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Received: Accepted: Published:	2018.04.29 2018.05.18 2018.06.20	-	Identification of Potenti Related Pseudogenes B Endogenous RNA Netwo	ial Prostate Cancer- ased on Competitive ork Hypothesis
Authors' C Stuc Data (Statistica Data Inter Manuscript Pr Literatu Funds (ontribution: dy Design A Collection B I Analysis C pretation D eparation E tre Search F Collection G	ABG 1 C 2 D 1 E 1 F 1 B 3	Tao Jiang Junjie Guo Zhongchun Hu Ming Zhao Zhenggang Gu Shu Miao	 Department of Urology, Third Affiliated Hospital of Qiqihar Medical University, Qiqihar, Heilongjiang, P.R. China Department of Pathogenic Biology, Qiqihar Medical University, Qiqihar, Heilongjiang, P.R. China Department of Pharmacology, Qiqihar Medical University, Qiqihar, Heilongjiang, P.R. China
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	Backţ Material/M	ground: ethods:	Long noncoding RNAs (IncRNAs) have been revealed which can seclude the common microRNAs (miRNAs) cestral gene. Nonetheless, the role of IncRNA-mediate Using The Cancer Genome Atlas (TCGA) database, In- cer tissues and 52 normal prostate tissues were ana entially expressed RNAs. GO and KEGG pathway an es "Clusterprofile." The ceRNA network in prostate TargetScan databases. Survival analysis was perform	d to function as competing endogenous RNAs (ceRNAs),) and hence prevent the miRNAs from binding to their an- ed ceRNAs in prostate cancer has not yet been elucidated. acRNA, miRNA, and mRNA profiles from 499 prostate can- alyzed with the R package "DESeq" to identify the differ- nalyses were performed using "DAVID6.8" and R packag- e cancer was constructed using miRDB, miRTarBase, and hed with Kaplan-Meier analysis.
	Const	Results:	A total of 376 lncRNAs, 33 miRNAs, and 687 mRNA. Based on the hypothesis that the ceRNA network (In tate cancer and forms competitive interrelations betw NA network that included 23 lncRNAs, 6 miRNAs, an cancer. Only 3 lncRNAs (LINC00308, LINC00355, and (P<0.05). The 3 prostate cancer-specific lncRNA were ing qRT-PCR.	as were identified as significant factors in tumorigenesis. ncRNA-miRNA-mRNA regulatory axis) is involved in pros- ween miRNA and mRNA or IncRNA, we constructed a ceR- id 2 mRNAs that were differentially expressed in prostate d OSTN-AS1) had a significant association with survival validated in prostate cancer cell lines PC3 and DU145 us-
	Conc	10510115:	for future studies of the ceRNA network and its regu	llatory mechanisms in prostate cancer.
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Background

The most common cancer in males worldwide is prostate cancer, accounting for 13% of cancer-related deaths. In 2016, prostate cancer resulted in 648 400 new cases and 80 900 deaths in developed countries [1]. Despite the rapid development of diagnosis and treatment of prostate cancer, poor therapeutic effect and high prevalence are still serious clinical challenges. Therefore, identification of new potential biomarkers and therapeutic targets is crucial to improving alternative therapies.

With the development of genome-wide analysis, up to 20 000 pseudogenes have been found in the human genome [2]. In general, pseudogenes are characterized by inaction in protein coding, such as long noncoding RNA (lncRNA). However, numerous studies suggest that they may execute important functions in carcinogenesis. Recently, a series of pseudogenes has been revealed to function as competing endogenous RNAs (ceRNAs), which can seclude the common microRNAs (miR-NAs) and hence prevent the binding of miRNAs to their target genes [3,4], such as PTENP1, the pseudogene of PTEN tumor suppressor that includes a poly-A tail and shares a common 5' and 3'UTR sequence with PTEN [5]. Zhang et al. showed that PTENP1 can act as a ceRNA to alter PTEN expression level by sponging miR-106b and miR-93 in gastric cancer [6]. In addition, Chen et al. suggested that the lncRNA ROR promotes radioresistance in hepatocellular carcinoma cells by acting as a ceRNA for microRNA-145 to regulate RAD18 expression [7].

In the present study, the expression profiles of lncRNAs, miR-NAs, and mRNAs were obtained from The Cancer Genome Atlas (TCGA) database. The lncRNA-miRNA-mRNA regulatory axis was positively correlated with prostate cancer. A ceR-NA network was subsequently constructed using miRDB, miR-TarBase, and TargetScan databases. Among the 23 lncRNAs, 6 miRNAs, and 2 mRNAs in the ceRNA network, 3 specific lncRNAs were found to have a strong association with the survival of prostate cancer patients. The results of this study help to describe the executive mechanisms of lncRNAs through the lncRNA-miRNA-mRNA network in prostate cancer, which may provide new insights for future research on prostate cancer.

Material and Methods

Patients and samples information

The RNA sequencing data from 499 prostate cancer tissues and 52 samples from non-tumorous prostate tissues were acquired from the TCGA database in 2018. The GDC Data Transfer Tool (*https://gdc.cancer.gov/access-data/gdc-data-transfertool*) was used to download the level 3 mRNASeq and miR-NAseq gene expression data, as well as clinical information of prostate patients. The RNA sequencing data were generated from Illumina HiSeqRNASeq and Illumina HiSeqmiRNASeq platforms. This study meets the publication guidelines provided by TCGA (*http://cancergenome.nih.gov/publications/publicationguidelines*). Ethics Committee approval was not required as the data were obtained from TCGA.

Analysis of differentially expressed RNA

The "DESeq" package [8] in R software was used to identify the differentially expressed mRNAs, lncRNAs, and miRNAs with thresholds of |log2FoldChange| >2, false discovery rate (FDR) or adjusted P value <0.01. In addition, mRNA and lncRNA annotation were performed with ENSEMBL to define and encode the differentially expressed RNAs (*htps://www.ensembl.org/*).

Go and KEGG functional enrichment analysis

In order to understand the potential biological processes and pathways of discriminatively expressed genes, we used the Annotate, Visualize, and Integrate Discovery Database (DAVID 6.8) (*http://david.abcc.ncifcrf.gov/*) [8] to perform Gene Ontology (GO) biological processes at the significant level (FDR <0.05). The KEGG Orthology-Based Annotation System 3.0 (KOBAS3.0) (kobas.cbi.pku.edu.cn/) was used to conduct KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway analysis at the significance level of adjusted P value<0.05. The "Goplot" package in R was used to conduct the chord plot. The network was assembled and globally visualized using Cytoscape v 3.6.1 [9].

Construction of the lncRNA-miRNA-mRNA ceRNA network

Based on the hypothesis that lncRNAs can sponge the common miRNAs and thereby prevent the miRNAs from binding to their target gene [10], a ceRNA network was constructed. StarBase v2.0 database (*http://starbase.sysu.edu.cn/*) was used to modify the miRNAs sequences, and the lncRNA-miRNA interactions were predicted by the miRanda database (*http:// www.microrna.org/*). miRDB (*http://www.mirdb.org/*), miRTar-Base (*http://mirtarbase.mbc.nctu.edu.tw/*) [11] and TargetScan (*http://www.targetscan.org/*) were used to predict the miRNAs target mRNAs. Also, in the present study, the aberrant expression data of the predicted miRNA were combined to select the intersecting lncRNA and mRNA. Construction and visualization of the lncRNA-miRNA-mRNA ceRNA network were performed by Cytoscape v3.6.1. lncRNA, miRNA, and mRNA with |log2Fold-Change| >2 and P<0.05 were analyzed.

Survival analysis

To determine the prognosis of TCGA prostate cancer patients in relation to differentially expressed RNA signatures, Kaplan-Meier survival curves of differentially expressed lncRNAs, microRNAs, and mRNAs were visualized using the "survival" package in R. Survival analysis was performed with log-rank test and P<0.05 was considered significant.

