

Identification of fatty acid oxidation-related subtypes by integrated analysis of bulk- and single-cell transcriptome profiling in colorectal cancer

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Background: As one of the major metabolic reprogramming pathways, fatty acid oxidation (FAO) contributes to rapid progression in tumor cells. Nevertheless, the genomic patterns of patients' FAO levels in colorectal cancer (CRC) remain unknown. Hence, it is crucial to identify the interplay mechanisms of molecular biochemical features of FAO in CRC.

Methods: Data of patients with CRC were accessed from The Cancer Genome Atlas (TCGA). Unsupervised consensus clustering related to FAO scores was conducted. The differentially expressed genes (DEGs) were screened by clustering according to FAO status polarized in TCGA, followed by the construction of the scores of genes related to FAO (GFAO_Score). Enrichment of FAO and carcinogenesis at the cell level were calculated based on the single-cell RNA (scRNA) sequencing analysis. The clinical values and drug analysis of GFAO_Score were evaluated by external validation cohorts from Gene Expression Omnibus (GEO) datasets.

Results: We classified patients into two distinct FAO clusters which indicated those with lower FAO levels had poor prognosis and high enrichment of carcinogenic-gene pathways. Further, the high FAO-enriched subtypes in epithelial cells revealed carcinogenesis. Three FAO-related genes (*ZFHX4*, *AQP8*, and *AKR1B10*) were screened to construct the GFAO_Score. The high GFAO_Score group leaned toward advanced CRC and unfavorable survival outcomes in the validation cohort. The low GFAO_Score group possessed a better response to immunotherapy and exhibited lower IC50 (50% inhibition concentration) values for certain chemotherapy drugs, such as 5-fluorouracil, irinotecan, oxaliplatin, paclitaxel, and camptothecin.

Conclusions: FAO patterns vary in patients with CRC. The GFAO_Score might contribute to the precise screening of patients according to metabolism reprogramming and optimization of strategies in clinical practice.

Keywords: Fatty acid oxidation (FAO); colorectal cancer (CRC); metabolic reprogramming; prediction; prognosis

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Introduction

Ranked third among the most common neoplasm categories, colorectal cancer (CRC), the main cause of cancer-related deaths, had approximately 1.9 million new occurrences in 2020 (1,2). As a standard treatment for resectable CRC, the radical operation followed by adjuvant chemotherapy has been unsatisfactory for advanced CRC (3). CRC is characterized by molecular alterations followed by the dysregulation of various carcinogenic pathways that lead to malignancy invasiveness (4). Therefore, markers related to prognosis are warranted, and it is needed to elucidate potential molecular mechanisms for CRC progression.

Metabolic reprogramming has been proven as a remarkable hallmark of malignant progression (5-7). As for tumor cells, dysregulation of lipid metabolism is one of the vital metabolic characteristics, which enables cancer cells to contend with limitations about energy sources (8,9). The abnormal alteration of fatty acid β -oxidation (FABO) is a frequent feature of metabolic reprogramming in carcinoma, in which fatty acids (FAs) are decomposed to produce acetyl-CoA, participate in Krebs' Cycle and produce ATP, NADPH, NADH, and FADH₂ (10-12). FAs are essential for energy consumption in the tumor microenvironment (TME) (13). TME plays an important role in the occurrence and metastatic progression of malignancy, which consists of numerous categories of

infiltrating cells, especially the immune cell types. They regulate tumor progress and metastasis by modifying the construction of TME. The previous research demonstrated that fatty acid oxidation (FAO) favors malignant cell proliferation, and impacts survival via drug resistance (14). It has been illustrated that a metabolic shift toward carbohydrate and lipid metabolism accounts for the adaptation to VEGF blockade. Restricting the lipid synthesis controls distal metastasis after withdrawal of antiangiogenic treatment in anti-tumor therapy (15). Besides, adipocytes facilitate the initial shelter of tumor cells to the omentum by providing FAs, fueling their progression (16). The promotion of self-renewal ability and drug resistance was related to FAO (17,18). Thus, the recognition of the status of FAO in CRC may predict the prognosis of individual patients. However, it is impossible to analyze such an amount of sequencing data to screen the specific patients who may benefit from adjuvant therapies in clinical practice. Therefore, identifying patients for concrete anti-tumor strategies is worthy of exploration in CRC.

In this study, we aimed to construct a novel signature related to FAO to identify certain patients with CRC based on bulk RNA sequencing and single-cell RNA (scRNA) sequencing data, which contributes to the following additional treatments. Furthermore, we explored the predictive capacity and adjuvant therapeutic performance of the signature by external validation cohorts. This study might help identify specific patients with CRC to optimize treatment strategies and enhance their prognosis in chemotherapy and immunotherapy. We present this article in accordance with the TRIPOD reporting checklist (available at <https://jgo.amegroups.com/article/view/10.21037/jgo-23-833/rc>).

Methods

Publicly databases collection and processing

Transcriptome data of 605 patients and clinical information of 536 patients with CRC were obtained from The Cancer Genome Atlas (TCGA)-Genomic Data Commons (GDC) (<https://cancergenome.nih.gov/>) and TCGA Pan-Cancer Clinical Data Resource respectively. The gene sets used in this study were all accessed from the molecular signatures database (MSigDB). In order to evaluate the FAO metabolism of patients in multiple dimensions, we collected all the gene sets related to FAO, totally seven gene sets (*Table 1*). In order to explore the relationship between the

Highlight box

Key findings

- This study found that patterns vary in patients with colorectal cancer (CRC) in terms of fatty acid oxidation (FAO), and developed a novel risk-scoring system that contributes to the personalized and stratified treatment of CRC.

What is known and what is new?

- The existing studies have proved that changes in FAO metabolites and gene expression levels in the FAO pathway are related to the progress of CRC.
- An efficient corresponding metabolic classifier to disclose the unclear phenotypes of FAO in patients with CRC is of well worth.

What is the implication, and what should change now?

- Patients with CRC were divided into high- and low-enrichment groups by FAO_Cluster. GFAO_Score risk scoring system can evaluate the metabolic enrichment profile of FAO in patients to some extent, which may be conducive to accurate treatment strategies in colorectal malignancy.

Table 1 Seven gene sets related to fatty acid oxidation from the MSigDB

FAO gene sets	Online source	Gene name
FATTY_ACID_OXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/FATTY_ACID_OXIDATION	ACADS, ACADVL, ADIPOR1, ADIPOR2, ALOX12, BDH2, CPT1A, CPT1B, ECH1, ECHS1, HACL1, HADHB, HAO1, HAO2, PPARA, PPARD, PPARGC1A
GOBP_FATTY_ACID_ALPHA_OXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/GOBP_FATTY_ACID_ALPHA_OXIDATION	HACL1, HAO1, ILVBL, PEX13, PHYH, SLC25A17, SLC27A2
GOBP_FATTY_ACID_BETA_OXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/GOBP_FATTY_ACID_BETA_OXIDATION	ABCB11, ABCD1, ABCD2, ABCD3, ABCD4, ACAA1, ACAA2, ACACB, ACAD10, ACAD11, ACADL, ACADM, ACADS, ACADVL, ACAT1, ACAT2, ACOT8, ACOX1, ACOX2, ACOX3, ACOXL, ADIPOQ, AKT1, AKT2, ALDH1L2, AMACR, AUH, BDH2, CNR1, CPT1A, CPT1B, CPT1C, CPT2, CRAT, CROT, DECR1, DECR2, ECH1, ECHDC1, ECHDC2, ECHS1, ECI1, ECI2, EHHADH, ETFA, ETFB, ETFBKMT, ETFDH, FABP1, GCDH, HADH, HADHA, HADHB, HSD17B10, HSD17B4, IRS1, IRS2, IVD, LEP, LONP2, MCAT, MFSD2A, MLYCD, MTLN, PEX2, PEX5, PEX7, PLIN5, PPARA, PPARD, SCP2, SESN2, SLC25A17, SLC27A2, TWIST1, TYSND1
GOBP_FATTY_ACID_OMEGA_OXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/GOBP_FATTY_ACID_OMEGA_OXIDATION	ADH4, ADH5, ADH7, CYP24A1, CYP4F2, CYP4V2
REACTOME_BETA_OXIDATION_OF_VERY_LONG_CHAIN_FATTY_ACIDS	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/REACTOME_BETA_OXIDATION_OF_VERY_LONG_CHAIN_FATTY_ACIDS	ABCD1, ACAA1, ACOT4, ACOT6, ACOT8, ACOX1, DECR2, ECI2, EHHADH, HSD17B4, MLYCD
WP_FATTY_ACID_BETAOXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/WP_FATTY_ACID_BETAOXIDATION	ACADL, ACADM, ACADS, ACADVL, ACAT1, ACSL1, ACSL3, ACSL4, ACSL5, ACSL6, ACSS2, CHKB, CPT1A, CPT1B, CPT2, CRAT, DECR1, DLD, ECHS1, ECI1, GCDH, GK, GK2, GPD2, HADH, HADHA, HADHB, LIPC, LIPE, LIPF, LPL, PNPLA2, SLC25A20, TPI1
WP_FATTY_ACID_OMEGAOXIDATION	https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/WP_FATTY_ACID_OMEGAOXIDATION	ADH1A, ADH1B, ADH1C, ADH4, ADH6, ADH7, ALDH1A1, ALDH2, CYP1A1, CYP1A2, CYP2A6, CYP2D6, CYP2E1, CYP3A4, CYP4A11

FAO, fatty acid oxidation; MsigDB, molecular signatures database.

colorectal carcinogenesis pathway and FAO metabolism, ten carcinogenic signaling pathway gene sets were collected (the supplementary table available at: <https://cdn.amegroups.cn/static/public/10.21037/jgo-23-833-1.xlsx>). Transcriptome data and survival information of 867 patients with CRC were downloaded from three Gene Expression Omnibus (GEO) datasets, including GSE39582, GSE17536, and GSE72970 (<https://www.ncbi.nlm.nih.gov/geo/>), as the external verification queues. For further scRNA sequencing analysis and verification, we selected the 10 tumor samples with their corresponding normal samples from GSE132465 (in a total of 23 samples 10 of which had both tumor and normal specimens) with a total of 22,793 cells. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

Construction and validation of the FAO score

Firstly, based on seven gene sets related to FAO, single-sample gene set enrichment analysis (ssGSEA) was used to evaluate the metabolism level of FAO in patients with CRC. We generated seven FAO scores for CRC individuals, which indicated the enrichment degree of gene sets in the samples. We determined the optimal cutpoints of seven FAO scores according to *survminer* package. Based on the optimal cutpoints, we stratified patients into high and low FAO score groups seven times and performed Kaplan-Meier (K-M) survival analyses to explore the difference in overall survival (OS) each time.

