy responses for breast cancer by integrating machine learning and bioinformatic analyses](https://pubmed.ncbi.nlm.nih.gov/36275774/) | Primary  breast cancer | RNA sequencing and clinical data were obtained from The Cancer Genome Atlas database and Gene Expression Omnibus. | Univariate Cox regression, random survival forest (RSF), and stepwise multivariate Cox regression analyses were employed to construct the hypoxia-lactate metabolism-related prognostic model (HLMRPM). | Prognostic Model Establishment: The HLMRPM was established using RSF and stepwise multivariate Cox regression analysis, incorporating five HLMRGs.  Risk Group Classification: Patients were divided into high- and low-risk groups based on the medium-risk score. Patients in the high-risk group had a worse prognosis than those in the low-risk group. |
| [Identification and validation of hypoxia-derived gene signatures to predict clinical outcomes and therapeutic responses in stage I lung adenocarcinoma patients](https://pubmed.ncbi.nlm.nih.gov/33754044/) | Primary  lung adenocarcinoma | The study analyzed transcriptome profiles and clinical parameters of 1,400 stage I LUAD patients from 14 public datasets, including 13 microarray datasets and 1 RNA-Seq dataset from The Cancer Genome Atlas (TCGA). | Bioinformatic and Machine Learning Approaches: These methods were combined to establish hypoxia-derived signatures to predict overall survival and immune checkpoint blockade (ICB) therapy response in stage I patients. Additionally, pathways, genomic, and copy number alterations were analyzed in different risk subgroups | Prognostic Risk Score (HPRS): The study developed a hypoxia-related prognostic risk score (HPRS), which showed a more powerful capacity for survival prediction compared to traditional clinicopathological features. |
| [Integrated analysis of hypoxia-associated lncRNA signature to predict prognosis and immune microenvironment of lung adenocarcinoma patients](https://pubmed.ncbi.nlm.nih.gov/34486476/) |  |  | Consensus cluster analysis characterized the hypoxia status of LUAD patients. Cox regression analysis with the least absolute shrinkage and selection operator (LASSO) method determined significantly prognosis-related lncRNAs which were used to create a prognostic model. |  |
| [A hypoxia-related signature for clinically predicting diagnosis, prognosis and immune microenvironment of hepatocellular carcinoma patients](https://pubmed.ncbi.nlm.nih.gov/32887635/) | hepatocellular carcinoma |  | consistent clustering analysis. Three DEGs closely related to overall survival (OS) were identified using Cox regression and LASSO analysis. |  |
| [A novel hypoxia gene signature indicates prognosis and immune microenvironments characters in patients with hepatocellular carcinoma](https://pubmed.ncbi.nlm.nih.gov/33616276/) |  |  | microarray analysis and a robust rank aggregation algorithm. |  |
| [A hypoxia-linked gene signature for prognosis prediction and evaluating the immune microenvironment in patients with hepatocellular carcinoma](https://pubmed.ncbi.nlm.nih.gov/35116696/) |  |  | Univariate along with multivariate Cox regression were adopted to create the prediction model. |  |
| [A 4-gene-based hypoxia signature is associated with tumor immune microenvironment and predicts the prognosis of pancreatic cancer patients](https://wjso.biomedcentral.com/articles/10.1186/s12957-021-02204-7) |  |  | univariable Cox regression analysis on the hypoxia core genes to obtain prognostic-related hypoxia genes. They were then analyzed by multivariable Cox regression |  |
| [Employing hypoxia characterization to predict tumour immune microenvironment, treatment sensitivity and prognosis in hepatocellular carcinoma](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8134035/) |  |  | 200 hypoxia-related genes were downloaded from Gene Set Enrichment Analysis (hallmark-hypoxia). The differentially expressed hypoxia-related genes (p < 0.05, |Log2-fold change (FC)| > 1) were analyzed by univariable and multivariable Cox regression. |  |
