

Identification of key candidate genes and small molecule drugs in cervical cancer by bioinformatics strategy

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Purpose: Cervical cancer (CC) is one of the most common malignant tumors among women. The present study aimed at integrating two expression profile datasets to identify critical genes and potential drugs in CC.

Materials and methods: Expression profiles, GSE7803 and GSE9750, were integrated using bioinformatics methods, including differentially expressed genes analysis, Kyoto Encyclopedia of Genes and Genomes pathway analysis, and protein–protein interaction (PPI) network construction. Subsequently, survival analysis was performed among the key genes using Gene Expression Profiling Interactive Analysis websites. Connectivity Map (CMap) was used to query potential drugs for CC.

Results: A total of 145 upregulated genes and 135 downregulated genes in CC were identified. The functional changes of these differentially expressed genes related to CC were mainly associated with cell cycle, DNA replication, p53 signaling pathway, and oocyte meiosis. A PPI network was identified by STRING with 220 nodes and 2,111 edges. Thirteen key genes were identified as the intersecting genes of the enrichment pathways and the top 20 nodes in PPI network. Survival analysis revealed that high mRNA expression of *MCM2*, *PCNA*, and *RFC4* was significantly associated with longer overall survival, and the survival was significantly better in the low-expression *RRM2* group. Moreover, CMap predicted nine small molecules as possible adjuvant drugs to treat CC.

Conclusion: Our study found key dysregulated genes involved in CC and potential drugs to combat it, which might provide insights into CC pathogenesis and might shed light on potential CC treatments.

Keywords: cervical cancer, bioinformatics, cell cycle, biomarker, drug

Introduction

Cervical cancer (CC) is the second most common malignant tumor among women, responsible for ~527,600 new cases and >265,700 deaths annually.¹ Despite advances in screening detection and new treatment strategies, CC is one of the leading causes of cancer death among females in many developing countries.^{2,3} Although most patients can be cured if diagnosed at an early stage, poor prognosis is observed with secondary metastatic cancer and tumor relapse.

Although human papillomavirus (HPV) is a prerequisite for CC, only a small number of women infected by this virus develop cancer. Thus, other risk factors should be considered as cofactors contributing to the progression of CC.⁴ Dysregulated genes play important roles in CC development.⁵ Several studies have used gene expression profiling to identify key genes between CC samples and normal cervix.^{6–9} Hundreds

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of differentially expressed genes (DEGs) were detected. However, DEGs reported in different studies vary enormously with only some of them consistently detected. Therefore, the discovery of novel effective therapeutic targets against CC is urgently required.

A number of chemotherapeutic agents have shown activity against CC, including cisplatin,¹⁰ bevacizumab,¹¹ carboplatin,¹² paclitaxel,¹³ ifosfamide,¹⁴ and topotecan.¹⁵ Various combinations of these agents are recommended as therapies.¹⁶ A recent systematic literature review found that carboplatin–paclitaxel is equally effective and less toxic than cisplatin–paclitaxel as the first-line therapy for metastatic CC.¹⁷ However, patients overall survival (OS) times remains short, indicating an urgent need to discover some molecular drugs that are more efficient and selective. Based on bioinformatics approaches, several studies found small molecules as potential anticancer agents.^{18–20}

In this study, we selected the following microarray datasets GSE7803 and GSE9750 from the Gene Expression Omnibus (GEO) database to identify DEGs. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis using the identified DEGs was investigated. A protein–protein interaction (PPI) network was constructed to elucidate the significant relationships among DEGs and to identify key genes. Furthermore, the Kaplan–Meier estimator was used on the Gene Expression Profiling Interactive Analysis (GEPIA) website. Candidate small molecules were identified for their potential use in the treatment of CC.

Materials and methods

Data collection

Two CC microarray datasets were downloaded from the GEO website (<http://www.ncbi.nlm.nih.gov/geo/>). GSE7803 microarray data contained 21 CC tissues and 10 normal cervical epithelia tissues.⁶ GSE9750 included 33 tumors samples and 24 healthy cervical samples.⁷ Both the profile datasets were based on the Affymetrix GPL96 platform (Affymetrix Human Genome U133A Array). Because Connectivity Map (CMap) strictly required all probesets obtained from the Affymetrix Human Genome U133A Array,²¹ we predicted the drugs for the DEGs measured only in this platform with high accuracy. GSE63514 data included 28 cancer cases and 24 normal cases⁸ and were chosen to validate *RRM2* mRNA expression in our analysis.

Data preprocessing and DEGs screening

The raw data were standardized and transformed into expression values using the *affy* package of Bioconductor

(<http://www.bioconductor.org/>).²² DEGs between cancer and normal samples were selected by significance analysis using the empirical Bayes methods within *limma* package.²³ False discovery rate (FDR) <0.05 and $|\log_2(\text{fold change})| > 1$ were set as the cutoff criteria for the identification of DEGs. Common dysregulated probesets between GSE7803 and GSE9750 were selected for subsequent analyzes.

KEGG pathway analysis

Pathway enrichment analysis was performed using the *clusterProfiler* package and a pathway with an adjusted *P*-value <0.05 was considered significantly enriched.²⁴ DEGs that we identified could be involved in multiple pathways. Thus, some overlap was observed among the pathways. We identified the significant pathways that shared the same DEGs and used Cytoscape (version 3.5.1) to construct graphical representations of the interactive relationships among the pathways.²⁵

PPI network construction and analysis

The PPI pairs of the screened DEGs were analyzed using the online database STRING version 10.5 (<https://string-db.org/>).²⁶ The pairs with combined scores >0.4 were used for the PPI network construction, then the Cytoscape software was used to construct the network and analyze the interaction relationship of the candidate DEGs encoding proteins in CC.

Validation of key genes

Key genes were identified as the intersecting genes of the enrichment pathways and top 20 nodes in PPI network. To confirm the reliability of these genes from our detection, we analyzed their prognostic and expression in CC using GEPIA.²⁷ GEPIA is an interactive web application for gene expression analysis based on 9,736 tumors and 8,587 normal samples from the Cancer Genome Atlas (TCGA) and the Genotype-Tissue Expression databases.^{28,29} We evaluated the expression of key genes in CC tissues and normal tissues. Then the survival curve and boxplot were performed to visualize the relationships.

Identification of candidate small molecules

The CC gene signature was used to query CMap to find potential drugs for use in patients.²¹ CMap is an *in silico* method to predict potential drugs that could possibly reverse, or induce, the biological state encoded in particular gene expression signatures. The common differently expressed probesets in GSE7803 and GSE9750 between CC samples and healthy controls were divided into upregulated and

downregulated groups. Then, these probesets were used to query the CMap database. Finally, the enrichment score representing similarity was calculated, ranging from -1 to 1. A positive connectivity score indicates that a drug is able to induce the input signature in human cell lines. Conversely, a negative connectivity score indicates that a drug is able to reverse the input signature. Negative connectivity scores were investigated, which indicate potential therapeutic value. After rank ordering all instances, the connectivity score of various instances were filter by the number of instances ($N > 10$) and P -value (< 0.05).

Results

DEGs identification

The two mRNA expression profiles, including 54 patients with CC and 34 healthy individuals, were included in our study. Using a FDR < 0.05 and $|\log FC| > 1$ as cutoff criteria, we extracted 443 and 848 differentially expressed probesets from the expression profile datasets GSE7803 and GSE9750, respectively. In GSE7803, 212 unregulated probes and 231 downregulated probes were identified. A total of 376 unregulated probes and 472 downregulated

probes were identified in GSE9750. After being overlapped, the common 149 upregulated and 146 downregulated probesets corresponding to 145 upregulated and 135 downregulated genes were identified from the two profile datasets (Table S1).

CC significant pathways evaluation

A total of 16 pathways with adjusted P -value < 0.05 were found enriched including 10 upregulated and 6 downregulated pathways (Table 1). The most significant upregulated pathway was cell cycle; the other significant pathways included DNA replication, oocyte meiosis, p53 signaling pathway, microRNAs in cancer, and cellular senescence. The downregulated pathways included arachidonic acid metabolism, serotonergic synapse, gap junction, estrogen signaling pathway, signaling pathways regulating pluripotency of stem cells, and proteoglycans in cancer (Figure 1A). In order to consider the potentially biological complexities in which a gene may belong to multiple pathways and provide information of numeric changes, we constructed pathway-gene networks to extract the complex association (Figure 1B, C). Cell cycle pathway contained the most significant genes in the network.