Unsupervised clustering algorithm was applied to cluster analysis of FAO scores in 511 CRC samples. FAO scores consist of seven different FAO scores (GO_FAAO, GO_

FABO, GO_FAOO, FAO, WP_FABO, WP_FAOO, and REACTOME_FAO scores) originated from seven gene sets related to FAO. We used the *ConsensusClusterPlus* package for the above steps and conducted 1000 repetitions to ensure the stability of the classification. Lastly, the patients were divided into two subtypes, Cluster 1 and Cluster 2, according to the parameter kappa 2. Taking the P value less than 0.05 as statistically significant, the OS and progression-free survival (PFS) analyses of the two subtypes were subsequently performed. In accordance with seven different FAO scores, patients with CRC were classified into high and low-score groups by the optimal cutoff value followed by K-M analysis for comparison of OS.

Based on seven FAO scores and the k-means clustering analysis of unsupervised learning, the patients were divided into two subtypes, Cluster 1 and Cluster 2, according to the parameter kappa 2. Taking the P value less than 0.05 as statistically significant, the OS and PFS analyses of the two subtypes were subsequently performed.

To assess the FAO metabolism status between the two subtypes, we additionally compared the enrichment scores of seven FAO metabolic pathways and the expression of key regulatory genes in FAO, including *ACADVL*, *CPT1A*, *ACADM*, *CPT2*, and *ACOX1*.

Gene set enrichment analysis (GSEA, <http://www.broadinstitute.org/gsea>) was used to identify the differences in enrichment degree between Cluster 1 and Cluster 2 of ten classical carcinogenic signaling pathways. Transcriptome data and survival information of 867 patients with CRC from GEO were collected as an external verification cohort, divided into two groups for further gene pathway enrichment and prognosis analyses based on FAO scores.

scRNA sequencing data analysis and validation

Seurat, R package (19) was applied to transfer scRNA-seq data into *Seurat* objects. We performed quality control (QC) by filtering out genes expressed in less than 3 cells and disregarded cells with less than 300 genes expressed. Cells with fewer than 1,000 or more than 20,000 unique molecular identifiers (UMI) were excluded. The expression of mitochondrial, ribosomal, and hemoglobin genes was calculated. To remove the low-activity cells, cells with a low ribosome (<3%), high mitochondria (>10%), and hemoglobin content (>0.1%) were discarded.

After filtering out poor-quality cells, a total of 16,658 cells were retained for further analysis (Figure S1). For clustering, highly variable genes were selected, and the

principal components based on those genes were used to build a graph, which was segmented with a resolution of 0.6. Single-cell clustering was visualized by t-distributed stochastic neighbor embedding (t-SNE). After data homogenization and batch effect removal, cells were clustered by resolution parameter (as 0.5), determined by *Clustree* package. Further, *singleR* package was applied to identify and name the clusters. Percentage, ssGSEA, AddModule, and AUC methods were used to calculate the FAO scores after clustering.

We collected 87 genes (FAO 87) from GOBP FATTY ACID OXIDATION in MsigDB (<https://amigo.geneontology.org/amigo/term/GO:0019395>) and further established a signature to evaluate the status of FAO at cell level. After the selection of the epithelial cells, we performed data normalization, dimensionality reduction, and re-clustering to classify the epithelial cells into two subtypes, C0 and C1, with a resolution of 0.2. The difference between C0 and C1 in terms of FAO 87-gene signature scores and enrichment of carcinogenic signaling pathways were analyzed.

Development and evaluation of GFAO_Score

To enhance the practicability of the classification based on FAO score, we decided to generate a more convenient signature to help detect certain patients with CRC. Therefore, we used three R packages with different methods (*DESeq2*, *edgeR*, and *Limma*) to detect differentially expressed genes (DEGs) by taking the intersection between C0 and C1 that met the screening parameters [\log_2 fold change $|\log_2 \text{FC}| > 1$, and false discovery rate (FDR) < 0.05]. Venn diagrams were used to determine the intersection of DEGs generated from three methods. DEGs in the above intersection were introduced into a univariate Cox regression along with survival information of patients with CRC to identify differentially expressed prognostic genes, which were defined as hub genes. Using the *glmnet* R package, least absolute shrinkage and selection operator (LASSO) regression analysis was further performed on hub genes in order to avoid multicollinearity and overfitting as well as develop the final model. Subsequently, scores of hub genes in FAO (GFAO_Score) were defined using the following formula: $\text{GFAO_Score} = \sum \text{Gene expression} \times \text{Coef}$.

Where *gene expression* is the expression profile of the hub genes, and *Coef* is the risk coefficient.

Divisions were established with high and low scores according to the medium value of GFAO_Score.

Subsequently, a prognostic assessment was calculated using the receiver operating characteristic (ROC) curve method in the *timeROC* package. K-M analysis revealed survival curves across the CRC training (TCGA) and validation cohort (GEO). To evaluate the independence of GFAO_Score in prognosis, multivariate Cox regression analyses were conducted. In addition, relationships between GFAO_Score and survival information [vital status and The American Joint Committee on Cancer (AJCC) stages] were also analyzed.

We explored the potential performance of GFAO_Score in anti-tumor treatments including immunotherapy and chemotherapy. To assess the immunotherapy effect, tumor immune dysfunction and exclusion (TIDE) analysis (<http://tide.dfci.harvard.edu>) web tool was used to predict the responses of patients with CRC. For an indication of systematical assessment of immunological activity and immunotherapy in CRC, we calculated the international prognostic scores (IPS) of high and low score groups of GFAO_Score. Furthermore, we collected 233 patients with CRC in total from GSE39582 who had received adjuvant chemotherapy after surgical resection and 133 patients underwent integrated therapy from GSE63216, in order to evaluate the predictivity of GFAO_Score. Later, the predictive efficacy of GFAO_Score in other solid tumors was also validated in the immunotherapy cohort of 348 patients with bladder cancer in IMvigor210.

The drug analysis datasets were collected from the Genomics of Drug Sensitivity in Cancer (GDSC) (<https://www.cancerrxgene.org/>) for the drug sensitivity assessment of GFAO_Score in patients with CRC using *Oncopredict* R package. Based on the GFAO_Score grouping, the relationships between the subgroups and drug sensitivity were determined in the aspect of chemotherapy and immunotherapy using the Wilcox test.

Statistical analysis

Data analyses and graphing were performed using R software (4.1.1). Cox regressions and K-M analyses were conducted using the *survival* R package with statistically significant differences assessed by the log-rank test. The comparison of count data was assessed by Fisher's precision probability test and chi-square test. Wilcox test was used to compare non-normal distribution data between subgroups. Spearman analysis was applied to assess the correlations between linearly related variables. The optimal cutoff value was formulated by the *survminer* package. The time-

dependent area under the ROC curve (AUC) for survival variables was plotted using the *timeROC* package. The value of two-tailed $P < 0.05$ indicates statistically significant differences.

Results

Construction and validation of the FAO score

Construction of the FAO score

Using the ssGSEA to illustrate individual metabolism levels of FA, we generated the seven FAO scores for each patient with CRC according to seven FAO pathway gene sets from MSigDB. The K-M survival curves between the high and low score groups implemented by an optimal cutoff value are depicted in [Figure S2](#). In total, the results indicated that patients with low FAO scores tended to have dismal survival outcomes compared to patients with high scores.

Unsupervised consensus clustering based on the FAO score

Screened by the standard parameters mentioned above, unsupervised consensus clustering was conducted to categorize patients into two clusters based on the seven FAO scores in the training set, with 304 patients in Cluster 1 and 232 patients in Cluster 2 respectively ([Figure 1A](#)). We appraised the survival curves by setting OS and PFS as the prognostic endpoints ([Figure 1B,1C](#)). It showed that there were significant statistical differences between the two groups of patients. Patients in Cluster 1 had a more favorable survival rate than those in Cluster 2.

Evaluation and validation of the clustering

The enrichment status of FAO in patients in Cluster 1 and Cluster 2 from the training dataset was assessed and calculated by the ssGSEA in seven FAO pathways. The heatmap of enrichment of FAO metabolism pathways showed that Cluster 1 has a rather higher FAO level, which had been in line with our preliminary results ([Figure 1D](#)). Additionally, to depict the expression profiles of key genes of FAO between Cluster 1 and Cluster 2, a boxplot was utilized to display the difference in *ACADVL*, *CPT1A*, *ACADM*, *CPT2*, and *ACOX1*, which indicated that the regularity genes were all highly expressed in Cluster 1 ([Figure 1E](#)).

