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ORIGINAL RESEARCH

Revealing IncRNA Biomarkers Related to Chronic Obstructive Pulmonary Disease Based on Bioinformatics

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Background: Chronic obstructive pulmonary disease (COPD) is a common chronic disease of the respiratory tract, with high prevalence, high disability, and poor prognosis. However, the molecular mechanism of COPD needs to be further revealed.

Methods: We obtained the gene expression profile and miRNA expression profile of COPD patients from Gene Expression Omnibus (GEO) database, and the differentially expressed genes (DEGs) and differentially expressed miRNAs (DEmis) in COPD were identified. Subsequently, the COPD-related ceRNA network was constructed based on the interaction between lncRNA, miRNA, and mRNA using the lncACTdb database. Finally, the Cytoscape software was used to analyze the network topology and COPD-related lncRNAs.

Results: Firstly, the 519 DEGs and 17 DEmis were identified from COPD GEO datasets. GO enrichment showed that leukocyte chemotaxis, cell chemotaxis, and myeloid leukocyte migration were upregulated, and muscle and membrane repolarization-related biological progress were downregulated in COPD. KEGG pathway enrichment shows that the p53 pathway was upregulated in COPD. Hallmark enrichment showed that chronic neutrophil inflammation was a sign of the pathogenesis of COPD. Next, a ceRNA network including 93 DEGs, 2 DEmi, 463 lncRNAs, and 1157 DEG-lncRNA, DEmi-lncRNA, and DEmi-DEG interactions were obtained. The hub-lncRNA (the network is ranked in the top 10) as the core marker of COPD, including SNHG12, SLFNL1-AS1, KCNQ10T1, XIST, EAF1-AS1, FOXD2-AS1, NORAD, PINK1-AS and RP11-69E11.4. And the cytoHubba analysis identified ATM, SMAD7 and HIF1A as hub genes of ceRNA network.

Conclusion: This study provides a landscape of ceRNA network of COPD, which help to reveal the underlying pathophysiological mechanisms of COPD and shed light on novel therapeutic strategies for COPD.

Keywords: chronic obstructive pulmonary disease, lncRNA, miRNA, bioinformatics

Introduction

Chronic obstructive pulmonary disease (COPD) is a common chronic bronchitis or emphysema hallmarked by chronic respiratory symptoms and airflow restriction, which can further develop into common chronic diseases of pulmonary heart disease and respiratory failure.¹ The prevalence of COPD is increasingly worldwide, which become a great individual and society burden.² As the COPD is often punctuated by rhinoviruses (RVs), the acute exacerbations frequently lead to morbidity and mortality of these patients.³ Although smoking and aging are the main causes of COPD.⁴ However, the pathological mechanism of COPD remains limited. The underlying pathophysiological mechanism is urgent for developing new therapies for COPD.

The dysregulation of mRNA and miRNA expression was also observed in COPD.⁵ A microarray of epithelium from COPD survey the TLR family gene expression and revealed that TLR5 is essential for the activation of innate immune responses in COPD. The aging-related genes were also differently expressed in COPD.⁶ The distinct miRNA profile was also observed in COPD.⁷ Moreover, the study showed that MicroRNA-218 regulated the overproduction of MUC5AC

and inflammation of COPD by targeting TNFR1-mediated NF-κB pathway. Recently, microRNA-21 was reported to mediate COPD pathogenesis by regulating SATB1/S100A9/NF-κB axis.⁸

Emerging studies showed that the genetic factors are also important determinants of COPD. Long non-coding RNA (lncRNA) is a type of single-stranded non-coding RNA with the length of longer than 200 nucleotides that participate in various biological processes by manipulating gene expression.⁹ Recently, lncRNAs have been documented to play a key role in diverse biological functions and be involved in various disease including COPD and airway disease.¹⁰ A recent study revealed the significant different lncRNA expression profiles in smokers with or without COPD. Moreover, lncRNAs was reported to perform essential functions in the progression of COPD. lncRNA TUG1 was reported to reduce proliferation in COPD by inducing $-\beta$.¹¹ Research by Li et al showed that lncRNA MIR155HG regulates/ macrophage polarization in COPD.¹² Zheng et al found that lncRNA COPDA1 promotes the proliferation of human bronchial smooth muscle cells in COPD.¹³ As the key regulator of miRNA, lncRNA was reported to regulate the COPD progression by targeting miRNA and mRNA.^{14,15} However, the landscape of COPD ceRNA network is limited.

In this study, we performed differential analysis of genes and miRNA expression profiles in COPD patients to obtain COPD-related genes and miRNAs, and constructed a COPD ceRNA network based on the interaction between genes, miRNAs and lncRNAs in the lncACTdb database. And then Cytoscape was used to perform topological analysis on the ceRNA network, and we obtained 10 lncRNAs as hub nodes, which were expected to become potential therapeutic targets for COPD.

Materials and Methods

Data Collection

We searched the mRNA and miRNA expression profiles of patients with COPD in the Gene Expression Omnibus (GEO) database based on the keywords "COPD", "Home sapiens", "mRNA profiles" and "miRNA profiles". A total of 16 items were identified. Finally, after screening for the presence or absence of normal samples and the source of the samples, 148 samples from the four studies were used for subsequent analysis. The detailed information of the data set is shown in Table 1.

Data Preprocessing and Differential Expression Analysis

The original data was downloaded and the R package "limma" was used for analysis. Firstly, the original data was normalized (log2), and then differently expressed genes between COPD and normal samples were analyzed (lmFit and eBay functions) with the threshold used is fold change (log2) cutoff of 1 and p value cutoff of 0.05. Each data set was analyzed separately. Volcano maps and gene expression heat maps were performed by R package "ggplot2 and pheatmap".

PPI Network Analysis

The protein–protein interaction (PPI) network can help us identify the key genes for the occurrence and development of COPD from the level of interaction. Get the PPI information of DEGs from the Search tool for the retrieval of Interacting Genes (STRING) database (<u>http://www.string-db.org/</u>).¹⁰ Then, Cytoscape v3.7.0 software was used to analyze the topology of the PPI network in COPD, and the PPI network was constructed.

Accession	Experiment	Platform	COPD	Normal	Mrna/microRNA
GSE38974	Array	GPL7723	19	8	microRNA
GSE38974	Array	GPL4133	23	9	mRNA
GSE103174	Array	GPL13667	37	16	mRNA
GSE135188	RNA-seq	GPL21290	18	18	mRNA

Table I Datasets

GO/KEGG Enrichment Analysis

In order to study the biological functions of DEG, the R package ClusterProfiler was used to analyze and visualize the functional map of DEGs (Gene Ontology (GO) annotation and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway) and the annotative R package (org.Hs.eg.db) was selected as background. P value <0.05 is statistically significant.

Hallmark Feature Enrichment

In order to explore the enrichment of DEG in the biological state and process, the Hallmark gene set was downloaded from the MsigDB database, and the gene set of each pathway in the hallmark and the overlap of DEG were calculated by hypergeometric analysis. The enrichment threshold is P value < 0.05.



Figure I The DEG in COPD samples and normal samples. (A) The volcano plots of DEGs in COPD using GSE38974 dataset. (B) The volcano plots of DEGs in COPD using GSE103174 dataset. (C) The volcano plots of DEGs in COPD using GSE135188 datasets. The upregulated gene were red and the down-regulated genes were blue. The filter parameter of DEGs were $|\log_2 (FC)| > 1$ and P <0.05. (D) The heat maps of DEGs in COPD samples and normal samples using GSE38974. (E) The heat maps of DEGs in COPD samples and normal samples in the GSE103174. (F) The heat maps of DEGs in COPD samples and normal samples in the GSE135188 datasets. (G) The network of DEGs in COPD.

