

Integrative genomics analysis of hub genes and their relationship with prognosis and signaling pathways in esophageal squamous cell carcinoma

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Abstract. The main purpose of the present study was to recognize the integrative genomics analysis of hub genes and their relationship with prognosis and signaling pathways in esophageal squamous cell carcinoma (ESCC). The mRNA gene expression profile data of GSE38129 were downloaded from the Gene Expression Omnibus database, which included 30 ESCC and 30 normal tissue samples. The differentially expressed genes (DEGs) between ESCC and normal samples were identified using the GEO2R tool. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses were performed to identify the functions and related pathways of the genes. The protein-protein interaction (PPI) network of these DEGs was constructed with the Search Tool for the Retrieval of Interacting Genes and visualized with a molecular complex detection plug-in via Cytoscape. The top five important modules were selected from the PPI network. A total of 928 DEGs, including ephrin-A1 (EFNA1), collagen type IV α 1 (COL4A1), C-X-C chemokine receptor 2 (CXCR2), adrenoreceptor β 2 (ADRB2), P2RY14, BUB1B, cyclin A2 (CCNA2), checkpoint kinase 1 (CHEK1), TTK, pituitary tumor transforming gene 1 (PTTG1) and COL5A1,

including 498 upregulated genes, were mainly enriched in the 'cell cycle', 'DNA replication' and 'mitotic nuclear division', whereas 430 downregulated genes were enriched in 'oxidation-reduction process', 'xenobiotic metabolic process' and 'cell-cell adhesion'. The KEGG analysis revealed that 'ECM-receptor interaction', 'cell cycle' and 'p53 signaling pathway' were the most relevant pathways. According to the degree of connectivity and adjusted P-value, eight core genes were selected, among which those with the highest correlation were CHEK1, BUB1B, PTTG1, COL4A1 and CXCR2. Gene Expression Profiling Interactive Analysis in The Cancer Genome Atlas database for overall survival (OS) was applied among these genes and revealed that EFNA1 and COL4A1 were significantly associated with a short OS in 182 patients. Immunohistochemical results revealed that the expression of PTTG1 in esophageal carcinoma tissues was higher than that in normal tissues. Therefore, these genes may serve as crucial predictors for the prognosis of ESCC.

Introduction

Esophageal squamous cell carcinoma (ESCC) is one of the most life-threatening types of cancer worldwide and the major histological type of esophageal cancer in East Asian countries (1). Approximately 455,800 new cases of esophageal cancer and 400,200 cases of esophageal cancer-related mortality occurred in 2012 worldwide; men with esophageal cancer have a three- to four-fold higher mortality rate than women (1). ESCC is an invasive tumor with a poor prognosis and is generally diagnosed only following the onset of symptoms. Although ESCC treatment has improved, the 5-year overall survival (OS) rate of patients with ESCC remains low due to insufficient understanding of its molecular pathogenesis and infrequent early-stage examination (2). Therefore, novel insights into the diagnosis and prognosis of ESCC can be obtained by increasing the level of understanding of its pathogenesis.

Similar to other types of cancer, the development of ESCC involves the gradual accumulation of vital gene mutations involved in cell cycle control, cell growth, differentiation,

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apoptosis, migration and invasion, or other functions, including the inactivation of tumor suppressor genes and activation of oncogenes (3). Zhang *et al* (4) found that ROC1 is expressed at a high level in ESCC and is associated with poor prognosis. Targeting the overexpressed ROC1 induces G2 cell cycle arrest and apoptosis in esophageal cancer cells. Hers *et al* (5) found that increasing the transduction of the Akt signaling pathway serves an important role in several types of cancer, including breast cancer (6), prostate cancer (7) and gastric cancer (5,8). P53 is one of the most commonly mutated genes in human cancer, the overexpression of epidermal growth factor receptor and P53 mutation induces tumor development, invasion and differentiation (9). Although certain genes or proteins are involved in the development of ESCC, the pathogenic mechanisms remain unclear. Therefore, determining the pathogenesis of esophageal cancer-related signaling pathways and predicting the prognosis of esophageal cancer are crucial.

The present study aimed to identify the hub genes (Table I) related to the occurrence and development of esophageal cancer through bioinformatics analysis, and then examine the signaling pathways involved in these hub genes and their relationship with the prognosis of esophageal cancer. The present study aims to further improve current understanding of the occurrence and development of esophageal cancer.

Materials and methods

Microarray data. The GSE38129 gene expression dataset was submitted by Hu *et al* (10) and can be obtained from the publicly accessible Gene Expression Omnibus (GEO) database. The dataset was downloaded and analyzed from the GEO at the National Center for Biotechnology Information website (<https://www.ncbi.nlm.nih.gov/geo/>). The study was based on the GPL571 platform (Affymetrix Human Genome U133A 2.0 Array, Affymetrix; Thermo Fisher Scientific, Inc.). The samples used for gene profile analysis were obtained from 30 patients with ESCC and paired adjacent normal tissues, the patients were from high-risk areas of China, and the most recent update was in April 2017.

Data processing of differentially expressed genes (DEGs). GEO2R online software was used for GSE38129 analysis to detect the DEGs between the tumor and normal tissues. GEO2R is an interactive networking tool that helps users to compare various groups of samples in the GEO series and identify DEGs under specific experimental conditions. The adjusted $P < 0.01$ and $|\log \text{fold change (FC)}| > 1$ values were used as the cut-off criteria for DEG identification. Subsequently, 928 DEGs were identified following GSE38129 analysis. Among these DEGs, 498 and 430 were upregulated and downregulated, respectively.

Gene Ontology (GO) function and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses. GO analysis (<https://david.ncifcrf.gov/>) (11), which is a bioinformatics tool that can be used to annotate genes and gene products and determine the biological characteristics of high-throughput genome or transcriptome data, includes three categories, namely, biological process (BP), cellular component (CC) and molecular function (MF). The KEGG knowledge

Table I. Eight hub genes with a high degree of connectivity.

Gene	Degree of connectivity	adj.P.Val
CHEK1	88	1.64E-08
BUB1B	84	2.10E-08
PTTG1	64	1.62E-04
COL4A1	16	2.26E-04
CXCR2	15	1.15E-08
ADRB2	12	2.15E-05
ACOX2	5	5.82E-06
EFNA1	4	1.27E-06

adj.P.Val, adjusted P-value.

database (12) is a group of databases used for all types of biological data and can be used to determine functional and metabolic pathways. $P < 0.05$ was set as the cut-off criterion and considered to indicate a statistically significant difference (Fig. S1). The Database for Annotation, Visualization and Integrated Discovery (DAVID) (13) is a web-based online bioinformatics resource and a functional interpretation tool with a large scale gene or protein dataset that can provide comprehensive functional annotation for genes.

