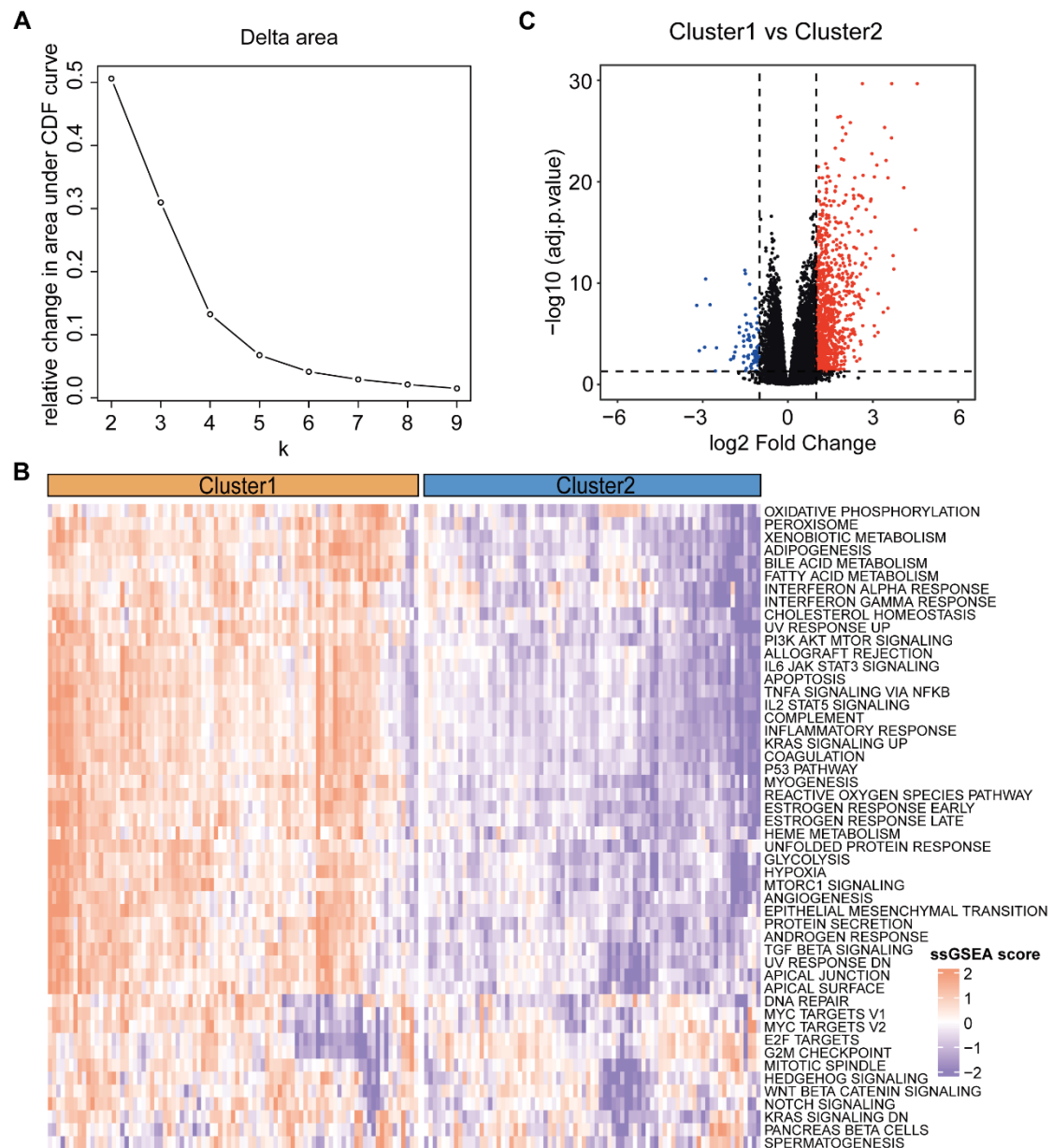


# Supplementary Figures

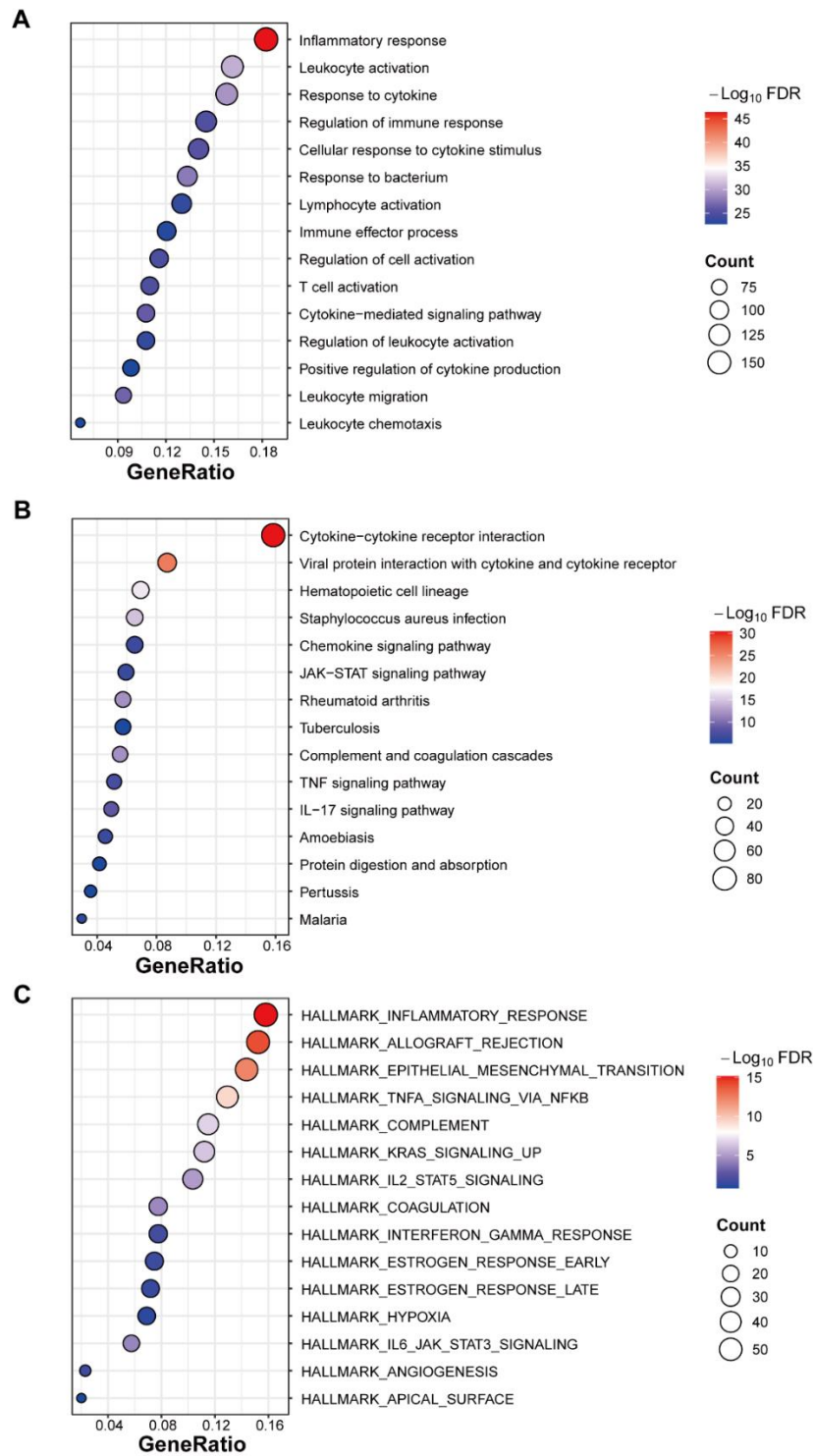
**Figure S1**



**Figure S1: Consensus clustering of FAMGs.**

(A) The line plot of relative change in area under CDF curve for each k. (B) The heatmap showed the hallmark function difference between the FAMGs cluster 1 and cluster 2. (C) The volcano plot showed the genes differently expressed between cluster 1 and cluster 2.

**Figure S2**



**Figure S2: The function enrichment analysis of upregulated genes in cluster 1.**

(A) the enrichment dot plot showed the enriched function of GO terms. (B) the enrichment dot plot showed the enriched function of KEGG pathways. (C) the enrichment dot plot showed the enriched function of cancer hallmark.