| [Development and validation of a hypoxia-associated signature for lung adenocarcinoma](https://pubmed.ncbi.nlm.nih.gov/35079065/) | Primary  lung adenocarcinoma | RNA sequencing was used to identify genes significantly differentially expressed under hypoxia (1% O2) in four LUAD cell lines | The identified genes were used for unsupervised clustering of a TCGA-LUAD training dataset (252 samples) and in a machine learning approach to build the hypoxia-related signature. | Prognostic Value: The 28-gene LUAD hypoxia-related signature was found to be prognostic in the TCGA training and test datasets, with hazard ratios (HR) indicating a significant association with overall survival.  Overall Survival Meta-analysis: In a meta-analysis of nine other datasets (1257 samples in total), the signature also showed prognostic value for overall survival.  Immune Response Association: The hypoxia-high group, as defined by the signature, was enriched in pathways involved in immune responses, indicating a potential link between hypoxia and immune activity in the tumor microenvironment. |
| [Establishment and External Validation of a Hypoxia-Derived Gene Signature for Robustly Predicting Prognosis and Therapeutic Responses in Glioblastoma Multiforme](https://pubmed.ncbi.nlm.nih.gov/35155681/) | Primary  Glioblastoma Multiforme | transcriptome profiling and clinicopathological characteristics of GBM from The Cancer Genome Atlas (TCGA) and Chinese Glioma Genome Atlas (CGGA) cohorts | receiver operator characteristic (ROC) and uni- and multivariate cox regression analysis | Among hallmarks of cancer, hypoxia acted as a prominent risk factor of GBM prognosis. A hypoxia-derived gene signature displayed efficient ability in predicting clinical outcomes. High risk score indicated undesirable prognosis, recurrence, and progression of GBM. Moreover, this risk score displayed positive correlations to immunity and stromal activation. Combining immunotherapeutic response predictors, high-risk patients more benefited from immunotherapy. ALDH3B1 and CTSZ expression had prominent upregulation in glioma cells than normal glial cells. |
| [Novel Immune-Related Gene-Based Signature Characterizing an Inflamed Microenvironment Predicts Prognosis and Radiotherapy Efficacy in Glioblastoma](https://pubmed.ncbi.nlm.nih.gov/35111196/) | / Immue related | K-mean, cox regression |  |  |
| [Integrative Analysis of KCNK Genes and Establishment of a Specific Prognostic Signature for Breast Cancer](https://pubmed.ncbi.nlm.nih.gov/35656548/) | /cox regression |  |  |  |
|  |  |  |  |  |
| [Development and validation of a hypoxia-stemness-based prognostic signature in pancreatic adenocarcinoma](https://pubmed.ncbi.nlm.nih.gov/25456371/) | Primary  pancreatic adenocarcinoma | The mRNA expression-based stemness index (mRNAsi) data of PAAD samples from The Cancer Genome Atlas (TCGA) database | one-class logistic regression (OCLR) machine learning algorithm. Univariate Cox regression and LASSO regression analyses were then performed to establish a hypoxia-mRNAsi-related gene signature, and its prognostic performance was verified in both the TCGA-PAAD and GSE62452 corhorts by Kaplan-Meier and receiver operating characteristic (ROC) analyses. | A novel prognostic risk model was successfully constructed based on the eight-gene signature comprising JMJD6, NDST1, ENO3, LDHA, TES, ANKZF1, CITED, and SIAH2, which could accurately predict the 1-, 3-, and 5-year OS of PAAD patients in both the training and external validation datasets. |
| [Development and Verification of the Hypoxia- and Immune-Associated Prognostic Signature for Pancreatic Ductal Adenocarcinoma](https://pubmed.ncbi.nlm.nih.gov/34691034/) | Pancreatic Ductal Adenocarcinoma |  | **Seven hypoxia and immune-associated signature genes (S100A16, PPP3CA, SEMA3C, PLAU, IL18, GDF11, and NR0B1) were identified to construct a risk score model using the Univariate Cox regression and the Least Absolute Shrinkage and Selection Operator (LASSO) Cox regression,** |  |
