

Identification of novel biomarkers and candidate small molecule drugs in non-small-cell lung cancer by integrated microarray analysis

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Background: Non-small-cell lung cancer (NSCLC) remains the leading cause of cancer morbidity and mortality worldwide. In the present study, we identified novel biomarkers associated with the pathogenesis of NSCLC aiming to provide new diagnostic and therapeutic approaches for NSCLC.

Methods: The microarray datasets of GSE18842, GSE30219, GSE31210, GSE32863 and GSE40791 from Gene Expression Omnibus database were downloaded. The differential expressed genes (DEGs) between NSCLC and normal samples were identified by limma package. The construction of protein–protein interaction (PPI) network, module analysis and enrichment analysis were performed using bioinformatics tools. The expression and prognostic values of hub genes were validated by GEPIA database and real-time quantitative PCR. Based on these DEGs, the candidate small molecules for NSCLC were identified by the CMap database.

Results: A total of 408 overlapping DEGs including 109 up-regulated and 296 down-regulated genes were identified; 300 nodes and 1283 interactions were obtained from the PPI network. The most significant biological process and pathway enrichment of DEGs were response to wounding and cell adhesion molecules, respectively. Six DEGs (PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5) which significantly up-regulated in NSCLC tissues, were selected as hub genes according to the results of module analysis. The GEPIA database further confirmed that patients with higher expression levels of these hub genes experienced a shorter overall survival. Additionally, CMap predicted the 20 most significant small molecules as potential therapeutic drugs for NSCLC. DL-thiorphan was the most promising small molecule to reverse the NSCLC gene expression.

Conclusions: Based on the gene expression profiles of 696 NSCLC samples and 237 normal samples, we first revealed that PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 could act as the promising novel diagnostic and therapeutic targets for NSCLC. Our work will contribute to clarifying the molecular mechanisms of NSCLC initiation and progression.

Keywords: non-small-cell lung cancer, novel biomarkers, candidate small molecules, prognosis, bioinformatics analysis

Introduction

Lung cancer remains the leading cause of cancer morbidity and mortality worldwide. In 2018, there are 234,030 newly diagnosed lung cancer patients, accounting for 13.5% of all types of malignant tumors. In addition, lung cancer results in approximately 154,050 death cases each year, accounting for 25.3% of all cancer-related deaths; 80–85% of all

lung cancer patients are diagnosed with non-small-cell lung cancer (NSCLC) subtype and 80% lung cancer-associated deaths are caused by NSCLC. The subtypes of NSCLC mainly consist of lung adenocarcinoma, lung squamous cell carcinoma and large cell lung cancer based on histological sub-classification.¹⁻⁴ Although great advance has been made in the therapeutic methods for NSCLC such as surgical resection, chemotherapy, radiotherapy and targeted therapy, the patients' prognosis is still far from ideal, with 5-year survival rate less than 20%. For advanced patients who are inoperable, chemotherapy such as platinum still remains the most ideal and important treatment strategy for NSCLC.⁵⁻⁷ The poor long-term survival rate of NSCLC patients is mainly attributed to the lack of specific symptoms and effective diagnostic methods at an early stage. In additionally, high metastasis rate and drug resistance are also vital factors that can not be ignored.⁸⁻¹⁰ In recent years, with our increased understanding of molecular characterization of NSCLC, molecular targeting therapies especially individualized precision treatment have undergone remarkable developments.^{11,12} Despite the prominent progress in the molecular diagnosis and treatment for NSCLC, substantive breakthroughs have not yet been made in patients' survival.¹³ Therefore, there is still an urgent demand to identify the novel biomarkers correlated with NSCLC diagnosis and prognosis to elucidate the precise molecular mechanism of NSCLC occurrence and progression. In this study, the microarray data of GSE18842, GSE30219, GSE31210, GSE32863 and GSE40791 from Gene Expression Omnibus (GEO) database was used to identify the differential expressed genes (DEGs) between NSCLC and adjacent normal tissues. Gene Ontology (GO) and pathway enrichment analysis were performed to better understand the biological functions of these DEGs. We also established a protein-protein interaction (PPI) network associated the DEGs. Furthermore, we also identified potential candidate small molecules for a better treatment of NSCLC. Six novel biomarkers were found to be related to the pathogenesis and prognosis of NSCLC. In summary, this study aimed to exploit promising novel biomarkers for NSCLC diagnosis, prognosis and molecular targeting therapies from new insights. Figure 1 shows the workflow of our study.

Materials and methods

Data resources

Series matrix files of GSE18842, GSE30219, GSE31210, GSE32863 and GSE40791 were downloaded from GEO database (<http://www.ncbi.nlm.nih.gov/geo/>). The platforms were

based on GPL9948 (Agilent Human 0.6 K miRNA Microarray G4471A; Agilent Technologies, Santa Clara, CA, USA) (GSE32863) and GPL570 (Affymetrix Human Genome U113 Plus 2.0 Array) (GSE18842, GSE30219, GSE31210 and GSE40791). A total of 696 NSCLC samples and 237 normal samples were included in our study, of which 46 tumor samples and 45 normal samples were in GSE18842 profile, 272 tumor samples and 14 normal samples in GSE30219 profile, 226 tumor samples and 20 normal samples in GSE31210 profile, 58 tumor samples and 58 normal samples in GSE32863 profile, and 94 tumor samples and 100 normal samples in GSE40791 profile.

Screening for DEGs

The matrix data of each dataset was performed log2 conversion and normalization using limma package of R/Bioconductor software.¹⁴ The limma package was also utilized to screen and identify the DEGs between NSCLC samples and normal tissue sample. Adjust *P*-value <0.05 and $|\log_2\text{FC}| > 1$ were considered the statistical significance of differential expression.

Functional enrichment analysis

GO and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis were performed to determine the biological functions of the overlapping DEGs. GO enrichment analysis is an extensively used method to investigate the molecular function (MF), cell component (CC) and biological process (BP) of genes or gene products. KEGG is a widely used database for systematic analysis of high-level gene functions. In this study, we carried out GO function and KEGG pathway enrichment analysis based on the platform of Database for Annotation Visualization and Integrated Discovery (DAVID, <http://david.ncifcrf.gov>), an online database rich in comprehensive annotation information of gene and protein functions. *P*-value <0.05 was considered statistically significant.¹⁵⁻¹⁹

Protein-protein interaction (PPI) network construction and module analysis

We used the online database STRING (Search Tool for the Retrieval of Interacting Genes, <https://string-db.org/>) to better illustrate the potential interactive relationships among the overlapping DEGs.²⁰ Then the Cytoscape software was utilized for analyzing the interactions with a combined score >0.4 (<http://www.cytoscape.org/>).²¹ Finally, the plug-in MCODE

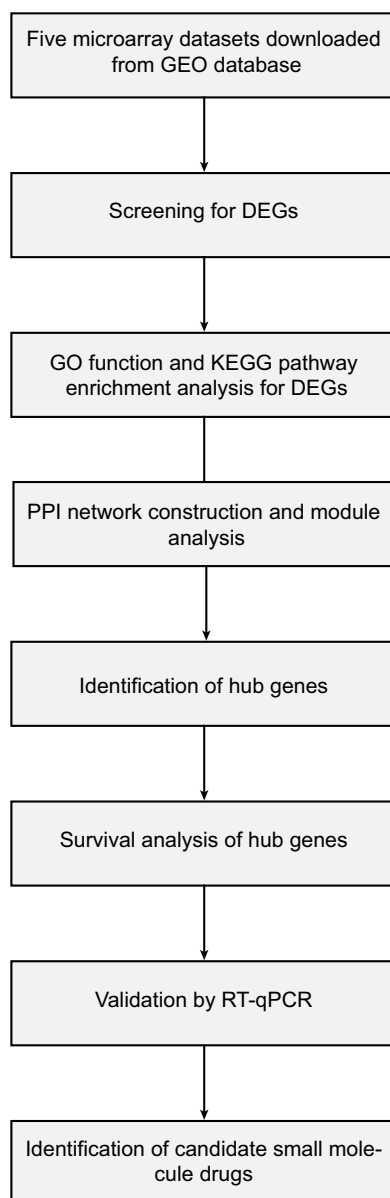


Figure 1 The workflow of this study.