Construction of ceRNA Network

The lncACTdb 2.0 (<u>http://www.bio-bigdata.net/LncACTdb/</u>) database contained the ceRNA interaction relationships from multiple documents. The DEGs and DEmis were submitted to the database, and then the related lncRNA, the interactions between DEGs and lncRNA, DEmi and lncRNA, and DEG and DEmiRNA were obtained. According to the ceRNA theory, the selected DEmi and DEG, DEmi and lncRNA, and DEG and lncRNA were integrated and interacted with each other, and the DEmi-DEG-lncRNA ceRNA network was constructed using Cytoscape v3.7.0 software.

Statistical Analysis

All data were analyzed using R (v 4.0.3). The different expression analysis was performed using R "limma" packages. Student's t-tests were used to calculate P-values by t.test function. The heatmaps were generated by pheatmap R package (v 1.0.12).

Result

DEG and DEmi Related to COPD Was Screened

Firstly, the 519 DEGs from the mRNA expression between COPD samples and normal samples from three GEO datasets were obtained with a threshold of p value <0.05 and |logFC|>1. Among them, 233 up-regulated DEGs, 240 down-regulated DEGs were identified in the data set GSE38974; 10 up-regulated DEGs and 12 down-regulated DEGs were identified in the data set GSE103174, and 16 up-regulated DEGs and 31 down-regulated DEGs were identified in the data set GSE135188. The DEGs volcano map of the above three datasets are shown in Figure 1A–C, and the heatmap is shown in Figure 1D–F. In the DEG expression heatmap, there was significant heterogeneity between the expression of DEGs in COPD samples and normal samples. Next, we use all 519 DEGs to construct a PPI network in Figure 1G. In the constructed PPI-DEG network, there were a total of 139 DEGs and 166 interaction relationships. Among them, UBD, H2AFX, BAG3, and CDKN1A were key genes in the network of COPD. Zhang et al determined the modular gene markers containing H2AFX by analyzing the protein interaction network as a marker for distinguishing COPD and NSCLC.¹⁶ Sun et al identified 40 potential COPD-related genes through bioinformatics analysis and found that HIF1A, CDKN1A, BAG3, ERBB2, and ATG16L1 may affect the development of COPD by regulating autophagy.¹⁷



Figure 2 The differential microRNAs (DEmi) in COPD samples and normal samples. (A) The volcano plots of DEmi obtained from the data set GSE38974 with P <0.05 and $|\log_2 (FC)| > 1$. The small diamond presents the microRNAs. (B) The heat map of DEmis of COPD samples and normal samples in the data set GSE38974.

We next selected 17 DEmis from the data set GSE38974 by using the same threshold as that used to obtain DEGs, including 11 up-regulated DEmis and 6 down-regulated DEmis. The volcano map and heatmap of DEmis are shown in Figure 2A and B, respectively.

Functional Enrichment of DEG in COPD

In order to explore the biological significance of COPD features, all DEGs from GSE38974, GSE103174 and GSE135188 were used for GO/KEGG analysis using the Hallmark gene sets in MSigDB. As shown in Figure 3A, GO enrichment showed that leukocyte chemotaxis, cell chemotaxis and myeloid leukocyte migration were upregulated, and muscle and membrane repolarization-related biological progresses were downregulated in COPD. The cytokine receptor CXCR2 antagonist (MK-7123) reduced the chemotaxis of neutrophils, which may alleviate the airway inflammation of COPD,¹⁸ and aerobic training combined with respiratory muscle stretching improved the functional exercise capacity of COPD patients and reduced dyspnea.¹⁹ In Figure 3B, KEGG pathway enrichment shows that p53 pathway was upregulated in COPD. The p53 signaling pathway polymorphism was associated with changes in emphysema in COPD patients,²⁰ and compared with non-smokers, healthy smokers and COPD smokers due to the apoptosis of active pulmonary capillary endothelial cells, the level of circulating endothelial cells increased.²¹ Dinesh et al also revealed the



Figure 3 The functional enrichment analysis of DEG in COPD. (A) GO_BP function enrichment of DEG in COPD. (B) KEGG function enrichment of DEG in COPD. The enrichment results of DEG up (C) and down (D) in Hallmark respectively. The abscissa was the number of intersections between DEG and the pathway gene set, and the ordinate was -log10 of the significance p-value of the hypergeometric test.

increased apoptotic cell death in airway epithelial cells in COPD.¹⁰ We also found in the Hallmark enrichment results of Figure 3C and D that chronic neutrophil inflammation was a sign of the pathogenesis of COPD, which persists after smoking cessation.²² And COPD patients may be particularly vulnerable to hypoxia-induced autonomic disorders.²³

IncRNA Marker is Screened Based on DEG and DEmi

We obtained the RNA interaction relationship from the database lncACTdb 2.0, and constructed the interaction relationship network containing 519 DEGs and 17 DEmis. The ceRNA network we obtained (Figure 4) contains 93 DEGs, 2 DEmi, 463 lncRNAs, and 1157 DEG-lncRNA, DEmi-lncRNA, and DEmi-DEG interactions. The network nodedegree is shown in Table 2. In the constructed ceRNA network, we selected hub-lncRNA (the network is ranked in the top 10) as the core marker of COPD, including SNHG12, SLFNL1-AS1, KCNQ1OT1, XIST, EAF1-AS1, FOXD2-AS1, NORAD, PINK1-AS and RP11-69E11.4. Next, basing on the cytoHubba analysis of cytoscape, ATM, SMAD7 and HIF1A were identified as hub genes in this network and are used for the treatment of COPD in the future (Figure 5).

Discussion

COPD is a chronic progressive inflammatory disease with poor prognosis and low long-term survival rate.²⁴ Pulmonary rehabilitation is traditionally recommended for patients with moderate to severe COPD. Although pulmonary rehabilitation, bronchodilators and anti-inflammatory agents provides the greatest improvement in dyspnea, exercise tolerance, and health-related quality of life,²⁵ it is very difficult to change physical activity and with poor outcome.²⁶ Therefore, COPD is a major heterogeneous disease and one of the world's leading causes of death, and it is urgent for diagnostic and prognostic biomarkers for COPD.



Figure 4 ceRNA network in COPD.