| A signature of hypoxia-related factors reveals functional dysregulation and robustly predicts clinical outcomes in stage I/II colorectal cancer patients | https://pubmed.ncbi.nlm.nih.gov/31572060/ |  | **Univariate** |  |
| [Determination of hypoxia signature to predict prognosis and the tumor immune microenvironment in melanoma](https://pubmed.ncbi.nlm.nih.gov/33624645/) |  |  | **Using Lasso Cox regression, a hypoxia model was constructed. The receiver operating characteristic and the Kaplan-Meier curve were used to evaluate the predictive capacity of the model. With the CIBERSORT algorithm, the abundance of 22 immune cells in the melanoma microenvironment was analyzed. A total of 20 hypoxia-related genes were significantly related to prognosis in the log-rank test. Lasso regression showed that FBP1, SDC3, FOXO3, IGFBP1, S100A4, EGFR, ISG20, CP, PPARGC1A, KIF5A, and DPYSL4 displayed the best features.** |  |
| [Centrosome amplification-related signature correlated with immune microenvironment and treatment response predicts prognosis and improves diagnosis of hepatocellular carcinoma by integrating machine learning and single-cell analyses](https://pubmed.ncbi.nlm.nih.gov/37154991/) | Primary  hepatocellular carcinoma  \not hypoxia | TCGA dataset, ICGC dataset was obtained for signature validation | using the LASSO-penalized Cox regression algorithm | 6 key prognostic genes (SSX2IP, SPAG4, SAC3D1, NPM1, CSNK1D, and CEP55) among them were screened out to construct a signature with both high sensitivity and specificity in diagnosis and prognosis of HCC patients |
| [Development of a Comprehensive Gene Signature Linking Hypoxia, Glycolysis, Lactylation, and Metabolomic Insights in Gastric Cancer through the Integration of Bulk and Single-Cell RNA-Seq Data](https://pubmed.ncbi.nlm.nih.gov/38001949/) |  |  | A HGLRG risk-score model was developed based on univariate Cox regression and a LASSO-Cox regression model and subsequently validated |  |
| [Characterizing the landscape of cervical squamous cell carcinoma immune microenvironment by integrating the single‐cell transcriptomics and RNA‐Seq](https://pubmed.ncbi.nlm.nih.gov/35634956/) | Primary  cervical squamous cell carcinoma | RNA Expression Data: From the Cancer Genome Atlas, Gene Expression Omnibus, and Genotype‐Tissue Expression databases. This included data for normal and tumor tissues in cervical squamous cell carcinoma (CSCC) | Univariate Cox Regression and Lasso Regression | The study identified six immune-related gene (IRG) signatures, four IRLs, and five IRHs that significantly influence the TIME. It was found that the expression level of immune checkpoint genes was significantly upregulated in certain T-cells and tumor-associated macrophages (TAMs) in tumor tissues. The study concluded that CD16+ monocyte-derived IFI30+ TAMs in the coexpression network regulate the TIME and have potential as novel immunotherapy target |
| [Identification and validation of a prognostic signature related to hypoxic tumor microenvironment in cervical cancer](https://pubmed.ncbi.nlm.nih.gov/35657977/) |  |  |  |  |
| Integrative Analysis of KCNK Genes and Establishment of a Specific Prognostic Signature for Breast Cancer | Primary  Breast Cancer | mRNA expression matrix and clinical data of breast cancer patients from the TCGA database.  Clinical samples and cell lines for experimental validation. | Construction of a prognostic signature using LASSO Cox regression analysis.  Univariate and multivariate Cox regression analyses for validating the prognostic signature.  Survival analysis using the Kaplan-Meier method and receiver operating characteristic (ROC) curve. | A specific prognostic signature comprising seven KCNK genes was developed, showing accuracy in predicting prognosis in both training and validation cohorts.  The study established a nomogram integrating the KCNK-based risk score with clinical features, showing great predictive performance.  KCNK genes were associated with the activation of various tumor microenvironment cells and the regulation of tumor immune responses. |