Cell culture

Normal myofibroblast stromal cell line WPMY1 and 2 prostate cancer cell lines (PC3 and DU145) were purchased from the American Type Culture Collection (USA). Cells were cultured in RPMI 1640 medium with 10% fetal bovine serum (Gibco, MA, USA), 100 mg/mL streptomycin, and 100 U/mL penicillin in a humidified atmosphere of 95% air and 5% CO₂ at a temperature of 37°C.

RNA extraction and the quantitative real-time PCR

Total RNA was extracted from cells with Trizol reagent (Invitrogen, Grand Island, CA, USA) according to the manufacturer's instructions. RNA was first reverse transcribed into cDNA using the PrimeScript RT kit (Takara, Japan) according to the manufacturer's protocol. qRT-PCR was then performed using an SYBR PrimeScript RT-PCR kit (Takara, Japan). The following primers were used:

LINC00308, 5'-CAGATAAGACTCTGTCTACCCT-3' (forward),

5'-ACTGAATAAAGGAATGATGCGT-3'(reverse);

LINC00355 5'-ACAGAGCTGGTGGGAGCTGGGAAT-3' (forward), 5'-AGTATCAATAGCTGAATAGAC-3'(reverse);

OSTN-AS1: 5'-CCTGCCTCAGCTTCCCAAGGAG-3' (forward), 5'-GTTGGCAATAAAAAGAAGAAGACAAT-3'.

U6 was used as endogenous control U6 (5'-CTCGCTTCGGCAGC ACA-3' (forward), and 5'-AACGCTTCACGAATTTGCGT-3' (reverse)). All samples were run in triplicates on the ABI 7900HT Real-Time PCR system (Applied Biosystems, CA, USA). Calculation of relative expression levels was performed using the $2^{-\Delta \Delta Ct}$ formula.

Statistical analysis

Statistical analyses were performed using SPSS 21.0 software (SPSS Inc., Chicago, IL, USA). Data are expressed as mean \pm SD. The *t* test was used for two-group comparisons and a P value <0.05 was considered statistically significant.

Results

Patient characteristics

The detailed clinical and pathological features of the TCGA prostate cancer study population are shown in Table 1. All 499 patients were pathologically diagnosed with prostate cancer. The median age was 61 years (range: 41–78 years). Follow-up time was 23–5024 days. The majority of patients were lymph node-free (69.9%) and at high risk according to Gleason score histologic grade (95.2%).

 Table 1. Clinicopathological characteristics of 499 patients with prostate cancer.

Characteristics	Subtype	Patinets n (%)	
A.c.o	>61	224	(44.9)
Аде	≤61	275	(55.1)
	Asian	2	(0.4%)
Race	Black or African American	7	(1.4%)
	White	147	(29.5%)
	Unknown	343	(68.7%)
Histological type	Acinar type	484	(97.0%)
HIStological type	Other subtype	15	(3.0%)
	T2a	13	(2.6%)
	T2b	10	(2.0%)
	T2c	145	(29.0%)
Tumor stage	T3a	158	(31.7%)
	T3b	136	(27.3%)
	T4	10	(2.0%)
	Unknown	7	(1.4%)
	NO	347	(69.6%)
Lymph node	N1	79	(15.8%)
	Unknown	73	(14.6%)
	With tumor	89	(17.8%)
Patients cancer status	Tumor free	347	(69.6%)
	Unknown	63	(12.6%)
Survival status	Alive	489	(98.0)
Survival Status	Dead	10	(2.0%)

Differentially expressed RNAs and their functional enrichment analysis

A total of 687 genes were identified as differentially expressed: 353 (51.38%) genes were downregulated and 334 (48.62%) were upregulated. The complete list of the differentially expressed genes is presented in Supplementary Table 1. The mRNA expression levels are visualized in the heatmap (Supplementary Figure 1). Using the same cut-off criteria of |log2FoldChange| >2 and adjusted P value <0.01, 376 lncRNAs (170 downregulated and 206 upregulated) and 33 miRNAs (11 downregulated and 22 upregulated) were identified as differentially expressed in prostate cancer tissues as compared to the normal tissues (Supplementary Figures 2, 3).



Figure 1. (A) Seven significant biological processes in GO analysis for differentially expressed mRNAs. (B) Chord diagram of all enriched genes in GO analysis. (C) Nineteen enrichment of KEGG pathways for differentially expressed mRNAs in prostate cancer.

To understand the mechanism of oncogenesis underlying prostate cancer, functional enrichment characterization of these 687 mRNAs was performed by GO and KEGG analysis with DAVID6.8 and KOBAS3.0, respectively. Enrichment of GO analysis showed that 8 significant functions are involved in prostate cancer (FDR<0.01) (Figure 1A). Among them, 133 genes were enriched in the extracellular region and represent the lowest FDR, followed by extracellular space with 108 enriched genes. All enriched gene-function relationships are shown in the chord diagram (Figure 1B). In the KEGG pathway analysis, a total of 19 pathways were genetically enriched (Table 2); salivary secretion was the most important cancer-related pathway, which contains 14 genes (Figure 1C). All the expressions related to these KEGG pathway-enriched genes were visualized using Cytoscape software. In the network diagram, the red genes represent upregulation in this pathway and green genes represent the opposite expression (Figure 2).

Construction of ceRNA network in prostate cancer

To further explore the mechanisms of these differentially expressed genes in prostate cancer, a lncRNA-miRNA-mRNA (ceRNA) network was constructed based on the above data. Consequently, 6 miRNAs targeted 24 key lncRNAs were described in the ceRNAs network (Table 3). The miRNA-targeted

mRNA was predicted through miRDB, miRTarBase, and TargetScan (Table 4). Only 2 differentially expressed mRNAs in the ceRNA network, PTGS2 and DUSP2, have previously been reported as tumor suppressor genes [10,12-14] (Figure 3). In the ceRNA network, 12 lncRNAs, 2 miRNAs, and 2 mRNAs are downregulated, while 12 lncRNAs and 4 miRNAs are upregulated (Table 5, Figure 4). Subsequently, we successfully constructed the dysregulated ceRNA network with differentially expressed RNAs, which included 24 lncRNAs, 6 miRNAs, and 2 mRNAs. Results indicate that differentially expressed IncRNAs indirectly interact with mRNAs through miRNAs in prostate cancer (Figure 5). To further identify the differentially expressed RNAs with prognostic significance, Kaplan-Meier survival analysis was used. As a result, 3 out of 24 differentially expressed lncRNAs (LINC00308, LINC00355, and OSTN-AS1) were significantly associated with overall survival (logrank P<0.05) (Figure 6A). However, no differentially expressed miRNA and mRNA in this ceRNA network were found to be associated with prognosis.

Characteristics of differentially expressed lncRNAs in prostate cancer

Based on the results of lncRNAs related to survival, we re-examined the expression data of prostate cancer tissues and

Pathway ID	Description	Adj. P-value	Number of DERNAs
hsa04970	Salivary secretion	0.00022	14
hsa05204	Chemical carcinogenesis	0.00022	13
hsa00982	Drug metabolism – cytochrome P450	0.00022	12
hsa00980	Metabolism of xenobiotics by cytochrome P450	0.00030	12
hsa04972	Pancreatic secretion	0.00075	13
hsa04918	Thyroid hormone synthesis	0.00591	10
hsa04971	Gastric acid secretion	0.00591	10
hsa00053	Ascorbate and aldarate metabolism	0.00593	6
hsa04610	Complement and coagulation cascades	0.00593	10
hsa00830	Retinol metabolism	0.00593	9
hsa04924	Renin secretion	0.00593	9
hsa00140	Steroid hormone biosynthesis	0.01369	8
hsa00040	Pentose and glucuronate interconversions	0.01440	6
hsa00590	Arachidonic acid metabolism	0.01642	8
hsa00983	Drug metabolism – other enzymes	0.01823	9
hsa04979	Cholesterol metabolism	0.01823	7
hsa04966	Collecting duct acid secretion	0.02425	5
hsa04923	Regulation of lipolysis in adipocytes	0.02566	7
hsa04974	Protein digestion and absorption	0.03680	9

 Table 2. KEGG pathways enriched by the differentially expressed mRNAs involved in ceRNA network.



