Supplementary Material

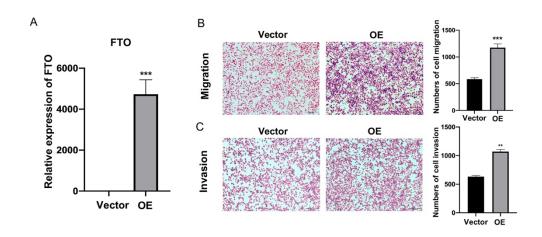


Figure S1 Overexpression of FTO promoted GC cell migration and invasion. **(A)** The overexpression efficiency of FTO in MKN7 cell was detected by qRT-PCR. **(B-C)** The migration and invasion ability of MKN7 cell after transfected with FTO overexpression plasmid was examined by transwell assay (original magnification, $100\times$). The columns on the right are quantified by counting 3 fields, and presented as the mean \pm standard deviation. *P<0.05, **P<0.01.

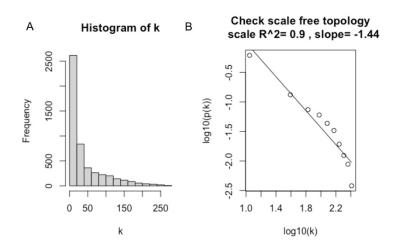


Figure S2 Determination of soft-thresholding power in the weighted gene coexpression network analysis (WGCNA). (A) The histogram of connectivity distribution when $\beta = 4$. (B) The check scale free topology when $\beta = 4$.

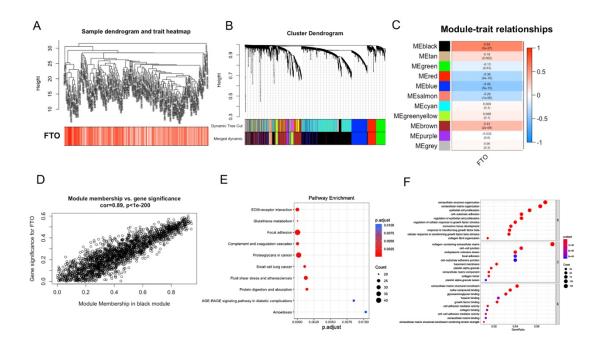


Figure S3 Construction of weight co-expression modules with FTO expression and functional enrichment analysis of FTO-related key module in GSE62254 dataset. (A) The clustering was based on the expression data from GSE62254 dataset. (B) A hierarchical clustering dendrogram was conducted by the Dynamic Tree Cutting method. The first color band indicates the modules detected by dynamic tree cut. The second color band indicates the modules after merging similar modules. (C) Heat map of the correlation between module eigengenes (ME) and the expression level of FTO. The black module was the most positively correlated with FTO high expression. (D) Scatter plot of the correlation between genes in black module and the expression level of FTO. (E) Significantly enriched KEGG pathways of black module. (F) Significantly enriched GO annotations of black module.

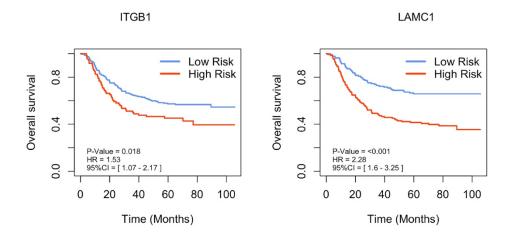


Figure S4 Overall Survival (OS) of ITGB1 and LAMC1 in GSE62254 dataset was analyzed by Kaplan–Meier analysis.

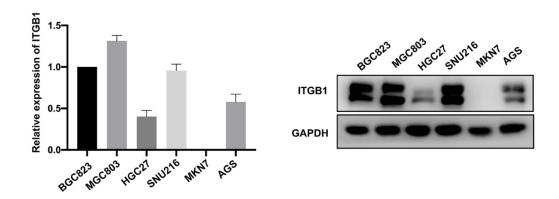


Figure S5 The relative mRNA and protein expression of ITGB1 in different gastric cancer cell lines were detected by qRT-PCR and Western blot. Data are presented as the mean \pm SD of three independent experiments. *P<0.05, **P<0.01.18S was used as an internal control for all qRT-PCR experiments. GAPDH was used as an internal control for all western blot assays.

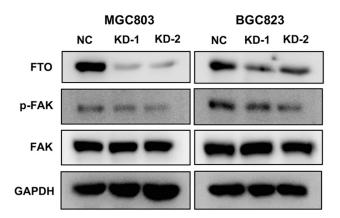


Figure S6 The downstream pathway protein in GC cells after transfected with siNC or FTO siRNAs were detected by Western blot. GAPDH was used as an internal control for all western blot assays.

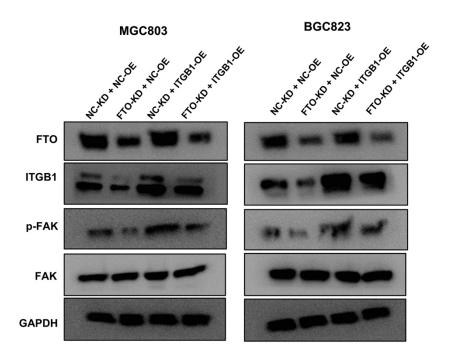


Figure S7 The downstream pathway protein in GC cells after co-transfected with siNC or FTO siRNAs and ITGB1 plasmids or empty vectors were detected by Western blot. GAPDH was used as an internal control for all western blot assays.