| [Establishment of Prognosis Model in Acute Myeloid Leukemia Based on Hypoxia Microenvironment, and Exploration of Hypoxia-Related Mechanisms](https://pubmed.ncbi.nlm.nih.gov/34777463/) |  |  |  |  |
| [A workflow combining single-cell CRISPRi screening and a supervised autoencoder neural network to detect subtle transcriptomic perturbations induced by lncRNA Knock-Down](https://www.biorxiv.org/content/10.1101/2023.07.11.548494v1.full.pdf+html) | Primary  the regulatory functions of hypoxia-regulated long non-coding RNAs (lncRNAs) | a mini-CROP-seq library with validated guide RNAs (gRNAs) targeting six lncRNAs known to be regulated by hypoxia and/or associated with poor prognosis, as well as the master transcription factors of the hypoxic response, HIF1A and HIF2/EPAS1, and negative control guides. | A supervised autoencoder neural network was developed to analyze fine-tuned regulations in the dataset. This method leveraged known cell labels corresponding to the received gRNA. It involved creating matrices for each target gene under different conditions, pooling cells based on their targeted gene, and using these matrices as inputs for the SAE classification workflow. | Validation of SAE Approach: The researchers first validated the SAE approach on HIF1A and HIF2/EPAS1 knock-down, demonstrating good sensitivity in detecting the known temporal switch between these regulators.  Identification of Transcriptomic Signatures: The SAE method was successful in detecting stable, short hypoxia-dependent transcriptomic signatures induced by the knock-down of some lncRNA candidates. This demonstrated the ability of the method to decipher weak perturbations in single-cell transcriptomic data, particularly in the context of CRISPR-based screening. |
| [Cell–cell communication inference and analysis in the tumour microenvironments from single-cell transcriptomics: data resources and computational strategies](https://academic.oup.com/bib/article/23/4/bbac234/6618236?login=true#no-access-message) | Primary  cell-cell communication in tumor microenvironments | single-cell RNA sequencing (scRNA-seq) data and spatial transcriptomic data | Deep Clustering-Based Cell-Type Identification, Ensemble Deep Learning, General Machine Learning Approach | Demonstration of Scoring Strategies: It demonstrates seven classical intercellular communication scoring strategies and highlights four types of representative intercellular communication inference methods. These include network-based approaches, machine learning-based approaches, spatial information-based approaches, and other approaches.  Analysis and Evaluation: The study summarizes evaluation and validation avenues for intercellular communication inference. It also analyzes the advantages and limitations of the four types of cell-cell communication methods mentioned. |
| [Pathomic Fusion: An Integrated Framework for](https://ieeexplore.ieee.org/abstract/document/9186053/?casa_token=fhfH727XNwIAAAAA:ePVATe2bnY8o3Y2ICoRQCvqbNB1h4UuJAGLVKT0DZBoUubhiGNXRWpUk8ioHv_hSlnDx3Gc)  [Fusing Histopathology and Genomic Features](https://ieeexplore.ieee.org/abstract/document/9186053/?casa_token=fhfH727XNwIAAAAA:ePVATe2bnY8o3Y2ICoRQCvqbNB1h4UuJAGLVKT0DZBoUubhiGNXRWpUk8ioHv_hSlnDx3Gc)  [for Cancer Diagnosis and Prognosis](https://ieeexplore.ieee.org/abstract/document/9186053/?casa_token=fhfH727XNwIAAAAA:ePVATe2bnY8o3Y2ICoRQCvqbNB1h4UuJAGLVKT0DZBoUubhiGNXRWpUk8ioHv_hSlnDx3Gc) | Primary  Cancer Diagnosis and Prognosis | Molecular Profiles: Genomic data, including mutations, copy number variations (CNV), and RNA sequencing (RNA-Seq), were