Figure S3

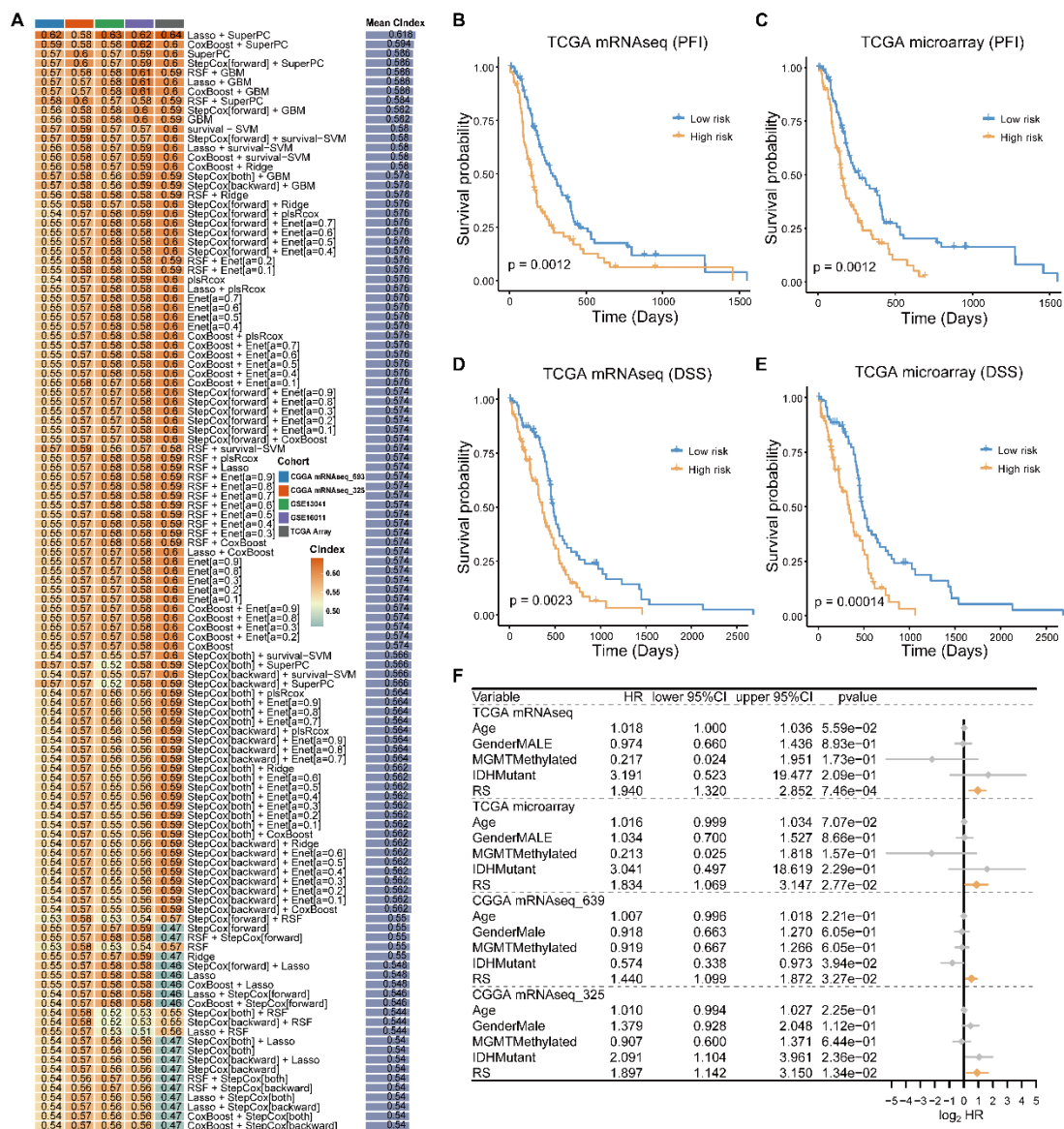


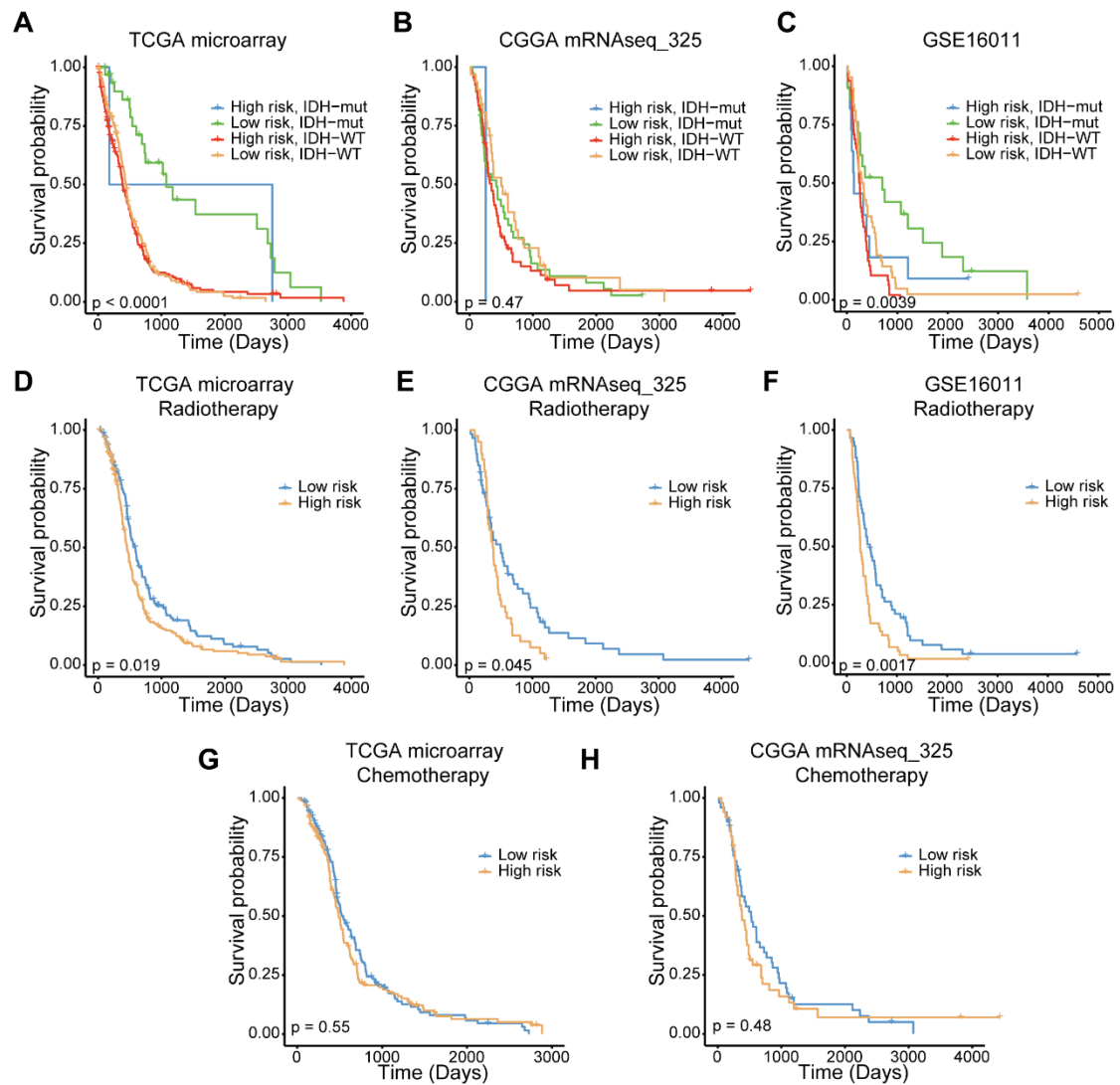
Figure S3: Calculation of FAMS using of machine learning algorithm combination.

(A) Total of 101 kinds of prediction models constructed by different algorithm combinations and further calculated the C-index of each model in all validation datasets.

(B-C) Kaplan-Meier curves of progression free interval (PFI) in TCGA GBM mRNA-seq and microarray dataset. (D-E) Kaplan-Meier curves of Disease Specific Survival (DSS) in TCGA GBM mRNA-seq and microarray dataset. (F) Multivariate Cox

regression analysis of FAMS in TCGA mRNA-seq, TCGA microarray, CGGA mRNAseq\_639, and CGGA mRNAseq\_325.