Table 1 Pathway enrichment analysis of DEGs function in CC

ID	Description	Adjusted P -value	Count	Gene symbol
Upregulated				
hsa04110	Cell cycle	2.02E-19	21	<i>BUB1B, CCNB1, CCNB2, CCNE2, CDC7, CDK1, CDKN2A, CDKN2C, E2F3, MAD2L1, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, ORC6, PCNA, PTTG1, SMC1A, TTK</i>
hsa03030	DNA replication	3.59E-11	10	<i>FEN1, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, RFC4, RFC5</i>
hsa04114	Oocyte meiosis	7.63E-04	8	<i>AURKA, CCNB1, CCNB2, CCNE2, CDK1, MAD2L1, PTTG1, SMC1A</i>
hsa04115	p53 signaling pathway	1.16E-03	6	<i>CCNB1, CCNB2, CCNE2, CDK1, CDKN2A, RRM2</i>
hsa05206	MicroRNAs in cancer	1.07E-02	10	<i>CCNE2, CDKN2A, DDIT4, DNMT1, E2F3, EZH2, MIR106B, MIR25, PLAU, STMN1</i>
hsa04218	Cellular senescence	1.44E-02	7	<i>CCNB1, CCNB2, CCNE2, CDK1, CDKN2A, CXCL8, E2F3</i>
hsa03430	Mismatch repair	2.09E-02	3	<i>PCNA, RFC4, RFC5</i>
hsa04914	Progesterone-mediated oocyte maturation	3.43E-02	5	<i>AURKA, CCNB1, CCNB2, CDK1, MAD2L1</i>
hsa05166	HTLV-I infection	3.43E-02	8	<i>BUB1B, CCNB2, CDKN2A, CDKN2C, E2F3, MAD2L1, PCNA, PTTG1</i>
hsa03410	Base excision repair	4.22E-02	3	<i>FEN1, MBD4, PCNA</i>
Downregulated				
hsa00590	Arachidonic acid metabolism	2.61E-02	5	<i>ALOX12, ALOX12B, ALOX15B, GPX3, PTGDS</i>
hsa04726	Serotonergic synapse	2.79E-02	6	<i>ALOX12, ALOX12B, ALOX15B, CYP2C18, DUSP1, ITPR2</i>
hsa04540	Gap junction	3.37E-02	5	<i>GJA1, ITPR2, PDGFD, TUBA1A, TUBB2A</i>
hsa04915	Estrogen signaling pathway	3.37E-02	6	<i>CALML3, ESRI, FOS, ITPR2, KRT10, KRT13</i>
hsa04550	Signaling pathways regulating pluripotency of stem cells	3.37E-02	6	<i>FGFR2, FZD1, ID4, IGF1, ISL1, KLF4</i>
hsa05205	Proteoglycans in cancer	3.70E-02	7	<i>CCND1, DCN, ESRI, FZD1, IGF1, ITPR2, PDCD4</i>

Abbreviations: CC, cervical cancer; DEGs, differentially expressed genes; HTLV-I, human T-lymphotropic virus type I.

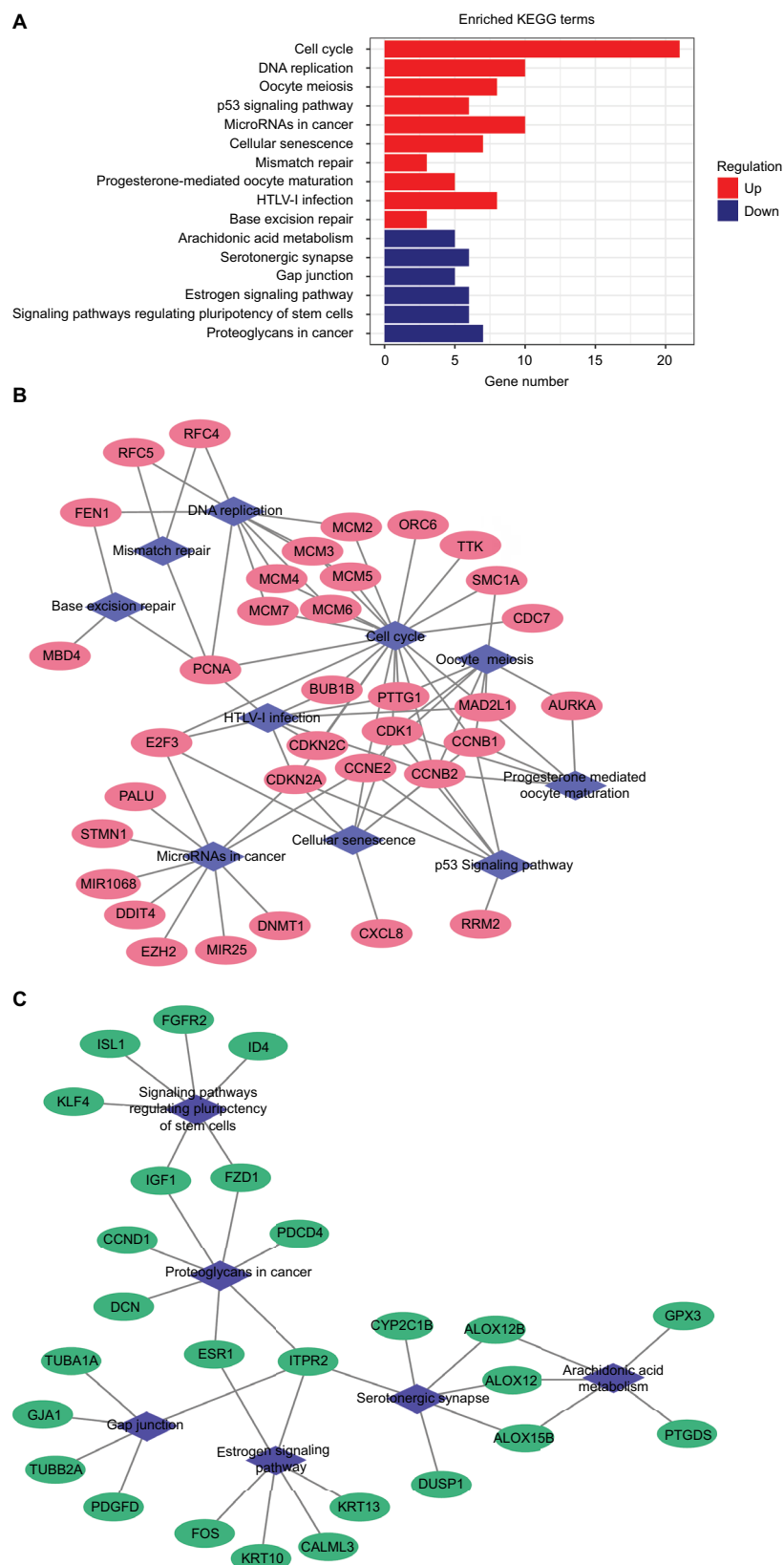


Figure I Significantly enriched pathway terms associated to DEGs in CC.

Notes: (A) KEGG pathways in CC DEGs enrichment analysis. (B) Upregulated pathway-gene network including 35 upregulated genes and 10 pathways. (C) Downregulated pathway-gene network including 26 downregulated genes and 6 pathways.

Abbreviations: CC, cervical cancer; DEGs, differentially expressed genes; KEGG, Kyoto Encyclopedia of Genes and Genomes; HTLV-I, human T-lymphotropic virus type I.

PPI network construction

STRING was used for mining proteins expressed by DEGs which can interact with others. At a combined score >0.4 , a total of 222 DEGs (118 upregulated and 104 downregulated genes) among the 280 commonly altered DEGs were filtered into the DEGs PPI network, containing 222 nodes and 2,111 edges (Figure 2A). NetworkAnalyzer app in Cytoscape was used to calculate the node degree.²⁵ The genes CDK1, PCNA, TOP2A, CCNB1, RFC4, MAD2L1, NDC80, CCNB2, AURKA, TYMS, MCM2, FEN1, RRM2, NCAPG, TTK, PRC1, MCM4, ZWINT, DTL, and MCM6 were the most significant 20 node degree genes and were selected as the hub nodes, since they might play important roles in CC progression (Figure 2B).