Protein-protein interaction (PPI) network construction and module analysis. The Search Tool for the Retrieval of Interacting Genes (STRING; <https://string-db.org/>) (14) database is an online tool that contains comprehensive information of various proteins and detects potential associations among the DEGs. The results were input into Cytoscape to visualize the PPI networks of the DEGs. A high combined score indicated reliable PPIs. In the present study, interactions with a combined confidence of > 0.7 were considered significant. The PPI network was constructed using Cytoscape software. The Molecular Complex Detection plug-in of Cytoscape (15) further indicated the essential modules in the PPI networks (degree node score cut-off=0.2, K-Core=2, degree cut-off=2).

Survival analysis. Gene Expression Profiling Interactive Analysis (GEPIA) (16) is a web-based server for cancer and normal gene expression analyses and interactive analysis on the basis of The Cancer Genome Atlas (TCGA) and Genotype-Tissue Expression (GTEx) data. Multiple types of analyses can be performed, including differential expression analysis, profiling plotting, correlation analysis and patient survival analysis. Through GEPIA analysis, ephrin-A1 (EFNA1) and collagen type IV $\alpha 1$ (COL4A1) were expressed at high levels in ESCC and were associated with a poor prognosis. The low expression of C-X-C chemokine receptor 2 (CXCR2) was not statistically significant.

Patients and samples. A total of 36 ESCC tissue samples and 35 normal esophageal tissue samples were collected for the present study, which had been surgically removed from Kazakh patients at the First Affiliated Hospital of Shihezi University (Xinjiang, China) between June 2018 to March 2019. The research protocol was approved by the Medical Ethics and

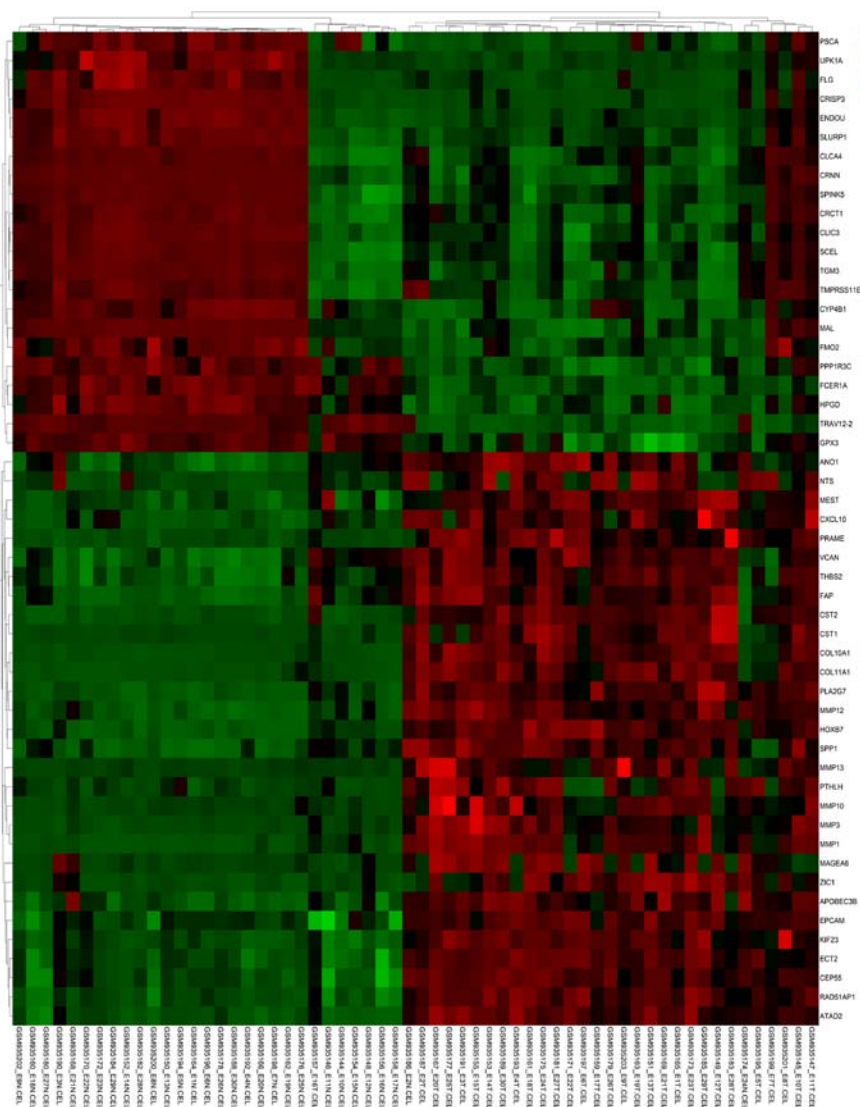


Figure 1. Heatmap of DEGs in ESCC and normal esophageal samples. The heatmap shows the DEGs between the ESCC and normal samples. When \log_2FCI was set to >2.5 and the P-value was adjusted to <0.01 , 52 differential genes, including 30 upregulated and 22 downregulated genes, were identified. The clustering of the samples is shown above the dendrogram and the level of gene expression signal us indicated by the color (red and green for high and low expression levels, respectively). ESCC, esophageal squamous cell carcinoma; DEGs, differentially expressed genes.

Human Clinical Trial Committee of Shihezi University School of Medicine (Xinjiang, China) and all recruited subjects were enrolled following the provision of written informed consent. All surgical samples were used as residual specimens following diagnostic sampling.

Immunohistochemistry (IHC). A total of 36 esophageal cancer tissue samples and 35 normal samples from Kazakh patients were selected from formalin-fixed and paraffin-embedded tissue chips. The sample tissue chips, with a diameter of 0.6 mm, were obtained using ALPHELYS. The tissue micro-arrays were heated in an oven at 65°C for 30 min, rehydrated with graded alcohols, immersed in ethylenediaminetetraacetic acid buffer (pH 9.0) at 130°C , and autoclaved in a microwave oven for 10 min. Following cooling to 30°C , the tissues were incubated at room temperature with 3% H_2O_2 solution for 10 min. The tissue sections were then incubated at 4°C with anti-securin antibody [also termed anti-pituitary tumor transforming gene 1 (PTTG1) antibody, Bioss antibodies,

rabbit polyclonal, cat. no. bs-1881R, dilution 1:400] overnight. The tissue sections were organized and washed in PBS three times for 5 min each and then incubated with secondary antibody [universal kit (mouse/rabbit polymer method detection system), cat. no. PV6000, ZSGB, Ready-to-use antibody] at 37°C for 30 min. Diaminobenzidine (DAB) solution was used for 5 min at room temperature and hematoxylin was used to counterstain the sections. The IHC score was performed independently by two pathologists using a light microscope (BX51; Olympus, Tokyo, Japan; magnification, x400) according to the color intensity as either negative (score 0), weak (score 1), moderate (score 2) or strong (score 3), and coloring area as negative (score 0), $\leq 10\text{-}25\%$ (score 2), $25\text{-}50\%$ (score 3) or $>50\%$ (score 4). The final score was determined as the coloring intensity multiplied by the coloring area. Scores 0-4 and 5-12 indicated low and high expression groups, respectively.