(Molecular Complex Detection) was used to filter the significant modules from the PPI network for the selection of hub genes (degree cutoff = 2, node score cutoff = 0.2, k-core = 2, and max. depth = 100).²² We also performed functional and pathway enrichment analysis for the genes in the significant modules. The heat map of module genes was constructed using UCSC Cancer Genomics Browser (<http://genome-cancer.ucsc.edu>). The Networks Gene Oncology tool (BiNGO), a plugin in Cytoscape, was used to explore and visualize the BP of the selected hub genes.²³

Survival analysis and validation of hub genes

To further explore the roles of module genes in the NSCLC occurrence and development, we predicted the co-expression genes of module genes and the co-expression network was constructed by cBioPortal online platform (<http://www.cbioportal.org>).^{24,25} The Gene Expression Profiling Interactive Analysis (GEPIA) database was utilized to assess the impact of hub genes on the patients' prognosis.²⁶ The NSCLC patients were divided into high expression and low expression groups

according to the median expression levels of hub genes. The hazard ratio (HR) with 95% CI of overall survival was calculated for each group. And the GEPIA platform was applied to further verify the expression level of hub genes between NSCLC and normal samples. We analyzed the protein expression of hub genes by using the human protein atlas (HPA, www.proteinatlas.org) database considering that gene expression was not always consistent with its protein level.²⁷

Identification of small molecules

The CMap database (<http://www.broadinstitute.org/cmap/>) was used to explore potential small molecule drugs for use in patients based on the gene signature of NSCLC. CMap collects >7,000 gene expression profile changes induced by various small molecular agents.²⁸ The overlapping differently expressed probesets among five datasets were classified into up-regulated and down-regulated groups. Then, these probesets from the two groups were uploaded into CMap database to match corresponding active small molecules. Finally, the enrichment scores between -1 and 1, which represent similarity, were calculated. A positive connectivity score (closer to +1) indicated the corresponding small molecule is able to induce the state of NSCLC cells, whereas a negative connectivity score (closer to -1) demonstrate greater similarity between the genes. We investigated and calculated negative connectivity scores with potential therapeutic value.

Real-time quantitative PCR

Total RNA from tumor tissues and non-tumorous tissues was extracted with Trizol reagent (Invitrogen, Carlsbad, CA, USA) according to the protocol. cDNA was synthesized using an Omniscript Reverse Transcription kit (Qiagen, Valencia, CA, USA). Quantitative real-time PCR (qPCR) assays were performed using EvaGreen Master Mix (Biotium Inc., Hayward, CA, USA). The conditions for qPCR amplification were as follows: 95°C for 120 s followed by 40 cycles of 95°C for 15 s, annealing temperature for 45 s. Each sample was run in triplicate. Relative expression level for each target gene was normalized by the Ct value of GAPDH (endogenous reference) using a $2^{-\Delta\Delta C_t}$ relative quantification method. The primers are as follows:

PTTG1 gene 5'-GACTCAGGCTGGAAGATTTG-3' (sense) and 5'-GGGAAGGTGGGAGAAGC-3' (anti-sense).

CDC45 gene 5'-TTTTCAGTTCCGTGGGTTTC-3' (sense) and 5'-CCCAACTAAGGCTCCCTACAT-3' (anti-sense).

TYMS gene 5'-AGCGAGAACCCAGACCTT-3' (sense) and 5'-AATAGTTGGATGCGGATTGTA-3' (anti-sense).

ECT2 gene 5'-AGGCGGAATGAACAGGA-3' (sense) and 5'-TTCATCTCCAAGCGGTAAA-3' (anti-sense)

COL1A1 gene 5'-CAAGGTGTTGTGCGATGACG-3' (sense) and 5'-CGACGCCGGTGGTTTCTT-3' (anti-sense)

SPP1 gene 5'-CTGCCAGCAACCGAAGT-3' (sense) and 5'-GTGATGTCCTCGTCTGTAGC-3' (anti-sense);

All reactions were performed on the Eppendorf Mastercycler ep realplex (2S; Eppendorf, Hamburg, Germany). using following cycling parameters, 95°C for 2 min, followed by 40 cycles of 95°C for 15 s, 60°C for 45 s.

Ethics statement

This study was performed with the approval of the institutional ethics committee of the Affiliated Hospital of Nantong University. And written informed consent had been provided for the NSCLC patients included in the present study, which was conducted in accordance with the Declaration of Helsinki.

Results

Identification of DEGs in NSCLC

After integrated bioinformatical analysis for GSE18842, GSE30219, GSE31210, GSE32863 and GSE40791 datasets, a total of 408 overlapping genes were found to be differentially expressed. The volcano plot showed the up-regulated and down-regulated DEGs in each dataset with the cutoff criterion of $P < 0.05$ and $|\log_2 FC| > 1$. The Venn diagrams showed the 408 overlap DEGs among the three datasets (Figure 2Ba) including 109 significantly up-regulated genes (Figure 2Bb) and 296 down-regulated genes (Figure 2Bc).

Enrichment analyses

In order to investigate the biological functions of these DEGs in NSCLC, GO and KEGG pathway, enrichment analysis was performed using DAVID. For BPs, GO analysis results indicated that up-regulated and down-regulated DEGs were significantly enriched in response to wounding, negative regulation of cell proliferation, regulation of cell proliferation, cell adhesion and response to

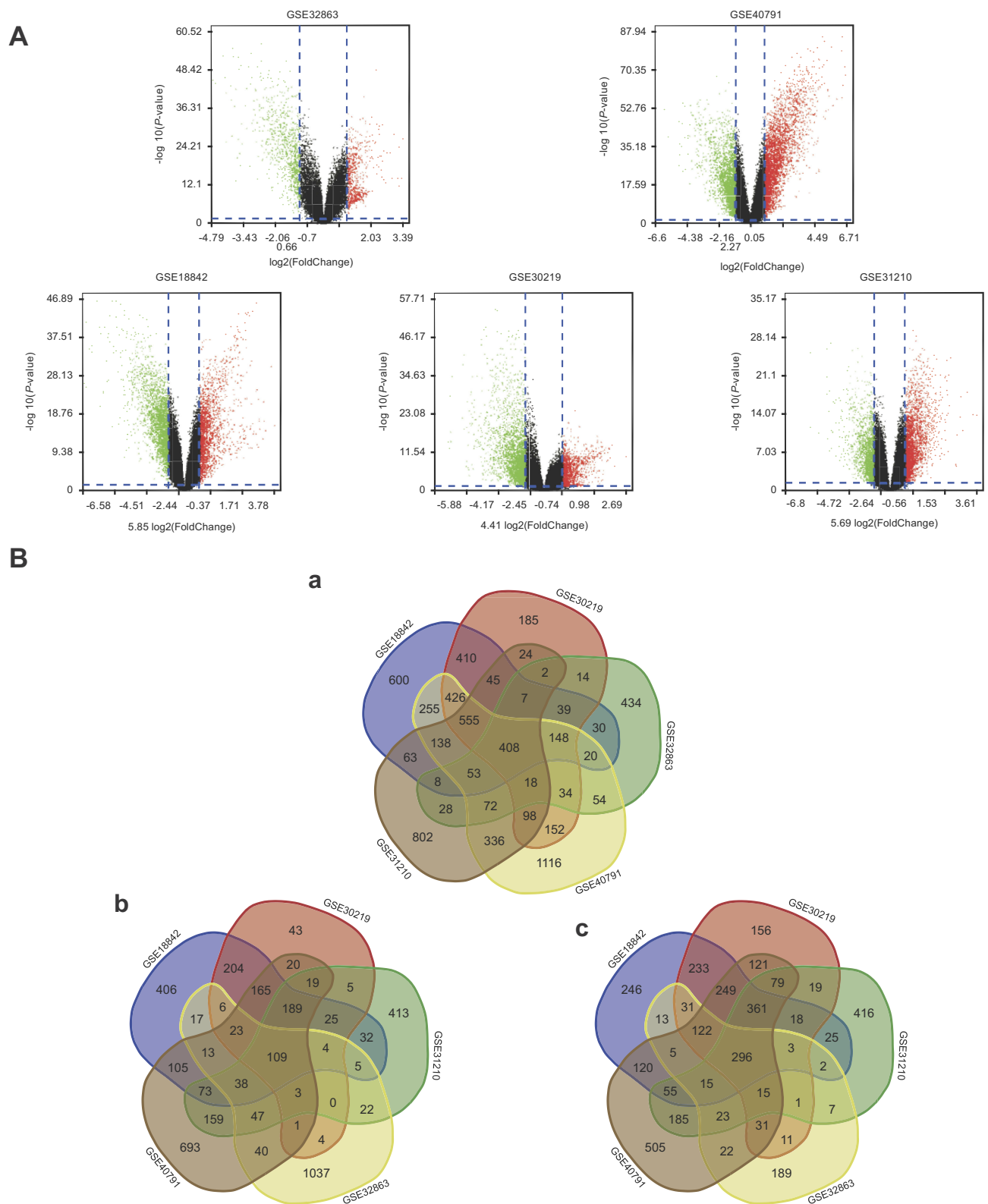


Figure 2 (A) Volcano plot of gene expression profile data between NSCLC and normal tissues in each dataset. Red dots: significantly up-regulated genes in NSCLC; green dots: significantly down-regulated genes in NSCLC; black dots: non-differentially expressed genes. Adj. $P < 0.01$ and $|\log_2 FC| > 1$ were considered as significant. **(Ba)** Venn diagram of 408 overlapping DEGs from GSE18842, GSE30219, GSE31210, GSE32863 and GSE40791 datasets. **(Bb)** Up-regulated DEGs **(Bc)** Down-regulated DEGs.