Key gene signatures identification in CC

Compared with KEGG enrichment genes, 13 of the top 20 nodes in the PPI network, including AURKA, CCNB1, CCNB2, CDK1, FEN1, MAD2L1, MCM2, MCM4, MCM6, PCNA, RFC4, RRM2, and TTK were found as key genes. Further survival analyses on these key genes were employed to evaluate their effects on CC patients' survival using GEPIA. Expression levels of *MCM2*, *PCNA*, *RFC4*, and *RRM2* were significantly related to the OS of patients with cervical squamous cancer ($P<0.05$). High expression of *MCM2*, *PCNA*, and *RFC4* could result in a high survival rate, and increased *RRM2* expression in CC was significantly associated with shorter patients' survival (Figure 3A–D). The expression of these four genes was significantly higher in CC tissues compared to that of normal tissues ($P<0.01$; Figure 3E–H). Together, the high level of these four genes might represent the important prognostic factor to predict the survival of CC. GSE63514 was used to validate *RRM2* mRNA expression. The results showed that *RRM2* expression was significantly higher in CC compared to that of normal tissues ($P<0.01$; Figure 4A). The PPI network based on *RRM2* found that *PCNA* and *RFC4* have a close relationship with *RRM2*, and most of the proteins in the network were related to cell cycle (Figure 4B).

Related small molecule drugs screening

In order to screen out small molecule drugs, consistent differently expressed probesets between CC samples and healthy controls were analyzed with CMap. The related small molecules with highly significant correlations are listed in Table 2. Among these molecules, trichostatin A (TSA), tanespimycin, vorinostat, trifluoperazine, prochlorperazine,

and thioridazine showed higher negative correlation and the potential to treat CC.

Discussion

Driver genes play vital roles during stages of cancer progression. Although many studies on CC development are available, more efforts are needed to identify driver genes and candidate drugs that may shed light on CC treatments. This study integrated two gene profile datasets based on Affymetrix Human Genome U133A Array, utilized bioinformatics methods to analyze these datasets, and identified 280 commonly changed DEGs (145 upregulated and 135 downregulated). Pathway enrichment analysis indicated that cell cycle, DNA replication, oocyte meiosis, p53 signaling pathway, cellular senescence, and DNA repair-relevant biological pathways were overrepresented among the upregulated genes. The PPI network was constructed including 222 nodes/DEGs and 2,111 edges. Thirteen key genes were identified and chosen for survival analysis. *MCM2*, *PCNA*, *RFC4*, and *RRM2* were clearly related to the prognosis of patients. In addition, small molecules that can provide new insights in CC therapeutic studies were identified.

Many researchers have found that four key genes were involved in cell cycle, participating in tumorigenesis and tumor proliferation. *MCM2* has been studied in a wide range of human malignancies and is associated with tumor histopathological grade in several malignancies, including colon, oral cavity, ovarian, urothelial, and non-small cell lung carcinoma.^{30–34} In cervical carcinoma and precancerous lesions, *MCM2* is overexpressed and positively correlated with high risk types of HPV.³⁵ Amaro Filho et al also reported an increasing expression of *MCM2* in invasive CC compared to control, but they suggested that *MCM2* is not a good biomarker when comparing the different clinical stages of CC.³⁶ *PCNA* acts as a central coordinator of DNA transactions by providing a multivalent interaction surface for factors involved in DNA replication and cell cycle regulation. Owing to its function, *PCNA* has been widely used as a tumor marker for cancer cell progression and patient prognosis.^{37–39} A recent systematic literature review found that the expression of *PCNA* is significantly associated with poor 5-year survival, International Federation of Gynecology and Obstetrics stage, or WHO grade, suggesting its use as a valuable prognostic and diagnostic biomarker in CC and gliomas.⁴⁰ *RFC4* is involved in cancer. Knockdown of *RFC4* in HepG2 cells induces apoptosis.⁴¹ Similar results were discovered in breast carcinoma.⁴² In colorectal cancer,

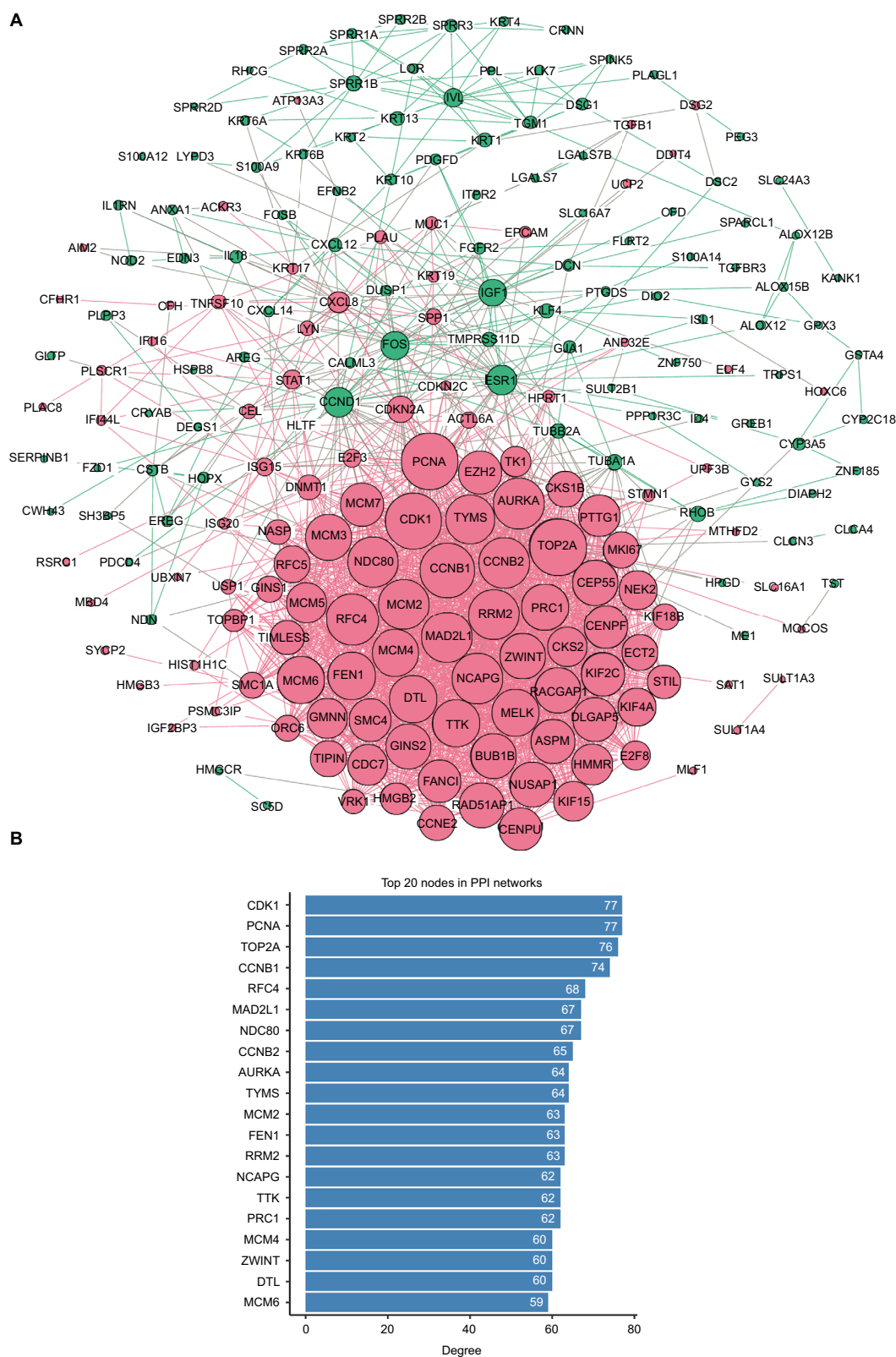


Figure 2 PPI network analysis.

Notes: (A) Using the STRING online database, a total of 222 DEGs (118 upregulated in red standing for upregulation and 104 downregulated genes in green standing for downregulation) were filtered into the DEGs PPI network. Bigger nodes represent genes with more links. (B) Degree of the top 20 nodes in the PPI network. All these nodes are upregulated genes.

Abbreviations: DEGS, differentially expressed genes; PPI, protein–protein interaction.