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	Gene	RNA	Upordown	Degree
	AADAC	mRNA	Down	0
	ABCG2	mRNA	Down	17
	AC002117.1	IncRNA	Plane	I
	AC002467.7	IncRNA	Plane	1
	AC003104.1	IncRNA	Plane	4
	AC003991.3	IncRNA	Plane	3
	AC004069.2	IncRNA	Plane	1
	AC004448.5	IncRNA	Plane	1
	AC005154.6	IncRNA	Plane	6
	AC005532.5	IncRNA	Plane	2
	AC007228.9	IncRNA	Plane	1
	AC007292.6	IncRNA	Plane	1
	AC008079.10	IncRNA	Plane	2
	AC008697.1	IncRNA	Plane	1
	AC009133.12	IncRNA	Plane	2
	AC009948.5	IncRNA	Plane	5
	AC010136.2	IncRNA	Plane	1
	AC010226.4	IncRNA	Plane	1
	AC012123.1	IncRNA	Plane	1
	AC015849.16	IncRNA	Plane	2
	AC015933.2	IncRNA	Plane	I
	AC016747.3	IncRNA	Plane	1
	AC017060.1	IncRNA	Plane	1
	AC017101.10	IncRNA	Plane	5
	AC018890.6	IncRNA	Plane	2
	AC023347.1	IncRNA	Plane	1
	AC034220.3	IncRNA	Plane	I
	AC058791.1	IncRNA	Plane	2
	AC069363.1	IncRNA	Plane	2
	AC073254.1	IncRNA	Plane	1
	AC073641.2	IncRNA	Plane	3
	AC074117.10	IncRNA	Plane	1
	AC074286.1	IncRNA	Plane	3
	AC074366.3	IncRNA	Plane	2
	AC084219.4	IncRNA	Plane	2
	AC092066.1	IncRNA	Plane	1
	AC093627.10	IncRNA	Plane	1
	AC097662.2	IncRNA	Plane	1
	AC104134.2	IncRNA	Plane	2
	AC107081.5	IncRNA	Plane	2
	AC108142.1	IncRNA	Plane	1
	AC116366.5	IncRNA	Plane	1
	AC139100.4	IncRNA	Plane	1
	AC141928.1	IncRNA	Plane	1
	ACAN	mRNA	Down	0
	ACSL5	mRNA	Up	0
	ACTA2	mRNA	Down	12
	ACTBL2	mRNA	Down	0
	ACTG2	mRNA	Down	0
	ACTN3	mRNA	Down	0
	ADAMTS4	mRNA	Up	1
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Gene	RNA	Upordown	Degree
ADHIA	mRNA	Down	0
ADHIC	mRNA	Down	0
ADORA2A-ASI	IncRNA	Plane	I
AF127936.9	IncRNA	Plane	I
AF146191.4	IncRNA	Plane	I
AGBLI	mRNA	Down	0
AGBL2	mRNA	Down	0
AGER	mRNA	Down	0
AGTR2	mRNA	Up	0
AK2P2	mRNA	Up	0
AKAPI4	mRNA	Down	0
AKIRINI	mRNA	Up	0
AL133243.1	IncRNA	Plane	I
ALAS2	mRNA	Up	0
ALG6	mRNA	Down	0
ALKBH3-ASI	IncRNA	Plane	I
ALMSI-ITI	IncRNA	Plane	I
ALOX12-ASI	IncRNA	Plane	2
AMOTL2	mRNA	Down	0
ANKMY2	mRNA	Down	0
ANKRD22	mRNA	Up	0
ANO8	mRNA	Up	0
ANXA2P3	mRNA	Down	0
ANXA5	mRNA	Down	0
ANXA6	mRNA	Up	0
AP001258.4	IncRNA	Plane	I
AP006621.8	IncRNA	Plane	I
APAFI	mRNA	Up	23
APOBEC3A	mRNA	Up	0
APOBEC3C	mRNA	Up	0
ARHGAP26	mRNA	Up	2
ARL4C	mRNA	Up	2
ARNTL2	mRNA	Up	0
ART4	mRNA	Down	0
ASPHDI	mRNA	Up	0
ASPN	mRNA	Down	0
ATF3	mRNA	Up	5
ATM	mRNA	Up	72
ATP1A2	mRNA	Down	0
ATP1B2	mRNA	Down	0
AXUDI	mRNA	Up	0
BACEI-AS	IncRNA	Plane	
BAG3	mRNA	Up	1
BAI3	mRNA	Down	0
BAIAP2-ASI	IncRNA	Plane	
BAX	mRNA	Up	22
BCDIN3D-ASI	IncRNA	Plane	1
BCHE	mRNA	Down	0
BCL2A1	mRNA	Up	0
BDKRBI	mRNA	Up	0
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Gene	RNA	Upordown	Degree
BPIFAI	mRNA	Down	0
BVES-ASI	IncRNA	Plane	1
CI0orfII6	mRNA	Down	0
C10orf28	mRNA	Down	0
CI IorfI0	mRNA	Down	0
CI lorf88	mRNA	Down	0
Cl3orf33	mRNA	Up	0
CL5orf48	mRNA	Un	0
Cl7orf102	IncRNA	Plane	1
Cl8orf32	mRNA	Un	0
Clorf105	mRNA	Up	0
Clorf132	IncRNA	Plane	1
Clorf195	IncRNA	Plane	
CIOTNE5	mRNA	Down	0
CIOTNF7	mRNA	Down	0
		Plane	4
C20orf46	mRNA	Down	0
C20orf85	mRNA	Down	0
C2orf40	mRNA	Down	0
C2orf54	mRNA		0
C2orf83	mRNA	Down	0
C4orf7	mRNA		0
C4	mRNA	Down	0
Cforfl 24	mRNIA	Lip	0
Cforf192	mRNA	Down	0
C7orf23	mRNIA	Down	0
C9orfU7	mRNIA	Down	0
C9orf171	mRNIA	Down	0
C9orf74	mRNIA	Down	0
CARPZ	mRNA	Down	0
	mRNIA	Lip	0
	mRNIA	Down	0
CAPS	mRNIA	Down	0
		Plano	U I
		Plane	י כ
CASC		Plane	3
CASE ASI		Plane	1
CASC-AST	mPNIA	Down	0
		Down	2
CAVI	mPNIA	Down	2
CRY		Down	25
CBAB		Down	0
CBTI		Down	0
		Down	0
CCDCI37		Op	0
		Down	0
		Fiane	0
		Down	0
		Down	0
		Down	0
	MKINA	Down	0

Table 2 (Continued).

Table 2 (Continued).
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Gene	RNA	Upordown	Degree
CCDC77	mRNA	Down	0
CCDC8I	mRNA	Down	0
CCL19	mRNA	Up	0
CCL20	mRNA	Up	4
CCL8	mRNA	Up	2
CCR6	mRNA	Up	0
CD70	mRNA	Up	0
CD86	mRNA	Down	4
CDC42EP2	mRNA	Up	0
CDH3	mRNA	Up	0
CDKNIA	mRNA	Up	70
CDKN2B-ASI	IncRNA	Plane	I
CESI	mRNA	Down	0
CFLAR-ASI	IncRNA	Plane	6
CGBI	mRNA	Down	0
CH25H	mRNA	Up	0
CHI3LI	mRNA	Up	0
CHI3L2	mRNA	Up	0
CHITI	mRNA	Up	0
CHMP4B	mRNA	Up	0
CHP2	mRNA	Up	0
CHST2	mRNA	Un	0
CKMT2-ASI	IncRNA	Plane	2
	mRNA		0
CLEC4E	mRNA	Un	0
	mRNA	Down	20
CMIP	mRNA		0
CNNI	mRNA	Down	0
	mRNA	Down	3
COLIAN	mRNA	Down	41
		Plane	7
		Plane	3
COX5A	mRNA		0
CPA3	mRNA	Down	ů 0
CPT2	mRNA		ů 0
CREB314	mRNA	Down	0
		Plane	2
CSE3	mRNIA		0
		Plane	U I
		Plane	6
CTC 351M121		Plane	7
		Plane	,
CTC 444N24.7		Plane	4
CTC 45954 3		Plane	т 1
CTC-459F4 9		Plane	י כ
CTC 479CE 10		Plano	۲ ۲
CTC 407M22 E		Plana	-+ E
		Plane	ა ე
CTD-204/H16.3		riane Diana	2 F
CTD-2075E4.5		riane	5
C1D-2292P10.4	INCKINA	riane	2