Statistical analysis. Data were assessed using the SPSS (version 17.0; SPSS, Inc.) statistical software package, and

Table II. Top 50 DEGs, including 19 upregulated and 31 downregulated genes.

ID	adj.P.Val	P-value	logFC	Gene
Downregulated				
207802_at	2.95E-08	5.42E-10	-5.38992228	CRISP3
220090_at	6.96E-06	4.36E-07	-4.46587146	CRNN
204777_s_at	1.29E-07	3.34E-09	-4.3672882	MAL
220620_at	8.69E-06	5.70E-07	-3.9442306	CRCT1
206004_at	4.68E-06	2.68E-07	-3.94095422	TGM3
209613_s_at	1.56E-08	2.40E-10	-3.67537874	ADH1B
220026_at	1.61E-04	1.80E-05	-3.65426494	CLCA4
214536_at	1.05E-06	4.61E-08	-3.56033721	SLURP1
206884_s_at	6.42E-05	6.13E-06	-3.51463756	SCEL
219529_at	3.15E-06	1.67E-07	-3.47635301	CLIC3
203914_x_at	1.03E-09	7.43E-12	-3.44800172	HPGD
206605_at	1.49E-08	2.28E-10	-3.43754016	ENDOU
215704_at	7.39E-07	2.90E-08	-3.37242552	FLG
213240_s_at	3.44E-04	4.35E-05	-3.31829107	KRT4
205185_at	1.44E-04	1.59E-05	-3.20158834	SPINK5
204284_at	2.66E-10	1.34E-12	-3.14636945	PPP1R3C
210096_at	1.07E-07	2.68E-09	-3.13376609	CYP4B1
220431_at	1.03E-04	1.08E-05	-3.13073801	TMPRSS11E
207008_at	1.15E-08	1.61E-10	-3.11373209	CXCR2
205783_at	4.37E-05	3.91E-06	-3.08906259	KLK13
206199_at	9.59E-06	6.39E-07	-3.06841828	CEACAM7
201348_at	1.59E-11	2.07E-14	-3.06249067	GPX3
205767_at	5.58E-08	1.22E-09	-2.96580978	EREG
212681_at	1.24E-11	1.40E-14	-2.9062456	EPB41L3
201325_s_at	9.91E-08	2.46E-09	-2.78110281	EMP1
209365_s_at	4.24E-07	1.47E-08	-2.72959968	ECM1
211726_s_at	7.83E-06	5.04E-07	-2.71946544	FMO2
205319_at	1.03E-06	4.47E-08	-2.67917377	PSCA
211026_s_at	4.92E-12	2.43E-15	-2.61375129	MGLL
207980_s_at	1.36E-10	5.35E-13	-2.57860425	CITED2
204614_at	1.34E-03	2.18E-04	-2.55597414	SERPINB2
Upregulated				
204620_s_at	4.60E-08	9.68E-10	2.57111875	VCAN
212353_at	8.15E-08	1.92E-09	2.57383841	SULF1
204779_s_at	2.10E-12	7.56E-16	2.57925018	HOXB7
214612_x_at	1.06E-03	1.66E-04	2.61538749	MAGEA6
209942_x_at	8.45E-04	1.27E-04	2.63065096	MAGEA6///MAGEA3
202859_x_at	1.18E-06	5.33E-08	2.6515207	CXCL8
205680_at	3.82E-06	2.11E-07	2.72388472	MMP10
206632_s_at	1.86E-08	3.05E-10	2.77430412	APOBEC3B
204475_at	1.12E-09	8.31E-12	4.8371858	MMP1
202404_s_at	1.57E-07	4.29E-09	2.84748214	COL1A2
202310_s_at	3.58E-08	6.90E-10	3.00373934	COL1A1
206224_at	1.58E-08	2.43E-10	3.04664986	CST1
206291_at	6.57E-04	9.38E-05	3.19271902	NTS
210809_s_at	4.97E-07	1.78E-08	3.22856265	POSTN
205157_s_at	3.12E-06	1.65E-07	3.32873111	KRT17///JUP
217428_s_at	1.24E-11	1.47E-14	3.34429678	COL10A1
204580_at	2.92E-09	2.93E-11	3.47409534	MMP12
37892_at	4.08E-11	8.94E-14	4.18462587	COL11A1
209875_s_at	3.55E-10	1.94E-12	4.46479482	SPP1

FC, fold change; adj.P.Val, adjusted P-value.

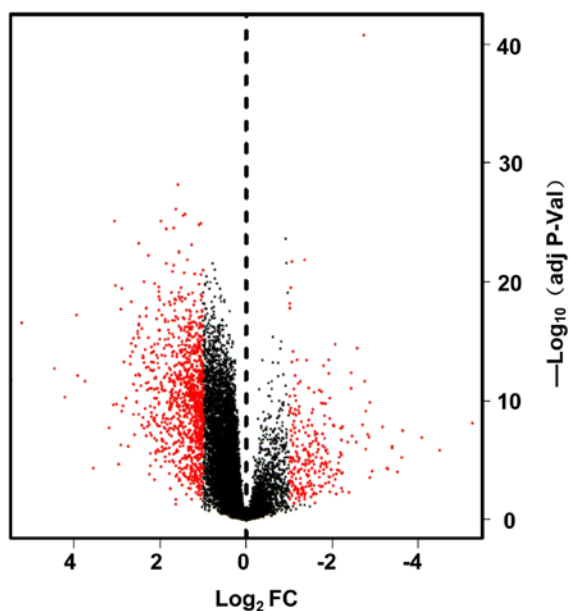


Figure 2. Volcano plot of all genes. A volcano plot of the differentially expressed genes between esophageal squamous cell carcinoma and normal samples is shown. The red dots on the left indicate upregulated genes, the red dots on the left and right and black dots indicate upregulated, downregulated and unregulated genes, respectively. FC, fold-change.

GraphPad Prism 5.0 (GraphPad Software, Inc.) was used to describe data. Comparisons of the expression levels of proteins between the ESCC (n=36) and normal tissues (n=35) were performed using the independent-samples t-test and χ^2 test. All data are presented as the mean \pm SD.