GSEA was applied to screen the differences in enrichment pathways between the two clusters through the cell cycle, and classical carcinogenic signaling pathways in the

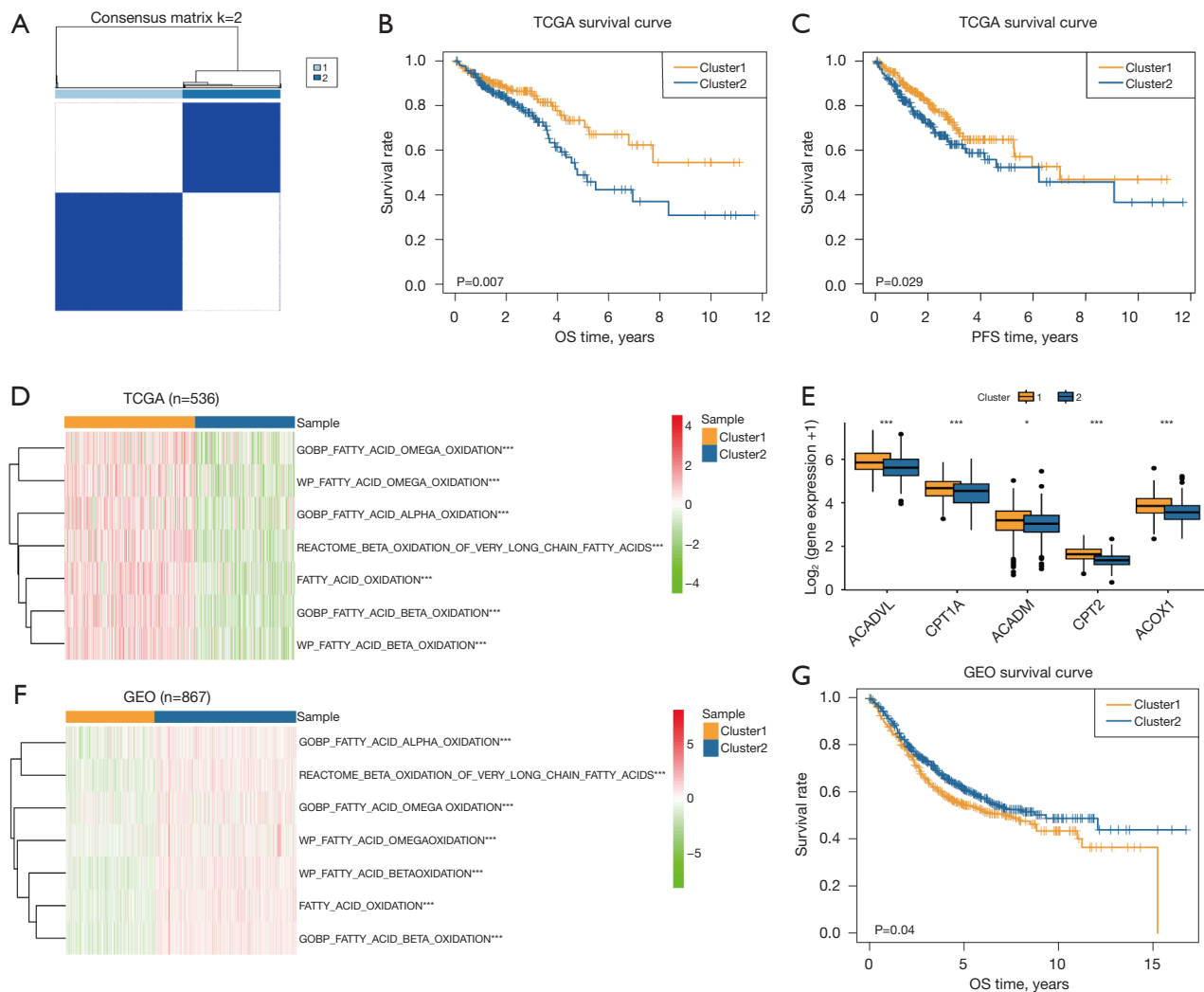


Figure 1 Construction and validation of FAO score. (A) Consensus heatmap of clustering with the robust classification (k=2). (B) Kaplan-Meier curves of OS between clusters in TCGA. (C) Comparison of PFS between clusters in TCGA. Log-rank test P values are shown. (D) k-means clustering of FAO metabolism in CRC based on FAO pathways calculated through the ssGSEA method in the TCGA training cohort. (E) The differences in expression of selected genes of FAO pathway (\log_2 intensity levels) in the TCGA cohort. Significance was determined by Wilcoxon rank-sum tests. (F) k-means clustering of FAO metabolism in CRC based on FAO pathways calculated through the ssGSEA method in the GEO validation cohort. (G) Comparison of Kaplan-Meier curves of OS in the GEO validation cohort. Log-rank test P value is shown. *, $P < 0.05$; ***, $P < 0.001$. FAO, fatty acid oxidation; TCGA, The Cancer Genome Atlas; OS, overall survival; PFS, progression-free survival; CRC, colorectal cancer; ssGSEA, single-sample gene set enrichment analysis; GEO, Gene Expression Omnibus.

MSigDB. We found that carcinogenic genes were enriched in different statuses between Cluster 1 and Cluster 2. The GSEA results suggested that Cluster 2 exhibited markedly higher transcriptional levels in the period of tumorigenesis, including CELL CYCLE, HIPPO, MAPK, NOTCH, PI3K-AKT, RAS, TGFB, and WNT signaling pathways (Figure S3).

In order to evaluate the stability of the results of our unsupervised consensus clustering, three datasets [GSE39582 (N=566), GSE17536 (N=177), and GSE72970 (N=124)] were collected from the GEO database as the external validation cohort after merging data and removing batch effect. Patients in the merged cohort were clearly categorized into two clusters. We used the heatmap to

show that the seven FAO pathways were rather more highly expressed and enriched in Cluster 2 than those in Cluster 1, indicating possession of the preferable survival time (Figure 1F). In addition, the survival analysis presented statistical differences in survival outcomes based on the FAO scores, which was consistent with the results of TCGA cohort (Figure 1G).

Identification of expression profile of FAO at scRNA sequencing analysis

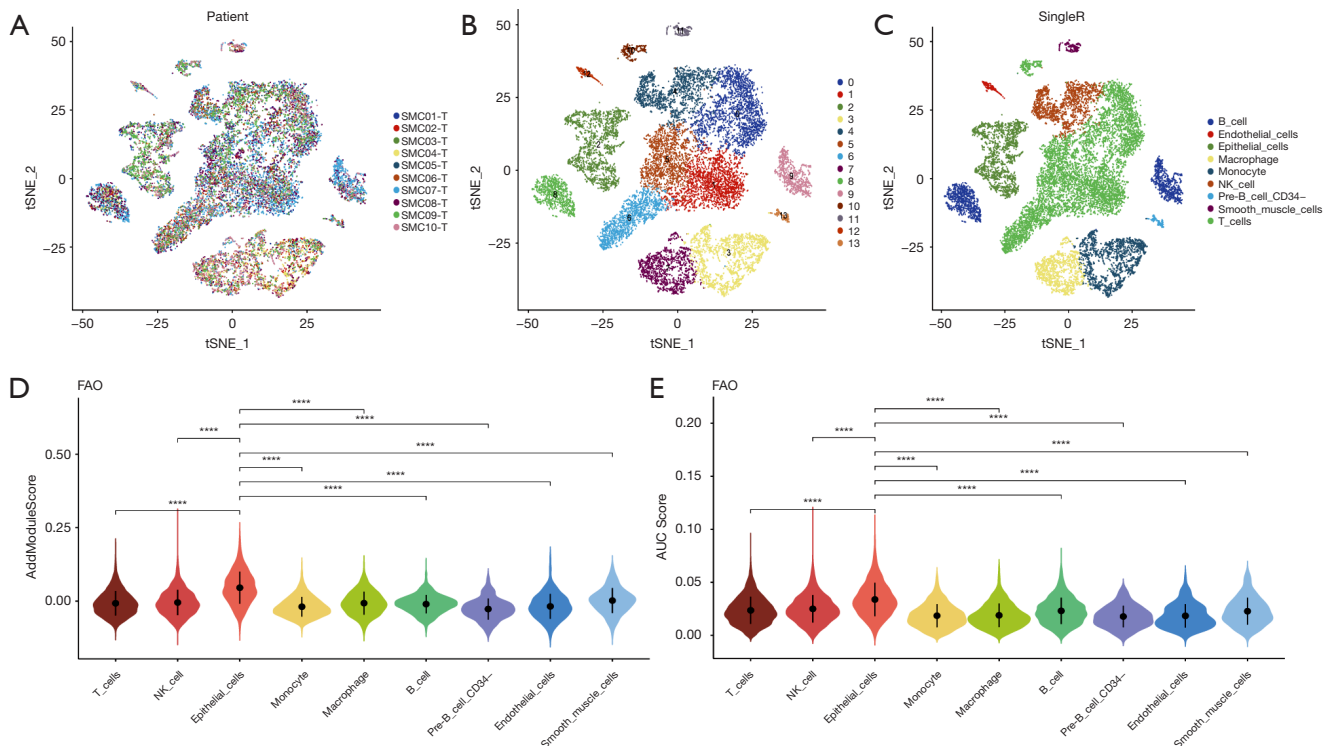
We then sought to determine whether the difference in FAO metabolism between the two clusters can be distinguished at the single-cell level. The single-cell resolution level assists in understanding the precise landscape of subclonal diversity. We selected ten CRC samples from GEO: GSE132465, a total of 22,793 cancer cells. We performed gene filtering, normalization, and dimensionality reduction and finally identified nine distinct clusters, including B cells, endothelial cells, epithelial cells, macrophage, monocyte, natural killer (NK) cell, pre-B cell CD34⁻, smooth muscle cells, and T cells (Figure 2A-2C). In order to evaluate the difference in FAO enrichment among cell clusters, we used a FAO 87-gene signature (FAO 87; see Methods section) and four common single-cell gene set scoring methods, and

it was found that the gene set enrichment score of epithelial cells was significantly higher than that of other cell clusters (Figure 2D,2E and Figure S3). In order to further explore the difference in FAO metabolism in tumor epithelial cells, we extracted epithelial cells and classified to Cluster 0 (C0) and Cluster 1 (C1) (Figure 2F-2H). We found that the FAO 87-gene signature score of the epithelial subtype was higher in C0 than those of C1, while the classical carcinogenic pathway enrichment score and epithelial-mesenchymal transition (EMT) score (AddModule, AUC) were both lower in C0, suggesting that FAO gene enrichment may be associated with better prognosis (Figure 2I-2N), which was consistent with the results in TCGA that patients with lower expression of FAO might lead poor survival outcomes.