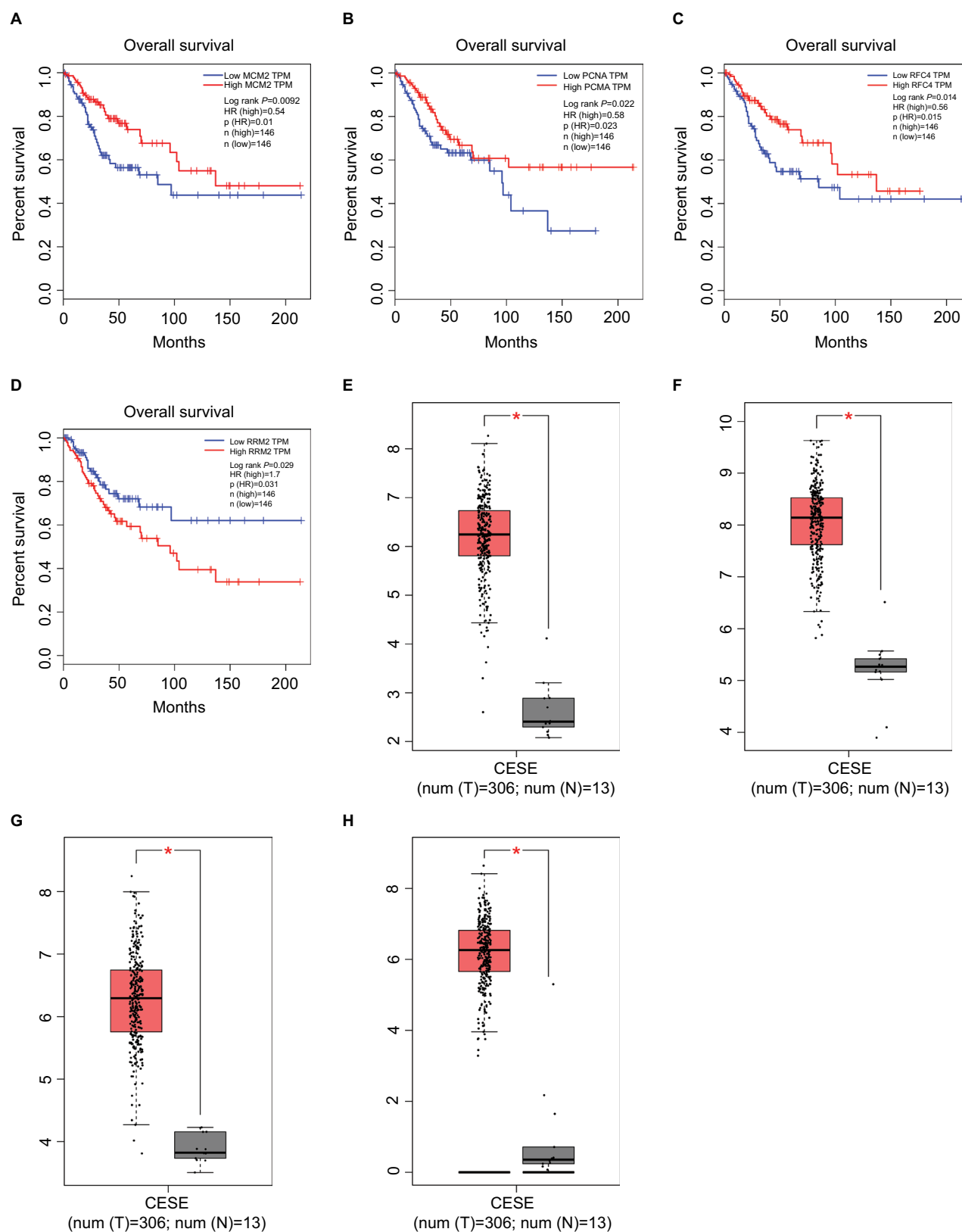


Figure 3 Survival curves and expression boxplots of key genes using GEPIA website.

Notes: (A–D) Expression level of *MCM2*, *PCNA*, *RFC4*, and *RRM2* was significantly related to the overall survival of patients with cervical squamous cancer ($P<0.05$). (E–H) *MCM2*, *PCNA*, *RFC4*, and *RRM2* were significantly upregulated in cervical squamous cancer compared with normal tissues ($P<0.01$).

Abbreviations: CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; GEPIA, Gene Expression Profiling Interactive Analysis; TPM, transcripts per million.

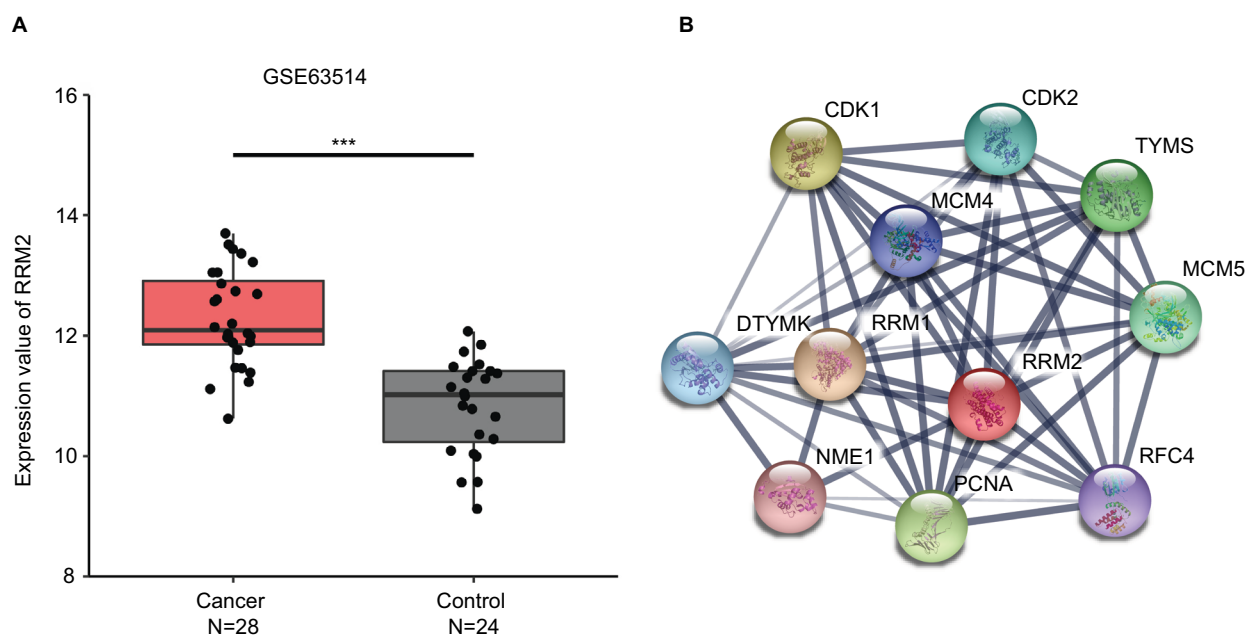


Figure 4 RRM2 validation using GSE63514 and PPI network.

Notes: (A) GSE63514 showed higher expression of RRM2 in CC tissues compared with normal cervical tissues ($P < 0.01$). (B) RRM2 PPI network based on STRING.

Abbreviations: CC, cervical cancer; PPI, protein-protein interaction.

Table 2 Results of CMap analysis

Rank	CMap name	Mean	N	Enrichment	P-value
1	Trichostatin A	-0.480	182	-0.419	0
2	Tanespimycin	-0.372	62	-0.301	0.00002
3	Vorinostat	-0.551	12	-0.571	0.00034
4	Trifluoperazine	-0.511	16	-0.488	0.00054
5	Prochlorperazine	-0.461	16	-0.436	0.00277
6	Thioridazine	-0.407	20	-0.375	0.00526
7	Alpha-estradiol	-0.367	16	-0.365	0.02104
8	Fluphenazine	-0.403	18	-0.326	0.03608
9	Chlorpromazine	-0.366	19	-0.310	0.04109

Abbreviation: CMap, Connectivity Map.

overexpression of RFC4 is associated with tumor progression and poor survival outcome.⁴³ Additionally, with gene network reconstruction, RFC4 is regarded as one of the main drivers in cell cycle network in CC.⁴⁴ Together with our results, *MCM2*, *PCNA*, and *RFC4* were significantly upregulated in CC compared with normal samples, and in CC patients, the survival rate was positively correlated with the high expression of these genes.