Figure 2. The KEGG network of differentially expressed mRNAs in prostate cancer. Downregulated genes are represented by a green ellipse and upregulated genes are represented by a red ellipse.

Table 3. miRNAs targeting cancer-specific lncRNAs in ceRNA network.

LncRNA	miRNA
C5orf64	miR-184; miR-122; miR-506
LINC00308	miR-137
LINC00313	miR-372; miR-187; miR-122
LINC00336	miR-506
UCA1	miR-184; miR-122; mir-506
PCA3	miR-137
LINC00355	miR-122; miR-506
HCG22	miR-122; miR-506
XIST	miR-372; miR-137; miR-122; miR-506
EMX2OS	miR-184; miR-506
AL161645.1	miR-184; miR-122
NALCN-AS1	miR-372; miR-506
ERVH48-1	miR-137; miR-184; miR-187
OSTN-AS1	miR-137; miR-506
DSCAM-AS1	miR-137; miR-122
GPC5-AS1	miR-372
ZBTB20-AS3	miR-122; miR-506
AL356133.2	miR-372
HNF1A-AS1	miR-372; miR-122
AL353803.1	miR-122
ALDH1L1-AS2	miR-372
LNX1-AS2	miR-506
PCAT1	miR-372; mir-122; mir-506
ANO1-AS2	mir-372

normal tissues. The results showed that the expression of LINC00308, LINC00355, and OSTN-AS1 was significantly higher in cancer tissues compared to the non-cancerous tissues (Figure 6B). In addition, we performed qRT-PCR in cell lines to examine the expression levels of LINC00308, LINC00355, and OSTN-AS1 in 2 prostate cancer cell lines, PC3 and DU145, as well as in the normal myofibroblast stromal cell line WPMY1. The results showed that LINC00308, LINC00355, and OSTN-AS1 are overexpressed in the prostate cancer cell line compared to the normal myofibroblast stromal cell line (Figure 6C).

 Table 4. miRNAs targeted cancer-specific mRNAs in ceRNA network.

miRNA	mRNA
miR-137	PTGS2
miR-122	DUSP2
miR-372	DUSP2



Figure 3. Venn diagram analysis of differentially expressed mRNAs in ceRNA network.

Discussion

Prostate cancer is known to be a multifactorial disease with miscellaneous genetic factors. Traditional prognostic and predictive factors for prostate cancer, including tumor size, histologic grade, TNM stage, and number of lymph node involvement, may correlate with the clinical prognosis of patients. However, due to molecular heterogeneity, they seem to have limitations in distinguishing clinical outcomes among cancer risk subgroups [15,16]. Interestingly, we found 687 significantly differentially expressed mRNAs in prostate cancer. The functional enrichment analysis demonstrated that these genes were mainly enriched in the "extracellular region." Several studies have revealed that DMBT1, ISG15, and EPPIN play an important role in the pathogenesis of prostate cancer [17-19]. The KEGG pathway analysis results showed that 14 genes were enriched in the salivary secretion pathway, including Cystatin, which has been shown to have a strong correlation with prostate cancer by modulating via the MAPK/Erk and androgen receptor pathways [20].

Many recent studies have revealed that various ncRNAs show great potential in the regulation of cancer. However, there have been few studies with large sample sizes (n=499) focusing on the identification of prostate cancer-related ncRNAs. Yang et al. revealed that lncRNA SNHG12 could be an oncogene in gastric

 Table 5. Differentially expressed RNAs involved in ceRNA network.

RNAs	Regulation	Fold change	P-value	FDR
C5orf64(IncRNA)	Down-regulation	-3.036662036	1.46E-30	7.31E-29
LINC00308(lncRNA)	Up-regulation	3.235382205	1.26E-10	9.30E-10
LINC00313(lncRNA)	Down-regulation	-2.476850161	1.82E-26	6.67E-25
LINC00336(lncRNA)	Down-regulation	-2.276139635	4.31E-18	7.72E-17
UCA1(lncRNA)	Down-regulation	-2.914678098	1.98E-47	2.4E-45
PCA3(lncRNA)	Up-regulation	3.331178572	5.63E-18	9.84E-17
LINC00355(lncRNA)	Up-regulation	3.435319383	9.65E-06	3.36E-05
HCG22(lncRNA)	Down-regulation	-3.277663954	2.48E-37	1.94E-35
XIST(lncRNA)	Down-regulation	-2.216949544	5.07E-11	3.99E-10
EMX2OS(lncRNA)	Down-regulation	-5.978725669	2.84E-215	2.21E-211
AL161645.1(lncRNA)	Down-regulation	-4.932391705	3.99E-151	6.2E-148
NALCN-AS1(IncRNA)	Up-regulation	2.337318012	9.23E-11	6.94E-10
ERVH48-1(lncRNA)	Up-regulation	2.606725757	5.73E-11	4.46E-10
OSTN-AS1(lncRNA)	Up-regulation	3.328039464	6.52E-07	2.79E-06
DSCAM-AS1(lncRNA)	Up-regulation	2.039530693	0.0001981	0.000546871
GPC5-AS1(lncRNA)	Up-regulation	4.291545148	1.31E-13	1.40E-12
ZBTB20-AS3(lncRNA)	Up-regulation	2.09029431	0.00131952	0.003071229
AL356133.2(lncRNA)	Up-regulation	4.946182739	5.14E-12	4.57E-11
HNF1A-AS1(lncRNA)	Up-regulation	2.202659839	1.29E-05	4.40E-05
AL353803.1(lncRNA)	Down-regulation	-2.924748531	3.83E-31	2.03E-29
ALDH1L1-AS2(lncRNA)	Down-regulation	-2.224445417	3.96E-39	3.31E-37
LNX1-AS2(lncRNA)	Down-regulation	-2.482616679	3.81E-32	2.16E-30
PCAT1(lncRNA)	Up-regulation	2.659207972	3.07E-22	8.05E-21
ANO1-AS2(IncRNA)	Down-regulation	-4.049375728	1.09E-50	1.81E-48
miR-184(miRNA)	Down-regulation	-2.560858037	4.86E-27	6.04E-26
miR-122(miRNA)	Up-regulation	3.84488164	1.24E-07	3.63E-07
miR-506(miRNA)	Up-regulation	3.111522156	0.000277343	0.000532199
miR-137(miRNA)	Up-regulation	2.357657061	1.76E-05	4.00E-05
miR-372(miRNA)	Up-regulation	3.819509783	2.81E-08	8.84E-08
miR-187(miRNA)	Down-regulation	-2.371598045	4.72E-33	9.78E-32
PTGS2(mRNA)	Down-regulation	-3.018672047	6.74E-64	1.08E-61
DUSP2(mRNA)	Down-regulation	-2.374155832	1.06E-51	1.22E-49



Figure 4. A list of differentially expressed 24 lncRNAs, 6 miRNAs, and 2 mRNAs in prostate cancer.



Figure 5. CeRNA network of prostate cancer. Downregulated genes are represented by a green ellipse and upregulated genes are represented by a red ellipse.

carcinoma cell by targeting miRNA-199a/b-5p [21]. Wu et al. showed that lncRNA-PAGBC acts directly on tumor-suppressive microRNAs by activating the AKT/mTOR pathway, thus promoting tumorigenesis [22]. Because of the strong correlation between ncRNA expression and tumor status, lncRNAs and miRNAs may be valuable as diagnostic and prognostic biomarkers [23,24].