Gene	RNA	Upordown	Degree
CTD-233717.1	IncRNA	Plane	1
CTD-2369P2.5	IncRNA	Plane	I
CTD-2410N18.4	IncRNA	Plane	3
CTD-2510F5.4	IncRNA	Plane	3
CTD-2517M22.14	IncRNA	Plane	4
CTD-2587H24.14	IncRNA	Plane	2
CTD-2619[13.14	IncRNA	Plane	1
CTD-2630F21.1	IncRNA	Plane	2
CTD-3032 10.2	IncRNA	Plane	I
CTD-3099C6.9	IncRNA	Plane	1
CTD-3131K8.2	IncRNA	Plane	5
CTGF	mRNA	Down	9
CTSS	mRNA	Up	0
CUL2	mRNA	Up	7
CXCL13	mRNA	Up	0
CYorf15B	mRNA	Un	0
CYPIBI	mRNA	Un	3
CYP3A4	mRNA	Down	3
CYP3A7	mRNA	Down	0
CYTOR		Plane	ů I
	mRNIA	Down	0
DAVVI	mRNIA	Down	U I
		Down	0
		Down	0
		Down	0
DES		Down	0
DUDGA ASI		Plane	3
DHR34-AST		Plane	
DLEUZL		Plane	
DLST		Up	0
DLX6-ASI		Plane	5
DINAJC5	MKINA	Up	0
DNAJC7	mRINA	Up	0
	mRINA	Down	0
DOHH	mRNA	Up	10
DPH6-AST	IncRNA	Plane	2
DPYD-ASI	IncRNA	Plane	5
DUSP15	mRNA	Down	0
DUSP2	mRNA	Up	4
DYNCIHI	mRNA	Down	0
DYNLRB2	mRNA	Down	0
EAFI-ASI	IncRNA	Plane	12
EBLN3P	IncRNA	Plane	8
EEFIAIPII	mRNA	Down	0
EFHB	mRNA	Down	0
EGFL7	mRNA	Down	0
EIFIB	mRNA	Up	0
EIF3J-AS1	IncRNA	Plane	2
ELOA-ASI	IncRNA	Plane	3
EMD	mRNA	Up	0
EML2-ASI	IncRNA	Plane	I

Table 2 (Continued).
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Gene	RNA	Upordown	Degree
ENPP2	mRNA	Down	0
ENPP4	mRNA	Down	0
ENTPD1-AS1	IncRNA	Plane	I
ERF	mRNA	Up	0
EXTL3-ASI	IncRNA	Plane	3
F8A1	mRNA	Down	0
FAM162B	mRNA	Down	0
FAM166B	mRNA	Up	0
FAM183A	mRNA	Down	0
FAM201A	IncRNA	Plane	5
FAM5C	mRNA	Down	0
FAM95C	IncRNA	Plane	I
FAM96B	mRNA	Down	0
FAT4	mRNA	Down	0
FENDRR	IncRNA	Plane	3
FGFBP2	mRNA	Down	0
FGG	mRNA	Up	2
FHLI	mRNA	Down	0
FIBIN	mRNA	Down	0
FILIPIL	mRNA	Down	0
FKBP10	mRNA	Up	0
FLI21511	mRNA	Down	0
FLI34515	mRNA	Down	0
FL 137453	IncRNA	Plane	3
FL 146284	IncRNA	Plane	3
FOLRI	mRNA	Down	0
FOXD2-ASI	IncRNA	Plane	-
FSTL I	mRNA	Down	8
FTX	IncRNA	Plane	9
FUS	mRNA	Un	0
GABBRI	mRNA	Down	0
GABRE	mRNA	Down	0
GADD45B	mRNA	Un	0
GAGE3	mRNA	Un	0
GASI	mRNA	Down	21
GAS5	IncRNA	Plane	2
GBP6	mRNA	Down	0
GDFI	mRNA	Un	0
GDEI0	mRNA	Down	0
GDF15	mRNA	Un	0
GFPT2	mRNA	Un	0
GIB2	mRNA	Un	0
GITIDI	mRNA	Un	0
GLT25D2	mRNA	Down	0
GLYCTK-ASI	IncRNA	Plane	-
GNALL	mRNA	Down	0
GNG12-ASI		Plane	2
GNGI3	mRNA	Down	2
GPC3	mRNA	Down	-
GPM6A	mRNA	Down	0
		DOWII	5

Gene	RNA	Upordown	Degree
GPR172A	mRNA	Up	0
GPR177	mRNA	Up	0
GRB14	mRNA	Down	0
GRM8	mRNA	Down	0
GSN	mRNA	Down	0
GSTA2	mRNA	Down	0
GSTA5	mRNA	Down	0
GSTMI	mRNA	Down	0
GSTTI	mRNA	Down	0
GUSBPII	IncRNA	Plane	1
H19	IncRNA	Plane	4
H2AFX	mRNA	Up	29
HAGLR	IncRNA	Plane	3
HASI	mRNA	Up	0
HCG18	IncRNA	Plane	3
HCRT	mRNA	Down	0
HELLPAR	IncRNA	Plane	I
HIFIA	mRNA	Up	79
HIRA	mRNA	Up	0
HIST I H2AB	mRNA	Down	0
HIST I H4B	mRNA	Down	0
НК3	mRNA	Up	0
HLA-U	mRNA	Up	0
HMBOXI	mRNA	Down	3
HMGB3L1	mRNA	Up	0
HMOXI	mRNA	Up	5
HNRNPA0	mRNA	Up	0
HNRNPAB	mRNA	Up	0
HORMAD2-ASI	IncRNA	Plane	1
HOTAIRMI	IncRNA	Plane	1
HOXA-AS2	IncRNA	Plane	4
HOXA-AS3	IncRNA	Plane	3
HOXA2	mRNA	Down	0
HOXC-AS2	IncRNA	Plane	I
HPR	mRNA	Up	0
HRASLS5	mRNA	Up	0
hsa-miR-105	miRNA	Up	0
hsa-miR-10a	miRNA	Up	0
hsa-miR-1274a	miRNA	Up	0
hsa-mi R-14 4	miRNA	Up	0
hsa-mi R-148 a	miRNA	Up	0
hsa-miR-223	miRNA	Up	0
hsa-miR-25*	miRNA	Down	0
hsa-miR-374a	miRNA	Up	0
hsa-miR-422a	miRNA	Down	0
hsa-miR-454	miRNA	Up	0
hsa-mi R-486-5 p	miRNA	Up	12
hsa-miR-513a-5p	miRNA	Down	3
hsa-miR-576-3p	miRNA	Down	0
hsa-mi R-664	miRNA	Up	0

Table 2 (Continued).

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Gene	RNA	Upordown	Degree
hsa-miR-766	miRNA	Up	0
hsa-miR-923	miRNA	Down	0
hsa-miR-937	miRNA	Down	0
HSPA2	mRNA	Down	0
HSPB3	mRNA	Down	0
HSPD1P6	mRNA	Up	0
ID4	mRNA	Down	4
IER3	mRNA	Up	0
IFITI	mRNA	Down	4
IFT20	mRNA	Up	0
IGFBP7-ASI	IncRNA	Plane	I
IGHM	mRNA	Up	0
IGSF6	mRNA	Up	0
ILIB	mRNA	Up	I
IL1R2	mRNA	Up	0
IL20RB	mRNA	Up	0
IL33	mRNA	Down	0
IL6	mRNA	Up	31
11.8	mRNA	Un	0
	mRNA	Down	0
IPO9-ASI	IncRNA	Plane	
	mRNA	Down	0
	mRNA		0
IRX5	mRNA	Down	0
	mRNA	Down	4
		Plane	т 4
ITGB2	mRNIA		0
	mRNA	Down	0
	mRNIA		0
	mRNIA	Up	0
		Dp	U I
	mPNIA		י ר
		Dp	2
		Plane	2
KB-1317D11.4		Plane Diana	1
		Plane Diana	ו ר
KB-1013E4.2		Plane Diana	3 2
KB-31868./		Plane Diana	3
		Plane	
		Down	0
KCNIP2-AST		Plane	
KCNQIOTI		Plane	16
KDM4A-ASI	IncKINA	Plane	10
KIAA0644	mRINA	Down	0
KII	mRNA	Down	56
KLK12	mKNA	Down	U
KPNA6	mRNA	Down	0
KRT17P3	mRNA	Up -	0
KRT4	mRNA	Down	0
KRT7	mRNA	Up	6
KRT7-AS	IncRNA	Plane	2