utilized. | Histology features were extracted using Convolutional Neural Networks (CNNs) and Graph Convolutional Networks (GCNs), or a combination of both. These networks were initially trained individually for their respective tasks. | Improvement Over Existing Models: The Pathomic Fusion approach outperformed existing models, including Cox models, unimodal networks, and previous deep learning-based feature fusion approaches for image-omic-based survival outcome prediction. Notably, it achieved better results than the WHO paradigm and previous state-of-the-art methods, with significant improvements in predictive accuracy (c-Index of 0.826)​​.  Fine-Grained Patient Stratification: Pathomic Fusion allowed for more detailed stratification of survival curves, which could be highly beneficial in clinical settings for defining treatment cohorts​ |
| [A combined hypoxia and immune gene signature for predicting survival and risk stratification in triple-negative breast cancer](https://pubmed.ncbi.nlm.nih.gov/34341184/) | breast cancer |  | Hypoxia-related genes (HRGs) and Immune-related genes (IRGs) were identified using the weighted gene co-expression network analysis (WGCNA) method and the single-sample gene set enrichment analysis (ssGSEA Z-score) with the transcriptomic profiles from Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) cohort. Then, prognostic hypoxia and immune based genes were identified in TNBC patients from the METABRIC (N = 221), The Cancer Genome Atlas (TCGA) (N = 142), and GSE58812 (N = 107) using univariate cox regression model. A robust hypoxia-immune based gene signature for prognosis was constructed using the least absolute shrinkage and selection operator (LASSO) method. |  |
| [A Hypoxia Gene-Based Signature to Predict the Survival and Affect the Tumor Immune Microenvironment of Osteosarcoma in Children](https://pubmed.ncbi.nlm.nih.gov/34337075/) |  |  | The genes related to hypoxia statistically relevant in univariate analysis were then shown to be significant in multivariate analysis which produced the risk score formula |  |
| [A Robust Hypoxia Risk Score Predicts the Clinical Outcomes and Tumor Microenvironment Immune Characters in Bladder Cancer](https://pubmed.ncbi.nlm.nih.gov/34484235/) |  |  | The hypoxia-related genes were collected from the Molecular Signatures Database. The TCGA-BLCA cohort was downloaded from the Cancer Genome Atlas and then was randomly divided into training and internal validation sets. Two external validation cohorts were gathered from Gene Expression Omnibus. Also, another independent validation cohort (Xiangya cohort) was collected from our hospital. The Cox regression model with the LASSO algorithm was applied to develop the hypoxia risk score. Then, we correlated the hypoxia risk score with the clinical outcomes, the tumor microenvironment (TME) immune characteristics, and the efficacy prediction for several treatments, which included cancer immunotherapy, chemotherapy, radiotherapy, and targeted therapies. |  |
| [Multi-omics data integration in upper gastrointestinal cancers research: A review of concepts, approaches, and application](file:///C:\Users\JCH\Desktop\Multi-omics%20data%20integration%20in%20upper%20gastrointestinal%20cancers%20research:%20A%20review%20of%20concepts,%20approaches,%20and%20application) | Review | \ | \ | upper gastrointestinal (GI) cancers, including esophageal, gastric, liver, and pancreatic cancers |
| [Machine Learning: A New Prospect in Multi-Omics Data Analysis of Cancer](https://www.frontiersin.org/articles/10.3389/fgene.2022.824451/full) | Review | \ | \ | Cancer Prevention/Early Detection/Treatment/Supervised Learning/Unsupervised Learning/Semi-Supervised Learning/Reinforcement Learning |
| [The Effect of Hypoxia and Hypoxia-Associated Pathways in the Regulation of Antitumor Response: Friends or Foes?](https://www.frontiersin.org/articles/10.3389/fimmu.2022.828875/full) |  |  |  |  |