steroid hormone stimulus. CC analysis showed that these DEGs were particularly involved in extracellular region part, extracellular region, extracellular space, proteinaceous extracellular matrix and extracellular matrix. Similarly, changes in MF of DEGs were significantly enriched in carbohydrate binding, growth factor binding, glycosaminoglycan binding, transforming growth factor beta binding and pattern binding. Furthermore, KEGG pathway enrichment analysis revealed that these DEGs were mainly enriched in cell adhesion molecules (CAMs), leukocyte transendothelial migration, TGF-beta signaling pathway, complement and coagulation cascades and ECM-receptor interaction (Figure 3 and Table 1).

PPI network construction and module analysis

The STRING database and Cytoscape were used to construct a PPI network of the potential interactions between the overlapping DEGs. As presented in Figure 4, there were 300 nodes and 1283 interactions found in the network. The top three significant modules were detected by MCODE (Figure 5). Pathway enrichment analysis suggested that the module1

genes were mainly enriched in DNA replication, cell cycle and oocyte meiosis (Figure 5A). The genes in module 2 were mainly enriched in tumor necrosis factor signaling pathway, CAMs and African trypanosomiasis (Figure 5B). The genes in module 3 were significantly enriched in PPAR signaling pathway, ECM-receptor interaction and Focal adhesion (Figure 5C) (Table 2). The heat map clearly showed the significant difference of module genes between cancer tissues and adjacent tissues (Figure 6A and B). Macromolecular complex subunit organization, S phase and cell cycle phase were the main BP of module genes (Figure 6C). Among the module genes, we selected PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 with high degree of connectivity as hub genes (Table 3). The expression of hub genes in NSCLC tissues was significantly up-regulated compared to normal tissues.

Analysis and validation of hub genes

The prognostic information of PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 was freely obtained from GEPIA database. A total of 962 NSCLC patients were available for survival analysis. It was found that the high expression level of PTTG1, TYMS, ECT2,

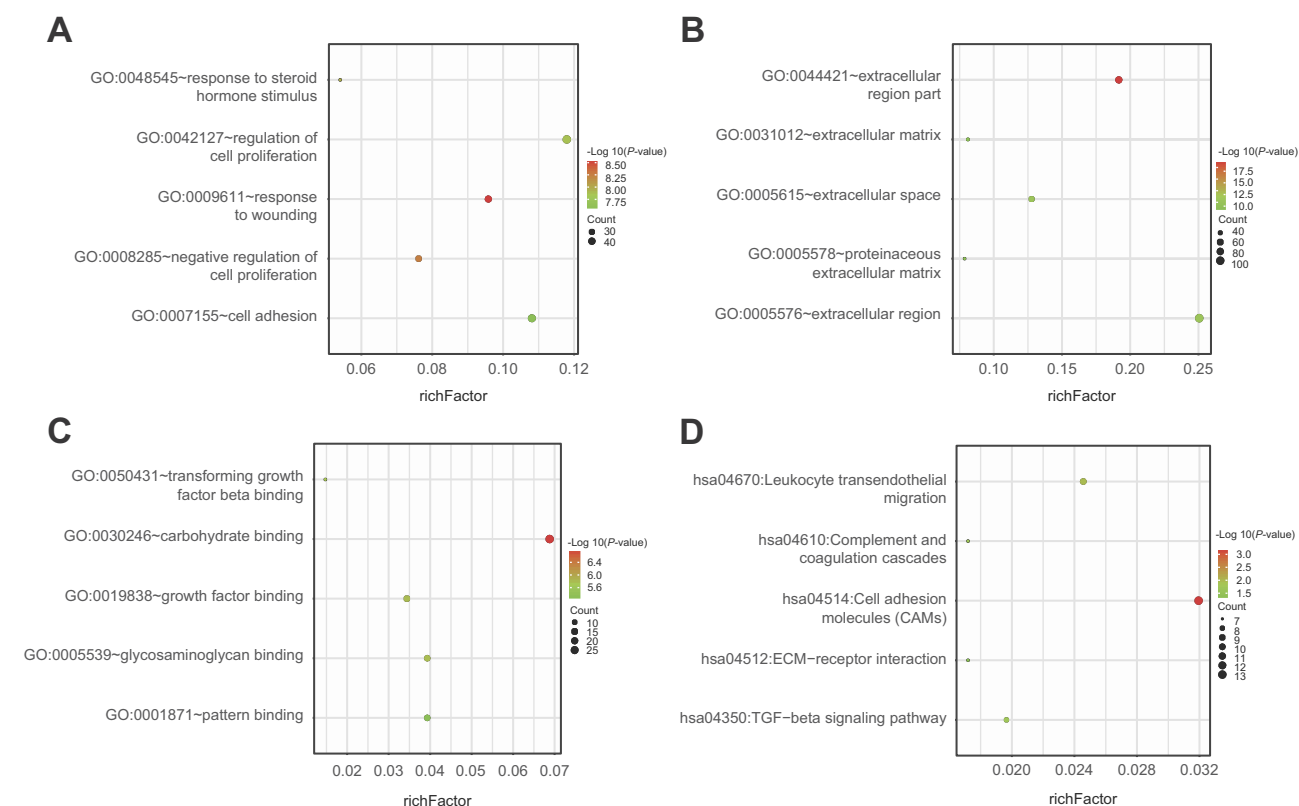


Figure 3 Functional and signaling pathway analysis of the overlapped DEGs in NSCLC. (A) Biological processes, (B) cellular components, (C) molecular function and (D) KEGG pathway.

Table 1. Functional and pathway enrichment analysis of the overlap DEGs

Category	Term	Count	PValue
GOTERM_BP_FAT	GO:0009611~response to wounding	39	3.00E-09
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	31	5.60E-09
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	22	1.08E-08
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	48	1.34E-08
GOTERM_BP_FAT	GO:0007155~cell adhesion	44	2.70E-08
GOTERM_CC_FAT	GO:0044421~extracellular region part	78	5.55E-20
GOTERM_CC_FAT	GO:0005576~extracellular region	102	5.06E-12
GOTERM_CC_FAT	GO:0005615~extracellular space	52	5.87E-12
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	32	2.19E-10
GOTERM_CC_FAT	GO:0031012~extracellular matrix	33	3.36E-10
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	28	1.64E-07
GOTERM_MF_FAT	GO:0019838~growth factor binding	14	1.59E-06
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	16	1.64E-06
GOTERM_MF_FAT	GO:0050431~transforming growth factor beta binding	6	1.92E-06
GOTERM_MF_FAT	GO:0001871~pattern binding	16	5.41E-06
KEGG_PATHWAY	hsa04514:Cell adhesion molecules (CAMs)	13	6.98E-04
KEGG_PATHWAY	hsa04670:Leukocyte transendothelial migration	10	0.010253
KEGG_PATHWAY	hsa04350:TGF-beta signaling pathway	8	0.017312
KEGG_PATHWAY	hsa04610:Complement and coagulation cascades	7	0.019019
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	7	0.044383

COL1A1, SPP1 and CDCA5 was markedly associated with worse overall survival for NSCLC patients (Figures 7 and 8A). This finding further confirmed the key role of these hub genes in the onset of NSCLC. Based on the immunohistochemical staining results from HPA database, the protein expression level of PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 was consistent with their gene expression, that is, the protein levels of hub genes were also in a higher expression state in NSCLC tissues compared to normal tissues (Figure 7B). In addition, we established a network of module genes and their co-expression genes (Figure 9A). In summary, PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 could represent the important diagnostic and prognostic biomarkers for NSCLC.