Gene	RNA	Upordown	Degree
LITDI	mRNA	Down	0
LA16c-358B7.3	IncRNA	Plane	1
LACTB2-ASI	IncRNA	Plane	1
LADI	mRNA	Up	0
LDB2	mRNA	Down	0
LEFTY2	mRNA	Down	0
LILRBI	mRNA	Up	0
LILRB2	mRNA	Up	0
LIMD1-AS1	IncRNA	Plane	1
LIMKI	mRNA	Up	24
LIMS2	mRNA	Down	0
LINC-PINT	IncRNA	Plane	6
LINC00158	IncRNA	Plane	1
LINC00304	IncRNA	Plane	1
LINC00339	IncRNA	Plane	4
LINC00461	IncRNA	Plane	1
LINC00472	IncRNA	Plane	1
LINC00511	IncRNA	Plane	3
LINC00525	IncRNA	Plane	2
LINC00630	IncRNA	Plane	I
LINC00641	IncRNA	Plane	2
LINC00645	IncRNA	Plane	I
LINC00661	IncRNA	Plane	I
LINC00664	IncRNA	Plane	I
LINC00665	IncRNA	Plane	9
LINC00667	IncRNA	Plane	3
LINC00670	IncRNA	Plane	2
LINC00707	IncRNA	Plane	1
LINC00869	IncRNA	Plane	7
LINC00893	IncRNA	Plane	2
LINC00894	IncRNA	Plane	7
LINC00907	IncRNA	Plane	1
LINC00909	IncRNA	Plane	1
LINC00910	IncRNA	Plane	1
LINC00958	IncRNA	Plane	10
LINC00960	IncRNA	Plane	2
LINC00963	IncRNA	Plane	6
LINC01085	IncRNA	Plane	1
LINC01090	IncRNA	Plane	2
LINC01116	IncRNA	Plane	1
LINC01128	IncRNA	Plane	10
LINC01134	IncRNA	Plane	2
LINC01140	IncRNA	Plane	7
LINC01184	IncRNA	Plane	I
LINC01197	IncRNA	Plane	1
LINC01257	IncRNA	Plane	1
LINC01278	IncRNA	Plane	2
LINC01358	IncRNA	Plane	2
LINC01362	IncRNA	Plane	2
LINC01521	IncRNA	Plane	I
	1	1	1

Table 2 (Continued).

Table 2 (Continue	d).
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Gene	RNA	Upordown	Degree
LINC01569	IncRNA	Plane	I
LINC01578	IncRNA	Plane	I
LINC01605	IncRNA	Plane	I.
LINC01619	IncRNA	Plane	I.
LINC01783	IncRNA	Plane	I.
LINC01934	IncRNA	Plane	4
LINC01965	IncRNA	Plane	1
LIPE-ASI	IncRNA	Plane	I
LIX I L-ASI	IncRNA	Plane	I
LLNLR-268E12.1	IncRNA	Plane	I
LLNLR-470E3.1	IncRNA	Plane	I
LMCDI	mRNA	Down	0
LMNBI	mRNA	Up	0
LMNB2	mRNA	Up	3
LMODI	mRNA	Down	0
LOC100128164	mRNA	Down	0
LOC100128178	mRNA	Down	0
LOC100128548	mRNA	Down	0
LOC100128977	mRNA	Up	0
LOC100131582	mRNA	Up	0
LOC100132247	mRNA	Down	0
LOC100134228	mRNA	Up	0
LOC23117	mRNA	Down	0
LOC338799	mRNA	Down	0
LOC389831	mRNA	Down	0
LOC391132	mRNA	Up	0
LOC391532	mRNA	Up	0
LOC402360	mRNA	Down	0
LOC51233	mRNA	Up	0
LOC595101	mRNA	Up	0
LOC646909	mRNA	Up	0
LOC646949	mRNA	Up	0
LOC649294	mRNA	Up	0
LOC650392	mRNA	Up	0
LOC728763	mRNA	Down	0
LOC728820	mRNA	Up	0
LOC729046	mRNA	Up	0
LOC729259	mRNA	Up	0
LOC729652	mRNA	Up	0
LOC780529	mRNA	Up	0
LRIGI	mRNA	Down	9
LRP5L	mRNA	Up	0
LRRC2	mRNA	Down	0
LRRC36	mRNA	Down	0
LRRC45	mRNA	Down	0
LRRC46	mRNA	Down	0
LRRC75A-ASI	IncRNA	Plane	2
LTBP2	mRNA	Down	0
LTBP4	mRNA	Down	0
LTC4S	mRNA	Down	0
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Table 2 (Continued).	
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Gene	RNA	Upordown	Degree
LTK	mRNA	Down	0
MACCI-ASI	IncRNA	Plane	1
MAGOH	mRNA	Up	0
MALATI	IncRNA	Plane	10
MAOB	mRNA	Down	0
MAP4K3	mRNA	Down	П
МАРКАРК3	mRNA	Up	0
MATNI-ASI	IncRNA	Plane	I
MBD4	mRNA	Up	0
MBNLI-ASI	IncRNA	Plane	I
MCF2L-ASI	IncRNA	Plane	1
MCM3AP-ASI	IncRNA	Plane	1
MED 18	mRNA	Up	2
MELTF-ASI	IncRNA	Plane	1
METTL7A	mRNA	Up	3
MFAP4	mRNA	Down	2
MGC70870	mRNA	Up	0
MIR124-2HG	IncRNA	Plane	
MIRISSHG	IncRNA	Plane	
MIR17HG		Plane	
MIR22HG		Plane	2
MIR4435-2HG		Plane	2
MIR4458HG		Plane	1
MIR583HG		Plano	
		Plano	4
		Plano	т 1
MMPI	mRNIA		
MMPIO	mRNA	Up	0
MMP14	mRNA	Down	12
MMPI9	mRNA	Lin	0
MMP9	mRNA	Up	49
MNIT	mRNA	Down	0
MOPI	mRNIA	Lip	0
	mPNIA	Up	0
MS4AD	mPNIA	Op	0
MS4A0D	mPNIA	Down	0
I'ISHAOD MSC		Down	7
MST		Op Davis	/
		Down	13
MTIC		Down	0
		Ор	0
мти		Ор	0
MITL	mRINA	Up	0
אין דיין אדער סער		Ор	/
MINDIP23	MKINA	Ор	0
MAD	MKINA	Op	13
MIR	mKNA	Down	59
MTHI	mKNA	Down	0
MYH2	mRNA	Down	
MYO15B	mRNA	Down	0
MYOC	mRNA	Down	