The expression of ncRNAs is low in the normal state but becomes increasingly upregulated in pathological states such as cancer. Hence, ncRNAs are also promising biomarker candidates for cancer [25] and numerous studies have focused on profiling RNA expression in relation to cancer state in search of potential biomarkers of cancer [26,27]. In the present study, we analyzed the public TCGA dataset based on human prostate



Figure 6. Characteristics of LINC00308, LINC00355, and OSTN-AS1 in prostate cancer. (A) LINC00308, LINC00355, and OSTN-AS1 were significantly associated with survival (P<0.05). (B) The expressions of LINC00308, LINC00355, and OSTN-AS1 was significantly upregulated in prostate cancer tissues (P<0.05). (C) Expressions of LINC00308, LINC00355, and OSTN-AS1 were significantly upregulated in prostate cancer cell lines (* p<0.05, ** p<0.01).</p>

cancer samples, which is extremely useful to find potential biomarkers. A total of 24 lncRNAs, 6 miRNAs, and 2 mRNAs were shown to harbor altered expression in the ceRNA network. One of the altered mRNAs was found to be PTGS2, also known as cyclooxygenase (COX-2). PTGS2 is an enzyme with a critical function in prostaglandin biosynthesis, and several reports have revealed its potential function in prostate cancer [28–30]. Our results confirm the function of PTGS2 in prostate cancer, and we also provide another potential mechanism: it may be regulated by XIST, PCA3, OSTN-AS1, DSCAM-AS1, LINC00308, and PCA3 in competing with mir-137. However, to the best our knowledge, the relationship between DUSP2 and prostate cancer has not been reported yet and our result suggest that DUSP2 may have a role in prostate carcinogenesis, but this remains to be elucidated mechanistically. Recently,

there have been many reports that miRNAs can act as oncogenes and tumor suppressor genes to play important roles in proliferation, invasion, migration, apoptosis, EMT, and other malignant biological behaviors of tumor cells [31,32]. MiR-372, one of the differentially expressed miRNAs in our study, has been shown to inhibit prostate cancer cells migration and invasion by targeting p65 [33]. In addition, mir-184, which was also found to be differentially expressed in our study, has previously been reported as a potential signaling pathway in prostate cancer, acting through the mir-184/Bcl-2 axis [34]. Several new targets and potential mechanisms can be found in our ceRNA network studies, which may provide the basis for future research. Although lncRNAs have received much attention in recent years, the study of miRNAs is still very important because it plays a pivotal role in ceRNAs.

However, in our ceRNA network, only 3 lncRNAs could predict patient survival. LINC00308 has been reported to be overexpressed in the testes, but the function of LINC00308 has not been studied [35]. Moreover, LINC00355, which has been reported as deregulated in patients with sepsis, shows central properties in the molecular pathways associated with disease pathogenesis and gene expression regulatory loops that may be involved in poor disease outcomes [36]. So far, none of the 3 differentially expressed lncRNA (LINC00355, LINC00308, and OSTN-AS1) reported in our study has been shown to be associated with cancer by other researchers. Hence, in the present study, the expression of these 3 lncRNAs was evaluated in prostate cancer lines. These lncRNAs were not only significantly associated with poor survival, but also were overexpressed *in vitro*.

Conclusions

To conclude, we have identified 3 novel lncRNAs – LINC00308, LINC00355, and OSTN-AS1 – associated with prognosis of prostate cancer, which could be clinically useful as potential prognostic biomarkers for prostate cancer. However, the underlying molecular mechanisms of action remain to be further elucidated in functional studies.

Conflicts of interests

None.

Supplementary Files

Supplementary Table 1. Differentially expressed mRNAs in prostate cancer.

Gene	logFC	logCPM	PValue	FDR
SERPIN	NA5 –6.7850686	73 4.397738393	0	0
MFSD2	2A -5.9667079	3.456236811	0	0
ACSL6	-4.9968765	96 2.406174962	4.98E-299	2.97E-295
MCF2	-5.2673428	95 0.929684863	1.59E-262	7.09E-259
EMX2	-6.7854448	01 2.244788495	8.95E-260	3.20E-256
HOXB	8 –6.2442681	43 1.047398016	4.88E-250	1.45E-246
CLDN2	-7.9112041	71 3.21684931	1.11E-247	2.82E-244
AKR1B	-3.8745471	87 5.715503602	6.03E-236	1.35E-232
SPINK	2 -7.4095284	96 2.678272683	7.41E-236	1.47E-232
CYP19	A1 -5.4060808	31 –1.222596337	2.05E-234	3.66E-231
KLHL1	4 –4.2474242	78 1.572359202	2.71E-206	4.41E-203
SPINK	13 -5.5284362	56 -0.392023032	2.65E-203	3.95E-200
PATE2	-5.4185135	76 0.297970005	1.42E-195	1.95E-192
TMEM	-8.9449780	33 0.54167799	2.54E-188	3.24E-185
NDRG	4 –3.3489673	14 2.992267305	3.41E-182	4.07E-179
WNT9	B –4.8777228	-0.703836945	1.10E-181	1.23E-178
CRTAC	1 –4.2923899	71 2.665559252	1.29E-177	1.35E-174
RASL1	0B -3.4659879	79 2.057893571	1.17E-166	1.16E-163
PIP	-7.3514085	95 6.495875509	3.33E-165	3.13E-162
ANXA1	-5.5153286	9 0.947383484	4.18E-165	3.74E-162
PATE4	-9.2136618	16 3.236652784	2.41E-157	2.05E-154
CYSLT	R2 -3.7221931	67 1.029914851	9.93E-155	8.07E-152
PAEP	-9.9224753	79 3.345532284	1.48E-151	1.15E-148
AQP2	-9.2951577	5 4.480800053	9.30E-151	6.93E-148
CA2	-4.4401924	91 2.780775663	5.54E-150	3.96E-147
CRISP1	1 –8.6679157	71 1.60380184	5.58E-149	3.84E-146
MGAN	-4.6922434	68 0.243483116	7.50E-149	4.97E-146
НОХВ	6 –4.5840925	75 1.419092909	1.02E-146	6.53E-144
SLC2A	9 –2.6962834	69 2.324688774	5.63E-140	3.47E-137
SPINT	3 -7.3573426	01 -1.907652893	5.44E-137	3.24E-134