Identification of related active small molecules

To identify candidate small molecule drugs targeting the gene expression of NSCLC, all the overlapping DEGs, which were divided into up-regulated and down-regulated groups, were submitted to the CMap database. The 20 most significant small molecules matched to the NSCLC gene expression changes are listed in Table 4

and Figure 9B. Among these small molecules, DL-thiorphan (enrichment score = -0.826) and phenoxybenzamine (enrichment score = -0.823) showed a highly significant negative correlation and have the potential to reverse the tumoral status of NSCLC. This analysis provided novel insights into the treatment of NSCLC. However, further studies were still needed to explore the molecular mechanism of these small molecules in NSCLC. To further investigate the molecular mechanism of the hub genes in NSCLC, we predicted potential transcription factors (Figure S1) and constructed a regulatory network of lncRNA, miRNA and mRNA (Figure S2) by Gene-Cloud Biotechnology Information (GCBI) database.

Evaluation of gene expression in NSCLC

To further verify the expression of PTTG1, CDCA5, TYMS, ECT2, COL1A1 and SPP1 genes in NSCLC tissues and corresponding adjacent normal tissues, we choose seven pairs of tumor tissues and corresponding adjacent tissues. Relative expression of PTTG1, CDCA5, TYMS, ECT2, COL1A1 and SPP1 mRNA in NSCLC and adjacent non-tumorous tissues were quantified by qPCR. The results showed that the average PTTG1, CDCA5, TYMS, ECT2, COL1A1 and SPP1 mRNA expression level in

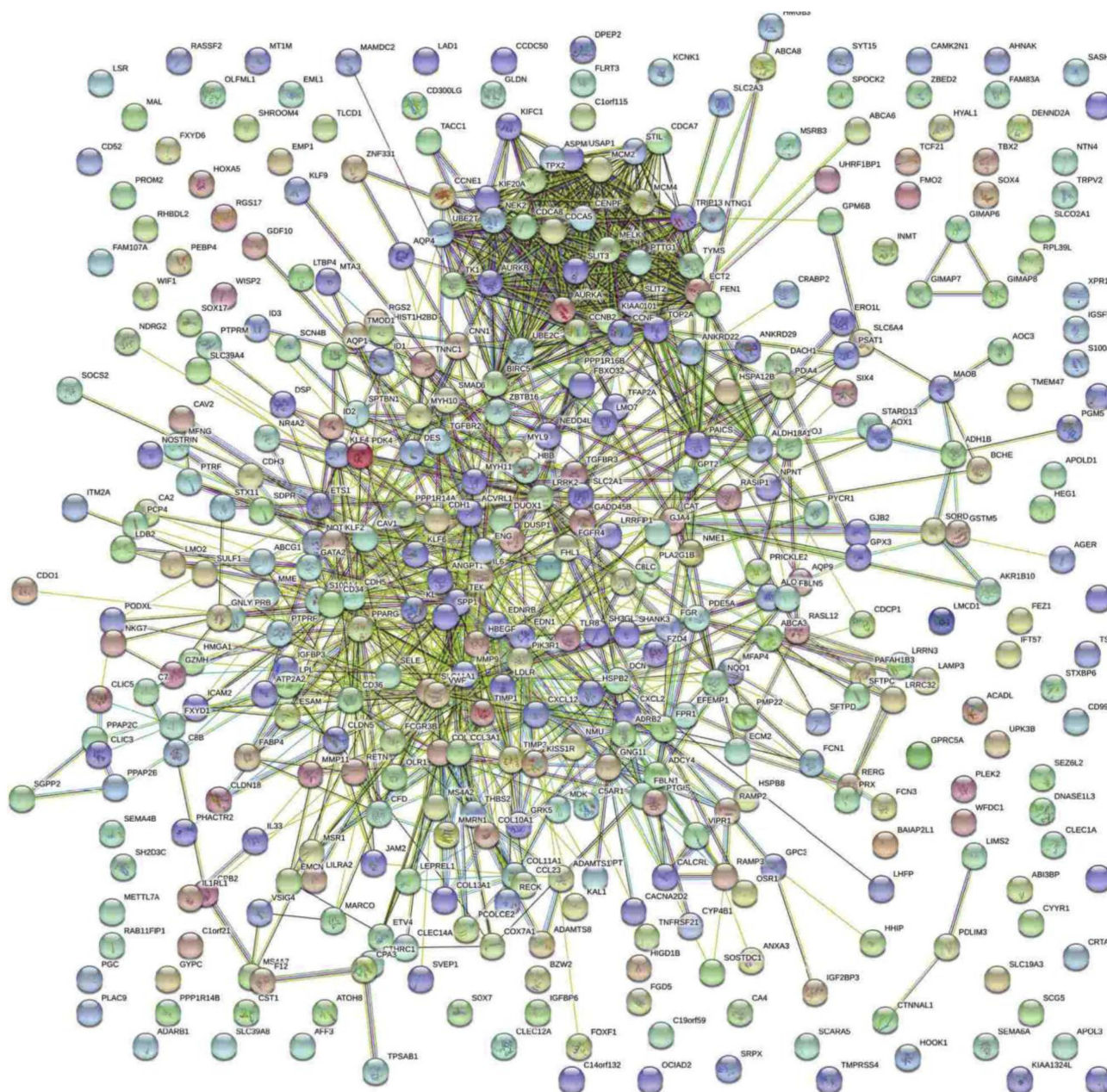


Figure 4 The protein-protein interaction networks of overlapping DEGs.

NSCLC tissues was significantly higher compared with non-tumorous tissues ($*p < 0.05$, compared with adjacent non-tumorous tissues, Figure 9C).

Discussion

Recently, the rapid advance in microarray and high-throughput technologies has expanded the application bio-medicine in clinical practice, such as cancer early diagnosis, novel targeted drug discovery and prognosis prediction.

GEO database, as a public repository for archiving high-throughput microarray experimental data, has provided the powerful tools to determine key genes and pathways associated with the pathogenesis of tumors.^{29,30} In the present study, based on the GEO database, five gene expression profiles including 696 NSCLC samples and 237 normal samples were integrated for a comprehensive bioinformatics analysis. The aim of our study was to find the potential small molecule drugs for the treatment of