Development and evaluation of the GFAO_Score

Construction and validation of the GFAO_Score

The differences in terms of biological behaviors and survival outcomes between Cluster 1 and Cluster 2 in TCGA were further explored. We applied three commonly used methods of differential gene expression analysis, which include DESeq2, edgeR, and Limma methods, to identify 355, 320, and 644 DEGs respectively (Figure S4).



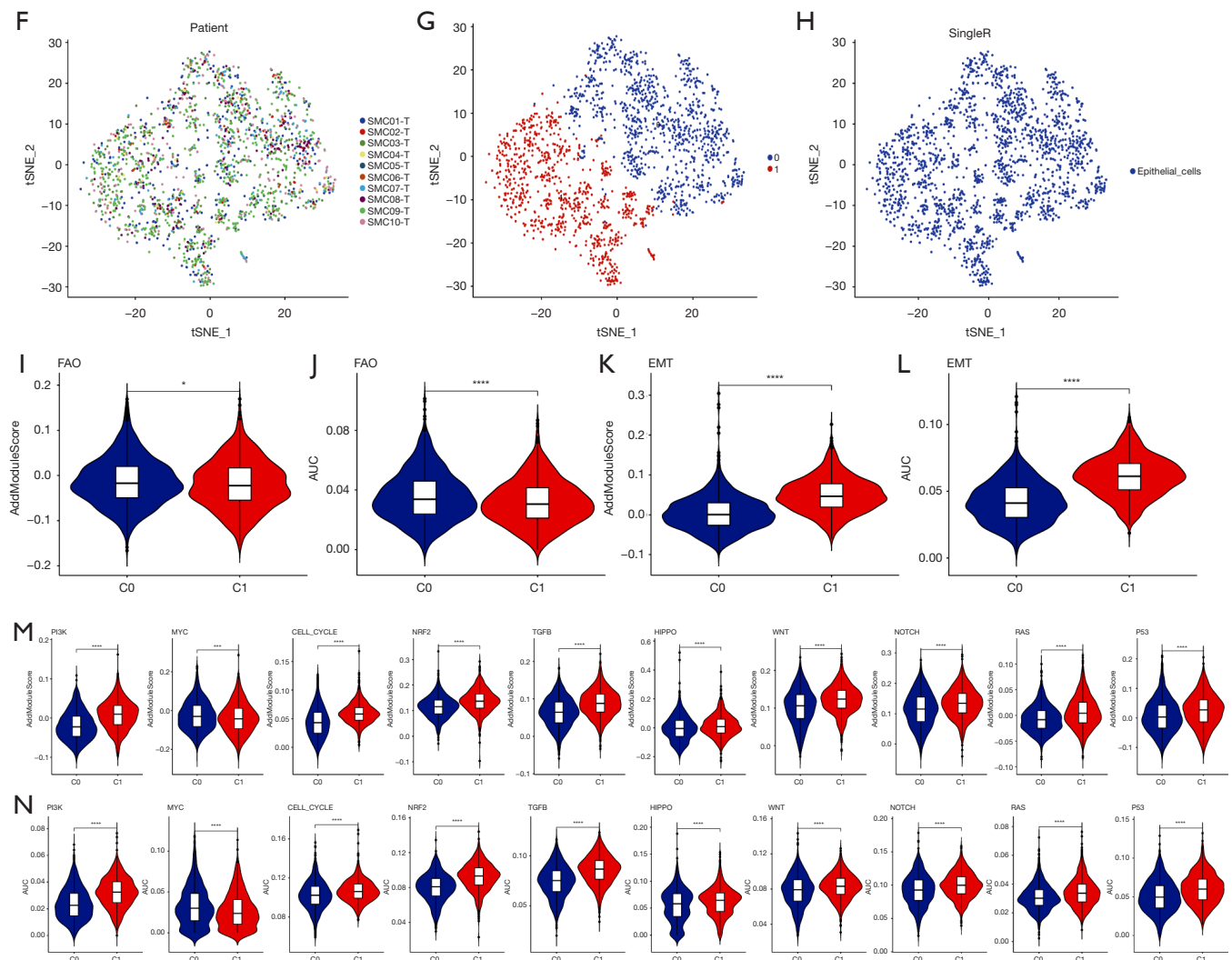


Figure 2 FAO at single-cell resolution. (A-C) t-SNE plot showing the nine major lineages of cells in CRC samples in GSE132465. (D,E) Comparison of the FAO 87-gene signature scores based on AddModule and AUC methods among the nine cell subsets. (F-H) The t-SNE plots presenting cell subpopulations in epithelial cell subcluster analysis based on FAO metabolism distribution. (I,J) Violin plots comparing the FAO 87-gene signature scores based on AddModule and AUC methods between C0 and C1. (K-N) The contrast of EMT and ten classical carcinogenic pathway enrichment scores based on AddModule and AUC methods in the two subclusters. *, $P < 0.05$; ***, $P < 0.001$; ****, $P < 0.0001$. FAO, fatty acid oxidation; t-SNE, t-distributed stochastic neighbor embedding; CRC, colorectal cancer; NK cell, natural killer cell; AUC, area under the curve; EMT, epithelial-mesenchymal transition; C0, Cluster 0; C1, Cluster 1.

Therefore, a total of 107 genes related to the FAO pathway were screened by taking the intersection of DEG results generated from three different methods between Cluster 1 and Cluster 2 (Figure 3A). Based on the intersection of DEG results, univariate Cox regression was performed to decrease redundancy and three prognosis-related DEGs remained. As a result, *ZFHX4*, *AQP8*, and *AKR1B10*

were further subjected to LASSO regression analysis for the construction of *GFAO_Score*. The formula for the prognostic risk assessment of the *GFAO_Score* was defined as follows: $GFAO_Score = (0.5323323498) \times \text{Exp}(ZFHX4) + (0.0058440605) \times \text{Exp}(AQP8) + (-0.0156539071) \times \text{Exp}(AKR1B10)$, where “Exp” represents the expression profile of the individual of selected DEGs. The *GFAO_Score* in

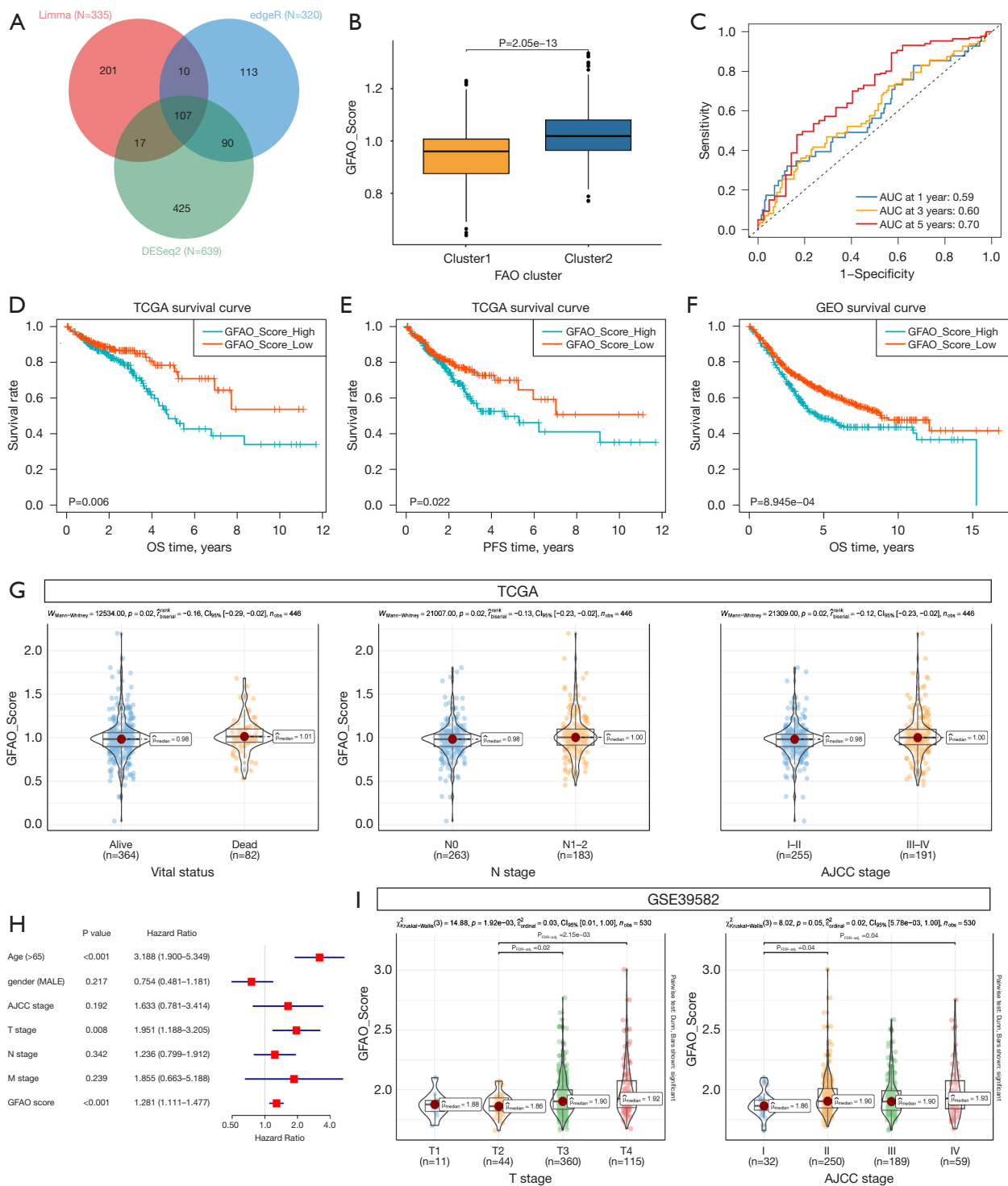


Figure 3 Development and evaluation of GFAO_Score. (A) Venn diagrams demonstrating the 107 DEGs identified by the intersection of *DESeq2*, *Limma*, and *edgeR* methods. (B) Comparison of GFAO_Score between Cluster 1 and Cluster 2. The Wilcoxon test was used to determine the statistical significance of the difference, and $P<0.05$ was considered statistically significant. (C) ROC curves and AUC of GFAO_Score in patients for 1-, 3-, and 5-year OS in TCGA cohort. (D) Comparison of OS between high and low GFAO_Score in TCGA. Log-rank test P value is shown. (E) Comparison of PFS between high and low GFAO_Score in TCGA. (F) Comparison of OS between high