Gene	logFC	logCPM	PValue	FDR
КСР	-3.487546788	0.465803728	4.69E-136	2.70E-133
ANO1	-2.868561416	5.461105992	9.81E-134	5.48E-131
C3orf36	-3.509127685	0.36085329	1.07E-131	5.80E-129
ATP13A4	-4.250554958	-0.531092553	1.48E-130	7.79E-128
SLC13A2	-6.292561769	1.033617138	4.23E-129	2.16E-126
KCNJ5	-3.119719349	3.007097953	7.69E-129	3.82E-126
PNMT	-4.667142036	1.022812758	2.83E-127	1.37E-124
STAC2	-4.416170051	3.417454375	8.66E-126	4.08E-123
ABCG2	-2.809960333	3.970415449	4.78E-124	2.19E-121
FAM83A	-5.078067363	-0.012191609	3.78E-123	1.69E-120
SLC16A12	-3.749170694	0.162005786	5.37E-121	2.34E-118
SEMG2	-9.505742358	10.32686946	8.68E-120	3.69E-117
C1orf186	-3.363933794	0.80475646	6.92E-119	2.88E-116
PAQR8	-2.568199676	3.692816808	4.02E-118	1.63E-115
UGT2B7	-5.583084346	-0.640545992	7.63E-118	3.03E-115
MRO	-3.090785129	-0.234389189	1.54E-116	5.97E-114
SLCO4C1	-4.798092265	-0.639044646	3.84E-116	1.46E-113
ACE2	-3.568169252	0.516117235	6.46E-114	2.41E-111
FUT3	-4.111844574	0.379086415	6.37E-113	2.33E-110
PTGES	-3.039801329	4.655930611	4.92E-112	1.76E-109
HS3ST5	-4.914778132	-1.407416204	2.03E-110	7.10E-108
KIRREL3	-3.012684881	-0.860795205	2.44E-109	8.40E-107
SEMG1	-9.757312184	11.35548942	3.89E-108	1.31E-105
DEFB129	-6.866593977	-2.315654961	2.00E-107	6.62E-105
PAX2	-4.064900582	0.376708484	2.81E-106	9.13E-104
PIK3C2G	-4.380016398	0.469725146	1.07E-102	3.40E-100
SLC46A2	-4.113213363	-1.409293159	3.17E-102	9.95E-100
SNAP25	-3.062100018	2.046817113	1.04E-96	3.21E-94
LPL	-3.698585	3.897033258	1.73E-96	5.25E-94
PLA2G4A	-2.306657328	3.506160074	5.45E-96	1.62E-93
НОХВ9	-3.738394139	1.187071894	6.96E-96	2.04E-93
POU3F3	-7.820353855	1.441534386	1.02E-93	2.93E-91
SLC28A3	-4.429709489	-0.22811352	4.13E-91	1.17E-88
GSTM3	-2.283273278	5.654161731	4.79E-91	1.34E-88
FRMD3	-2.232713406	2.362727796	5.80E-91	1.60E-88
EVA1A	-2.609102352	0.046188518	6.32E-91	1.71E-88
PRDM16	-2.585618819	0.810572803	5.09E-90	1.36E-87
FBP2	-3.625501212	-0.395808669	9.04E-90	2.38E-87
GCNT4	-2.419664765	1.308525087	2.55E-89	6.62E-87
CLU	-2.575286197	9.076442775	1.20E-88	3.06E-86
EDDM3A	-9.915750757	0.930978027	1.71E-88	4.30E-86
KCNJ16	-5.300617001	1.33688112	9.23E-88	2.29E-85
KCNJ15	-3.274002031	1.948780543	1.64E-87	4.02E-85
PATE1	-8.559529455	4.39114703	4.70E-87	1.14E-84
KRT24	-4.993860718	-2.05900135	1.41E-86	3.36E-84
SULT2A1	-6.511620056	-1.487548002	1.54E-84	3.58E-82
NPFFR2	-4.628734826	-1.871185299	1.24E-82	2.84E-80
GNAO1	-2.487785948	3.631013922	4.77E-81	1.08E-78
DEFB131A	-7.992232167	-2.717399459	1.12E-79	2.51E-77

Gene	logFC	logCPM	PValue	FDR
PDK4	-3.01435869	6.971020626	2.35E-79	5.19E-77
UNC5B	-2.199076184	5.027632209	2.67E-79	5.83E-77
 CAMP	-3.53381043	-1.328045181	9.63E-78	2.08E-75
 SLC31A2	-2.111149911	0.324281459	2.44E-77	5.20E-75
 PON3	-3.31897902	-0.714040817	1.52E-76	3.20E-74
 ADCY8	-4.727507179	-2.378656903	2.96E-76	6.15E-74
 TMEM238L	-3.460883798	0.330286585	3.96E-76	8.14E-74
 EDDM3B	-9.095154357	-1.282761718	1.53E-75	3.08E-73
 LHX1	-6.152126939	-2.569155343	2.06E-75	4.09E-73
 TMEM171	-2.978213867	-2.490124781	2.99E-73	5.88E-71
 ELSPBP1	-5.964830301	-2.613099778	9.37E-73	1.82E-70
 QPRT	-2.396260233	2.787898063	2.12E-72	4.07E-70
 FAM167A	-2.899049257	2.215708554	1.58E-71	3.00E-69
 RASAL1	-3.075775921	0.258555744	1.90E-71	3.57E-69
 G0S2	-2.281974698	2.740748523	1.01E-70	1.89E-68
 SLC26A3	-4.713543952	4.255428037	4.42E-70	8.15E-68
 GLIS3	-2.10224676	3.141701783	5.68E-69	1.04E-66
 ADTRP	-3.145256188	1.796113975	1.34E-67	2.38E-65
 PATE3	-5.878495255	-2.049038515	6.54E-67	1.12E-64
 PAX8	-3.163424949	2.312640932	4.67E-66	7.95E-64
 PALM3	-2.862055728	1.75017837	2.61E-65	4.36E-63
 SLPI	-3.550360086	5.950826934	3.38E-65	5.60E-63
 SCGB1D4	-6.616957825	-3.643904883	1.38E-64	2.27E-62
 CA14	-2.628944503	1.565656785	1.41E-64	2.29E-62
 GRXCR1	-7.152527699	-1.442456622	4.35E-64	7.00E-62
 PTGS2	-3.018672047	6.0997409	6.74E-64	1.08E-61
 DEFB125	-7.823009219	-3.088436223	1.21E-63	1.90E-61
 SP6	-2.048223343	2.495992609	1.74E-63	2.70E-61
 LIPG	-2.797035036	2.502758674	2.57E-63	3.96E-61
 HOXB7	-2.538554469	1.469159627	4.12E-63	6.24E-61
 AOX1	-2.401455097	4.820050441	7.83E-63	1.18E-60
 SIM1	-5.801689063	-1.342000003	8.05E-63	1.20E-60
 TRIM9	-2.21544454	-0.284214026	1.28E-60	1.86E-58
 MUCL1	-3.994926646	1.918418391	1.13E-59	1.61E-57
 TEDDM1	-3.162014508	-2.397478949	1.84E-59	2.62E-57
 GDPD2	-2.614839978	-2.578615619	1.32E-58	1.84E-56
 CYP4F8	-4.234944216	5.957323259	4.62E-58	6.40E-56
 HSPA6	-3.56230163	3.163452791	1.40E-57	1.93E-55
 PTGS1	-2.488186912	4.442555664	1.50E-57	2.05E-55
 HOXB5	-3.507475786	-0.118278523	2.93E-57	3.94E-55
 ARC	-2.791928795	1.302315162	5.92E-57	7.79E-55
 C2orf88	-2.342319604	2.417718221	7.27E-57	9.48E-55
 APOBEC3C	-2.037731259	4.968381179	1.06E-56	1.37E-54
 TFAP2B	-3.887211428	-2.562766626	2.07E-56	2.66E-54
 PADI3	-4.318296193	0.033579355	5.97E-56	7.63E-54
 CES5A	-5.399715292	-2.273300712	6.88E-55	8.60E-53
 ATP1A4	-2.650615554	-0.8604139	1.12E-54	1.39E-52
 CCDC27	-2.230774182	-2.116580292	4.27E-54	5.27E-52
 WFDC9	-7.370447463	-3.418331864	1.29E-53	1.59E-51