RRM2 is markedly upregulated in many patients' cancer types and indeed acts as an oncogene.⁴⁵ RRM2 knockdown reduces cell proliferation and invasive ability in gastric cancer and pancreatic adenocarcinoma.^{46,47} Wang et al reported that RRM2 expression inhibition significantly increases apoptosis, promotes cell cycle arrest at the G1 phase, and inhibits tumor formation in CC nude mice transplant models.⁴⁸ Several studies showed that RRM2 is an independent

prognostic factor and may predict poor survival in ovarian cancer, bladder cancer, breast cancer, and CC.^{49–52} In this study, according to the PPI network, RRM2 closely interacts with PCNA and RFC4 involved in CC progression. Therefore, a further exploration of cell cycle and related genes was of enormous significance.

Consistent with our results, recent studies have also reported the identification of DEGs in CC. van Dam et al used three publicly available Affymetrix gene expression datasets (GSE5787, GSE7803, and GSE9750) and identified five cancer hallmarks enriched pathways in CC, showing that cell cycle deregulation is the major component of CC biology. They also identified seven probesets that were highly expressed in both CIN3 samples compared to normal samples and in cancer samples compared to CIN3 samples. From these probesets, six genes (*AURKA*, *DTL*, *HMGB3*, *KIF2C*, *NEK2*, and *RFC4*) were overexpressed in CC cell lines compared to cancer samples, suggesting their potential role as biomarkers in CC early diagnosis.⁵³ One of these genes, such as *RFC4*, was also identified in our study. Furthermore, our conclusion generated from both expression and survival analysis suggested that *RFC4* might have a prognostic value. Another report from Li et al was based on TCGA data.⁵⁴ They found that *MCM2*, *MCM4*, *MCM5*, *PCNA*, and *RNASEH2A* participating in DNA replication pathway might be prognostic biomarkers in CC patients. *MCM2* and *PCNA* were also found in our results.

Several small molecules with potential therapeutic efficacy against CC were identified. The most significant

small molecules in our result have been reported to display anticancer activity. TSA, as a histone deacetylase (HDAC) inhibitor, shows a potential therapeutic effect in various types of cancer cells, when combined with radiotherapy or chemotherapy.^{55,56} In particular, TSA and its hydroxamate analogs can effectively and selectively induce tumor growth arrest at very low concentrations.⁵⁷ Additionally, TSA can inhibit HeLa cells growth via Bcl-2-mediated and caspase-dependent apoptosis.⁵⁸ Vorinostat is a hydroxamate-based pan-HDAC inhibitor also known as suberoylanilide hydroxamic acid used for the treatment of cutaneous T-cell lymphoma.⁵⁹ In HeLa cell, both mRNA and protein levels of HPV18 E6 and E7 were reduced after vorinostat treatment.⁶⁰ Furthermore, vorinostat promotes SiHa apoptosis through upregulation of p21 and Bax mRNA and protein, leading to cell cycle arrest in G0/G1 phase.⁶¹ Thioridazine, a derivative of phenothiazine, displays anticancer abilities in a variety of cancer types and can reverse multidrug resistance.^{62–64} Kang et al found that thioridazine can inhibit the PI3K/Akt/mTOR/p70S6K signaling pathway and exert cytotoxic effect on CC cells by inducing cell cycle arrest and apoptosis.⁶⁵ Thus, we might suppose that these identified drugs could play certain roles to combat CC.

Conclusion

Using bioinformatics analysis, 280 DEGs were identified, which were significantly enriched in several pathways, mainly associated with cell cycle, DNA replication, oocyte meiosis, p53 signaling pathway, and cellular senescence. We also identified key genes including *MCM2*, *PCNA*, *RFC4*, and *RRM2* that might play important roles in CC and that might represent novel biomarkers in CC diagnosis, prognosis, and therapy. Additionally, a group of small molecules was identified that might be exploited as adjuvant drugs for improved therapeutics for CC. However, further investigations are required to validate the predicted drugs.

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Disclosure

The authors report no conflicts of interest in this work.

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Supplementary material

Table S1 Common dysregulated probes identified in GSE7803 and GSE9750

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
Upregulated						
1	200783_s_at	STMN1	1.0912	1.0985	4.11E-05	1.25E-04
2	201202_at	PCNA	1.8714	1.3752	4.41E-09	2.87E-05
3	201291_s_at	TOP2A	2.4680	2.4862	1.05E-08	5.16E-06
4	201292_at	TOP2A	1.2403	2.0680	1.71E-06	2.30E-04
5	201506_at	TGFB1	1.1157	1.1297	2.21E-02	1.60E-02
6	201555_at	MCM3	1.0145	1.2759	3.14E-07	5.41E-07
7	201589_at	SMC1A	1.3907	1.0445	5.43E-06	8.52E-05
8	201650_at	KRT19	1.5763	2.3797	2.89E-02	8.95E-05
9	201663_s_at	SMC4	1.4923	1.5673	1.60E-06	4.31E-05
10	201664_at	SMC4	1.7038	1.8408	9.71E-06	7.08E-06
11	201697_s_at	DNMT1	1.0219	1.2128	1.05E-08	4.10E-09
12	201761_at	MTHFD2	1.6111	1.3783	4.73E-05	4.37E-05
13	201839_s_at	EPCAM	1.6182	2.2101	3.36E-04	1.82E-04
14	201890_at	RRM2	1.7698	2.3342	1.05E-05	1.44E-06
15	201897_s_at	CKS1B	1.3398	1.2246	1.04E-06	4.26E-05
16	201930_at	MCM6	1.5487	1.4628	6.91E-09	1.25E-08
17	201970_s_at	NASP	1.3464	1.1522	1.38E-08	9.44E-09
18	202107_s_at	MCM2	1.7296	2.2864	1.91E-08	7.29E-10
19	202219_at	SLC6A8	1.4325	1.8698	5.38E-03	2.75E-05
20	202234_s_at	SLC16A1	1.3561	1.2683	4.70E-03	7.50E-04
21	202338_at	TK1	1.1038	1.2846	2.40E-06	2.91E-06
22	202412_s_at	USP1	1.0775	1.2056	3.24E-04	3.54E-04
23	202430_s_at	PLSCR1	1.2889	1.1148	1.29E-04	7.10E-05
24	202446_s_at	PLSCR1	1.6150	1.5934	1.16E-06	1.41E-06
25	202503_s_at	PCLAF	2.0118	1.9842	2.33E-10	1.18E-04
26	202589_at	TYMS	1.5263	2.2375	1.95E-04	8.52E-08
27	202619_s_at	PLOD2	1.8339	2.0812	1.44E-06	1.41E-07
28	202620_s_at	PLOD2	2.8767	2.2084	3.54E-09	5.09E-07
29	202625_at	LYN	1.1767	1.4027	1.20E-03	2.09E-03
30	202626_s_at	LYN	1.5737	1.7521	1.07E-03	8.51E-05
31	202633_at	TOPBP1	1.6677	1.4670	3.67E-07	7.76E-07
32	202666_s_at	ACTL6A	1.5525	1.1292	9.46E-07	1.46E-03
33	202688_at	TNFSF10	1.0878	1.1141	3.63E-02	3.00E-02
34	202705_at	CCNB2	1.0405	1.7114	7.17E-05	8.58E-06
35	202854_at	HPRT1	1.0911	1.2618	2.75E-04	7.59E-05
36	202859_x_at	CXCL8	1.5100	2.7989	1.66E-02	3.86E-04
37	202887_s_at	DDIT4	1.0791	2.1221	4.05E-02	3.21E-04
38	202983_at	HLTF	2.0242	1.2271	4.08E-07	2.36E-03
39	203046_s_at	TIMELESS	1.1641	1.4554	1.96E-08	1.55E-07
40	203209_at	RFC5	1.5612	1.2914	1.93E-07	7.95E-06
41	203213_at	CDK1	1.5427	1.9989	1.11E-05	9.35E-06
42	203358_s_at	EZH2	1.6144	1.6656	3.31E-07	3.91E-05
43	203362_s_at	MAD2L1	1.0749	1.2051	4.94E-03	1.40E-02
44	203554_x_at	PTTG1	1.2746	1.3424	1.32E-05	3.11E-03
45	203693_s_at	E2F3	1.2182	1.2321	1.16E-06	1.28E-04
46	203744_at	HMGB3	1.1938	1.6479	3.01E-04	1.41E-07
47	203755_at	BUB1B	1.0860	1.8703	3.34E-07	1.96E-06
48	203764_at	DLGAP5	1.4536	2.2334	3.73E-05	9.69E-05