Table S1 The univariate and multivariate Cox regression of prognostic factors for OS in GSE62254 dataset

| | Univariate Cox | | | | Multivariate Cox | | | |
|--------|----------------|-----|----------|---------|------------------|------|-----------|---------|
| Gene | Coef | HR | 95% CI | P | Coef | HR | 95% CI | P |
| Gender | 0.042 | 1 | 0.73-1.5 | 0.82 | | | | |
| Age | 0.2 | 1.2 | 0.87-1.7 | 0.25 | | | | |
| T | 0.61 | 1.8 | 1.5-2.3 | < 0.001 | 0.36 | 1.44 | 1.13-1.83 | 0.003 |
| N | 0.72 | 2.1 | 1.7-2.5 | < 0.001 | 0.57 | 1.77 | 1.45-2.15 | < 0.001 |
| M | 1.4 | 4 | 2.5-6.3 | < 0.001 | 0.84 | 2.31 | 1.44-3.69 | < 0.001 |
| FTO | 0.54 | 1.7 | 1.2-2.4 | 0.0021 | 0.36 | 1.43 | 1.01-2.03 | 0.041 |

Table S2 KEGG pathway enrichment analysis of turquoise module

| Category | ID | Term | p.adjust | Count |
|----------|----------|--|----------|-------|
| KEGG | hsa04360 | Axon guidance | 1.60E-07 | 54 |
| KEGG | hsa04510 | Focal adhesion | 2.23E-07 | 57 |
| KEGG | hsa04512 | ECM-receptor interaction | 1.03E-06 | 32 |
| KEGG | hsa00480 | Glutathione metabolism | 4.85E-05 | 22 |
| KEGG | hsa04810 | Regulation of actin cytoskeleton | 0.0002 | 51 |
| KEGG | hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 0.0002 | 25 |
| KEGG | hsa05205 | Proteoglycans in cancer | 0.0006 | 48 |
| KEGG | hsa04151 | PI3K-Akt signaling pathway | 0.0008 | 72 |
| KEGG | hsa04015 | Rap1 signaling pathway | 0.0009 | 48 |
| KEGG | hsa01230 | Biosynthesis of amino acids | 0.0010 | 23 |
| KEGG | hsa05414 | Dilated cardiomyopathy (DCM) | 0.0011 | 27 |
| KEGG | hsa04530 | Tight junction | 0.0013 | 40 |
| KEGG | hsa05410 | Hypertrophic cardiomyopathy (HCM) | 0.0021 | 25 |
| KEGG | hsa05146 | Amoebiasis | 0.0026 | 27 |
| KEGG | hsa04010 | MAPK signaling pathway | 0.0035 | 59 |
| KEGG | hsa04520 | Adherens junction | 0.0069 | 20 |
| KEGG | hsa00561 | Glycerolipid metabolism | 0.0069 | 18 |
| KEGG | hsa04022 | cGMP-PKG signaling pathway | 0.0069 | 37 |
| KEGG | hsa01200 | Carbon metabolism | 0.0090 | 28 |
| KEGG | hsa00220 | Arginine biosynthesis | 0.0090 | 9 |

Table S3 Correlation of FTO and coexpression genes in FA and ECM signaling pathway

| Gene | R | P | Gene | R | P |
|--------|----------|-----------|-------|----------|-----------|
| COL4A4 | 0.3778 | 4.661e-12 | ITGB4 | -0.1108 | 0.05014 |
| COL4A5 | 0.4154 | 1.738e-14 | ITGB6 | -0.00458 | 0.9357 |
| COL9A2 | -0.2226 | 7.105e-05 | LAMA3 | 0.001415 | 0.9801 |
| ITGA1 | 0.5322 | 2.719e-24 | LAMA5 | 0.3346 | 1.267e-09 |
| ITGA2 | -0.06198 | 0.2743 | LAMB2 | 0.4445 | 1.372e-16 |
| ITGA3 | 0.03187 | 0.5743 | LAMB3 | -0.2172 | 0.0001069 |
| ITGA5 | 0.3946 | 4.21e-13 | LAMC1 | 0.5006 | 2.963e-21 |
| ITGA6 | -0.1639 | 0.003631 | LAMC2 | -0.07985 | 0.1587 |
| ITGA7 | 0.5265 | 1.013e-23 | THBS3 | 0.4346 | 7.528e-16 |
| ITGA8 | 0.3236 | 4.602e-09 | THBS4 | 0.4934 | 1.318e-20 |
| ITGA9 | 0.5239 | 1.857e-23 | TNC | 0.49 | 2.61e-20 |
| ITGAV | 0.3893 | 9.024e-13 | TNXB | 0.4783 | 2.661e-19 |
| ITGB1 | 0.508 | 6.126e-22 | VTN | 0.05902 | 0.2979 |