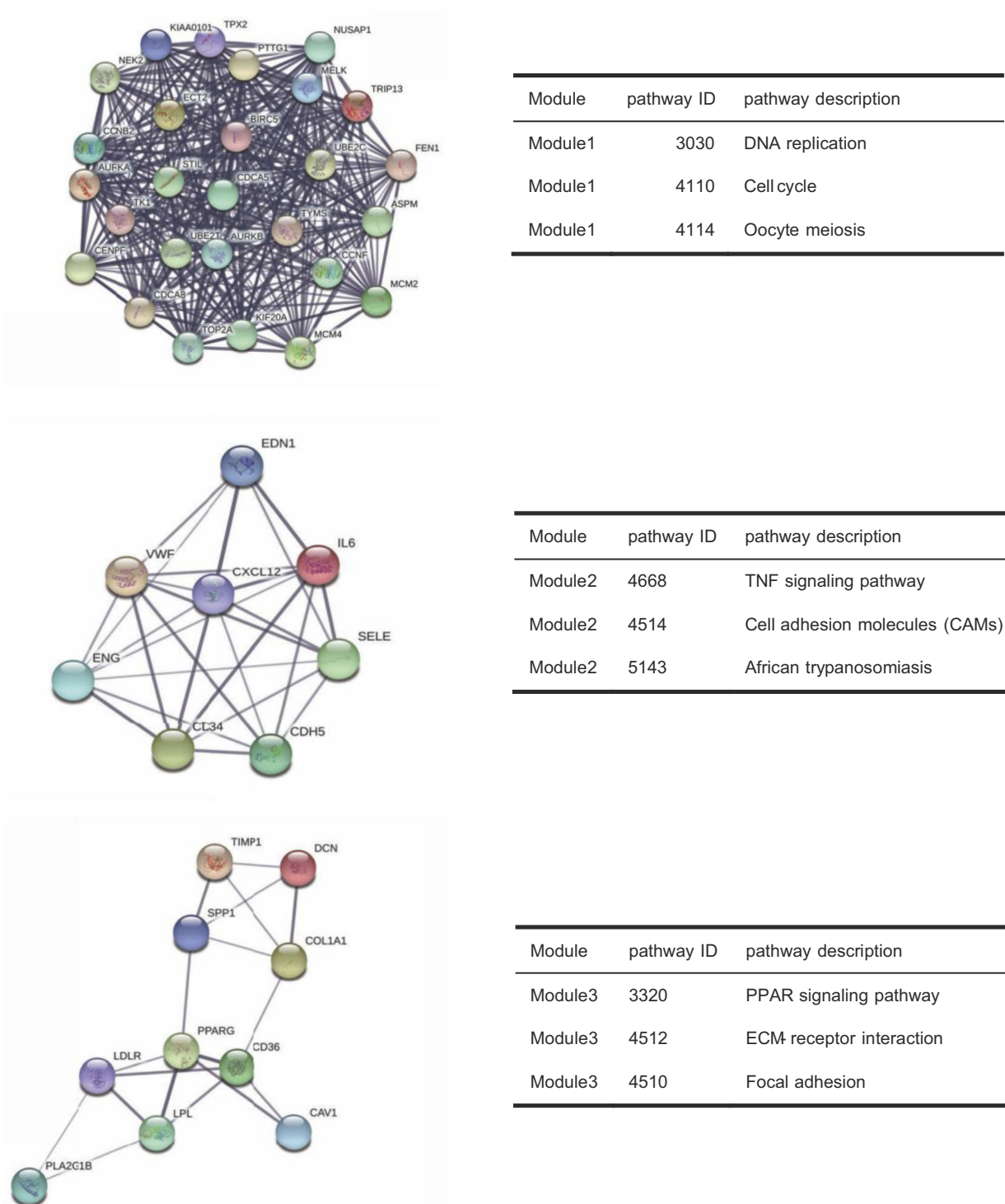


Figure 5 The three most significant modules extracted from PPI network and KEGG pathway analysis of module genes.

NSCLC and to identify the novel biomarkers correlated with the pathogenesis and prognosis of NSCLC. A total of 408 overlapping DEGs between tumor tissues and corresponding adjacent normal tissues were identified, which consisted of 109 up-regulated genes and 296 down-regulated genes. For a better in-depth understanding of these

overlapping DEGs, the GO function and KEGG pathway enrichment for these DEGs were performed. GO term analysis was carried out via the following aspects: BP, MF and CC. The BP analysis showed that these DEGs were mainly enriched in response to wounding, negative regulation of cell proliferation and regulation of cell

Table 2 The pathway enrichment analysis of module genes

Module	pathway ID	pathway description	observed gene count	false discovery rate
Module1	hsa3030	DNA replication	3	0.00264
Module1	hsa4110	Cell cycle	4	0.00264
Module1	hsa4114	Oocyte meiosis	3	0.0336
Module2	hsa4668	TNF signaling pathway	3	0.00213
Module2	hsa4514	Cell adhesion molecules (CAMs)	3	0.00225
Module2	hsa5143	African trypanosomiasis	2	0.00672
Module3	hsa3320	PPAR signaling pathway	3	0.00117
Module3	hsa4512	ECM-receptor interaction	3	0.00117
Module3	hsa4510	Focal adhesion	3	0.0103

proliferation. MF analysis indicated that these DEGs were significantly associated with carbohydrate binding, growth factor binding and glycosaminoglycan binding. Changes in CC were mainly enriched in extracellular region part, extracellular region and extracellular space. The KEGG pathway enrichment analysis revealed nine significant signaling pathways including CAMs, leukocyte transendothelial migration, TGF-beta signaling pathway, complement and coagulation cascades and ECM-receptor interaction. Multiple CAM are involved in the tumor growth, metastasis and angiogenesis. Vascular CAM-1 was first noted as an endothelial cell adhesion receptor for more than two decades, which plays a key role in leukocyte recruitment in cellular immune responses. The L1 cell adhesion molecule (L1CAM), as neural adhesion molecules, extensively participates in the progression of human malignant tumors.^{31,32} Targeting the TGFβ pathway has been used for various cancer therapy.^{33,34} An increasing number of studies reveal that the ECM-receptor interaction pathway is significantly associated with the various cancer cells proliferation and invasion. Zhang et al demonstrated that Twist2 is involved in the proliferation and invasion of kidney cancer cells through regulating the expression of two molecules in the ECM-receptor interaction pathway: ITGA6 and CD44.³⁵ In summary, the above theories strongly supported our findings from bioinformatics analysis. The PPI network complex based on DEGs-encoding proteins was constructed and 300 nodes with 1283 interactions were obtained. The MCODE plug-in extracted three modules with the most significant degree from the PPI network. TTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 with high degree of connectivity were selected as hub genes. Survival analysis for 962 NSCLC patients from GEPIA database showed that patients with high expression

levels of PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 experienced a worse prognosis than those with low expression. To validate the results of bioinformatics analysis, we performed qPCR analysis to evaluate the expression of hub genes expression in seven paired NSCLC tissues. The qPCR analysis showed the same gene expression trend as found in the GEO database, thereby verifying the reliability of our results. Additionally, the establishment of a network of lncRNA–miRNA–mRNA and the prediction of transcription factors will enhance our understanding of the mechanism of PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 in the pathogenesis of NSCLC. Previous studies have proved that PTTG1 protein is abundantly expressed in various invasive tumors and hematopoietic malignant tumors, but its expression level is low or undetectable in most normal tissues. Several studies have further emphasized the role of PTTG1 in the growth and metastasis of tumors. They have shown that ectopic expression of PTTG1 enhances proliferation or invasiveness in various histologically derived cancer cell lines, whereas silencing of PTTG1 produces the opposite result.^{36,37} CDCA5 plays a key role in ensuring the accurate separation of sister chromatids in S and G2/M phases of cell cycle by interacting with coherents and cdk1. Additionally, CDCA5 also interacts with the key regulatory factors ERK and cyclin E1 of G1/Smitotic checkpoint. Recent studies have shown that the expression of CDCA5 in oral squamous cell carcinoma, urothelial cell carcinoma and gastric cancer, which is related to tumorigenesis and tissue invasion.^{38,39} ECT2 is a guanine nucleotide exchange factor (GEF), which is related to tumor cell differentiation, TNM stage, prognosis and lymph node metastasis, such as breast cancer, osteosarcoma cells, gastric cancer, and gliomas.^{40,41} COL1A1 is a