Gene	logFC	logCPM	PValue	FDR
DCAF12L1	-3.039717642	-2.084125111	3.70E-53	4.50E-51
SBSPON	-2.274088177	3.432870313	1.42E-52	1.70E-50
DUSP2	-2.374155832	4.249770546	1.06E-51	1.22E-49
EPHA10	2.181110197	3.496632325	5.18E-51	5.87E-49
GSTP1	-2.053371722	6.920002831	1.40E-50	1.55E-48
LMO3	-2.170273005	3.259518865	5.16E-50	5.52E-48
CXCR2	-2.604659545	-0.234591526	1.54E-49	1.62E-47
LYVE1	-2.250739542	1.531070033	6.82E-49	7.09E-47
VWA5B2	-2.355784274	1.103997608	1.52E-48	1.56E-46
ANGPT1	-2.047422403	3.901247666	1.86E-48	1.90E-46
MUC6	-4.984635603	7.087473698	2.08E-48	2.10E-46
WFDC8	-4.53427633	-4.039274837	2.45E-48	2.46E-46
DEFB127	-6.707184857	-3.923081354	6.20E-48	6.16E-46
LCN15	-3.320802889	-0.939497584	6.94E-48	6.86E-46
AL163195.3	-3.923578432	-4.064090252	7.69E-48	7.55E-46
DEFB132	-2.327019581	2.024711463	1.45E-46	1.39E-44
TNMD	-3.2653763	-1.061318979	2.36E-46	2.24E-44
TMEM132C	-2.486194486	1.508679117	2.43E-46	2.30E-44
HRASLS5	-2.182632517	0.139647911	2.89E-46	2.72E-44
SI C9A4	-3.17506859	-2.826706326	3.82F-46	3.58F-44
SCN11A	-2.21835192	-1.749469071	9.22E-46	8.54F-44
DUOX1	-2.137499241	4.097778228	1.46F-45	1.34F-43
MUC15	-2.661608288	1.132262497	2.45F-44	2.19F-42
TRPM5	-3 176120461	-0.890607598	3 48F-44	3 10F-42
SIC39A2	-3 854360669	2 020647601	5 33F-44	4 72F-42
TRPM3	-2 29500896	-0.137630395	6 04F-44	5 32F-42
	-2.893980809	_2 015181875	3 56F-43	3.05F_41
TPIM61	_2.0293200009	_2.615101075	J.JOE-43	3.05E-41
HPN	2.020527421	8 064534927	1.06E-42	8 01F_41
KI HI A	_2.030001565	_0.004334927	1.002-42	1 555-10
CATA3	_2.057771	3 782637/70	2 305-42	1.015-40
GPD1	-2.202255741	_0.21002/8/0	2.302-42	3.245-40
	-2.390403013	-0.219024049	J.92E-42	2 00E 40
	-3.436723776	-3.034312029	4.04E-42	J.99E-40
	-2.107/90425	1 102274077	6 205 42	4.92E-40
	-2.976905257	-1.102574977	1 505 41	1 105 20
MATIA C20arf202	-2.84/22049/	-1.240774796	1.50E-41	2.205.20
C200ff202	-2.009368734	-2.563236881	2.80E-41	2.20E-39
HCAR2	-2.004843097	1.194232598	6.33E-41	4.94E-39
ASPA	-2.0/852/2//	1.495235978	6.77E-41	5.26E-39
KUNJI	-2./62883/64	-2.903446081	1.75E-40	1.33E-38
STAC	-2.388338573	2.991906842	1.81E-40	1.36E-38
GPX2	-2.515514209	2.45210946	1.96E-40	1.4/E-38
DCHS2	-2.148971591	0.710909297	5.37E-40	3.95E-38
C10ort99	-3.579716304	-2.223557443	6.29E-40	4.59E-38
PCP4L1	-2.206007918	1.907712695	8.99E-40	6.45E-38
DMRT2	-2.991089671	-2.296521924	1.56E-39	1.11E-37
CLDN19	-2.531145647	-2.60827072	1.71E-39	1.22E-37
IVL	-3.726131389	-1.441202673	2.34E-39	1.66E-37
SLC34A2	-3.167340855	3.466038276	5.84E-39	4.05E-37

Gene	logFC	logCPM	PValue	FDR
SLC18A2	-2.562912473	1.63627357	1.20E-38	8.23E-37
 NKX2-3	4.295926347	0.960315432	1.82E-38	1.24E-36
 PLCZ1	-3.528460242	-4.111131902	2.16E-38	1.46E-36
 SH2D1B	-2.070812969	-2.247153696	2.30E-38	1.55E-36
 CCNI2	-2.393120663	-0.757806717	4.32E-38	2.89E-36
 OVCH2	-2.474604409	-1.229899903	4.36E-38	2.91E-36
 FOXQ1	-2.113706442	2.340709388	1.77E-37	1.15E-35
 KCNS1	-2.740616324	0.817741242	1.92E-37	1.24E-35
 REG3G	-5.362768922	-3.996026989	2.04E-37	1.31E-35
 C21orf62	-2.497748317	0.055828895	2.58E-37	1.65E-35
 LCN1	-6.139941235	-1.286853617	4.00E-37	2.53E-35
 EPHB1	-2.071871109	1.406334339	4.28E-37	2.69E-35
 КҮ	-2.334715222	-0.154030942	4.95E-37	3.09E-35
 SLC6A2	-2.10678614	-1.995090013	6.49E-37	4.03E-35
 KCNH5	-3.179639439	-2.263489674	1.54E-36	9.37E-35
 SIM2	2.246683676	6.39245743	2.10E-36	1.26E-34
 SIAH3	-2.391041994	-2.100220433	2.26E-36	1.36E-34
 TMEM213	-2.938009836	-0.973458402	3.77E-36	2.25E-34
 HOXB4	-2.013128998	0.556074277	4.13E-36	2.44E-34
 WFDC2	-2.278298566	5.691380285	6.46E-36	3.76E-34
 SYT8	-2.62796781	-0.04504407	9.39E-36	5.40E-34
 RAD21L1	-3.931426302	-4.029582937	1.14E-35	6.49E-34
 JPH4	-2.032898156	3.896512339	1.52E-35	8.59E-34
 CLCA2	-2.99069792	1.679389133	2.18E-35	1.22E-33
 GSTM1	-3.348712796	3.902420778	2.36E-35	1.31E-33
 LY6D	-3.253162593	0.960481773	4.33E-35	2.40E-33
 LRCOL1	-2.383609469	-2.229173553	4.98E-35	2.74E-33
 KRT222	-2.281961674	-0.980864847	8.50E-35	4.62E-33
 CST4	-3.656991558	1.448466198	9.21E-35	4.96E-33
 NEFM	-2.864624272	0.554358796	1.63E-34	8.52E-33
 DUOX2	-2.585503889	2.635300446	1.67E-34	8.69E-33
 OPCML	-2.590292577	-1.566109784	2.15E-34	1.11E-32
 DUOXA2	-2.845461401	-0.495623973	2.55E-34	1.29E-32
 PDE1C	-2.216681928	0.951037818	4.56E-34	2.27E-32
 MSLN	-2.673143906	2.312078872	9.59E-34	4.63E-32
 ATP6V1G3	-3.407739337	-2.880382936	1.15E-33	5.49E-32
 PRSS1	-4.522834207	-1.662313282	3.21E-33	1.50E-31
 FOXI2	-2.306900792	-2.155968961	3.52E-33	1.64E-31
 DCC	-2.459225535	-0.956958564	4.76E-33	2.20E-31
 DUOXA1	-2.155945912	2.560577531	2.07E-32	9.23E-31
 EMX1	-2.835853169	-3.197852638	2.31E-32	1.03E-30
 LVRN	-2.019593234	-2.758757798	4.93E-32	2.12E-30
 CYP4B1	-2.165077764	3.831392901	5.23E-32	2.24E-30
 TRH	-2.994128142	-3.124637854	8.51E-32	3.59E-30
 HCAR3	-2.221534692	-1.323656559	9.86E-32	4.13E-30
 ITLN1	-2.679097356	-0.945384899	1.00E-31	4.18E-30
 SYT10	-2.319711561	-1.05820299	3.21E-31	1.29E-29
 ADRA1A	-2.022518109	2.151912159	4.83E-31	1.93E-29
 CDH8	-2.263389081	-0.939571117	5.72E-31	2.28E-29