Table 2 (Continued).
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Gene	RNA	Upordown	Degree
MYOZI	mRNA	Down	0
MYRIP	mRNA	Down	0
NBPF14	mRNA	Down	0
NBPF20	mRNA	Up	0
NCR2	mRNA	Up	0
NEATI	IncRNA	Plane	7
NEUROGI	mRNA	Up	0
NFKBIZ	mRNA	Up	0
NFYC-ASI	IncRNA	Plane	2
NKILA	IncRNA	Plane	I
NKX2-8	mRNA	Down	0
NLRP2	mRNA	Up	0
NMNAT3	mRNA	Down	0
NNT-ASI	IncRNA	Plane	1
NORAD	IncRNA	Plane	11
NOV	mRNA	Down	0
NPHP4	mRNA	Up	0
NPIP	mRNA	Down	0
NPM3	mRNA	Un	0
NPNT	mRNA	Down	15
NPPA-ASI	IncRNA	Plane	I
NPTN	mRNA	Down	0
NR2FI-ASI		Plane	3 7
NB2F2	mRNA	Down	, 5
NB4A1	mRNA		0
NR4A2	mRNA	Up	18
NSBPI	mRNA	Down	0
NTE3	mRNA	Down	8
NTM	mRNA		i i
	mRNA	Up	0
		Plane	i i
		Plane	2
OGN	mRNA	Down	0
		Plane	5
	mRNIA	Down	0
	mRNA		0
	mRNA	Down	0
	mRNA		0
		Plane	2
OKZAT-AST OSM	mRNIA		2
OSThota	mRNIA	Op Down	0
	mRNIA	Down	0
	mPNIA	Dowii	0
		Op Plana	0
PCA2		Plane	1
			י ב
		rialle Deur	5 0
		Down	0
		Down	0
		Down	0
FUATI	IIIKINA	Ор	U

	Gene	RNA	Upordown	Degree
	PDCD4-ASI	IncRNA	Plane	I
	PF4	mRNA	Up	0
	PFDN6	mRNA	Up	0
	PHFI	mRNA	Down	0
	PHF5A	mRNA	Up	0
	PHLDAI	mRNA	Up	0
	PHLDA2	mRNA	Up	0
	PHLDA3	mRNA	Down	0
	PI16	mRNA	Down	0
	PI3	mRNA	Up	0
	PIK3CD-ASI	IncRNA	Plane	I
	PIK3CD-AS2	IncRNA	Plane	I
	PIMI	mRNA	Up	19
	PINK I-AS	IncRNA	Plane	П
	PLA2G1B	mRNA	Down	0
	PLA2G2A	mRNA	Up	0
	PLA2G7	mRNA	Up	0
	PLEKHG4	mRNA	Up	0
	PLEKHH3	mRNA	Down	0
	PLN	mRNA	Down	0
	PMAIPI	mRNA	Up	5
	POLR2C	mRNA	Up	0
	POLR2J4	IncRNA	Plane	I
	POU2AFI	mRNA	Up	0
	PPIB	mRNA	Up	0
	PPPIRI4A	mRNA	Down	0
	PPP1R3C	mRNA	Down	0
	PPP3CB-ASI	IncRNA	Plane	5
	PRDM6	mRNA	Down	0
	PRKCB	mRNA	Up	3
	PRKT	MRINA	Down	0
	PROST		Down	1
	PROSERZ-ASI		Plane	0
		mRNA	Up Up	0
		mRNIA	Ор Цр	0
		mRNIA	Op Down	0
	PRSS36	mRNIA		0
	PSMA3_ASI		Op Plane	7
			Plane	,
			Plane	
	PTPNI	mRNA		2
	PTPRD	mRNA	Down	12
	PTX3	mRNA	 Up	3
	PVTI	IncRNA	- r Plane	2
	QTRTI	mRNA	Up	0
	RABI3	mRNA	Up	3
	RAB20	mRNA	Up	0
	RAB23	mRNA	Down	4
	RAETIE-ASI	IncRNA	Plane	I
J.				

Table 2 (Continued).

Table 2 (C	ontinued).
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Gene	RNA	Upordown	Degree
RANBP6	mRNA	Down	0
RAPIGAP	mRNA	Down	0
RAPGEF5	mRNA	Down	0
RBM26-ASI	IncRNA	Plane	I
RERG	mRNA	Down	0
RFX3-ASI	IncRNA	Plane	4
RGL2	mRNA	Down	0
RGL4	mRNA	Up	0
RGSI	mRNA	Up	0
RGS22	mRNA	Down	0
RNDI	mRNA	Up	0
RNFI25	mRNA	Up	0
RNFI45	mRNA	Up	0
RPI-117O3.2	IncRNA	Plane	I
RP1-118j21.5	IncRNA	Plane	6
RP1-158P9.1	IncRNA	Plane	I
RPI-191J18.66	IncRNA	Plane	10
RPI-193H18.2	IncRNA	Plane	I
RP1-199J3.7	IncRNA	Plane	4
RP1-224A6.9	IncRNA	Plane	I
RP1-253P7.4	IncRNA	Plane	I
RP1-27K12.2	IncRNA	Plane	I
RP1-283E3.8	IncRNA	Plane	2
RPI-37C10.3	IncRNA	Plane	2
RP1-92014.6	IncRNA	Plane	3
RP11-1000B6.5	IncRNA	Plane	I
RP11-1007O24.3	IncRNA	Plane	4
RP11-106M3.3	IncRNA	Plane	I
RP11-108M9.3	IncRNA	Plane	2
RP11-108M9.6	IncRNA	Plane	2
RP11-10K16.1	IncRNA	Plane	I
RP11-1149O23.2	IncRNA	Plane	I
RP11-120D5.1	IncRNA	Plane	2
RP11-120E11.2	IncRNA	Plane	I
RP11-133K1.11	IncRNA	Plane	I
RP11-140H17.2	IncRNA	Plane	I
RP11-147L13.12	IncRNA	Plane	2
RP11-154D6.1	IncRNA	Plane	I
RP11-156E6.1	IncRNA	Plane	3
RP11-157P1.4	IncRNA	Plane	3
RP11-158K1.3	IncRNA	Plane	I
RP11-160H22.5	IncRNA	Plane	I
RP11-161H23.9	IncRNA	Plane	I
RP11-161M6.2	IncRNA	Plane	3
RP11-16E12.2	IncRNA	Plane	I
RP11-186B7.4	IncRNA	Plane	I
RP11-197N18.2	IncRNA	Plane	I
RP11-197N18.8	IncRNA	Plane	I
RP11-228B15.4	IncRNA	Plane	2
RP11-244H3.1	IncRNA	Plane	I

RP11-267M23.1 IncRNA Plane	I
RPII-277PI2.20 IncRNA Plane	I
RP11-278C7.3 IncRNA Plane 3	3
RP11-288L9.4 IncRNA Plane 3	3
RP11-295P9.3 IncRNA Plane	I
RP11-299J3.8 IncRNA Plane 3	3
RP11-29G8.3 IncRNA Plane 3	3
RP11-2C24.3 IncRNA Plane	I
RP11-2C24.4 IncRNA Plane 2	2
RPII-303E16.2 IncRNA Plane 2	2
RPII-304L19.13 IncRNA Plane	I
RP11-305E6.4 IncRNA Plane 7	7
RPII-314B1.2 IncRNA Plane 7	7
RP11-317N8.5 IncRNA Plane 8	8
RP11-328C8.4 IncRNA Plane 7	7
RPII-334C17.5 IncRNA Plane 4	4
RPII-342K2.I IncRNA Plane 2	2
RPII-342MI.3 IncRNA Plane 2	2
RPII-345P4.4 mRNA Down (0
RPII-348N5.7 IncRNA Plane	I
RPII-348PI0.2 IncRNA Plane	I
RPII-352G18.2 IncRNA Plane 3	3
RPII-355BII.2 IncRNA Plane	I .
RPII-357HI4.17 IncRNA Plane 5	5
RPII-359B12.2 IncRNA Plane	I
RPII-360N9.2 IncRNA Plane	I
RPII-372K14.2 IncRNA Plane 4	4
RPII-373N22.3 IncRNA Plane	I
RPII-378JI8.8 IncRNA Plane	I
RPII-380LII.4 IncRNA Plane	I
RPII-381N20.1 IncRNA Plane 3	3
RPII-386GII.5 IncRNA Plane 5	5
RP11-394O2.3 IncRNA Plane	I
RP11-395G23.3 IncRNA Plane 3	3
RP11-399K21.14 IncRNA Plane 2	2
RP11-405O10.2 IncRNA Plane	I
RPII-412PII.I IncRNA Plane	I
RP11-415J8.3 IncRNA Plane 5	5
RPII-416N4.4 IncRNA Plane 2	2
RPII-421L21.3 IncRNA Plane 6	6
RPII-446H18.5 IncRNA Plane	I
RP11-452F19.3 IncRNA Plane	I
RPII-45PI5.4 IncRNA Plane 3	3
RP11-468E2.5 IncRNA Plane 7	7
RP11-46O21.2 IncRNA Plane	I
RP11-477D19.2 IncRNA Plane	I
RP11-478C19.2 IncRNA Plane 2	2
RP11-481C4.2 IncRNA Plane	I
RP11-493P1.2 IncRNA Plane 3	3
RPII-519G16.3 IncRNA Plane I	I

Table 2 (Continued).