(Continued)

Table S1 (Continued)

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
49	203819_s_at	IGF2BP3	1.2319	1.4909	2.75E-02	2.22E-02
50	203856_at	VRK1	1.1485	1.1641	4.00E-06	2.15E-04
51	204023_at	RFC4	1.5116	2.1996	7.47E-08	2.54E-07
52	204026_s_at	ZWINT	1.5906	1.8649	2.05E-04	2.07E-05
53	204092_s_at	AURKA	1.1672	1.0470	1.39E-07	2.36E-05
54	204146_at	RAD51API	1.6216	1.6478	4.26E-07	8.74E-05
55	204159_at	CDKN2C	1.5231	1.2248	2.07E-03	3.73E-03
56	204162_at	NDC80	1.5684	1.3280	9.05E-05	1.03E-03
57	204170_s_at	CKS2	1.4786	1.5687	6.24E-05	5.32E-03
58	204416_x_at	APOC1	1.0620	1.3204	8.58E-03	9.07E-04
59	204439_at	IFI44L	1.5993	1.4595	4.00E-02	5.25E-02
60	204510_at	CDC7	1.3374	1.6750	1.88E-06	2.38E-06
61	204580_at	MMP12	1.6409	2.9620	2.22E-03	2.97E-05
62	204641_at	NEK2	1.3957	2.1694	6.79E-08	2.33E-07
63	204698_at	ISG20	1.0250	1.3923	6.87E-04	1.78E-05
64	204767_s_at	FEN1	1.4080	1.7083	1.31E-09	3.37E-07
65	204784_s_at	MLF1	1.6420	1.6891	6.24E-05	3.01E-04
66	204822_at	TTK	1.4460	1.4235	7.52E-08	2.45E-03
67	204825_at	MELK	1.8745	1.9957	2.90E-07	3.60E-07
68	205034_at	CCNE2	1.3408	1.7091	4.18E-04	5.08E-04
69	205157_s_at	KRT17	1.5725	3.3509	2.32E-02	1.54E-05
70	205339_at	STIL	1.0641	1.5078	1.16E-06	9.67E-08
71	205449_at	SAC3D1	1.3483	1.1408	4.86E-05	2.80E-04
72	205479_s_at	PLAU	1.2262	1.4554	1.65E-03	4.38E-04
73	205483_s_at	ISG15	1.3717	2.0505	1.65E-02	5.73E-04
74	205569_at	LAMP3	1.7550	1.2873	4.09E-04	2.57E-02
75	205691_at	SYNGR3	1.2198	1.4950	5.72E-04	3.29E-04
76	205910_s_at	CEL	1.8737	1.2510	1.62E-02	3.08E-02
77	206102_at	GINS1	1.6544	1.9896	6.95E-05	4.57E-06
78	206332_s_at	IFI16	1.5947	1.2876	8.99E-07	2.56E-04
79	206513_at	AIM2	2.0306	2.3769	1.22E-03	2.74E-03
80	206546_at	SYCP2	1.3491	2.3512	2.17E-03	5.99E-05
81	206632_s_at	APOBEC3A, APOBEC3B	2.9688	1.9572	1.68E-08	2.46E-04
82	206858_s_at	HOXC6	2.1365	1.4749	1.66E-05	1.02E-03
83	207039_at	CDKN2A	4.6085	4.0377	3.50E-14	1.62E-14
84	207165_at	HMMR	1.4593	1.0523	2.62E-06	1.30E-02
85	207332_s_at	TFRC	1.2833	1.3954	4.66E-04	5.87E-03
86	207828_s_at	CENPF	1.4100	1.9877	1.36E-07	9.05E-08
87	208079_s_at	AURKA	2.2857	2.0803	1.85E-09	5.77E-08
88	208691_at	TFRC	1.5192	1.4901	6.53E-06	5.22E-04
89	208795_s_at	MCM7, MIR25, MIR93, MIR106B	1.1151	1.3206	1.55E-07	2.44E-05
90	208808_s_at	HMGB2	1.5215	1.1577	8.56E-07	7.41E-04
91	208965_s_at	IFI16	1.4542	1.3939	2.56E-05	6.32E-04
92	208966_x_at	IFI16	1.7717	1.3388	4.13E-07	6.92E-05
93	208998_at	UCP2	1.9521	1.1262	2.31E-05	2.83E-03
94	209398_at	HIST1H1C	1.1786	1.2497	5.37E-03	7.31E-03
95	209408_at	KIF2C	1.4768	1.5638	1.85E-09	4.49E-09
96	209579_s_at	MBD4	1.2877	1.1884	6.26E-07	6.34E-05
97	209773_s_at	RRM2	1.2805	1.9504	2.40E-03	6.29E-05
98	209875_s_at	SPPI	2.5457	3.4037	3.80E-04	3.18E-06
99	209900_s_at	SLC16A1	1.5149	1.2504	1.45E-03	1.73E-03
100	209969_s_at	STAT1	1.8886	2.1349	6.82E-04	4.07E-04

(Continued)

Table S1 (Continued)

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
101	210580_x_at	SLX1A-SULT1A3, SLX1B-SULT1A4, SULT1A3, SULT1A4	1.0598	1.0491	1.80E-03	1.19E-03
102	212022_s_at	MKI67	1.4831	1.5781	8.11E-07	1.81E-06
103	212236_x_at	KRT17	1.3508	2.7588	3.84E-02	7.95E-06
104	212255_s_at	ATP2C1	1.0824	1.0588	1.60E-04	8.54E-05
105	212297_at	ATP13A3	1.4423	1.1315	1.69E-06	6.46E-05
106	212621_at	NEMPI	1.4685	1.2100	1.63E-07	2.29E-07
107	212840_at	UBXN7	1.0252	1.0213	1.25E-04	1.36E-03
108	212977_at	ACKR3	2.0327	1.2298	4.91E-03	5.31E-02
109	213007_at	FANCI	1.3983	1.6034	2.79E-07	2.80E-07
110	213008_at	FANCI	1.0861	1.6205	4.34E-05	4.91E-08
111	213164_at	SLC5A3	1.0329	1.0596	2.97E-05	4.04E-04
112	213457_at	MFHAS1	1.0606	1.0186	3.06E-02	2.25E-03
113	213693_s_at	MUC1	1.2200	1.9901	3.72E-02	4.37E-04
114	213951_s_at	PSMC3IP	1.2274	1.2423	1.92E-07	2.52E-07
115	213988_s_at	SAT1	1.1293	1.0600	2.52E-03	7.87E-04
116	214329_x_at	TNFSF10	2.3354	1.2571	6.72E-06	1.12E-02
117	214710_s_at	CCNB1	1.2879	1.7956	3.73E-05	1.97E-04
118	215388_s_at	CFH, CFHRI	1.4348	1.0577	1.61E-02	4.50E-02
119	216237_s_at	MCM5	1.5683	2.0746	1.77E-08	8.15E-11
120	217885_at	IPO9	1.1126	1.0339	1.76E-07	1.89E-05
121	217901_at	DSG2	1.3065	2.5311	6.24E-05	3.60E-07
122	218009_s_at	PRC1	1.6401	2.1259	5.88E-08	1.78E-06
123	218039_at	NUSAP1	2.1401	2.3735	7.34E-09	5.69E-06
124	218350_s_at	GMNN	1.7878	1.8225	3.13E-07	2.66E-06
125	218355_at	KIF4A	1.0153	1.7434	2.38E-06	2.89E-07
126	218542_at	CEP55	1.3865	2.4903	2.46E-06	2.29E-07
127	218585_s_at	DTL	1.3800	2.8428	2.32E-06	4.81E-09
128	218662_s_at	NCAPG	1.6736	1.5539	4.30E-06	1.30E-04
129	218757_s_at	UPF3B	1.3448	1.0318	6.72E-05	2.68E-05
130	218883_s_at	CENPU	1.2494	1.5454	7.55E-04	3.91E-03
131	219014_at	PLAC8	1.2330	1.4057	2.84E-02	3.55E-02
132	219105_x_at	ORC6	1.0780	1.0908	2.10E-04	5.03E-07
133	219258_at	TIPIN	1.1365	1.4832	3.91E-07	1.27E-06
134	219306_at	KIF15	1.0990	1.0348	1.84E-04	1.03E-03
135	219507_at	RSRC1	1.3864	1.2573	3.27E-05	3.86E-04
136	219787_s_at	ECT2	2.8139	2.5551	1.00E-08	1.37E-06
137	219918_s_at	ASPM	1.2168	1.9490	4.36E-05	2.25E-04
138	219959_at	MOCOS	1.0344	1.9971	3.59E-03	1.67E-05
139	219978_s_at	NUSAP1	1.1780	1.6455	8.94E-04	6.82E-05
140	219990_at	E2F8	1.4188	1.1301	1.17E-04	1.10E-03
141	220239_at	KLHL7	1.0503	1.0053	3.05E-03	1.40E-03
142	221046_s_at	GTPBP8	1.0722	1.0602	1.44E-06	4.04E-04
143	221521_s_at	GINS2	1.4631	1.8407	8.85E-06	3.27E-06
144	222036_s_at	MCM4	1.0134	1.8445	1.71E-06	1.67E-06
145	222039_at	KIF18B	1.5126	1.0619	7.17E-09	2.91E-06
146	222077_s_at	RACGAP1	1.5482	1.6939	2.69E-06	5.07E-05
147	222380_s_at	PDCD6	1.0922	1.0579	3.96E-04	1.18E-02
148	31845_at	ELF4	1.2212	1.0448	2.96E-05	1.00E-05
149	33304_at	ISG20	1.1281	1.1279	1.62E-04	7.59E-05
Downregulated						
1	200795_at	SPARCL1	-2.6933	-2.5139	3.39E-04	2.05E-04
2	201012_at	ANXA1	-1.6637	-1.2447	1.15E-03	1.28E-03