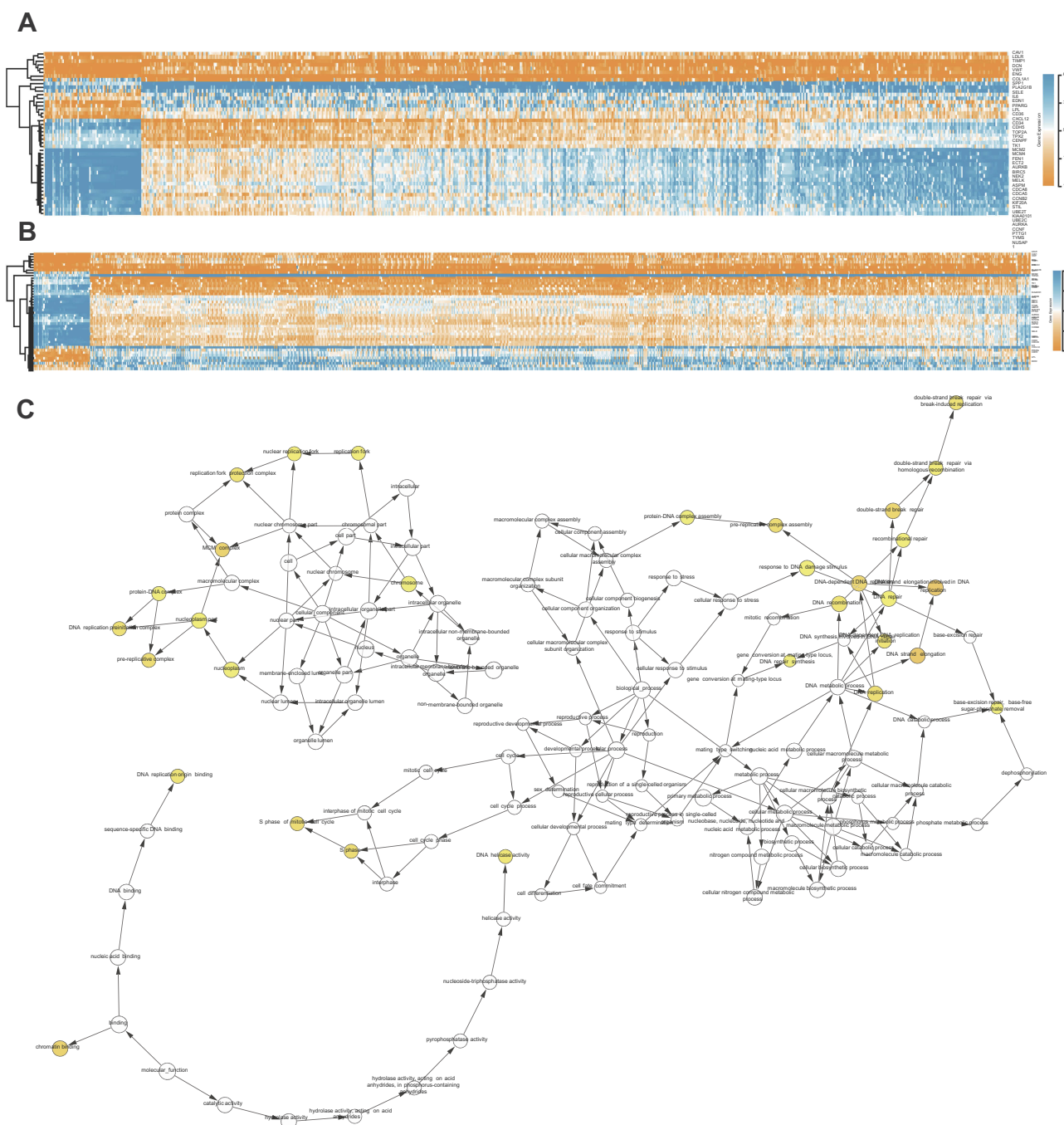


Figure 6 (A, B) The heatmap of module genes between NSCLC (LUAD and LUSC) and normal samples. **(C)** The BiNGO revealed the biological process of module genes. The color depth of nodes represents the corrected *P*-value. The size of nodes represents the number of genes involved.

target gene of miR-133a-3p in oral squamous cell carcinoma and miR-129-5p in gastric cancer^{42,43} However, no studies have reported the potential mechanism of ITGB5 and RGS4 in the initiation and progression of NSCLC. The above studies indicated PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 may also play an important role in the occurrence and development of NSCLC.

In additionally, analyzed with the overlapping DEGs and CMap database, we determined a set of small molecule drugs that had potential to reverse the gene expression changes of NSCLC. The small molecules with a highly significant negative enrichment value may become new targeted drugs for the treatment of NSCLC. DL-thiorphan, as the most significant small molecule

Table 3 The full name and functional roles of hub genes

Gene symbol	Full name	Function
PTTG1	Pituitary Tumor-Transforming 1	The encoded protein is a homolog of yeast securin proteins, which prevent separins from promoting sister chromatid separation. It is an anaphase-promoting complex (APC) substrate that associates with a separin until activation of the APC. The gene product has transforming activity in vitro and tumorigenic activity in vivo, and the gene is highly expressed in various tumors. The gene product contains 2 PXXP motifs, which are required for its transforming and tumorigenic activities, as well as for its stimulation of basic fibroblast growth factor expression. It also contains a destruction box (D box) that is required for its degradation by the APC. The acidic C-terminal region of the encoded protein can act as a transactivation domain. The gene product is mainly a cytosolic protein, although it partially localizes in the nucleus. Three transcript variants encoding the same protein have been found for this gene.
CDCA5	Cell Division Cycle Associated 5	CDCA5 (Cell Division Cycle Associated 5) is a Protein Coding gene. Diseases associated with CDCA5 include Cornelia De Lange Syndrome. Among its related pathways are Cell Cycle, Mitotic and MicroRNAs in cancer. Gene Ontology (GO) annotations related to this gene include <i>chromatin binding</i> .
TYMS	Thymidylate Synthetase	Thymidylate synthase catalyzes the methylation of deoxyuridylate to deoxythymidylate using, 10-methylenetetrahydrofolate (methylene-THF) as a cofactor. This function maintains the dTMP (thymidine-5-prime monophosphate) pool critical for DNA replication and repair. The enzyme has been of interest as a target for cancer chemotherapeutic agents. It is considered to be the primary site of action for 5-fluorouracil, 5-fluoro-2-prime-deoxyuridine, and some folate analogs. Expression of this gene and that of a naturally occurring antisense transcript, mitochondrial enolase superfamily member 1 (GeneID:55556), vary inversely when cell-growth progresses from late-log to plateau phase. Polymorphisms in this gene may be associated with etiology of neoplasia, including breast cancer, and response to chemotherapy.
ECT2	Epithelial Cell Transforming 2	The protein encoded by this gene is a guanine nucleotide exchange factor and transforming protein that is related to Rho-specific exchange factors and yeast cell cycle regulators. The expression of this gene is elevated with the onset of DNA synthesis and remains elevated during G2 and M phases. In situ hybridization analysis showed that expression is at a high level in cells undergoing mitosis in regenerating liver. Thus, this protein is expressed in a cell cycle-dependent manner during liver regeneration, and is thought to have an important role in the regulation of cytokinesis. Several transcript variants encoding different isoforms have been found for this gene.
COL1A1	Collagen Type I Alpha 1 Chain	This gene encodes the pro-alpha1 chains of type I collagen whose triple helix comprises two alpha1 chains and one alpha2 chain. Type I is a fibril-forming collagen found in most connective tissues and is abundant in bone, cornea, dermis and tendon. Mutations in this gene are associated with osteogenesis imperfecta types I-IV, Ehlers-Danlos syndrome type VIIA, Ehlers-Danlos syndrome Classical type, Caffey Disease and idiopathic osteoporosis. Reciprocal translocations between chromosomes 17 and 22, where this gene and the gene for platelet-derived growth factor beta are located, are associated with a particular type of skin tumor called dermatofibrosarcoma protuberans, resulting from unregulated expression of the growth factor. Two transcripts, resulting from the use of alternate polyadenylation signals, have been identified for this gene.
SPPI	Secreted Phosphoprotein 1	The protein encoded by this gene is involved in the attachment of osteoclasts to the mineralized bone matrix. The encoded protein is secreted and binds hydroxyapatite with high affinity. The osteoclast vitronectin receptor is found in the cell membrane and may be involved in the binding to this protein. This protein is also a cytokine that upregulates expression of interferon-gamma and interleukin-12. Several transcript variants encoding different isoforms have been found for this gene.

(enrichment score = -0.826), was the most promising small molecule to reverse the abnormal NSCLC gene expression. It is worth noting that so far no research has focused on the potential role of this small molecule in NSCLC. Similarly, the relationship between phenoxylbenzamine (enrichment score = -0.823) and NSCLC was

also not investigated. This information is beneficial for the development of novel targeted drugs for the treatment of NSCLC. Given the emergence of these candidate biomarkers in silico, in vitro studies (with cell lines, etc.) and then in vivo experiments could be worth of interest in functional validation.

