

# Transcriptome profiling analysis reveals biomarkers in colon cancer samples of various differentiation

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**Abstract.** The aim of the present study was to investigate more colon cancer-related genes in different stages. Gene expression profile E-GEOD-62932 was extracted for differentially expressed gene (DEG) screening. Series test of cluster analysis was used to obtain significant trending models. Based on the Gene Ontology and Kyoto Encyclopedia of Genes and Genomes databases, functional and pathway enrichment analysis were processed and a pathway relation network was constructed. Gene co-expression network and gene signal network were constructed for common DEGs. The DEGs with the same trend were clustered and in total, 16 clusters with statistical significance were obtained. The screened DEGs were enriched into small molecule metabolic process and metabolic pathways. The pathway relation network was constructed with 57 nodes. A total of 328 common DEGs were obtained. Gene signal network was constructed with 71 nodes. Gene co-expression network was constructed with 161 nodes and 211 edges. ABCD3, CPT2, AGL and JAM2 are potential biomarkers for the diagnosis of colon cancer.

## Introduction

Colon cancer together with lung, prostate and breast cancer constitute a threat to human health worldwide (1). Notably, previous findings showed that surgery had minimal adverse reaction in stage 2 patients (2). In addition, some treatment strategies such as adjuvant chemotherapy, were found to be effective, especially for stage 3 colon cancer (3). Thereby, the known critical genes in different stages of colon cancer was necessary for the diagnosis and treatment of this disease.

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Various studies have been previously performed to investigate the molecular mechanism of colon cancer. For example, Yu *et al* found that methylated TBX5 may be a functional tumor suppressor gene for the diagnosis of malignancy of colon cancer (4). Moreover, the metachronous distant metastasis of colon cancer was ensured to be correlated with the downregulation of SASH1 (SAM- and SH3-domain containing 1) expression (5). Schepeler *et al* showed that the expression level of miR-320 and miR-498 was closely related to the recurrence-free survival of colon cancer (6). miR-21 was also confirmed to be upregulated in stage 2 colon cancer by participating in the immune process (7). In addition, transforming growth factor  $\beta$ 1 could prevent an organized hyperplasia in the early transition, and further suppress colon cancer (8). Although these genes, miRNAs and pathways were identified, differentially expressed genes (DEGs) in different staging and their potential mechanism remain to be determined.

In order to investigate more colon cancer-related genes in different stages, DEGs in four stages compared with controls were identified in this study, and series test of clusters were processed. In addition, functional and pathway enrichment analysis was used for these DEGs. Finally, various networks including a pathway relation network, gene signal network and gene co-expression network were constructed.

## Materials and methods

**Microarray data.** The gene expression profile E-GEOD-62932 was extracted from the ArrayExpress Archive, including 64 colon cancer tissues and 4 healthy control samples (9). The 64 colon cancer tissues included 12 samples in stage 1, 17 in stage 2, 20 in stage 3, and 15 in stage 4. Platform information of this profile was GPL570 [HG-U133\_Plus\_2] Affymetrix Human Genome U133 Plus 2.0 Array.

**Data preprocessing and DEGs screening.** The obtained probe sets were converted into expression value matrix and background correction, normalization and summarizing were performed using the Robust Multi-chip Average algorithm. Based on the information of Affymetrix (\*.transcript.csv), the probe sets were annotated. The annotated data were screened with the threshold of >0.8 median (normalized unscaled standard errors) <1.2 and >0.25 median (relative log expression) <0.25.

Table I. Top 5 GO terms of differentially expressed genes.

GO ID	GO Name	Diff gene counts in GO	Enrichment Score	P-value	FDR
GO:0044281	Small molecule metabolic process	129	3.905874858	5.67E-40	1.57E-36
GO:0051301	Cell division	56	7.834124719	7.24E-33	1.00E-29
GO:0000278	Mitotic cell cycle	59	6.707641713	9.84E-31	9.07E-28
GO:0000236	Mitotic prometaphase	28	11.55533396	7.75E-22	5.36E-19
GO:0000087	M phase of mitotic cell cycle	35	7.295034066	7.28E-20	4.02E-17

GO, Gene Ontology; FDR, false discovery rate.

DEGs between colon cancer in various stages and normal tissues were identified by significance analysis of microarrays method with the cut-off criteria of  $P < 0.05$  (10).

*Series test of clusters.* The gene expression profiles were always changed with tumor development. In the present study, series test of cluster (STC) analysis was used to obtain the significant trending models related to tumor stage and their involved DEGs (11). Clusters with  $P < 0.05$  were regarded as statistically significant.