Table 2 (Continued)).
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Gene	RNA	Upordown	Degree
RP11-531A24.7	IncRNA	Plane	I
RP11-539I5.1	IncRNA	Plane	2
RP11-54515.3	IncRNA	Plane	4
RP11-5407.1	IncRNA	Plane	I
RP11-54O7.3	IncRNA	Plane	10
RP11-574K11.29	IncRNA	Plane	I
RP11-57H12.5	IncRNA	Plane	5
RPI1-588H23.3	IncRNA	Plane	I
RP11-588K22.2	IncRNA	Plane	4
RP11-58K22.5	IncRNA	Plane	I
RP11-5C23.1	IncRNA	Plane	I
RP11-60A24.3	IncRNA	Plane	I
RP11-626G11.5	IncRNA	Plane	I
RP11-631M21.2	mRNA	Down	0
RP11-656D10.6	IncRNA	Plane	I
RP11-656D10.7	IncRNA	Plane	2
RP11-65L3.2	IncRNA	Plane	2
RP11-661A12.5	IncRNA	Plane	I
RP11-661A12.8	IncRNA	Plane	I
RP11-677118.3	IncRNA	Plane	1
RP11-677M14.8	IncRNA	Plane	3
RP11-69E11.4	IncRNA	Plane	II.
RP11-69E11.8	IncRNA	Plane	3
RP11-701H24.4	IncRNA	Plane	
RP11-702F3.1	IncRNA	Plane	1
RP11-714G18.1	IncRNA	Plane	
RP11-715F3.2	IncRNA	Plane	3
RP11-73M18.8	IncRNA	Plane	1
RP11-77H9.2	IncRNA	Plane	
RP11-793H13.3	IncRNA	Plane	2
RP11-799B12.4	IncRNA	Plane	-
RP11-802E16.3	IncRNA	Plane	
RP11-815121.4	IncRNA	Plane	
RP11-819C21.1	IncRNA	Plane	2
RP11-81K13.1	IncRNA	Plane	2
RP11-822F23.8	IncRNA	Plane	5
RP11-829H16.3	IncRNA	Plane	1
RP11-834C11.4	IncRNA	Plane	6
RP11-843B15 4		Plane	3
BP11-84G211		Plane	1
RP11-861F21 2		Plane	
RP11-968A15.8		Plane	
RP11-96D1 10		Plane	2
RP11-983P16 4		Plane	-
RP13-143G15.4	IncRNA	Plane	
RP13-36C9.6	mRNA	Down	0
RP13-39P12 3		Plane	
RP13-516M141	IncRNA	Plane	•
RP3-323NI 2		Plane	•
RP3-467114		Plane	י כ
N J-70/LI.7		i ialle	2

Table	2	(Continued).
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Gene	RNA	Upordown	Degree
RP4-569M23.2	IncRNA	Plane	I
RP4-605O3.4	IncRNA	Plane	1
RP4-613B23.1	IncRNA	Plane	1
RP4-622L5.7	IncRNA	Plane	I
RP4-625H18.2	IncRNA	Plane	I
RP4-635E18.7	IncRNA	Plane	2
RP4-639F20.1	IncRNA	Plane	1
RP4-665N4.8	IncRNA	Plane	2
RP4-669K10.8	IncRNA	Plane	3
RP4-671G15.2	IncRNA	Plane	2
RP4-671014.6	IncRNA	Plane	3
RP4-758118.13	IncRNA	Plane	
RP4-758118.2	IncRNA	Plane	1
RP4-761114.8	IncRNA	Plane	1
RP4-794H19.1	IncRNA	Plane	1
BP5-1021120.5	IncRNA	Plane	1
RP5-1024G6 2	IncRNA	Plane	2
RP5-1024G65		Plane	6
RP5-1033H22 2		Plane	Ŭ I
RP5-1039K5 19		Plane	3
RP5-1071N3 1		Plane	J
RP5 1074114		Plano	3
		Plano	5
		Plane	י ז
		Plane	о О
		Plane	0 7
NF3-004N17.7		Plane	/
		Plane	1
		Plane	4
RF3-877E7.1		Plane	4
RF3-991G20.1		Plane	1
RF5-79/D16.2		Plane	1
RF6-24A23.7		Plane	
RPA4	MRINA	Down	0
RPS14P8	MRINA	Op	0
RPS6P1	mRNA	Down	0
RRP12	mRNA	Up	0
RSPHIOB	mRNA	Down	0
STOUAT2	mRNA	Up	0
S100A8	mRNA	Up	0
S100A9	mRNA	Up	
STOOB	mRNA	Up	3
SAAI	mRNA	Up	0
SAPSI	mRNA	Down	0
SCAMPI-ASI	IncRNA	Plane	I
SCN4B	mRNA	Down	0
SEC14L3	mRNA	Down	0
14-Sep	mRNA	Up	0
SERPINDI	mRNA	Up	0
SERTADI	mRNA	Up	0
SETBPI	mRNA	Down	0

Gene	RNA	Upordown	Degree
SFN	mRNA	Up	0
SFTPAIB	mRNA	Down	0
SGCE	mRNA	Down	0
SGMS1-AS1	IncRNA	Plane	I
SGPP2	mRNA	Up	5
SH3BP5-AS1	IncRNA	Plane	I
SH3GL3	mRNA	Down	0
SHANK3	mRNA	Down	0
SHC2	mRNA	Down	0
SLAMF7	mRNA	Up	0
SLC16A1-AS1	IncRNA	Plane	I
SLC25A22	mRNA	Up	0
SLC26A4	mRNA	Up	0
SLC2A1-AS1	IncRNA	Plane	3
SLC39A7	mRNA	Up	0
SLC44A5	mRNA	Down	0
SLC45A4	mRNA	Down	0
SLC6A19	mRNA	Up	0
SLC6A4	mRNA	Down	10
SLC7A8	mRNA	Up	0
SLCO4A1	mRNA	Up	0
SLFNL1-AS1	IncRNA	Plane	17
SLIT2	mRNA	Down	0
SLITRK6	mRNA	Down	0
SMAD7	mRNA	Down	75
SMARCADI	mRNA	Down	0
SMG7	mRNA	Down	0
SNAII	mRNA	Up	41
SNHGI	IncRNA	Plane	2
SNHG12	IncRNA	Plane	22
SNHG14	IncRNA	Plane	I
SNHG15	IncRNA	Plane	2
SNHG16	IncRNA	Plane	6
SNHG17	IncRNA	Plane	I
SNHG20	IncRNA	Plane	I
SNHG22	IncRNA	Plane	2
SNHG3	IncRNA	Plane	3
SNHG5	IncRNA	Plane	3
SNHG7	IncRNA	Plane	5
SNORA70	mRNA	Down	0
SNTN	mRNA	Down	0
SOCS3	mRNA	Up	15
SOD2	mRNA	Up	7
SOSTDCI	mRNA	Down	0
SPAG8	mRNA	Down	0
SPARCLI	mRNA	Down	0
SPEG	mRNA	Down	0
SPPI	mRNA	Up	10
SPSB2	mRNA	Down	0
SRD5A3-ASI	IncRNA	Plane	

