66+20+4=90

1+4+8 = 13

hypoxia signature cancer microenvironment: 386/82,900

hypoxia signature cancer microenvironment autoencoder: 0/294

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 ((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

(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

((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and

((develop) or (autoencoders) or (AE) or (machine learning) or (deep learning)) ) and

(transcriptomic):

66/1

(hypoxia) and (signature) and

((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and

((autoencoders) or (machine learning) or (deep learning)) and

(transcriptomic):

4/8

(hypoxia) and (signature) and

((cancer) or (tumour)) and ((micro-environment) or (TME) or (microenvironment)) and

((autoencoders) or (AE) or (machine learning) or (deep learning)):

20/4

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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| index | Title | Type/Topic | Data/ Data Availability | Method/ Performance Metrics/ | Result |
| 1 | [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. |
| 2 | [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. |
| 3 | [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 |  |
| 4 | [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. |
| ~~5~~ | [~~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.~~ | ~~Clustering 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.~~ |
| 6 | [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. |
| 7 | [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). | Hypoxia-derived signatures using bioinformatic and machine learning approaches including WGCNA and LASSO Cox algorithm | 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. |
| 8 | [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. |  |
| 9 | [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. |  |
| 10 | [A novel hypoxia gene signature indicates prognosis and immune microenvironments characters in patients with hepatocellular carcinoma](https://pubmed.ncbi.nlm.nih.gov/33616276/) |  |  | multivariable LASSO Cox regression |  |
| 11 | [Employing hypoxia characterization to predict tumour immune microenvironment, treatment sensitivity and prognosis in hepatocellular carcinoma](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8134035/) |  |  | Kmean 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. |  |
| 12 | [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. |
| 13 | [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 LASSO | 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. |
| 14 | [Development and validation of a hypoxia-stemness-based prognostic signature in pancreatic adenocarcinoma](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9350896/) | 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 15TCGA-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. |
| 15 | [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,** |  |
| 16 | [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.** |  |
| 17 | [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 |  |
| 18 | [Identification and validation of a prognostic signature related to hypoxic tumor microenvironment in cervical cancer](https://pubmed.ncbi.nlm.nih.gov/35657977/) |  |  | LASSO |  |
| 19 | [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/) |  |  | LASSO cox |  |
| 20 | [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. |  |
| 21 | [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. |  |
| 22 | [Identification of a Hypoxia-Associated Signature for Lung Adenocarcinoma](https://www.frontiersin.org/articles/10.3389/fgene.2020.00647/full) | LUDA | LASSO Cox Regression |  |  |