Gene	logFC	logCPM	PValue	FDR
TMEM252	-2.122053299	0.986298859	8.91E-31	3.52E-29
AQP5	-2.201067826	-0.242796203	9.48E-31	3.74E-29
РҮҮ	-2.304539289	-2.689358214	9.95E-31	3.91E-29
HOXD4	-2.010658856	-1.667951124	1.07E-30	4.18E-29
ASTL	-2.271544473	-2.255063905	1.29E-30	4.99E-29
FOLR1	-2.267963855	0.443328675	1.60E-30	6.16E-29
MGAT4C	-2.127179772	-1.600917474	2.23E-30	8.48E-29
LRRC3B	-2.226821286	-3.265920448	2.37E-30	8.95E-29
KCNF1	-2.008639046	-1.489871946	2.41E-30	9.07E-29
CRNN	-4.196298519	-3.602598059	3.11E-30	1.16E-28
IL1RL1	-2.164943372	0.580067069	4.59E-30	1.69E-28
IGSF1	-2.205150167	1.353299712	5.01E-30	1.84E-28
CDO1	-2.25897076	3.975578364	6.05E-30	2.21E-28
UCN	2.225028987	0.886371038	6.40E-30	2.32E-28
AMACR	3.271375874	7.272807932	1.43E-29	5.08E-28
GLRA4	-2.291078633	-3.061966898	1.61E-29	5.68E-28
CAPN6	-2.167733352	3.083222877	1.67E-29	5.88E-28
KCNJ13	-2.677244912	-2.098731552	2.33E-29	8.06E-28
ROS1	-2.664547966	-1.41857366	2.56E-29	8.87E-28
MEI4	-2.157511068	-3.504964788	2.79E-29	9.63E-28
SLC45A2	5.233859283	3.020506268	3.11E-29	1.07E-27
CYP4F22	-2.48815109	1.361704428	4.42E-29	1.50E-27
CLPSL1	-3.884589239	-3.179552875	7.45E-29	2.49E-27
EVX2	-2.201786126	0.147793705	1.24E-28	4.07E-27
KRT16	-2.392624596	2.060345166	1.80E-28	5.83E-27
FAM83C	-2.840632484	-1.823672187	2.44E-28	7.86E-27
CHIA	-4.044693208	-3.761939133	2.80E-28	8.97E-27
CFAP65	2.17924865	1.923214285	4.94E-28	1.57E-26
IL20	-2.734032718	-2.568179433	1.09E-27	3.38E-26
HSD17B13	-2.59308437	2.765460154	1.20E-27	3.67E-26
ATP6V0D2	-2.062948021	-0.049347798	1.43E-27	4.33E-26
FNDC10	2.189675352	3.1851198	1.43E-27	4.34E-26
CLPSL2	-2.9526799	-3.435156672	4.32E-27	1.25E-25
LGR6	-2.077080456	2.417215605	6.96E-27	1.99E-25
S100A14	-2.094417081	2.768825991	7.06E-27	2.01E-25
SFRP5	-2.760385146	0.642123766	7.15E-27	2.04E-25
NETO2	2.090951916	3.425360608	1.14E-26	3.22E-25
LMX1B	2.910958396	1.214627903	1.29E-26	3.60E-25
GJB4	-2.106346704	-0.022277162	2.07E-26	5.69E-25
SLITRK3	-2.314417037	0.590359859	2.24E-26	6.13E-25
CDH16	-3.658293176	-2.481108891	2.75E-26	7.49E-25
ACTC1	-2.549775894	5.199099142	3.86E-26	1.03E-24
IL19	-2.963272464	-4.136314081	4.35E-26	1.16E-24
LINGO2	-2.353643152	-1.61961467	2.36E-25	5.84E-24
TGM5	-2.041707954	-1.130721222	2.51E-25	6.21E-24
FAM83B	-2.016553537	0.635021108	3.30E-25	8.00E-24
DNAH5	2.32012031	5.526858819	4.15E-25	1.00E-23
CYP3A5	-2.005756625	3.220640626	4.78E-25	1.15E-23
KRT13	-2.974414253	5.283076591	5.95E-25	1.42E-23

Gene	logFC	logCPM	PValue	FDR
LINC00694	-2.00291498	-2.423117021	7.37E-25	1.75E-23
SCARA5	-2.212531236	1.054207669	7.76E-25	1.84E-23
PLA2G3	-2.484369479	-2.123775808	8.97E-25	2.12E-23
SLIT1	2.991124143	4.235802648	9.13E-25	2.15E-23
ADAMTS18	-2.485445465	-1.555485261	9.65E-25	2.26E-23
ATP4B	-2.170350626	-3.615853337	2.04E-24	4.61E-23
MATN4	-2.253033183	-1.39482938	3.30E-24	7.32E-23
C2orf72	2.352501555	6.112412268	3.37E-24	7.45E-23
CBLN4	-2.282088492	-2.141588262	3.46E-24	7.64E-23
HRASLS	-2.750037652	-2.668890752	4.62E-24	1.01E-22
PENK	-2.157694308	2.279458961	5.35E-24	1.17E-22
CCDC198	-3.361534597	-3.550866101	6.39E-24	1.38E-22
 BTN1A1	-2.058438498	-3.223659882	8.65E-24	1.84E-22
TG	-2.866055894	5.040539624	9.02E-24	1.91E-22
 SMR3B	-4.345403915	-1.407810214	9.65E-24	2.04E-22
 C2CD4C	2.365102335	1.292132594	1.03E-23	2.16E-22
ATP6V0A4	-2.469261417	-0.171828266	1.44E-23	2.99E-22
C1orf61	-2.037014861	-1.442631941	2.23E-23	4.54E-22
 SERPINB5	-2.026028458	3.221299557	2.88E-23	5.82E-22
 OR7C1	-2.022970619	-2.050624749	3.09E-23	6.23E-22
 KBTBD13	-2.109275337	-3.695224421	3.30E-23	6.63E-22
 TH	-2.763714651	-1.950206659	3.39E-23	6.81E-22
 MATK	2.589971629	3.389770366	3.57E-23	7.14E-22
 ARHGAP19-SLIT1	3.000318492	-2.097085148	4.54E-23	9.00E-22
 PAQR6	2.309347403	3.648588239	7.11E-23	1.37E-21
 CIDEC	-2.214864174	-1.468234676	7.64E-23	1.47E-21
 FADS6	-2.326944554	-3.777201655	1.38E-22	2.59E-21
 DPP6	-2.186696088	0.124736584	1.39E-22	2.61E-21
 WIF1	-2.21507643	2.513039346	1.94E-22	3.57E-21
 CPB2	-2.040650414	-2.684359228	2.11E-22	3.86E-21
 APOC1	2.315598498	4.432027844	2.22E-22	4.06E-21
 NLRP12	2.474330308	1.187055602	2.27E-22	4.14E-21
 CPNE6	-2.170399828	1.772299025	2.49E-22	4.53E-21
 HOXC6	2.328170608	3.774272822	2.79E-22	5.03E-21
 HOXC4	2.31331291	2.665774136	2.79E-22	5.03E-21
 ARSF	-2.138562635	-2.870411011	2.97E-22	5.34E-21
 CERS1	2.553768773	1.469026165	3.80E-22	6.80E-21
 TRIM31	-2.091716954	0.490285758	5.70E-22	1.00E-20
 ATP2B3	-2.394530451	-3.269639342	7.38E-22	1.29E-20
 ANKRD66	2.801025739	-0.784999268	9.06E-22	1.57E-20
 MMP26	3.066474235	1.352487044	9.41E-22	1.62E-20
 KCNA4	-2.346476072	-2.699325651	1.18E-21	2.01E-20
 MUC21	-3.114340581	-2.477022768	1.22E-21	2.08E-20
 CLEC18B	2.167387184	-1.095435957	1.69E-21	2.84E-20
 TMEM196	-2.596176551	-3.648797811	2.57E-21	4.24E-20
 CCDC78	2.642490882	2.309466825	2.97E-21	4.87E-20
 EPGN	-2.120950779	-2.692080174	3.34E-21	5.46E-20
 DEFB134	-2.58614525	-4.035042203	3.75E-21	6.09E-20
 GAS2L2	-2.487311305	-1.119961385	5.49E-21	8.72E-20