*Functional and pathway enrichment analysis.* Gene Ontology (GO) is a cross-species and comprehensive database, which was constructed by the GO Consortium (12). Similarly, the Kyoto Encyclopedia of Genes and Genomes (KEGG) is a powerful tool for analysis of biological metabolism and metabolic network (13). Based on the abovementioned databases, GO functional and KEGG pathway enrichment analysis were processed for identified DEGs with the threshold of  $P < 0.05$ . The Fisher's exact test and multiple comparisons were used to calculate the significance of GO terms and pathways, and false discovery rate (FDR) was the adjusted P-value.

*Construction of pathway relation network.* The pathway relation network was constructed based on information from the KEGG database. From this network, a signal transduction relationship was obtained. In addition, upstream regulatory pathways and downstream effective pathways were identified.

*Gene signal and gene co-expression network construction for common DEGs.* DEGs in GO terms and KEGG pathways were inserted based on the same symbol. The obtained DEGs were regarded as common DEGs. Gene signal information was collected from the KEGG database. The common DEGs were mapped into the whole network and the gene signal network of common DEGs in colon cancer was generated. Additionally, the gene co-expression network was a weighted network that was constructed based on gene expression value and their correlation indexes. The two networks were visualized by Cytoscape (14).

## Results

*DEG screening and series test of cluster.* Based on the threshold of DEGs, 1,543 DEGs were screened to be associated with

colon tumor development compared with control samples. Then, the DEGs with the same trend were clustered. A total of 16 clusters with statistical significance were obtained, including profile 14, 67, 5 and 2 (Fig. 1).

*Functional and KEGG pathway enrichment.* The screened DEGs were enriched into various GO terms, such as small molecule metabolic process (FDR=1.57E-36), cell division (FDR=1.00E-29) and mitotic cell cycle (FDR=9.07E-28) (Table I). In addition, the DEGs were gathered into different pathways including metabolic pathways (FDR=1.57E-21), cell cycle (FDR=8.23E-12) and progesterone-mediated oocyte maturation (FDR=3.56E-09) (Table II).

*Construction of the pathway relation network.* The pathway relation network was constructed with 57 nodes and 158 edges. The hub nodes were glycolysis/gluconeogenesis (Degree=17), apoptosis (Degree=17), citrate cycle (TCA cycle) (Degree=16) and pathways in cancer (Degree=13). Notably, pathways in cancer (Outdegree=13), phenylalanine metabolism (Outdegree=4) and gap junction (Outdegree=4) were upstream pathways, while cytokine-cytokine receptor interaction (Indegree=5) and oxidative phosphorylation (Indegree=4) were downstream pathways (Fig. 2).

*Gene signal network and gene co-expression network construction for common DEGs.* Based on the same gene symbol, a total of 328 common DEGs were obtained, such as adenosylhomocysteinase-like 2, oxytocin receptor, aquaporin 8 and hedgehog interacting protein. As shown in Fig. 3, the gene signal network was constructed with 71 nodes and 146 edges. The hub nodes were adenylate cyclase 9 (Degree=18), ectonucleoside triphosphate diphosphohydrolase 5 (Degree=18) and protein kinase, cAMP-dependent, catalytic,  $\beta$  (Degree=14).

The gene co-expression network was constructed with 161 nodes and 211 edges (Fig. 4). In this network, the hub nodes with a higher degree were ATP-binding cassette, sub-family D, member 3 (ABCD3, Degree=19), carnitine palmitoyltransferase 2 (CPT2, Degree=17) and amylo- $\alpha$ -1, 6-glucosidase, 4- $\alpha$ -glucanotransferase (AGL, Degree=15). Moreover, this network showed that ABCD3 has a positive relationship with various DEGs, including ankyrin 3, adenylate cyclase 9 and acyl-coA dehydrogenase, and short/branched chain.

Table II. The top 5 pathways of differently expressed genes.

Pathway ID	Pathway name	Diff gene counts in pathway	Enrichment score	P-value	FDR
1,100	Metabolic pathways	95	3.297358904	6.37E-24	1.57E-21
4,110	Cell cycle	23	7.654743119	6.66E-14	8.23E-12
4,914	Progesterone-mediated oocyte maturation	17	8.157835437	5.00E-11	3.56E-09
4,114	Oocyte meiosis	19	7.00099953	5.76E-11	3.56E-09
5,200	Pathways in cancer	29	3.659946318	5.29E-09	2.61E-07

FDR, false discovery rate.