Results

DEG identification. The DEGs were detected using the GEO2R online analytical tool with adjusted $P < 0.01$ and $|\log_2 FC| > 1$ as cut-off criteria. A total of 928 DEGs were obtained between the ESCC and normal samples, including 498 upregulated and 430 downregulated genes. Eight core genes were selected on the basis of the degree of connectivity and adjusted P-value (Table I), including checkpoint kinase 1 (CHEK1), BUB1B, PTTG1, COL4A1, CXCR2, adrenoreceptor $\beta 2$ (ADRB2), acyl-CoA oxidase 2 (ACOX2) and EFNA1. The top 50 DEGs are shown in Table II (19 upregulated and 31 downregulated genes). Additionally, by setting $|\log_2 FC| > 2.5$ and adjusted $P < 0.01$, 52 DEGs were selected, of which 30 and 22 were upregulated and downregulated, respectively. The heat maps and volcano plots show the different DEG samples (Figs. 1 and 2). These volcano plots and heat maps indicate all genes, and the top 52 DEGs, respectively.

GO and KEGG pathway analyses of DEGs. To appreciate the functions of the DEGs further, DAVID (<https://david.ncifcrf.gov/>) was used to apply the GO function and KEGG pathway for enrichment analysis. The BPs, CCs and MFs of the DEGs were annotated and classified by GO analysis. The present study identified 39 GO terms on the basis of the DEGs of modules with a false discovery rate (FDR) < 0.05 and count of > 2 as thresholds and these terms were then sorted by the P-value. The top five enriched GO terms for the BPs, CCs and

MFs were selected from the GO terms (Fig. 3 and Table III). The signaling pathways were obtained through the KEGG database, and the major signaling pathways included 'cell cycle', 'ECM-receptor interaction', 'p53 signaling pathway', 'protein digestion and uptake', 'small cell lung cancer' and 'proteoglycans in cancer' (Table IV).

PPI network construction and module analysis. The STRING database was used to predict the interaction between 928 DEGs (minimum required interaction score of > 0.7). To select important modules in the PPI network, the MCODE plug-in was used and 25 modules were found. The top five modules were also selected for further analysis, which included 60, 15, 13, 32 and 7 genes (Table V). The DEGs in the top five modules were also enriched in important pathways (Fig. 4A-J). Module A had 60 nodes and 1,643 interactions, and all of the DEGs were upregulated in this module. The genes in this module, including CHEK1, cyclin A2 (CCNA2) and TTK, were considerably enriched in the cell cycle and p53 signaling pathway-related functions (Fig. 4B).

Survival analysis. Gene expression and survival analyses were performed by GEPIA in the TCGA database. The resulting box plots (Fig. 5A-H) showed that EFNA1 and COL4A1 were expressed at a high level in ESCC (Fig. 5B and C), whereas the expression of CXCR2 was low in ESCC (Fig. 5E). Survival analysis (Fig. 6A-H) further showed that EFNA1 and COL4A1 were associated with poor prognosis and exhibited statistically significant differences (Fig. 6B and C).

IHC features. According to the degree of connectivity and adjusted P-value, eight core genes were selected (Table I), among which the most strongly correlated genes were CHEK1 (degree of connectivity=88, adjusted $P = 1.64E-08$), BUB1B (degree of connectivity=84, adjusted $P = 2.10E-08$), PTTG1 (degree of connectivity=64, adjusted $P = 1.62E-04$), COL4A1 (degree of connectivity=16, adjusted $P = 2.26E-04$), and CXCR2 (degree of connectivity=15, adjusted $P = 1.15E-08$). No significant prognostic significance was found for CHEK1 or BUB1B (Fig. 6G and H). Relevant references were also reviewed and it was found that PTTG1 is an oncogene that is overexpressed in several tumors. The high expression of PTTG1 also exhibited a relatively poor prognosis through GEPIA survival analysis (Fig. 6A). Therefore, PTTG1 was selected for IHC analysis. IHC was used to detect the expression of PTTG1 in 36 ESCC tissue samples and 35 normal tissue samples of the Kazakh patients. The results showed that the expression of PTTG1 (Fig. 7A and B) in esophageal cancer tissues was significantly higher than that in normal tissues, and the difference was statistically significant ($P = 0.002$). In addition, the PTTG1 IHC staining scores in the ESCC and normal tissues were compared using independent-samples t-test analysis, and the difference was statistically significant ($P < 0.001$; Fig. 7C).

Discussion

ESCC is a digestive tract tumor, is the fourth highest cause of cancer-associated mortality and is one of the most aggressive malignancies in China (17). In the present study, the online

Table III. Top five BPs, CCs and MFs in the analysis of differentially expressed genes between ECSS and normal tissues.

Term	Count	P-value	FDR	Functional group
GO:0051301 cell division	59	4.21E-16	8.10E-13	BP
GO:000008 G1/S transition of mitotic cell cycle	30	7.47E-15	1.36E-11	BP
GO:0030198 Extracellular matrix organization	41	1.50E-14	2.75E-11	BP
GO:0006260 DNA replication	35	1.60E-13	2.93E-10	BP
GO:0030574 collagen catabolic process	22	1.79E-12	3.28E-09	BP
GO:0070062 extracellular exosome	229	1.55E-17	2.27E-14	CC
GO:0005615 extracellular space	127	1.20E-13	1.76E-10	CC
GO:0031012 extracellular matrix	47	1.32E-12	1.93E-09	CC
GO:0005737 cytoplasm	333	3.71E-10	5.43E-07	CC
GO:0005654 nucleoplasm	199	1.59E-09	2.32E-06	CC
GO:0005515 protein binding	515	2.55E-09	4.07E-06	MF
GO:0005201 extracellular matrix structural constituent	17	1.07E-07	1.71E-04	MF
GO:0043142 single-stranded DNA-dependent ATPase activity	7	2.46E-06	0.003918	MF
GO:0005518 collagen binding	14	5.39E-06	0.008585	MF
GO:0003678 DNA helicase activity	9	1.20E-05	0.019143	MF

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; FDR, false discovery rate; Count, enriched gene number in the category.

Table IV. KEGG pathway analysis of differentially expressed genes.

Category	Term	Count	P-value	FDR
hsa04110	Cell cycle	29	3.86E-10	5.05E-07
hsa03030	DNA replication	16	4.92E-10	6.43E-07
hsa04512:	ECM-receptor interaction	23	3.24E-09	4.24E-06
hsa05146	Amoebiasis	19	3.94E-05	0.051506178
hsa04974	Protein digestion and absorption	17	4.48E-05	0.058547669
hsa04510	Focal adhesion	28	6.69E-05	0.087469624
hsa04115	p53 signaling pathway	14	1.16E-04	0.151932901
hsa05222	Small cell lung cancer	14	0.001286708	1.670849429
hsa03430	Mismatch repair	7	0.001721063	2.229032091
hsa05200	Pathways in cancer	38	0.002816977	3.624393493
hsa05202	Transcriptional misregulation in cancer	19	0.009704623	11.98140955
hsa04114	Oocyte meiosis	14	0.011336843	13.861154
hsa04151	PI3K-Akt signaling pathway	31	0.019748427	22.97410608
hsa04972	Pancreatic secretion	12	0.020140081	23.37588312
hsa05144	Malaria	8	0.023512051	26.75579741
hsa05205	Proteoglycans in cancer	20	0.026031699	29.1909003
hsa00590	Arachidonic acid metabolism	9	0.027995297	31.03652764
hsa04914	Progesterone-mediated oocyte maturation	11	0.031059516	33.82807896
hsa05219	Bladder cancer	7	0.03140939	34.14009186
hsa00410	beta-Alanine metabolism	6	0.033090282	35.62023199
hsa03320	PPAR signaling pathway	9	0.041960173	42.93477387
hsa00071	Fatty acid degradation	7	0.042590557	43.42421223

KEGG, Kyoto Encyclopedia of Gene and Genome; FDR, false discovery rate; Count, enriched gene number in the category.