and low GFAO_Score in the GEO validation cohort. Log-rank test P value is shown. (G) Volcano plots showing the tendency of GFAO_Score in terms of vital status and clinical stage. (H) Forest plots of multivariate Cox regression analyses, including GFAO_Score, age, gender, TNM, and clinical stage in TCGA. (I) Volcano plots exhibiting the distribution of GFAO_Score in terms of T and clinical stages in GSE39582. GFAO_Score, the scores of genes related to FAO; FAO, fatty acid oxidation; DEGs, differentially expressed genes; ROC, Receiver operating characteristic; AUC, Area under curve; TCGA, The Cancer Genome Atlas; OS, Overall survival; PFS, Progression-free survival; GEO, Gene Expression Omnibus; AJCC, The American Joint Committee on Cancer.

Cluster 2 was significantly higher than that in Cluster 1 (Figure 3B), which indicated that the GFAO_Score could represent the FAO level and detect certain patients with CRC. ROC analysis was performed to assess the efficiency of GFAO_Score with the AUCs for 1-, 3-, and 5-year OS prediction, which was 0.59, 0.60, and 0.70, respectively (Figure 3C). Furthermore, patients in the TCGA training cohort were assigned into two groups, with 255 and 256 patients in high and low GFAO_Score groups sorted by the medium value. Additionally, K-M analysis revealed an unfavorable OS and PFS in the high GFAO_Score group (Figure 3D, 3E). In the GEO validation cohort, patients with high GFAO_Score also had the unfavorable prognosis (Figure 3F). Patients in death revealed significantly higher GFAO_Score in vital status analysis. Patients classified in the high GFAO_Score group leaned towards the more advanced AJCC stage and lymph node status with statistical significance (Figure 3G). The multivariate Cox regression analyses including age, gender, AJCC, and TNM, were calculated to show that GFAO_Score was an independent risk factor for CRC ($P < 0.05$) (Figure 3H). In addition, we collected GSE39582 as the validation cohort from the GEO database to evaluate the performance of GFAO_Score. The results also showed that patients in advanced clinical stages in AJCC classification were detected with higher GFAO_Score (Figure 3I), consistent with the previous validation in the TCGA cohort.

Immunological assessment of the GFAO_Score

The IPS score was used to evaluate the potential treatment outcomes of immunotherapy. Patients with higher IPS values received better responses to immunotherapy with CTLA-4 monoclonal antibody or PD-1 monoclonal antibody. The results showed a tendency for patients with higher IPS to obtain lower GFAO_Score (Figure 4A).

The TIDE score was applied as a predictor of treatment outcomes after immune checkpoint blockade was used. There was a higher proportion of patients possessing lower response rates to the immunotherapy in the high GFAO_Score group (Figure 4B). The violin plots revealed that the

TIDE scores, exclusion scores, and dysfunction scores in the low GFAO_Score group were lower than that in the high GFAO_Score group, which meant that patients with high GFAO_Scores might tend to expose to the immune escape and worse response to immune checkpoint therapies (Figure 4C-4E).

Analysis of adjuvant therapies and drug sensitivity

In order to evaluate the value of the GFAO_Score in integrated anti-tumor therapy, 233 and 133 patients with CRC from GSE39582 and GSE63216 were collected for survival analysis respectively. The results illustrated that in GSE39582, patients with lower GFAO_Scores would prefer a better prognosis in adjuvant chemotherapy (Figure 5A). Besides, patients with low GFAO_Score tended to possess longer survival time receiving capecitabine, oxaliplatin, and bevacizumab treatments in GSE63216 (Figure 5B). In order to evaluate the predictive performance in other tumors, we also assessed the GFAO_Score of 348 patients with bladder cancer in the IMvigor210 cohort. Patients with low GFAO_Score had better survival outcomes, whereas those with high GFAO_Score presented the opposite results in K-M analysis (Figure 5C).

In addition, we calculated the IC50 (50% inhibition concentration) of 198 medications from GDSC for high and low GFAO_Score groups in the training cohort. Filtering the abnormalities, six widely applied chemotherapy drugs are shown in Figure 5D, including 5-fluorouracil, irinotecan, oxaliplatin, cisplatin, paclitaxel, and camptothecin in the low GFAO_Score group had significantly lower IC50 values than those in the high GFAO_Score group, which revealed that patients with lower GFAO_Score might benefit from chemotherapy. Inhibitors of tumor activation pathways were further explored to identify the differences between the two subgroups. Screening for target drugs, we analyzed the IC50 and found the lower values of sorafenib (the anti-VEGFR drug), lapatinib (the anti-EGFR/HER2 drug), dabrafenib (the anti-BRAF drug), gefitinib (the EGFR-TKI drug) in the low GFAO_Score group (Figure 5D), indicating the preferable vital status in patients in target therapy.

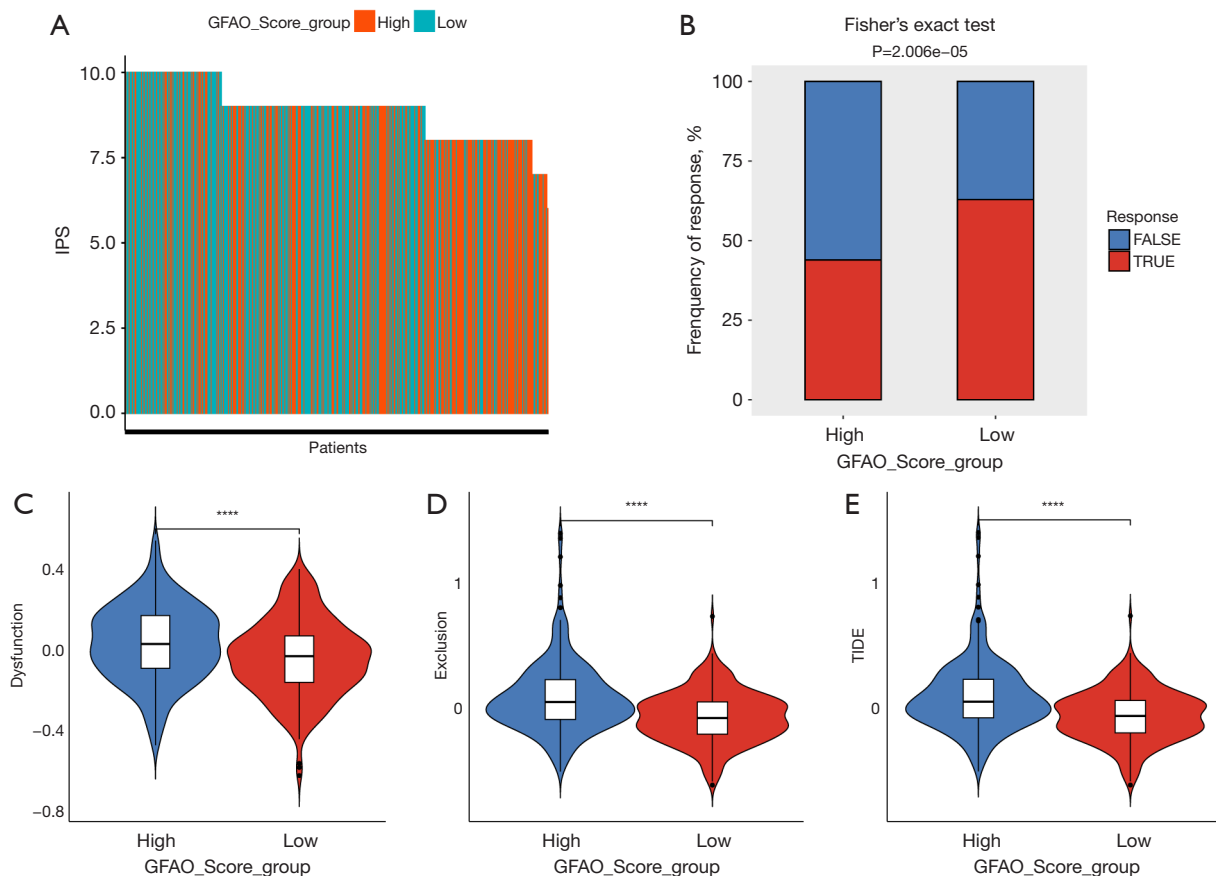


Figure 4 Immunological assessment of GFAO_Score. (A) Barplots showing the distribution of patients from high and low GFAO_Score groups in IPS. (B) The proportion of response rates to ICI therapy in the high and low GFAO_Score groups based on TIDE prediction. (C-E) Violin plots exhibiting the difference in dysfunction and exclusion scores between high and low GFAO_Score groups. ****, $P < 0.0001$. GFAO_Score, the scores of genes related to FAO; FAO, fatty acid oxidation; IPS, international prognostic scores; ICI, immune checkpoint inhibitors; TIDE, tumor immune dysfunction and exclusion.