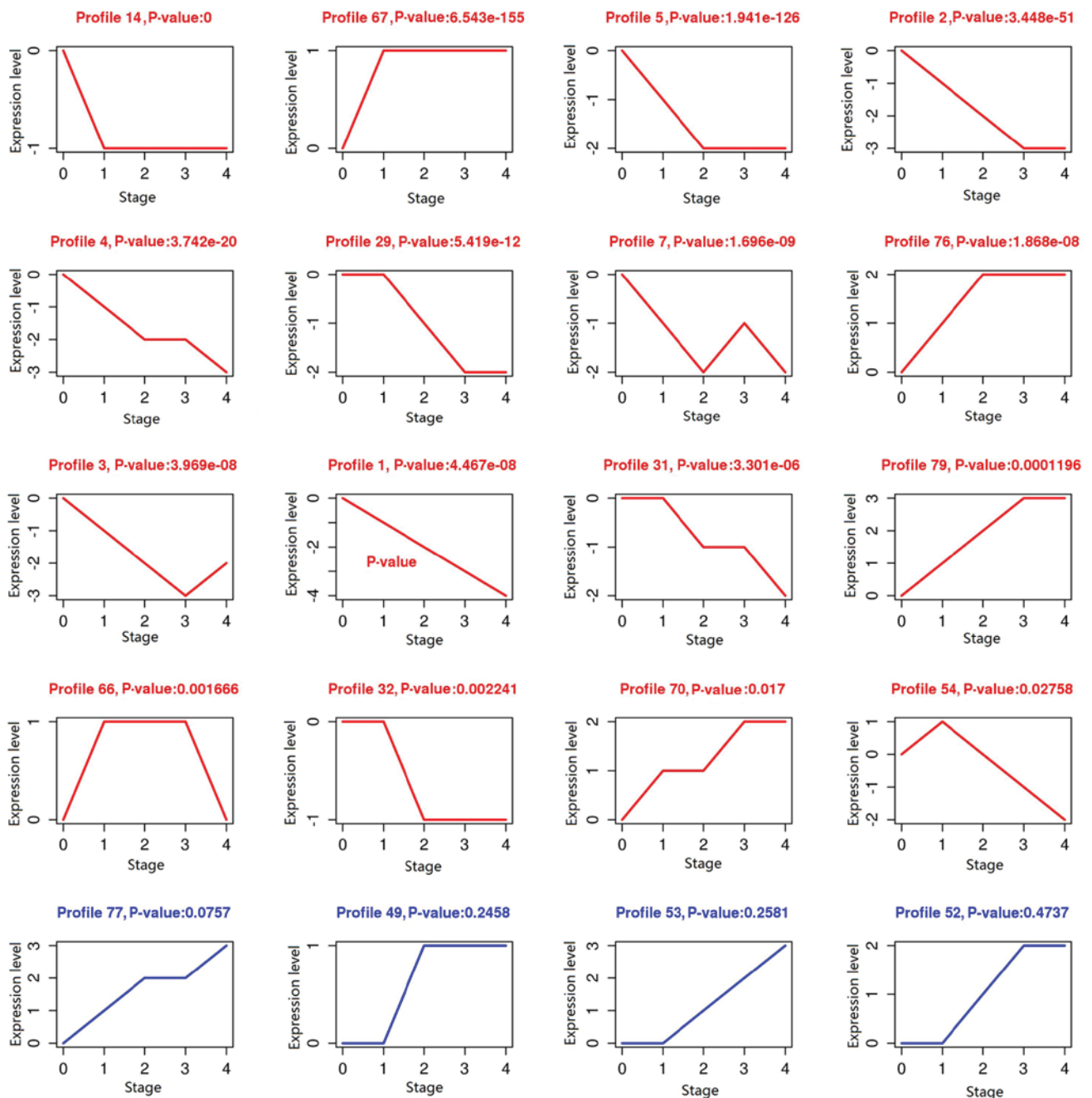


Figure 1. Cluster of the screened differentially expressed genes. The red profiles are statistically significant, but the blue profiles have no statistical significance.