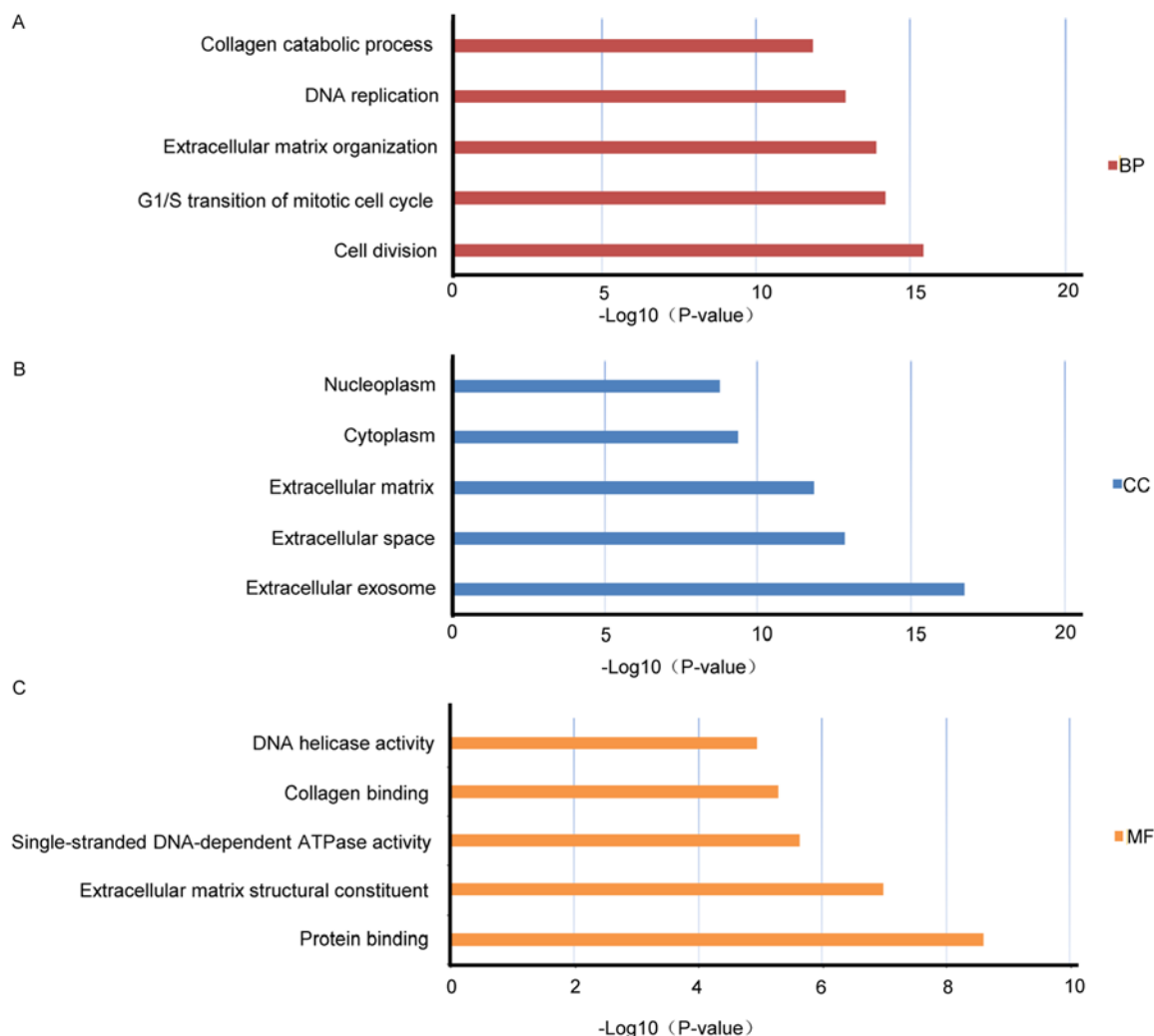


Figure 3. GO term enrichment analysis. (A) Top five clusters of DEGs in BPs (red). (B) Top five clusters of DEGs in CCs (blue). (C) Top five clusters of DEGs in MFs (orange). These groups are ranked and presented as bar plots according to their Fisher's exact P-value. DEGs, differentially expressed genes; GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function.

Table V. Modules of networks.

Module name	Nodes	Edges	Cluster scores
A	60	1643	55.695
B	15	102	14.571
C	13	78	13.000
D	32	144	9.290
E	7	20	6.667

GEO2R tool was used between ESCC and normal samples to detect 928 DEGs, including 498 upregulated and 430 down-regulated genes. Using several bioinformatics tools, the DEGs were found to be mainly related to cell cycle, DNA replication and ECM-receptor interactions. A PPI network of the DEGs was also constructed, and the first five modules were selected for further analysis. All the genes enriched in module 1, including BUB1B, CCNA2, CHEK1, BUB1, CCNB1 and CCNB2, were upregulated. These genes were mainly related to cell cycle, progesterone-mediated oocyte, and the p53 signaling pathway.

The COL family of genes was mainly enriched in module 2, including COL11A1, COL1A1, COL1A2, COL5A1, COL5A2 and COL6A3, which was involved in the ECM-receptor interaction and PI3K-Akt signaling pathways. EFNA1 and COL4A1 were also associated with the prognosis of patients with ESCC.

EFNA1 is an angiogenic factor. EFNA1 was originally separated from human umbilical vein endothelial cells as a secretory protein and treated with tumor necrosis factor- α . Tumor necrosis factor- α -induced (18) EFNA1 and its receptor, Eph receptor 2, are associated with various types of cancer, including bladder cancer (19) and gastric cancer (20). High expression of EFNA1 is also involved in colorectal cancer (21) and its low expression is associated with a poor prognosis in clear cell renal cell carcinoma (22). High expression of COL4A1 is associated with advanced tumors and poor OS and disease-free survival in patients with HCC (23). COL4A1 knockdown decreases cell viability and cell cycle in breast cancer cells (24). Therefore, EFNA1 and COL4A1 may be associated with the prognosis of esophageal cancer. The GEPIA database in the TCGA was used in the present study for the survival analysis and it was found that EFNA1 and COL4A1 were associated with a poor prognosis in ESCC.