Discussion

The incidence of CRC in younger adults has increased in recent years (1). Inconclusive conventional approaches may lead to inappropriate prescription-making and surveillance (20). Personalized assessment approaches exhibited various survival outcomes in CRC. With an in-depth understanding of the complexity of tumors, it was found that metabolic reprogramming is an important marker of tumors. In recent years, the change in energy metabolism is generally regarded as an important sign of cancer occurrence, development, and treatment resistance, in which the imbalance of lipid metabolism has been proven to be an important feature of tumor cell metabolism (19).

FA metabolism influences biological behaviors in different ways, typically including the synthesis

of lipid building blocks for membranes, that is, glycerophospholipids, and signaling intermediates such as phosphatidylinositol (4,5)-biphosphate, diacylglycerol (DAG) and phosphatidate to facilitate mitogenic and/or oncogenic signaling (21). FAs are a large, essential, energy source that can meet the substantial fuel needs of rapid invasiveness of carcinoma (22). Plenty of epidemiological evidence reveals that the recurrence and mortality rates of patients with CRC increase in obese people (23). The obesity-related impacts on tumor incidence, progression, and therapeutical efficacy will increasingly challenge malignant disease arrangement, which underscored the significance of FAO in CRC pathogenesis. Abnormal expression levels of metabolic enzymes involved in FA uptake, synthesis, and FAO have been found in many

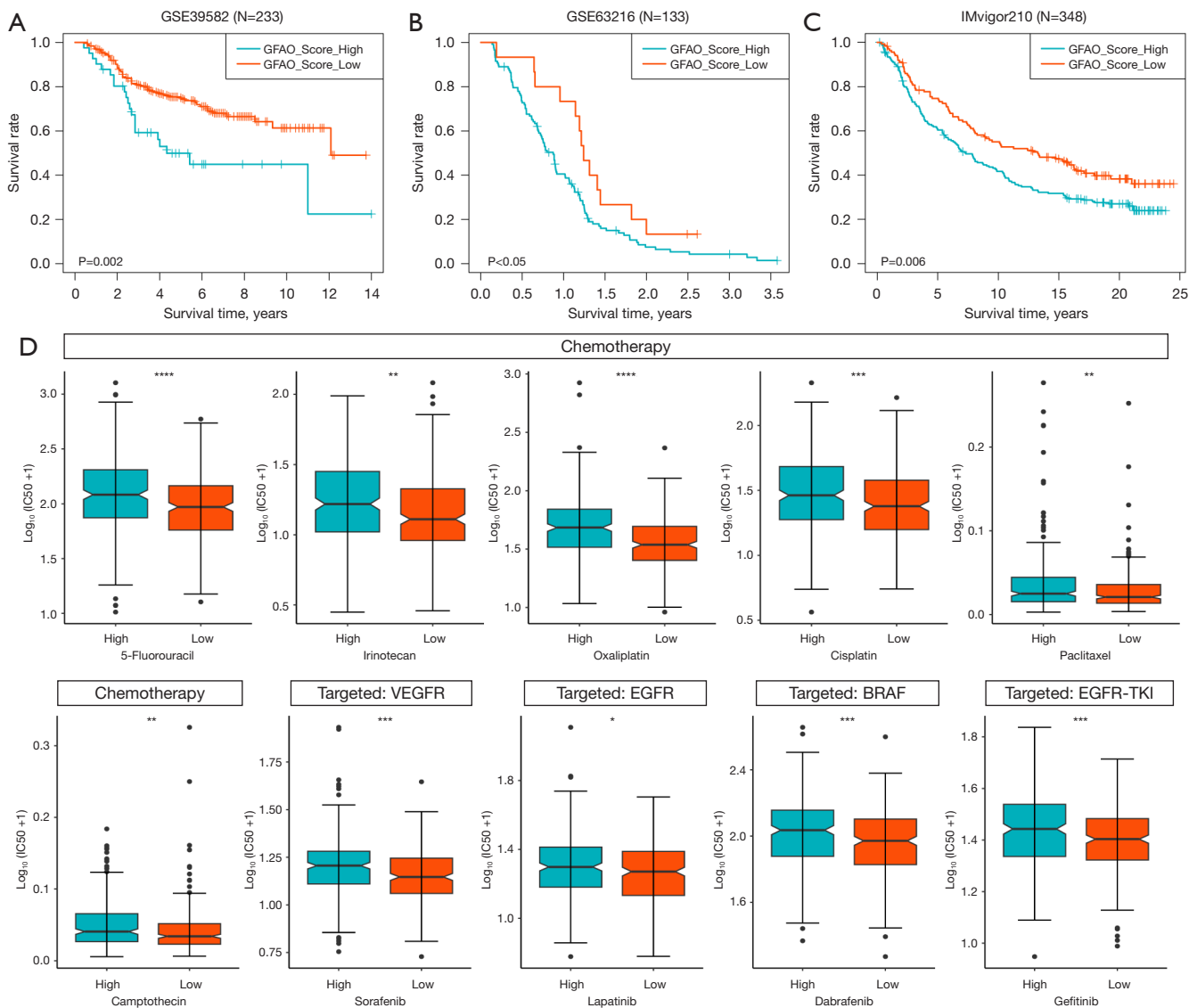


Figure 5 Analysis of adjuvant therapies and drug sensitivity. (A) Comparison of survival outcomes in external chemotherapy cohorts. (B) Comparison of survival outcomes in the external cohort treated by capecitabine, oxaliplatin, and bevacizumab. (C) K-M curves presenting survival outcomes in high and low GFAO_Score groups in the iMvigor210 cohort. Log-rank test P value is shown. (D) Boxplots for evaluation of drug sensitivity including traditional chemotherapy agents and targeted inhibitors between the two subtypes based on GFAO_Score. Chemotherapeutics including 5-fluorouracil, irinotecan, oxaliplatin, paclitaxel, and camptothecin exhibit significantly lower IC50 in the low GFAO_Score group than in the high GFAO_Score group. Targeted inhibitors, including sorafenib, lapatinib, dabrafenib, and gefitinib are illustrated with preferable treatment outcomes in low GFAO_Score. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$. GFAO_Score, the scores of genes related to FAO; FAO, fatty acid oxidation; IC50, 50% inhibition concentration.

tumors, leading to FA metabolism reprogramming and promoting tumorigenesis and development (24). However, the mechanism of lipid metabolism reprogramming in CRC has not been fully explored, especially the alteration in FAO metabolism in patients with CRC. In this study,

we identified the enrichment and inner interaction of FAO in individuals with CRC via TCGA and GEO databases. Development of the classifications according to bulk RNA and scRNA sequencing analysis indicated that patients who differed in levels of FAO tended to possess a variety of

prognoses.

The role that FA metabolism plays in carcinogenesis has been illustrated in many studies. Tumor FA metabolism adapts to ‘macro-level’ host attributes and, at the local microenvironment level, influences disease behavior. Recent research related to gynecologic malignancy showed that adipocytes provide FAs to procedures of metastasis and activate the FAO pathway, which serves as an energy source to facilitate distal metastasis. Many categories of tumors co-localize with adipose tissue and exhibit a close relationship, such as breast cancer, prostate cancer, and ovarian cancer that grow or invade the adipose-rich areas (25–28). FAs can act as substrates for lipid synthesis and storage in cancer cells which serve as the energy pool. Some research showed that *CPT1A*, one of the key proteins of the FAO pathway, whose expression profile in breast cancer was required to metabolize adipocyte-derived FAs and supported the further invasion and EMT induced by adipocytes (29). In melanoma cancer cells, the increase of *CPT1A* remained more stable, which might remind the differences among cancer types (30). It has been suggested that the accumulation of FAs can promote the growth of CRC cells and liver metastasis. Among them, saturated FAs can participate in the tumor-related inflammatory microenvironment and promote the occurrence and development of CRC. Reducing the content of ultra-long chain FAs can inhibit the growth of tumor cells. In addition, FA metabolism is also closely related to immune cells in the TME. Tumor cells can release FAs for lipid communication with tumor-related macrophages, making tumor-related macrophages become “accomplices” to assist tumor cells in liver metastasis.

In CRC, we calculated the enrichment status of FAO in individuals using ssGSEA and classified patients into two subgroups by unsupervised consensus clustering. In order to verify its stability and repeatability, we conducted validation in several aspects: visualizing the differences in enrichment scores; clarifying the expression profile of key genes in FAO; exploring the enrichment of some gene pathways; and requiring other external data to support and verify the conclusion. According to the results, patients with high enrichment levels in FAO (Cluster 1) showed more favorable OS and PFS. The heterogeneity and vitro experimental model design may contribute to such a situation. However, we generated the FAO scores to evaluate the individual level via the bulk RNA sequencing data, which focused on the integrity of the genomic landscape and inner interaction

about the enrichment of lipid metabolism in bioinformatics. To unclothe the differences between Cluster 1 and Cluster 2, we drew a systematic analysis in terms of the clinical characteristics, and biological behaviors related to the FAO metabolism. The results suggested that compared to Cluster 1, Cluster 2 possessed higher transcriptional profiles about tumorigenesis, including CELL CYCLE, HIPPO, MAPK, NOTCH, PI3K-AKT, RAS, TGFB, and WNT pathways. Similar situations have been found in other cancer types like non-small cell lung cancer. A metabolic transition that inhibited FA synthesis and promoted energy provision has been identified as a crucial component of TGFβ1-induced EMT and metastasis (31). We subsequently used GEO data for external verification. The results suggested that the samples could also be clearly divided into two groups. Cluster 2 in GEO had a better prognosis than Cluster 1, labeled by a higher FAO enrichment score. It was also the case that the group with a high enrichment score in TCGA cohorts had a better survival outcome. Therefore, the performance of our clustering was stable and repeatable. Animal models are indispensable work in the study of CRC, which helps explore the biological progress of tumor growth and subsequently develop anti-tumor drugs. The mouse CRC model has been widely used in various malignancy research in the world. A previous study has verified that the alteration of FAO affects the progress of CRC through experiments of the mouse model *in vivo* (32). In addition, the signaling pathways of intestinal development, regeneration, and disease between drosophila and mammals are highly conserved (33). The previous study has proved that the change of expression of FAO-related genes has a significant influence on intestinal stem cells (ISC) based on a new CRISPR-Cas9 fly model, in which ISC is the established cell of origin for CRC in the mammalian intestine (34).