Table 2	(Continued).
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Gene	RNA	Upordown	Degree
SRGN	mRNA	Up	0
SSBP3-AS1	IncRNA	Plane	4
SSPN	mRNA	Down	0
ST20-ASI	IncRNA	Plane	2
ST6GALNAC3	mRNA	Down	0
ST6GALNAC5	mRNA	Down	0
STARD13-AS	IncRNA	Plane	3
STARD4-AS1	IncRNA	Plane	4
STC2	mRNA	Up	5
STK32C	mRNA	Up	0
STOML3	mRNA	Down	0
STX18-AS1	IncRNA	Plane	1
SULTIAI	mRNA	Down	0
SVIL	mRNA	Down	0
TAF5L	mRNA	Up	0
TARID	IncRNA	Plane	I
TBCID9	mRNA	Down	1
tcag7.873	mRNA	Up	0
TCEAL4	mRNA	Down	0
TCF21	mRNA	Down	2
TCTN2	mRNA	Down	0
	mRNA	Down	0
TFPI	mRNA	Un	0
TFX41	IncRNA	Plane	2
THBSI	mRNA	Un	-
THCAT158	IncRNA	Plane	1
		Plane	5
TIXINB		Plane	J I
TMC3-ASI		Plane	
TMED9	mRNA	Un	0
TMFM100	mRNA	Down	2
TMEM120B	mRNA	Un	0
TMEM147-ASI	IncRNA	Plane	2
TMFM178	mRNA	Down	0
TMEM201	mRNA	Un	0
TMEM212	mRNA	Down	0
TMEM254-ASI		Plane	ĩ
	mRNA		3
	mRNIA	Up	0
TNIFRSFAR	mRNIA	Up	0
		Plane	U U
TPTEPI	mRNIA		0
TRAM2 ASI		Plano	U I
TREM2	mRNIA		2
		Plane	7
		Plano	,
		Plane	2
	mDNIA		3
		Dana	с Г
		Fiane	5
111115	MKINA	Down	U

able z (Conunueu).

Gene	RNA	Upordown	Degree
TUBA4B	mRNA	Down	0
TUFM	mRNA	Down	0
TUGI	IncRNA	Plane	6
TXLNGY	mRNA	Down	0
TYRPI	mRNA	Down	0
UBD	mRNA	Up	5
UNK	mRNA	Up	0
UNQ6494	IncRNA	Plane	I
UNQ9419	mRNA	Up	0
UPFI	mRNA	Up	0
URB2	mRNA	Up	0
USP36	mRNA	Up	0
VCAN-ASI	IncRNA	Plane	3
VLDLR-ASI	IncRNA	Plane	I
VPS18	mRNA	Down	I
VPS9D1-AS1	IncRNA	Plane	2
WDR67	mRNA	Down	0
WFDCI	mRNA	Down	0
WFDC21P	IncRNA	Plane	2
XAGEID	mRNA	Un	0
XIST		Plane	16
XX-FW83563B9 5		Plane	1
XXbac-B461K10.4		Plane	5
YFATS2_AS1		Plane	1
74CN	mRNIA	Down	0
ZBBX	mRNA	Down	0
	mRNA	Down	0
		Plane	1
ZC3H12A	mRNIA		2
		Plane	2
		Plano	2
	mPNIA	Down	0
		Down	7
		Plane	/
ZII'12-A31 ZNELLZ		Flane	0
		Op Diana	0
		Plane	2
	MRINA	Up D	0
		Down	0
ZNF337-AST	IncKINA	Plane	4
ZNF426	mRNA	Up	0
	mKNA	Down	U
	mRNA	Up	2
ZNF674-ASI	IncRNA	Plane	3
ZNF675	mRNA	Up	0
ZNF728	mRNA	Up	0
ZNF790-ASI	IncRNA	Plane	8
ZRANB2-AS2	IncRNA	Plane	I
ZSCAN10	mRNA	Up	0



Figure 5 The hub genes of COPD in ceRNA network.

High-throughput sequencing technologies have implied in various disease for detecting potential diagnostic and prognostic biomarkers at the transcriptome level. Accumulation of studies revealed the disease-related RNAs which correlated with disease pathology. lncRNAs and miRNAs regulated mRNAs network implied in the various diseases, and some of them was identified as potentially suitable biomarkers.²⁷ In this study, we identified the differentially expressed RNAs, which have significant associations with immune and cancer-related signaling pathway. Among of these, the cytokine receptor CXCR2 antagonist (MK-7123) reduced the chemotaxis of neutrophils, which may alleviate the airway inflammation of COPD.¹⁸ The p53 signaling pathway polymorphism was associated with changes in emphysema in COPD patients.²⁰

In addition, ceRNAs network related to COPD was evaluated, implying new molecular mechanism and potential therapeutic target for COPD. Among of the network genes, 10 lncRNAs might be used as COPD marker including SNHG12, SLFNL1-AS1, KCNQ1OT1, XIST, EAF1-AS1, FOXD2-AS1, NORAD, PINK1-AS and RP11-69E11.4. Among them, SNHG12 participated in the unfolded protein response and function as a potential therapeutic target and biomarker for human cancer.²⁸ Many tumor cells avoided immune-mediated attacks and enhanced the polarization of effector immune cells (such as macrophages and T cells) via SNHG12.²⁹ SNHG12 also actED as a competitive endogenous RNA (ceRNA) by containing multiple miRNA binding sites, thereby "sponging" these miRNAs to regulate its downstream targets.³⁰ Recent studies have described the emerging role of ceRNAs in the etiology of cancer, where various ncRNA molecules including lncRNAs, miRNAs, pseudogenes and circular RNAs (circRNAs) share common miRNA response elements (MREs), thereby passing through complex RNA networks Mutual regulation through cellular processes.³¹ XIST/miR-200c-3p/EGR3 axis promotes 16HBE cell apoptosis and inflammatory response stimulated by cigarette smoke extract. These findings may provide new insights for the treatment of COPD by reducing lung inflammation.³²

In conclusion, our research has revealed the DEGs and DEmis related to COPD, and constructed the ceRNA network in COPD, which may provide potential new insights for the treatment of COPD. However, we have some limitations on the mechanism of action of lncRNA involved in the progression of chronic obstructive pulmonary disease. Next, we will further study the related functions and mechanisms through cell, tissue and animal experiments.

Abbreviations

COPD, Chronic obstructive pulmonary disease; GEO, Gene Expression Omnibus; DEGs, differentially expressed genes; DEmi, differentially expressed miRNAs; lncRNA, Long non-coding RNA; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Data Sharing Statement

The datasets generated during and/or analyzed during the current study are available in the Gene Expression Omnibus (GEO) datasets (http://www.ncbi.nlm.nih.gov/geo/).

Ethical Approval

This study has been exempted from the medical ethics committee of the Affiliated Hospital of Inner Mongolia Medical University. The public database mentioned in this study is publicly available for re-analyzing, and no ethical approval was required by the local ethics committees, so that this study does not require ethics approval.

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Disclosure

The authors declare that they have no competing interests in this work.

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