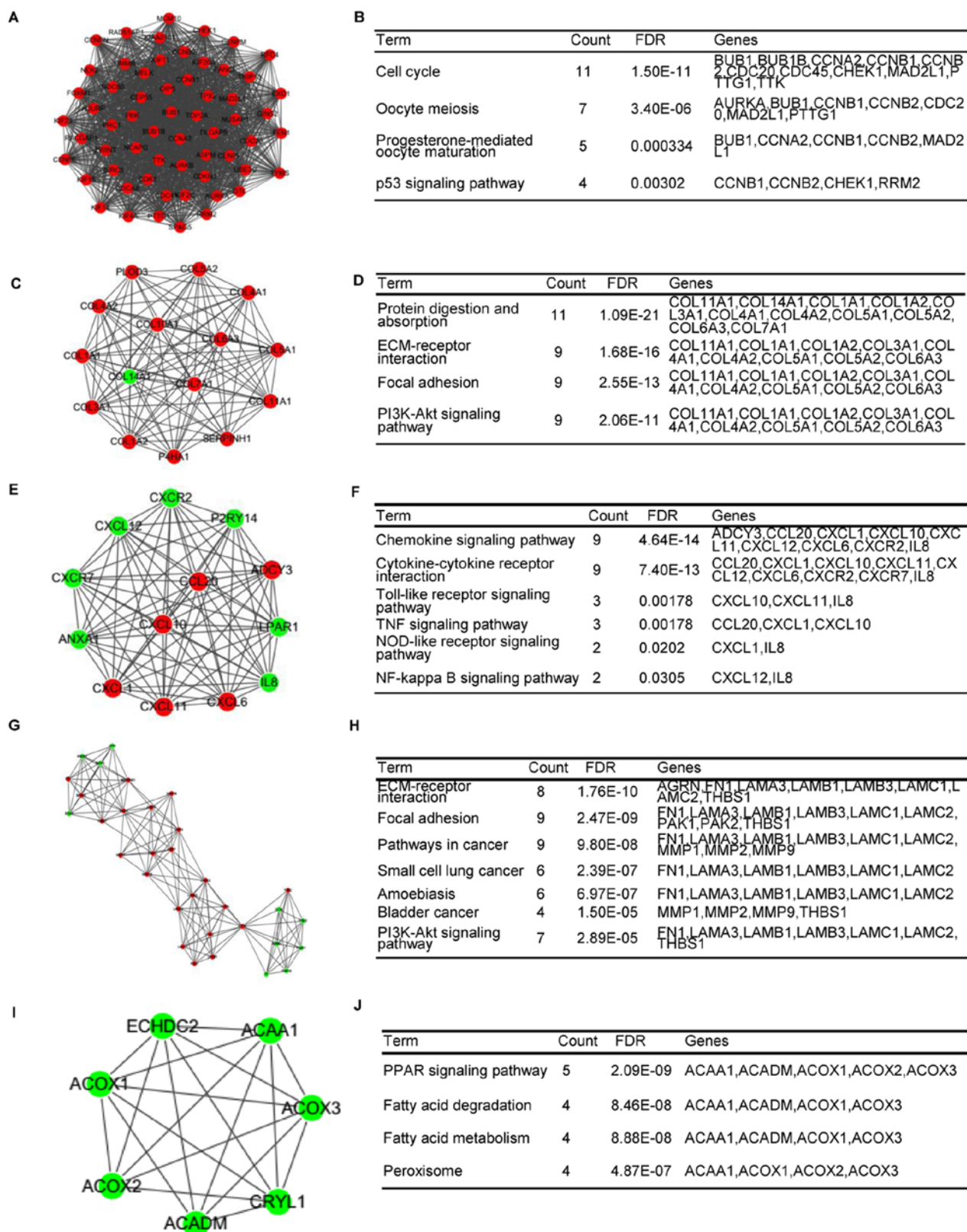


Figure 4. Top five modules from the protein-protein interaction network. (A) Module 1, (B) enriched pathways of module 1; (C) module 2, (D) enriched pathways of module 2; (E) module 3, (F) enriched pathways of module 3; (G) module 4, (H) enriched pathways of module 4; (I) module 5, (J) enriched pathways of module 5. Green and red nodes represent downregulated and upregulated genes, respectively.

The cell cycle is a process in which a cell completely divides, including interphase and division phases. The mechanism of cell cycle disorder in any condition causes the development of cancer, as cancer is closely associated with cell proliferation

and growth (25). An important hallmark of cancer is uncontrolled cell proliferation. Tumor cells generally exhibit damage to genes that directly regulate cell cycle (26). In the present study, several DEGs were enriched in the cell cycle. COL1A1