(Continued)

Table S1 (Continued)

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
3	201041_s_at	DUSP1	-1.7177	-1.2448	7.16E-03	3.26E-02
4	201201_at	CSTB	-1.6745	-1.0817	6.75E-04	2.05E-04
5	201312_s_at	SH3BGRL	-1.0735	-2.0334	1.43E-02	3.28E-04
6	201324_at	EMPI	-2.5006	-2.0144	1.69E-05	7.39E-05
7	201325_s_at	EMPI	-2.8729	-2.3264	2.29E-08	3.96E-06
8	201348_at	GPX3	-1.6408	-2.9297	1.32E-05	9.66E-08
9	201667_at	GJA1	-2.1421	-2.0359	3.83E-03	6.21E-03
10	201735_s_at	CLCN3	-1.1179	-1.0850	1.09E-03	1.89E-03
11	201811_x_at	SH3BP5	-1.2423	-1.3642	3.25E-03	5.04E-03
12	201893_x_at	DCN	-1.2951	-2.2495	1.17E-03	7.34E-04
13	202539_s_at	HMGCR	-1.0673	-1.3111	2.12E-03	1.05E-02
14	202575_at	CRABP2	-1.1350	-1.9855	2.03E-07	1.63E-03
15	202660_at	ITPR2	-1.2894	-1.0723	6.71E-07	2.03E-04
16	202668_at	EFNB2	-1.0648	-1.0430	2.83E-03	1.00E-02
17	202768_at	FOSB	-1.6730	-2.2309	6.70E-03	5.21E-03
18	202967_at	GSTA4	-1.4779	-1.8389	4.26E-07	2.57E-04
19	203407_at	PPL	-1.5681	-1.8813	3.47E-05	3.27E-06
20	203535_at	S100A9	-1.9766	-1.2926	8.14E-03	1.86E-02
21	203585_at	ZNF185	-1.3599	-1.3991	1.52E-03	4.20E-05
22	203638_s_at	FGFR2	-1.3240	-1.5564	3.23E-04	7.27E-04
23	203700_s_at	DIO2	-1.3828	-1.1342	1.94E-03	4.10E-02
24	203913_s_at	HPGD	-1.7678	-2.7646	5.41E-05	3.98E-05
25	203914_x_at	HPGD	-2.4427	-2.7244	1.11E-05	2.65E-05
26	203961_at	NEBL	-1.4367	-1.5881	2.34E-03	5.38E-03
27	204141_at	TUBB2A	-1.7240	-1.5928	1.18E-03	1.89E-04
28	204256_at	ELOVL6	-1.3219	-1.1355	4.57E-03	4.75E-02
29	204284_at	PPP1R3C	-2.6784	-3.7692	4.26E-07	2.33E-09
30	204359_at	FLRT2	-1.1097	-2.2141	5.71E-03	4.36E-05
31	204451_at	FZD1	-1.1135	-1.0997	1.15E-05	1.01E-04
32	204731_at	TGFBR3	-1.3493	-1.8325	7.17E-03	4.04E-04
33	204750_s_at	DSC2	-2.0225	-1.1059	2.83E-04	4.70E-02
34	204751_x_at	DSC2	-1.9548	-2.2472	2.98E-04	1.15E-04
35	204777_s_at	MAL	-4.8179	-5.7789	9.50E-07	1.62E-14
36	204952_at	LYPD3	-1.5886	-1.7448	1.08E-04	4.43E-04
37	205064_at	SPRR1B	-2.2769	-2.7744	1.39E-03	1.20E-02
38	205185_at	SPINK5	-3.8683	-3.6665	3.46E-07	3.15E-05
39	205225_at	ESR1	-3.0458	-2.7160	9.37E-06	1.54E-05
40	205239_at	AREG	-1.8099	-1.5361	3.96E-02	1.14E-03
41	205363_at	BBOX1	-1.8640	-2.8822	2.54E-09	1.27E-05
42	205382_s_at	CFD	-2.1856	-2.5747	9.39E-07	1.20E-06
43	205470_s_at	KLK11	-1.9196	-2.3007	8.84E-08	1.78E-03
44	205726_at	DIAPH2	-1.0814	-1.4450	1.17E-03	1.34E-04
45	205759_s_at	SULT2B1	-1.2047	-1.2198	1.04E-06	5.73E-03
46	205765_at	CYP3A5	-1.8262	-1.1731	3.95E-06	5.05E-03
47	205767_at	EREG	-1.6854	-2.1525	1.38E-04	8.11E-05
48	205778_at	KLK7	-1.3998	-1.7611	4.35E-03	1.13E-02
49	205862_at	GREB1	-1.5579	-1.8147	1.16E-03	1.94E-06
50	205863_at	S100A12	-1.2720	-2.0771	4.51E-03	6.18E-04
51	205900_at	KRT1	-4.8450	-5.1604	9.91E-10	1.22E-06
52	206008_at	TGM1	-1.3988	-1.4672	3.53E-03	2.12E-02
53	206104_at	ISL1	-1.8146	-1.8069	4.46E-05	4.23E-06
54	206295_at	IL18	-1.8318	-1.1817	9.99E-08	1.78E-02

(Continued)

Table S1 (Continued)