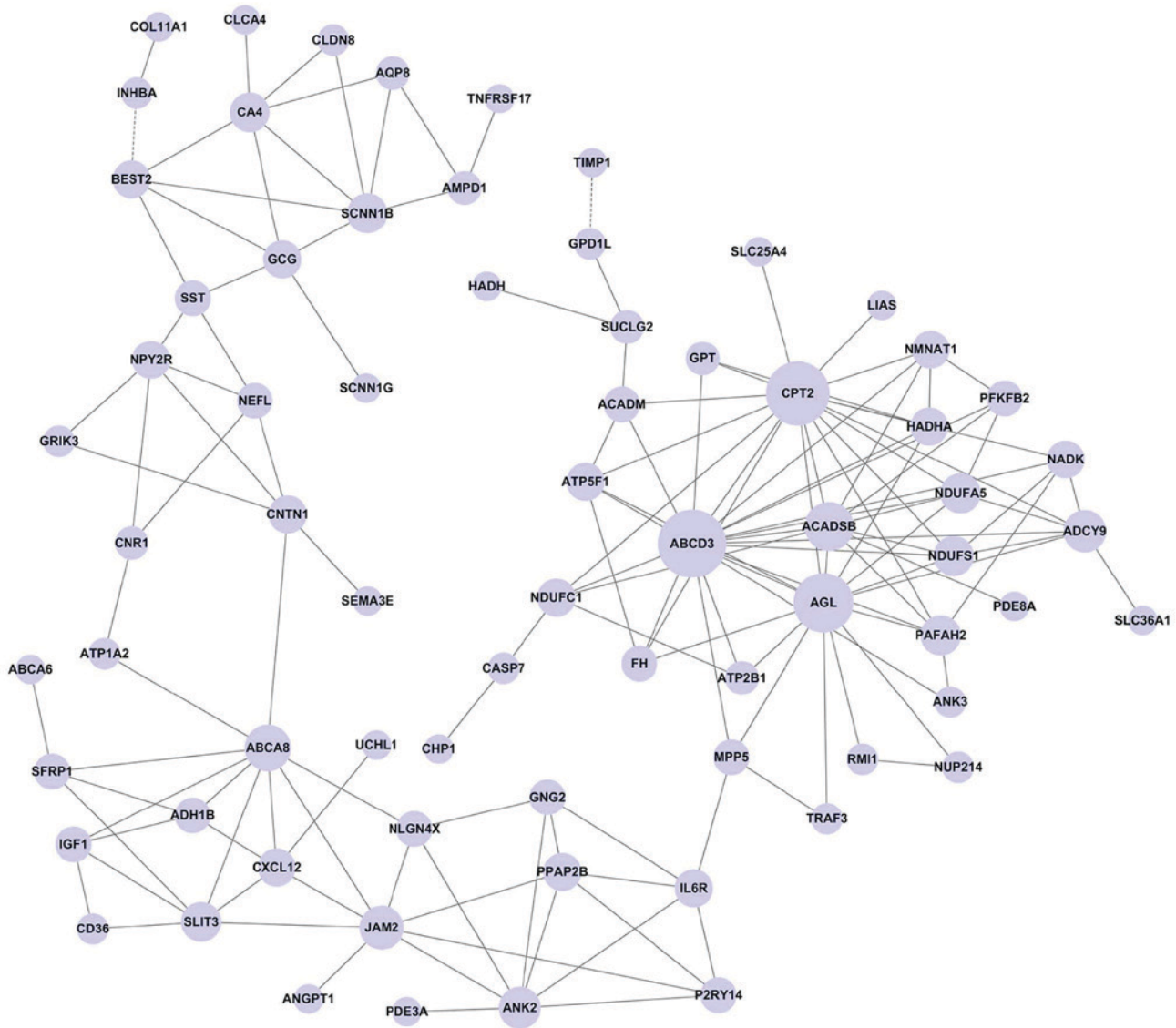


Figure 4. Gene co-expression network of common differentially expressed genes (DEGs). The nodes and edges are common DEGs and their regulation and relationships, respectively. The solid lines show the positive correlation while the dashed lines show the negative correlation.

hypothesized that AGL was a potential biomarker for the diagnosis of colon cancer.

JAM2 encodes a type I membrane protein that functions as an adhesive ligand for interacting with the number of immune cell types (29). The findings of a previous study revealed that JAM2 played an important role in motility and its adhesion process of colon cancer cells (30). In addition, Royse *et al.* found that JAM2 altered the expression in early- and late-stage colon tumors, and is also closely associated with PTEN, which is a tumor suppressor (31). In the present study, JAM2 was gathered into tight junction, cell adhesion molecules and in blood coagulation. Consistent with previous studies, the indexes of blood coagulation were closely associated with the progression of colon cancer (32). Moreover, various blood coagulation inhibitors were found to be beneficial for colon cancer patients (33). Thus, JAM2 may be involved in the pathogenesis of colon cancer by participating in cell adhesion molecules and blood coagulation.

In summary, the identified DEGs including ABCD3, CPT2, AGL and JAM2 constitute potential biomarkers for the diagnosis of colon cancer by participating in various functions and pathways. The validation of these biomarkers identified is to be conducted in future studies.

### Competing interests

Authors declare they have no competing interests.

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