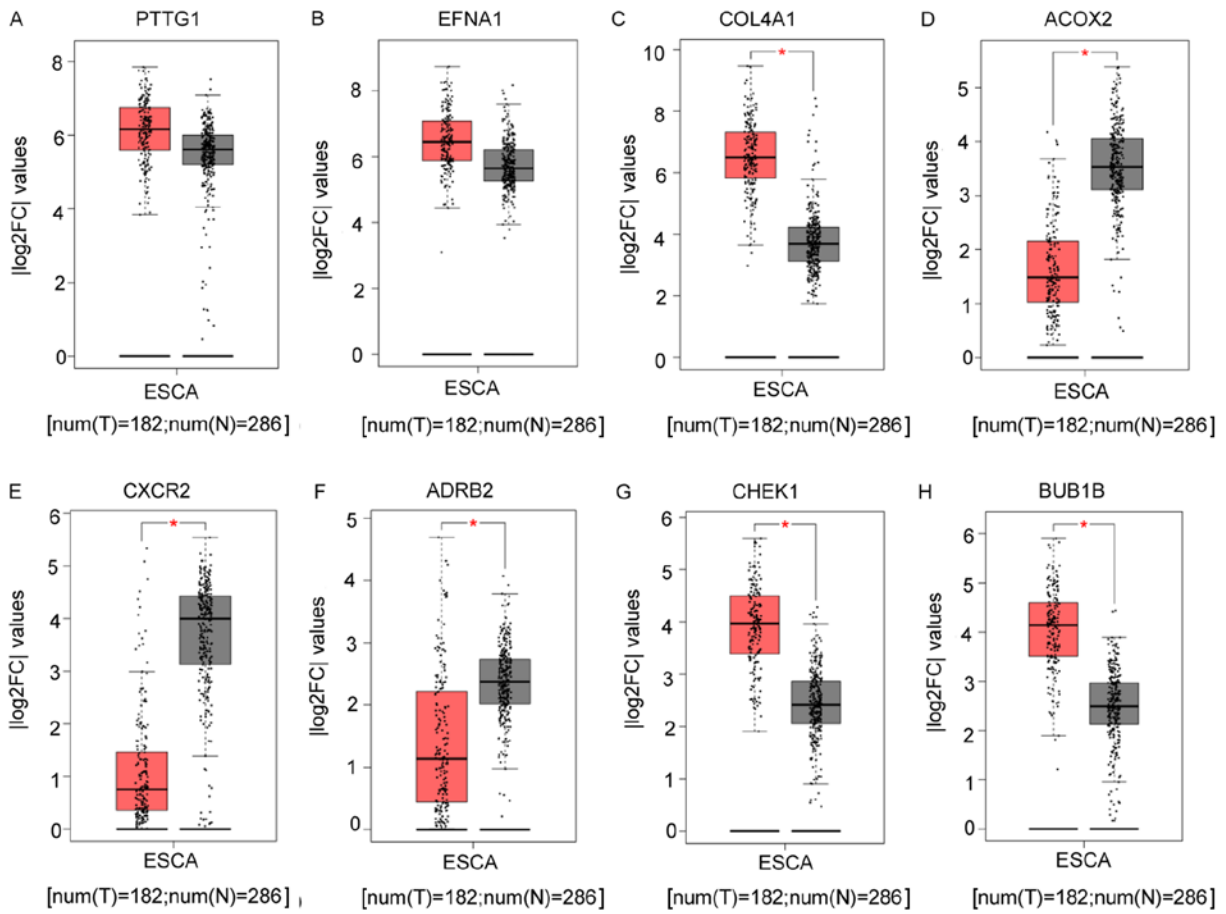


Figure 5. Box plots of ESCC and normal tissue expression levels in The Cancer Genome Atlas database. Box plots indicate the expression of different genes in tumor and normal tissues. The expression levels of (A) PTTG1 and (B) EFNA1 in ESCC tissues were higher than those in normal tissues, although there was no statistical significance. (C) COL4A1, (D) ACOX2, (E) CXCR2, (F) ADRB2, (G) CHEK1 and (H) BUB1B exhibited statistically significant differences. * $P < 0.05$ between ESCC and normal tissues. ESCC tissues are shown in red, normal tissues are shown in black. Y-axis: $|\log_2FC|$ cut-off. X-axis: num (T)=182, num (N)=286. ESCC, esophageal squamous cell carcinoma; FC, fold-change; T, tumor; N, normal tissues.

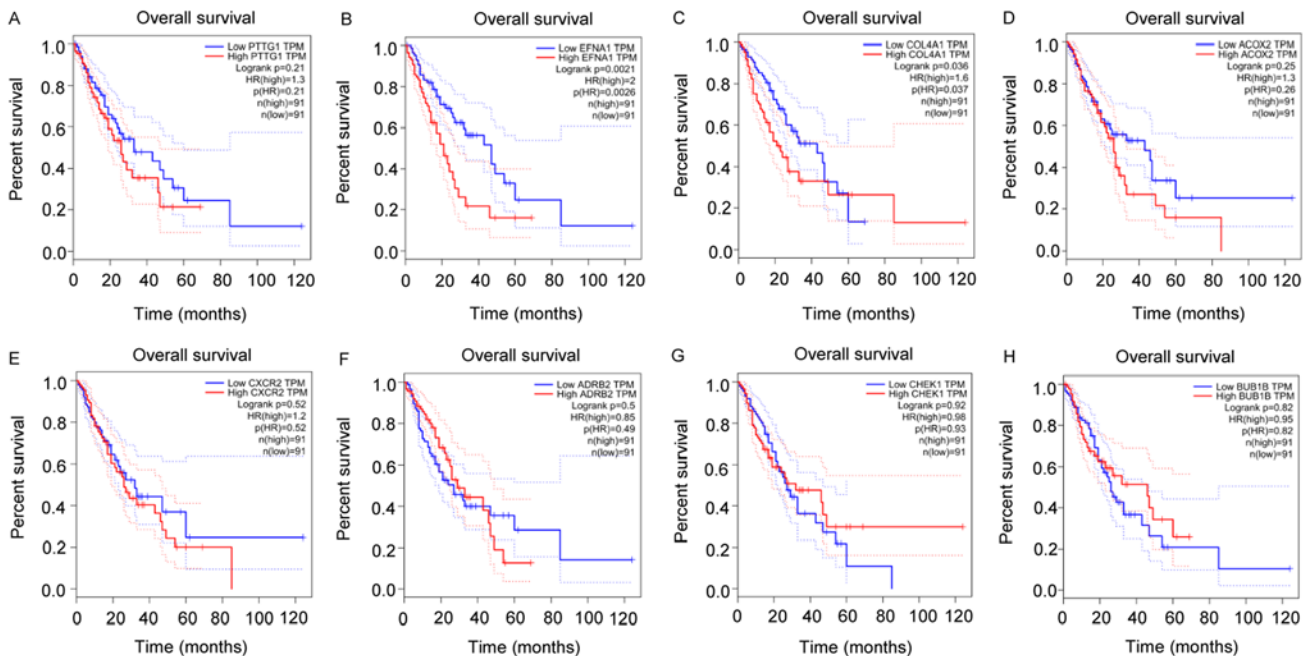


Figure 6. Prognostic value of eight hub genes in GSE38129. Relationships between gene expression and OS in 182 patient prognostic values in the GSE38129 of (A) PTTG1, (B) EFNA1, (C) COL4A1, (D) ACOX2, (E) CXCR2, (F) ADRB2, (G) CHEK1 and (H) BUB1B were obtained from Gene Expression Profiling Interactive Analysis. The results showed that the patients with high expression levels of EFNA1 ($P = 0.0026$) and COL4A1 ($P = 0.037$) had a poorer prognosis than those with low expression levels of EFNA1 and COL4A1. * $P < 0.05$. OS, overall survival; HR, hazard ratio; TPM, number of transcripts per million reads.