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
55	206400_at	LGALS7, LGALS7B	-1.2508	-1.7496	1.50E-02	2.32E-02
56	206605_at	ENDOU	-2.0623	-3.5113	1.38E-10	3.61E-09
57	206642_at	DSGI	-3.6072	-4.3758	2.39E-09	6.70E-07
58	206714_at	ALOX15B	-1.2685	-1.0664	8.35E-04	2.03E-02
59	206884_s_at	SCEL	-2.4970	-3.2369	4.84E-05	3.50E-06
60	207002_s_at	PLAGL1	-1.1346	-1.2887	9.02E-03	5.44E-04
61	207023_x_at	KRT10	-1.6054	-1.6701	5.50E-03	1.32E-03
62	207057_at	SLC16A7	-1.5167	-1.0148	2.07E-06	2.86E-02
63	207206_s_at	ALOX12	-2.4692	-2.9129	2.60E-07	5.89E-06
64	207381_at	ALOX12B	-1.8250	-1.5189	8.81E-07	1.92E-02
65	207463_x_at	PRSS3	-1.6595	-2.2675	1.69E-05	7.14E-04
66	207480_s_at	MEIS2	-1.1053	-1.4587	8.12E-03	3.86E-03
67	207602_at	TMPRSS11D	-1.7796	-2.2185	1.94E-04	1.24E-03
68	207720_at	LOR	-1.5659	-1.7321	9.03E-03	5.54E-03
69	207761_s_at	METTL7A	-1.4377	-1.7274	1.64E-02	1.54E-03
70	207802_at	CRISP3	-3.5353	-4.9186	8.56E-07	2.03E-08
71	207908_at	KRT2	-1.0700	-1.7438	7.77E-06	2.44E-04
72	207935_s_at	KRT13	-3.3723	-3.4606	6.80E-04	5.75E-03
73	208126_s_at	CYP2C18	-1.0287	-1.2034	3.17E-04	2.53E-02
74	208228_s_at	FGFR2	-1.1180	-1.5103	5.59E-03	2.23E-03
75	208399_s_at	EDN3	-1.7159	-2.7146	2.90E-07	1.83E-07
76	208539_x_at	SPRR2A, SPRR2B, SPRR2D	-1.0258	-3.4094	4.88E-03	2.74E-04
77	208650_s_at	CD24	-1.6380	-1.0461	5.52E-03	9.70E-03
78	208712_at	CCND1	-1.7584	-1.3400	1.85E-09	1.70E-04
79	209118_s_at	TUBA1A	-1.1814	-1.6618	3.70E-03	8.97E-04
80	209126_x_at	KRT6A, KRT6B	-1.0109	-1.7619	7.83E-03	3.16E-03
81	209189_at	FOS	-1.2550	-1.7443	6.40E-03	1.23E-02
82	209242_at	PEG3	-1.1185	-1.7051	1.60E-04	4.77E-05
83	209250_at	DEGS1	-1.6475	-1.0716	1.68E-04	4.35E-03
84	209283_at	CRYAB	-1.4519	-2.9331	4.29E-07	1.48E-09
85	209291_at	ID4	-2.2617	-1.7203	2.32E-06	1.04E-03
86	209318_x_at	PLAGL1	-1.0631	-1.5734	2.80E-02	1.87E-03
87	209335_at	DCN	-1.6677	-2.5536	2.57E-03	3.04E-04
88	209540_at	IGF1	-1.1470	-2.0332	1.72E-02	5.42E-03
89	209541_at	IGF1	-1.4871	-2.5855	1.91E-03	2.83E-03
90	209550_at	NDN	-1.1674	-1.7010	4.80E-05	3.81E-04
91	209569_x_at	NSG1	-1.3910	-1.9295	8.88E-08	1.28E-04
92	209570_s_at	NSG1	-1.6985	-1.3952	1.95E-04	2.86E-05
93	209605_at	TST	-1.5512	-1.0193	1.42E-07	1.02E-02
94	209687_at	CXCL12	-1.6878	-3.5983	1.05E-03	1.57E-05
95	210020_x_at	CALML3	-1.2936	-1.5506	2.22E-03	2.33E-02
96	211423_s_at	SC5D	-1.0341	-1.1407	2.63E-04	2.14E-02
97	211548_s_at	HPGD	-2.2811	-2.9565	9.06E-06	1.77E-05
98	211549_s_at	HPGD	-1.5563	-1.6731	1.97E-05	2.01E-05
99	211597_s_at	HOPX	-3.4727	-3.8543	1.85E-09	6.16E-10
100	211748_x_at	PTGDS	-1.1759	-2.8281	6.75E-04	3.00E-05
101	211813_x_at	DCN	-1.0371	-2.4546	5.80E-03	8.88E-05
102	211896_s_at	DCN	-1.7222	-2.8559	4.39E-05	6.65E-04
103	212099_at	RHOB	-1.2852	-1.4439	1.59E-02	9.09E-03
104	212187_x_at	PTGDS	-1.0762	-2.8519	1.63E-03	2.66E-05
105	212230_at	PLPP3	-1.2267	-1.8056	4.59E-03	2.70E-03
106	212268_at	SERPINB1	-2.0739	-1.0263	1.49E-06	1.91E-02

(Continued)

Table S1 (Continued)

Number	Probe name	Gene symbol	logFC		Adjusted P-value	
			GSE7803	GSE9750	GSE7803	GSE9750
107	212593_s_at	PDCD4, MIR4680	-1.0203	-1.0249	1.71E-06	6.53E-04
108	213005_s_at	KANK1	-1.3237	-1.4490	2.32E-06	1.01E-04
109	213240_s_at	KRT4	-4.3954	-3.6606	1.22E-05	4.69E-03
110	213287_s_at	KRT10	-1.4603	-1.5958	6.51E-03	7.27E-04
111	213421_x_at	PRSS3	-1.3548	-1.8542	1.74E-05	2.02E-03
112	213680_at	KRT6B	-1.9134	-1.6133	1.08E-02	4.60E-02
113	213796_at	SPRR1A	-2.5895	-3.5348	1.67E-02	2.67E-03
114	213895_at	EMPI	-1.5169	-1.8942	7.08E-07	1.20E-06
115	214091_s_at	GPX3	-1.6787	-3.0400	6.10E-06	7.67E-08
116	214247_s_at	DKK3	-1.7619	-1.4292	4.50E-04	1.56E-02
117	214549_x_at	SPRR1A	-2.7653	-3.2505	1.35E-04	6.67E-04
118	214599_at	IVL	-2.6075	-2.2661	3.08E-05	4.70E-05
119	214621_at	GYS2	-1.6288	-1.5121	1.62E-04	9.55E-06
120	214624_at	UPK1A	-3.4453	-2.3695	1.95E-11	4.10E-09
121	214696_at	MIR22, MIR22HG	-1.2503	-1.0092	9.91E-04	6.55E-04
122	217845_x_at	HIGD1A	-1.1969	-1.1395	4.79E-04	1.22E-03
123	218002_s_at	CXCL14	-2.3615	-2.3685	5.25E-03	2.29E-03
124	218312_s_at	ZSCAN18	-1.5418	-1.8495	2.07E-06	4.65E-06
125	218502_s_at	TRPS1	-1.0972	-1.8370	2.27E-04	1.42E-06
126	218677_at	SI00A14	-1.2332	-1.0900	4.46E-05	2.11E-03
127	218990_s_at	SPRR3	-3.8102	-4.0176	5.84E-05	5.09E-04
128	219090_at	SLC24A3	-1.4945	-1.8096	2.33E-05	3.51E-05
129	219267_at	GLTP	-1.9362	-1.2742	5.88E-07	2.51E-03
130	219304_s_at	PDGFD	-1.2399	-2.5374	1.71E-05	1.89E-09
131	219554_at	RHCG	-2.3009	-3.4518	1.07E-05	3.81E-05
132	219648_at	MREG	-1.1721	-1.0151	3.34E-06	2.70E-02
133	219836_at	ZBED2	-1.8152	-1.6920	4.01E-07	4.37E-04
134	219995_s_at	ZNF750	-1.3202	-1.4628	3.99E-03	6.24E-03
135	220026_at	CLCA4	-1.7727	-2.3287	2.21E-02	2.67E-03
136	220066_at	NOD2	-1.2609	-1.3621	1.70E-05	8.88E-05
137	220090_at	CRNN	-4.8078	-6.4682	1.02E-11	7.05E-15
138	220266_s_at	KLF4	-1.1657	-2.2531	4.46E-05	1.27E-04
139	220403_s_at	TP53AIP1	-1.2074	-1.2307	1.17E-03	1.28E-03
140	220431_at	TMPRSS11E	-1.1214	-2.9572	3.59E-04	5.14E-04
141	220620_at	CRCT1	-2.6450	-4.1521	1.60E-06	6.43E-05
142	220723_s_at	CWH43	-1.7748	-2.6534	4.41E-09	7.02E-07
143	221667_s_at	HSPB8	-1.6989	-1.8139	7.42E-06	5.09E-07
144	221841_s_at	KLF4	-2.1774	-2.2756	3.11E-05	2.90E-04
145	221896_s_at	HIGD1A	-1.1638	-1.1978	7.06E-04	9.97E-04
146	57588_at	SLC24A3	-1.1619	-1.5407	2.29E-05	1.32E-05

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