**Figure S4**

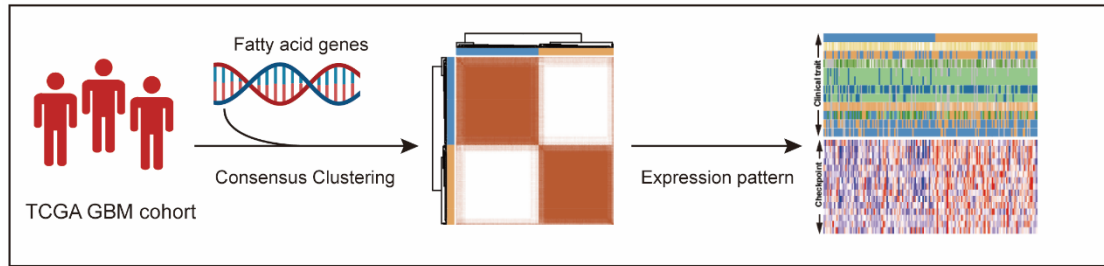


**Figure S4: The stratified analysis of IDH mutation and treatment with FAMS.**

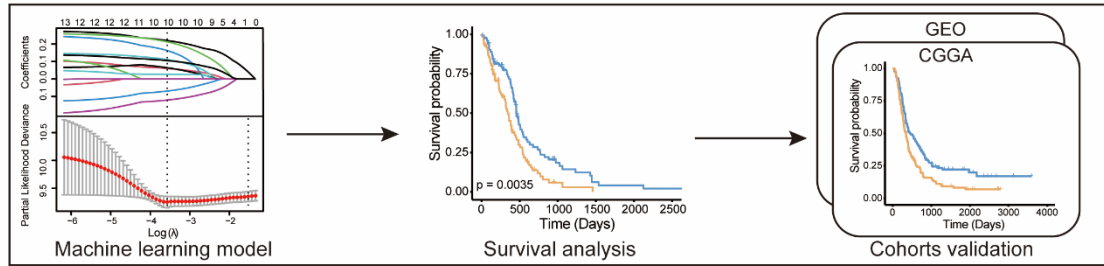
(A-C) Kaplan–Meier overall survival analysis of FAMS combined with IDH status in TCGA microarray, CGGA mRNAseq\_325, and GSE16011 dataset. (D-F) Kaplan–Meier overall survival analysis of FAMS among patients with radiotherapy in TCGA microarray, CGGA mRNAseq\_325, and GSE16011 dataset. (G, H) Kaplan–Meier overall survival analysis of FAMS among patients with chemotherapy in TCGA microarray, CGGA mRNAseq\_325 dataset.

**Figure S5**

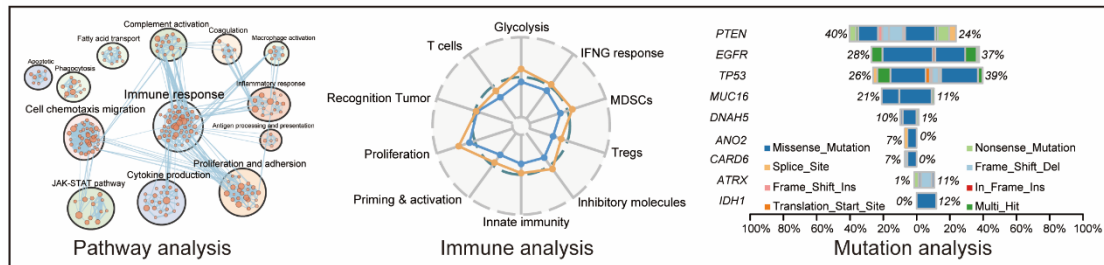
**① Identification of fatty acid gene expression patterns in TCGA GBM cohort**



**② Construction of fatty acid metabolism related gene signature (FAMS)**



**③ Functional analysis of gene signature**



**Figure S5: The workflow of the present study.**

(1) Identification fatty acid metabolism related genes expression pattern in TCGA GBM cohort. (2) Constructing fatty acid metabolism-related prognostic signature (FAMS) based on machine learning model. (3) Functional characterization of FAMS through pathway analysis, immune infiltration analysis and mutation analysis.