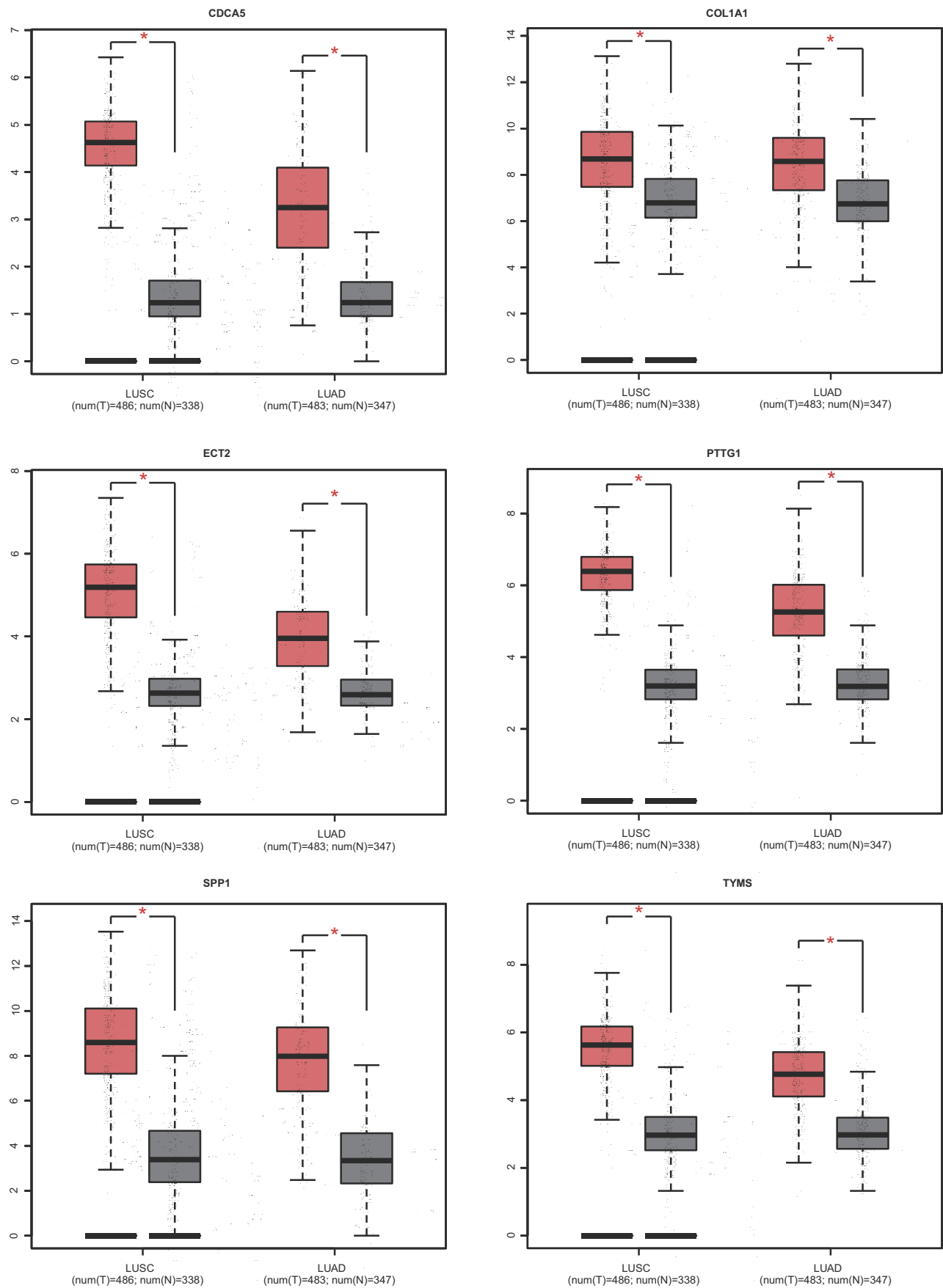


Figure 7 The expression level of hub genes according to the GEPIA database.

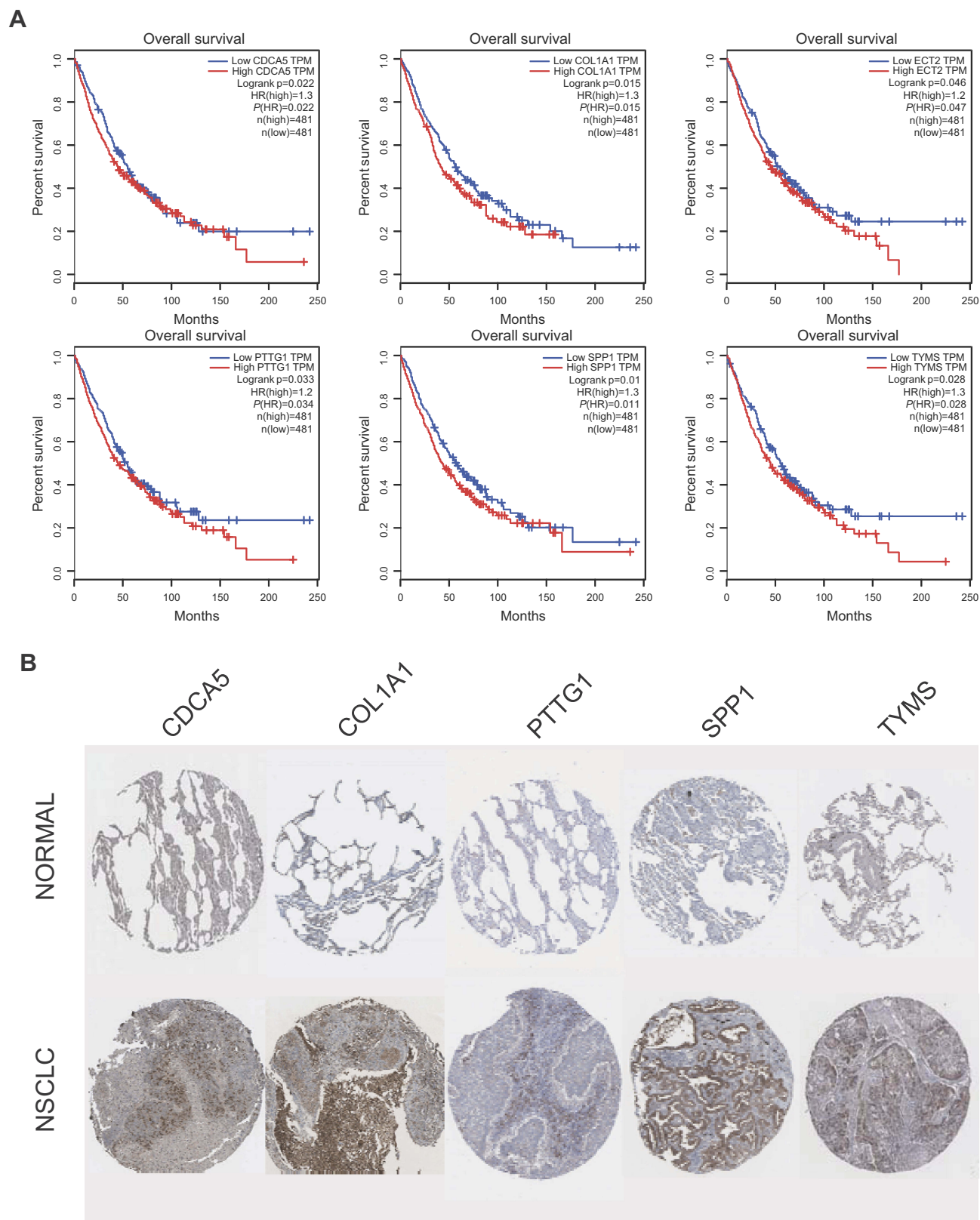


Figure 8 (A) The survival analysis for hub genes according to the GEPIA database. (B) The protein level expression of hub genes in NSCLC and normal tissues using immunohistochemistry.