Following the previous analysis, we further focused on the scRNA sequencing method to clarify the correlation between FAO and tumor progression in CRC. The epithelial cells were screened for high expression of the FAO 87-gene signature, related to the oxidation of FAs in mitochondria. The epithelial cells were then extracted and clustered again into two clusters. The classical carcinogenic pathway label enrichment score and EMT score were apt to be lower in C0, suggesting that poor FAO enrichment may lead to disease deterioration.

However, it is of high cost and unavailable to conduct the bulk RNA sequencing procedure for the whole seven FAO gene sets to perform detection for patients with

CRC. Considering the clinical practicality, we decided to generate a new signature based on the unsupervised consensus clustering of FAO. Therefore, three genes, *ZFHX4*, *AQP8*, and *AKR1B10* were identified and subjected to the LASSO algorithm for the development of GFAO_Score, which showed excellent efficacy in prognosis and treatment response in chemotherapy and target therapy. According to the classification of GFAO_Score, we found that the high GFAO_Score group had an unoptimistic survival time compared to the low-score group. Adjuvant therapy response and external validation were subsequently evaluated.

Besides, considering the relationship between heterogeneity and clinical benefits of the two groups, the predictive performance of GFAO_Score in chemotherapy and target therapy was further assessed. Patients in the low-score group who had higher IPS values received better responses to immunotherapy with CTLA-4 or PD-1 application. In addition, we calculated the GFAO_Score in order to evaluate the immunotherapy response in the IMvigor210 cohort as external validation data, which also indicated that patients in the high GFAO_Score group presented unfavorable survival outcomes and poor sensitivity to immunotherapy. The resistance to immunotherapy challenges the standard treatment strategies nowadays. A long-chain fatty acyl-CoA synthetase inhibitor, triacsin C, that blocks FA activation and thereby lipid droplet biogenesis, which means lower the status of FAO, can enhance the sensitivity of chemotherapy of CRC cells *in vitro* and in mouse xenografts (35). Tumoral CPT1A expression was associated with poorer OS in patients with gastric cancer, a similar situation in CRC (18). Pharmacological regulation of FAO like CPT1 inhibitors, might consistently chemosensitized tumor cells. While further shreds of evidence in the real world are necessary to validate the efficacy of GFAO_Score.

As for drug sensitivity analysis, six commonly utilized chemotherapy drugs including 5-fluorouracil, irinotecan, oxaliplatin, paclitaxel, and camptothecin, were screened with the lower IC50 values in the low-score group, suggesting that patients who obtained the lower GFAO_Score might benefit from chemotherapy. GFAO_Score also showed a good performance in the discrimination of patients sensitive to tumor pathway inhibitors in our study. Our signature has the potential to be a surrogate for prognostic and predictive assessment and drug benefit selection. This may also offer guidance for clinical medicine, such as decision-making strategies for immunotherapy based on our medication

sensitivity analysis.

Moreover, we identified the three genes related to FA metabolism in CRC, which included *ZFHX4*, *AQP8*, and *AKR1B10*. With the max coefficient and highest expression level in the signature, *AKR1B10*, a member of the aldosterone reductase superfamily, is mainly expressed in the human small intestine and colon epithelial tissues. It has been previously mentioned that high expression of *AKR1B10* in breast cancer is significantly positively correlated with genes related to FAO (36). In breast cancer, *AKR1B10* can promote tumor migration and metastasis by activating the MAPK pathway (37) but regulates FAO to enhance the prognosis of CRC. However, there is no research exploring the regulation mechanism of FAO mediated by *AKR1B10* in patients with CRC.

ZFHX4 is one of the DNA repair pathway genes, and somatic mutations in this gene are associated with poor survival in esophageal squamous cell carcinoma and multiple myeloma (38,39). Moreover, *ZFHX4* encodes a zinc finger protein and is associated with the maintenance of tumor-initiating cells in glioblastoma (40). However, the role of this gene in CRC is not clear. Based on the derivation of GFAO_Score, patients with overexpression of *ZFHX4* are more likely to be stratified into the high-risk group. It will be a valuable research direction to explore the relationship between *ZFHX4* mutation and the prognosis of CRC. Besides, the aquaporins are a family of small membrane transport proteins, and *AQP8* functions as water-selective transporters (41). The dysregulation of *AQP8* has been proven to be involved in tumorigenesis. For example, *AQP8* increases viability, inhibits apoptosis, and facilitates metastasis in cervical cancer cells (42). In CRC, *AQP8* represses progression by regulating PI3K/AKT signaling and PCDH7 expression (43). However, the association between *AQP8* expression and FA metabolism pathways in CRC remains unexplored.

Although the remarkable prognosis and prediction of GFAO_Score in CRC have been evaluated in this study, some limitations remain to be addressed. First, because the datasets were collected from online retrospective public databases, it is anticipated that large prospective clinical studies and experiments *in vivo* and *in vitro* should be validated. Second, real immunotherapy and target therapy cohorts were recruited by the study, which limited its efficacy in prediction. The subsequent downstream mechanism of FAO needs to be explored at cellular or subcellular levels to clarify the underlying bio function of *AKR1B10*.

Conclusions

We explored the predictive efficacy and prognostic performance of the clustering related to FAO metabolism. Using the bulk RNA and scRNA sequencing analysis, a promising prognostic signature was constructed, the GFAO_Score, based on three determined DEGs related to the enrichment of FAO, which showed good evaluation of survival outcomes and adjuvant therapies. Our research provided a new angle to connect the inner interaction of lipid metabolism and tumor progression, serving as a tool for precise screening and strategy-making in chemotherapy and immunotherapy in patients with CRC when transferred to actual application in the future.

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Footnote

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Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at <https://jgo.amegroups.com/article/view/10.21037/jgo-23-833/coif>). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. Ethics approval is not required since the data of transcriptome expression in this study were accessed from online available databases. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

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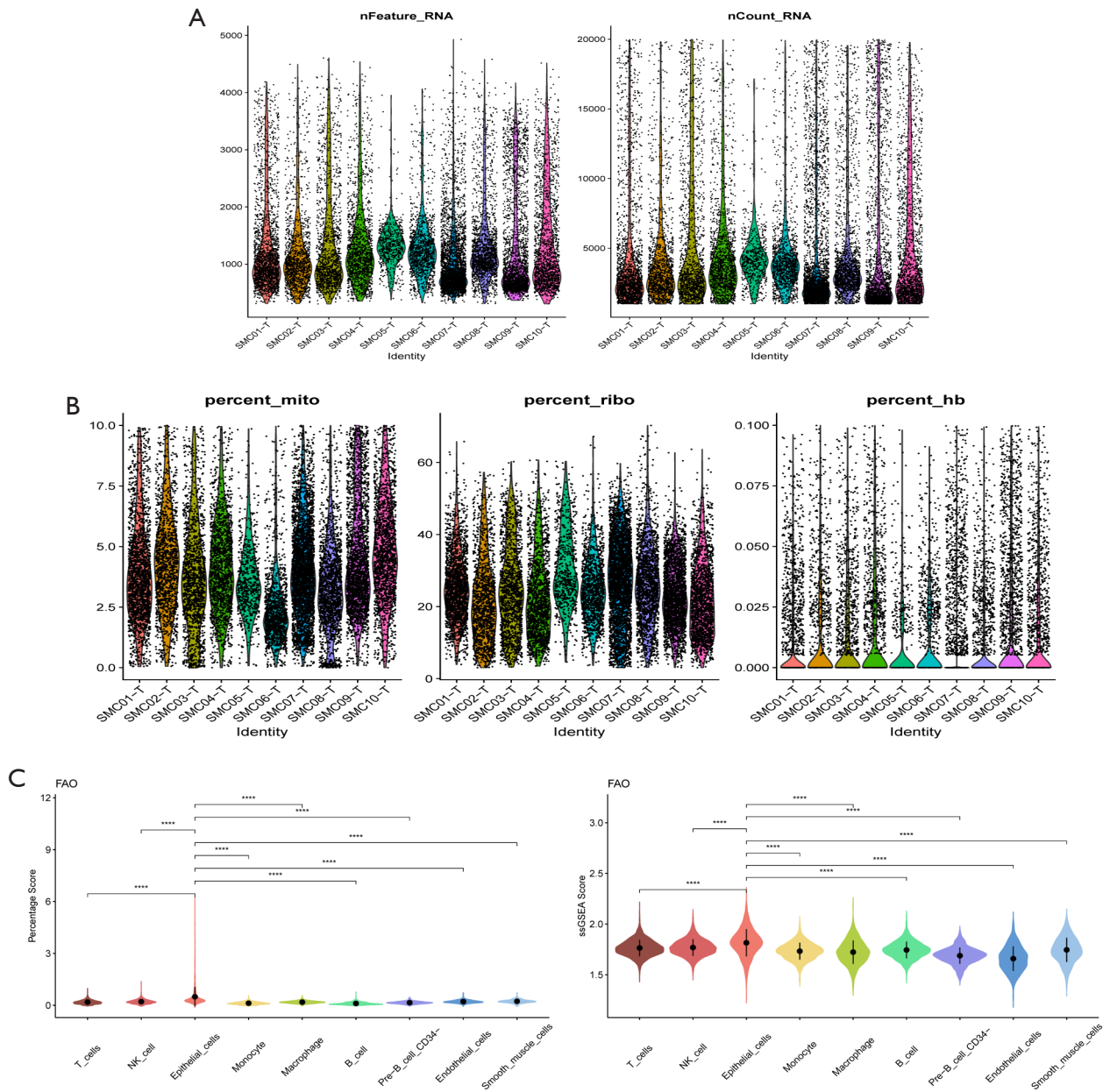


Figure S1 Quality control and enrichment score of FAO at the single-cell level. (A,B) Visualization after performing quality control. (C) Violin plots comparing the FAO 87-gene signature scores based on Percentage and ssGSEA methods between C0 and C1. ****, $P < 0.0001$.