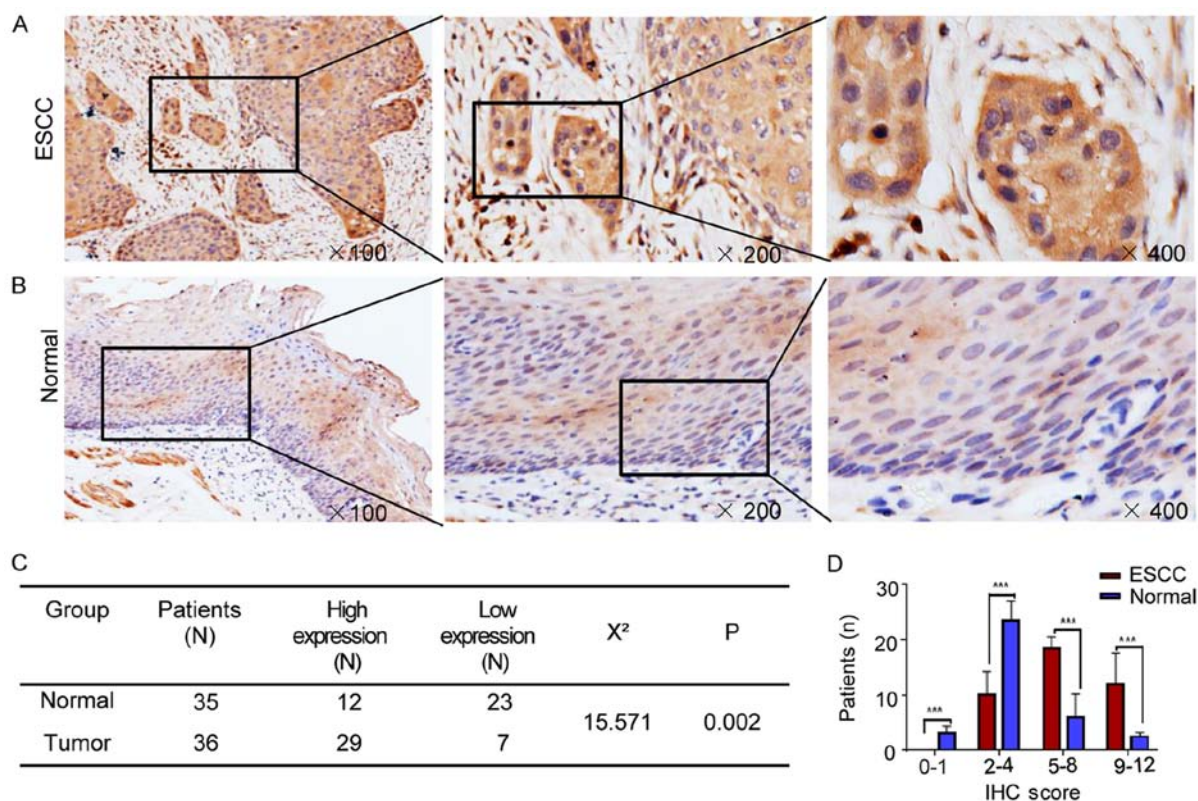


Figure 7. Protein expression of PTTG1 in ESCC and normal tissues. (A) Expression of PTTG1 in ESCC, cytoplasmic staining (magnification, x100, x200, x400). (B) Expression of PTTG1 in normal tissues, cytoplasmic staining (magnification, x100, x200, x400). (C) Expression of PTTG1 in ESCC tissues (n=36) was significantly higher than that in normal tissues (n=35), and the difference was statistically significant (P=0.002). (D) PTTG1 IHC staining score in ESCC and normal tissues using independent-samples t-test analysis; each bar represents the mean \pm SD. ***P<0.001. ESCC, esophageal squamous cell carcinoma; IHC, immunohistochemistry.

and COL1A2 encode the $\alpha 1$ and $\alpha 2$ chains of type I collagen, respectively (27). The cell adhesion molecule COL1A1 is expressed at a high level in ESCC, which is essential for ESCC carcinogenesis (28). CHEK1 is also type of protein-coding gene. The protein encoded by CHEK1 belongs to the Ser/Thr protein kinase family. Checkpoints that mediate cell cycle arrest require the presence of DNA damage or unreplcated DNA. The high cytoplasmic expression of phosphorylated CHEK1 was associated with the poor prognosis of breast cancer (29) and also exhibited high expression in ovarian and oral squamous cell carcinoma (30,31). Therefore, the targeted regulation of CHEK1 may become a novel method for cancer treatment.

PTTG1 is an oncogene that is overexpressed in several tumor types. The expression of PTTG1 is high in bladder cancer. PTTG1 knockdown significantly inhibits bladder cancer cell migration, invasion, metastasis and growth, and induces G0/G1 phase senescence and cell cycle arrest (32). Feng *et al* (33) reported that PTTG1, via activating the expression of GLI1 in ESCC, was involved in the epithelial-mesenchymal transformation (EMT) process, and promoted the metastasis in ESCC cell lines and tissues by inducing EMT. Particularly in cells with lymph node metastasis. TTK, also referred to as Mps1, is overexpressed in human pancreatic cancer and primary liver cancer (34,35). BUB1B, which is a mitotic checkpoint serine/threonine kinase B, is a member of the spindle assembly checkpoint protein family and is involved in various types of cancer. The expression of BUB1B is high in prostate cancer and associated with poor prognosis (36). BUB1B is also expressed at a high level

in lung adenocarcinoma, and the overexpression of BUB1B is associated with poor disease progression and poor survival rates in patients with lung adenocarcinoma (37). Certain transcription factors can regulate ESCC cancer cell cycle by regulating BUB1B, which is a cell cycle-related DEG, thereby promoting the development of ESCC (38). Therefore, BUB1B may promote the development of ESCC by deregulating the cell cycle.

The present study identified DEGs through bioinformatics analysis, some of which may serve an important role in the development, progression and prognosis of ESCC. CHEK1 and BUB1B are primarily related to the cell cycle, and COL5A1, COL11A1 and COL1A1 are related to the main ECM-receptor interaction pathway. Through KEGG analysis, these differentially expressed genes were mainly related to cell cycle and ECM receptors. CHEK1, BUB1B, COL5A1, PTTG1, TTK and COL1A1 have also been associated with the development of various types of cancer. EFNA1 and COL4A1 were associated with the prognosis of ESCC. The IHC results showed that the expression of PTTG1 in ESCC tissues was significantly higher than that in normal esophageal tissues, with statistical significance. However, the present study used mostly consultation cases from the People's Hospital of Xinjiang Uyghur Autonomous Region, and the Xinjiang Yili Prefecture Friendship Hospital; ESCC fresh samples are difficult to obtain due to the lack of patients in this region, therefore, it is difficult to collect proteins for further analysis. In future research, when additional fresh tissue samples are collected, reverse transcription-PCR and western blot analyses will be performed for the validation of

these identified target genes in clinical samples. In conclusion, the genes identified may serve an important role in the occurrence and prognosis of ESCC. However, their mechanism in ESCC requires further investigation.

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Availability of data and materials

The datasets analyzed in the present study are available from the GEO repository (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38129>).

Authors' contributions

XBC and FFC conceived and designed the study. YZC, HP and SRZ collected the expression data and screened for the differentially expressed genes. FFC and HP analyzed and interpreted the data. FFC wrote the manuscript. XBC and YZC reviewed and edited the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

The present study was approved by the Medical Ethics and Human Clinical Trial Committee of Shihezi University School of Medicine, and all recruited subjects were enrolled following the provision of written informed consent.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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