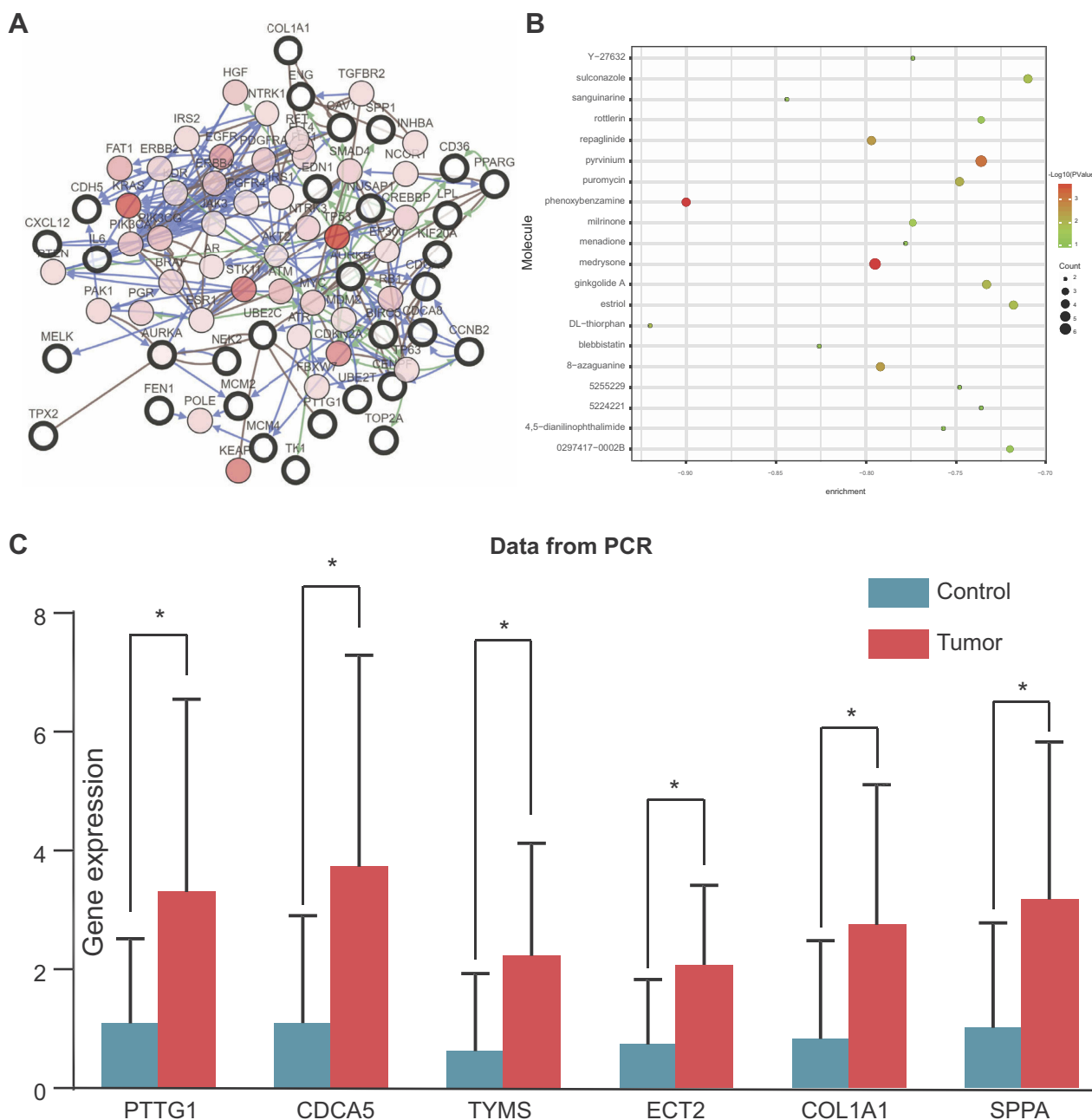


Figure 9 (A) The network of module genes and their co-expression genes constructed by cBioPortal. Nodes with thick outline: hub genes; nodes with thin outline: co-expression genes. (B) The 20 most small molecule drugs identified by CMap database. (C) qPCR validation of these six hub genes in seven paired NSCLC samples. * $P < 0.05$.

Conclusion

In this study, six key genes were identified for the first time in NSCLC by integrated bioinformatics analysis. Survival analysis revealed that high expression levels of PTTG1, TYMS, ECT2, COL1A1, SPP1 and CDCA5 were markedly associated with worse prognosis of patients. These hub genes could act as the promising novel biomarkers for the diagnosis, prognosis and

treatment of NSCLC. We also revealed several crucial signaling pathways correlated with the NSCLC initiation and progression. Furthermore, we identified a set of candidate small molecule drugs which could reverse the abnormal gene expression of NSCLC. We hope the present study could provide powerful evidence for the future development of genomic individualized treatment in NSCLC.

Table 4 List of the 20 most significant small molecule drugs

cmap name	enrichment	p
DL-thiorphan	-0.92	0.01312
phenoxybenzamine	-0.9	0.00016
sanguinarine	-0.844	0.04873
blebbistatin	-0.826	0.05964
repaglinide	-0.797	0.00334
medrysone	-0.795	0.00016
8-azaguanine	-0.792	0.00378
menadione	-0.778	0.09664
milrinone	-0.774	0.02354
Y-27632	-0.774	0.10102
4,5-dianilinophthalimide	-0.757	0.11651
puromycin	-0.748	0.00806
5255229	-0.748	0.12557
pyrvinium	-0.736	0.0007
roscovitine	-0.736	0.03758
5224221	-0.736	0.13802
ginkgolide A	-0.733	0.01011
0297417-0002B	-0.72	0.04521
estriol	-0.718	0.01281
sulconazole	-0.71	0.01428

Disclosure

The authors report no conflicts of interest in this work.

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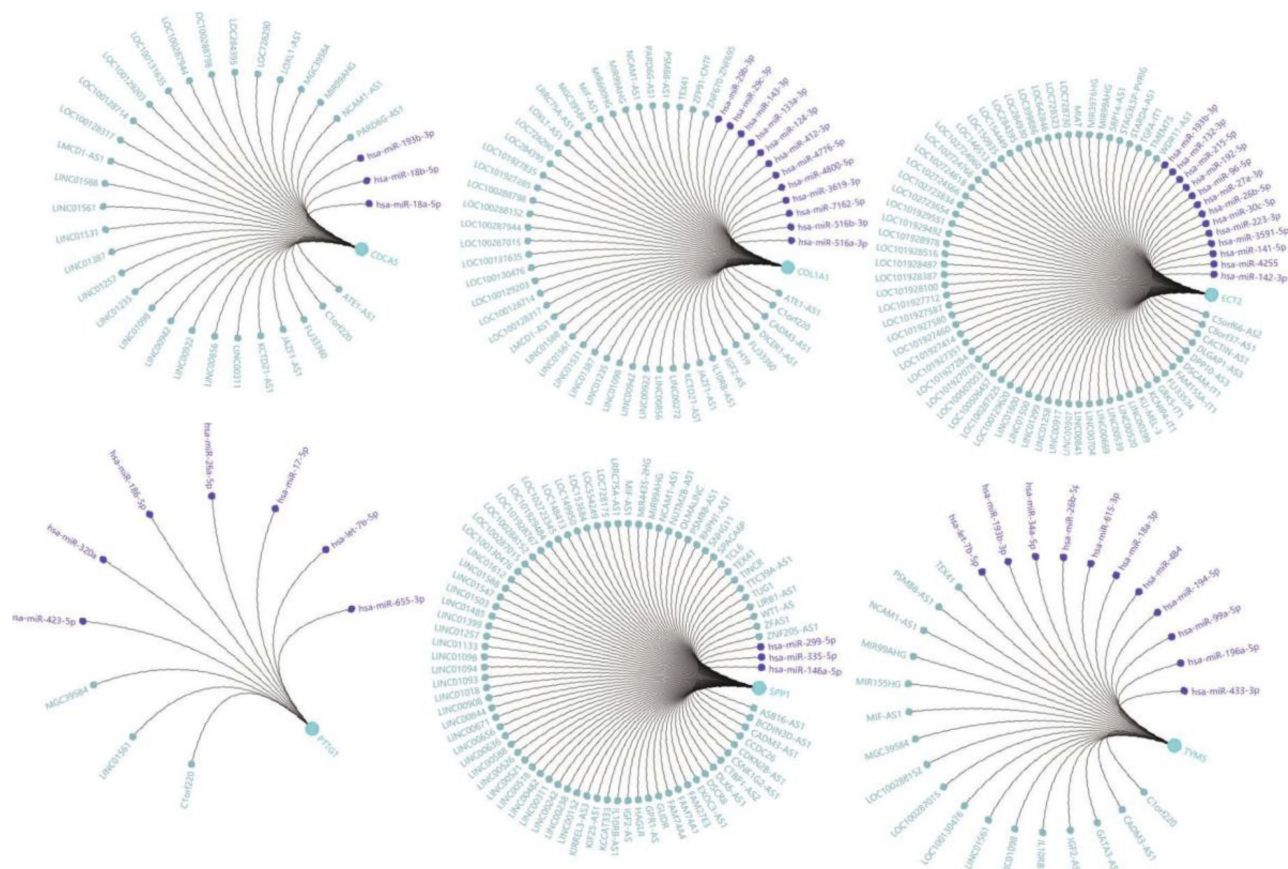


Figure S2 A regulatory network of lncRNA-miRNA-mRNA constructed by GCBI. Purple nodes: related lncRNA; Blue nodes: targeted miRNA.

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