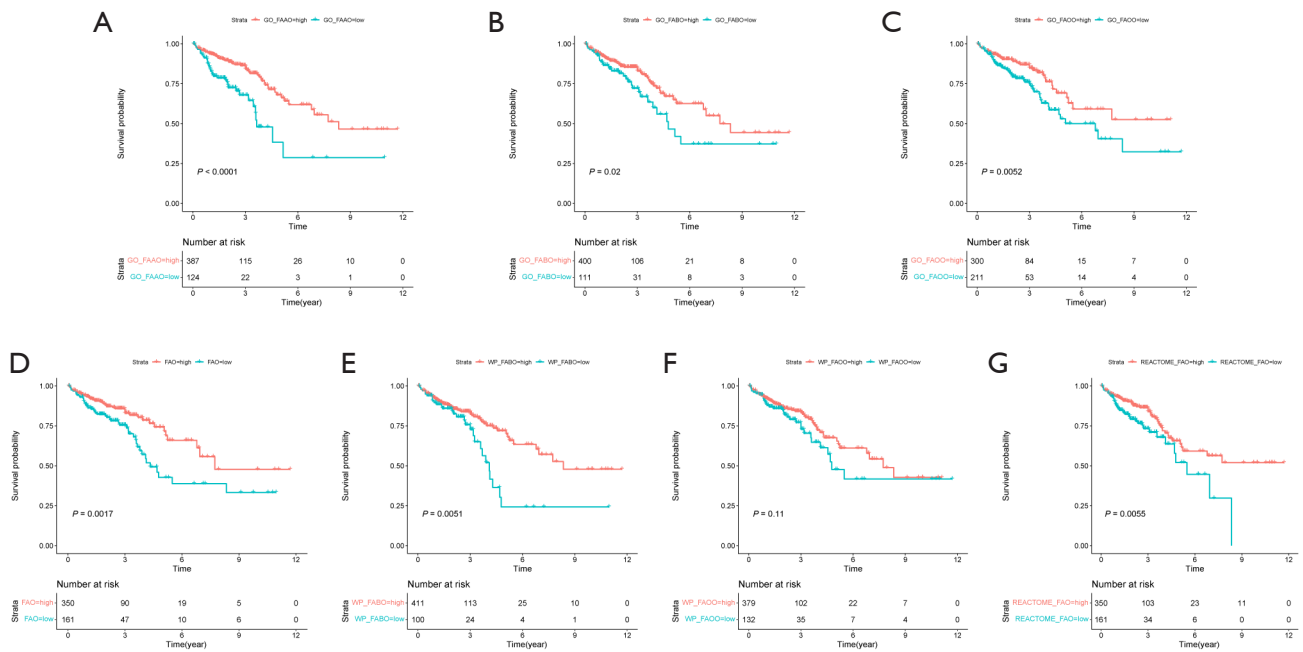


Figure S2 Survival analysis in seven gene sets related to FAO. (A-G) In the seven gene sets related to FAO, the K-M curves show that high-FAO patients tend to have favorable OS.

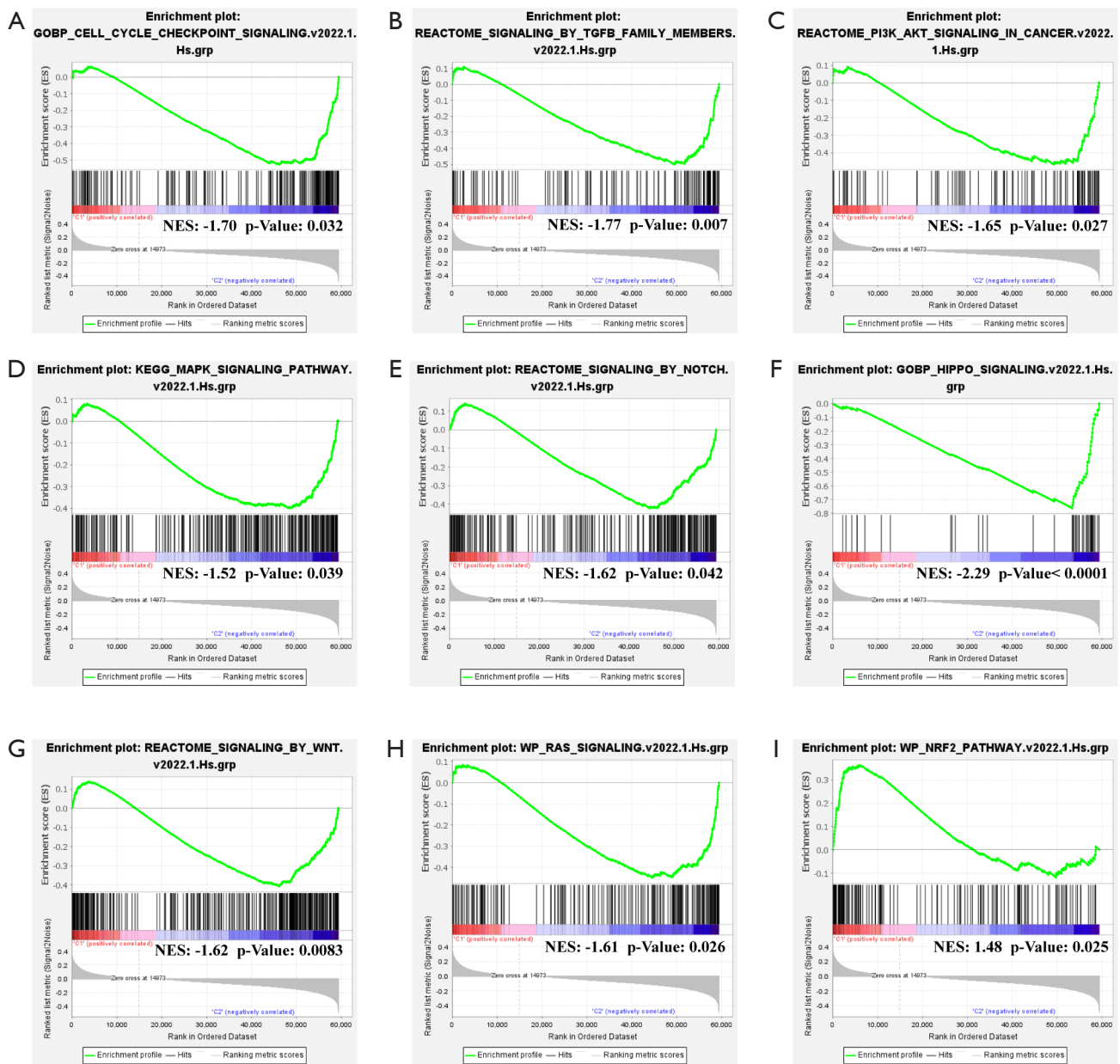


Figure S3 Enrichment analysis of carcinogenetic pathways in two clusters. (A-I) Gene set enrichment analysis (GSEA) of TCGA dataset in classical tumor pathways in Cluster 1 and Cluster 2.

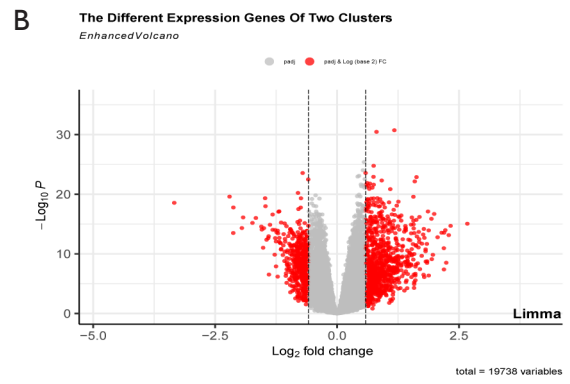
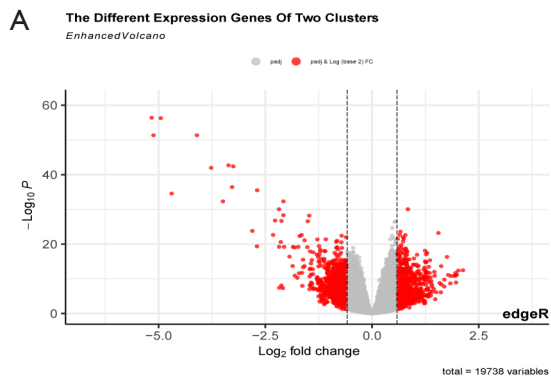


Figure S4 Differential gene expression analysis. (A,B) Volcano plots presenting the differential expression genes between Cluster 1 and Cluster 2 in TCGA based on *edgeR* and *limma* methods, red dots on the left side of the 0 axis represent downregulated genes, and the right-side red dots represent upregulated genes.