Gene	logFC	logCPM	PValue	FDR
CHP2	-2.13935326	1.031772412	5.59E-21	8.87E-20
FAM163A	-2.082472426	-2.065990547	9.75E-21	1.52E-19
TNFSF11	-2.003738684	-2.569011336	1.24E-20	1.90E-19
KRT27	-2.305026411	-3.966447429	1.69E-20	2.55E-19
SCGB1A1	-2.475823685	3.909002352	2.53E-20	3.75E-19
COLEC10	-2.558276109	-2.501754928	3.26E-20	4.77E-19
APOF	2.433781339	3.137119857	4.46E-20	6.45E-19
PDIA2	4.280402557	2.013335255	4.70E-20	6.77E-19
ADRB3	-2.365978611	-2.540179574	5.72E-20	8.14E-19
FLG2	-2.599596026	-2.865814995	6.83E-20	9.67E-19
SHISA8	2.993519423	-0.189202204	6.86E-20	9.69E-19
TMPRSS11A	-2.790567956	-1.570310054	9.22E-20	1.29E-18
RPE65	-2.175383876	-0.00527736	1.31E-19	1.80E-18
HJURP	2.068082168	2.187879526	1.34E-19	1.85E-18
CCDC83	3.229819171	-1.017747147	1.44E-19	1.96E-18
ACSM1	2.868523218	6.613879148	1.57E-19	2.13E-18
CLCA4	-2.496145495	1.627115296	1.66E-19	2.25E-18
C10orf82	-2.135397958	-0.911355049	2.24E-19	2.98E-18
KCNK10	-2.011525621	-2.711656881	2.32E-19	3.08E-18
TERT	2.688569503	-1.772060648	2.39E-19	3.16E-18
EPPIN	-2.691805498	-3.769965344	2.52E-19	3.32E-18
DMBT1	-2.236532941	0.1096238	3.62E-19	4.67E-18
ONECUT2	2.681251387	3.221606201	3.64E-19	4.69E-18
SFTPC	-2.25322321	-3.281266307	5.39E-19	6.82E-18
TWIST1	2.177091444	3.574725101	9.65E-19	1.19E-17
FAM196B	-2.217220736	-1.695478869	1.03E-18	1.27E-17
PHGR1	3.386311578	1.820119662	1.36E-18	1.66E-17
MOV10L1	2.27846602	1.581465328	1.41E-18	1.71E-17
TBX4	-2.17375547	2.268146306	1.58E-18	1.92E-17
АМН	3.230456823	1.135656782	1.79E-18	2.16E-17
ZIC2	3.465784012	2.099443841	1.95E-18	2.35E-17
REN	-2.010856028	-1.82427371	2.05E-18	2.46E-17
ARL14	-2.041449796	-2.836582438	2.77E-18	3.27E-17
GPR149	-3.565113736	-2.173936635	2.97E-18	3.49E-17
CACNA1D	2.177413498	5.843737038	3.34E-18	3.89E-17
NOX4	2.005839671	1.199904726	4.41E-18	5.07E-17
SCGB3A1	-2.174104533	2.495869638	7.08E-18	8.03E-17
FOXN4	2.808885496	-0.819378366	8.85E-18	9.88E-17
DLX1	2.964944227	5.245627	1.43E-17	1.56E-16
ARHGDIG	2.722116583	1.951835142	1.80E-17	1.94E-16
F2RL2	2.081512112	0.759279249	2.12E-17	2.26E-16
LCN8	-2.945514338	-3.234638837	2.79E-17	2.94E-16
OTX1	2.103182365	3.115942657	2.93E-17	3.08E-16
KRT4	-2.137873946	2.801389922	4.58E-17	4.75E-16
ALB	4.431655563	3.09043822	6.92E-17	7.03E-16
TSPAN19	3.208847265	0.730279277	9.00E-17	9.05E-16
GNG13	2.803827842	0.126341753	1.01E-16	1.01E-15
DSG4	-2.466048424	-2.345854057	1.03E-16	1.03E-15
EFNA2	3.057267493	-1.886740535	1.45E-16	1.43E-15

Gene	logFC	logCPM	PValue	FDR
CCER2	2.000918092	-0.3544635	1.48E-16	1.45E-15
FAM163B	-2.321266796	-2.413589392	1.63E-16	1.60E-15
WFDC13	-2.806598091	-3.536010249	1.88E-16	1.83E-15
ULBP1	2.15541201	-1.028236929	1.89E-16	1.84E-15
OR51E2	2.414972238	9.179968408	2.69E-16	2.59E-15
TGM3	2.329959919	3.971772096	3.43E-16	3.25E-15
MIOX	2.023651528	-0.851072617	6.30E-16	5.82E-15
VGF	2.505950604	1.28386305	6.83E-16	6.28E-15
OR51S1	3.289112641	-3.044498407	1.27E-15	1.14E-14
KISS1R	3.422260325	-2.414859811	1.44E-15	1.28E-14
HTR1E	-2.206015072	-3.426655036	1.62E-15	1.42E-14
GLYATL1B	2.200776254	-0.628848988	1.84E-15	1.60E-14
KLK15	2.046781312	2.991115701	1.94E-15	1.67E-14
THRSP	-2.470893848	-0.92431372	2.09E-15	1.80E-14
ANGPTL3	3.829532766	1.319655772	2.86E-15	2.43E-14
TDRD1	2.968954599	4.312041873	4.32E-15	3.60E-14
TNN	2.314343045	-0.352090036	4.70E-15	3.90E-14
FOXD1	2.796864479	1.801714027	4.83E-15	4.00E-14
DEFB126	-2.714005591	-1.975045093	6.47E-15	5.29E-14
MYH6	-2.531908454	0.826728283	1.06E-14	8.52E-14
OR51H1	3.267819899	-3.615043094	1.09E-14	8.69E-14
SPON2	2.315586856	10.45792138	1.10E-14	8.78E-14
ZMYND10	2.085925052	1.832701834	1.13E-14	9.04E-14
ZP1	2.210730897	0.676381856	1.32E-14	1.04E-13
KRTAP5-1	2.140411485	-1.919084242	1.36E-14	1.07E-13
SLC22A10	3.112889405	0.336771949	1.63E-14	1.27E-13
NUTM2F	2.599677343	-2.440419577	1.81E-14	1.40E-13
C11orf87	-2.120433611	-3.11909289	2.06E-14	1.59E-13
SMIM28	2.307959645	-1.425734172	2.32E-14	1.77E-13
AC233992.2	2.188468656	-2.988603347	2.55E-14	1.94E-13
TRPC5	-2.627768694	-3.195666087	2.61E-14	1.99E-13
ADGRG4	-2.227928687	-4.008538955	3.07E-14	2.32E-13
DLX2	2.520792049	1.771274957	3.45E-14	2.59E-13
AC013470.2	2.37626599	-2.264634427	3.74E-14	2.80E-13
12-Sep	2.32842503	-1.614438692	3.83E-14	2.87E-13
CHRM2	-2.627807986	-0.761918657	4.63E-14	3.42E-13
PLPPR5	-2.051535096	-3.828879148	4.65E-14	3.44E-13
KLB	2.917388689	2.020757836	5.17E-14	3.79E-13
KRT20	3.970669871	-0.213705133	5.31E-14	3.90E-13
SRARP	3.763182115	4.202486163	5.51E-14	4.04E-13
BAIAP2L2	2.226024178	2.628704883	5.96E-14	4.35E-13
HIST1H4E	2.159254954	1.043399573	7.18E-14	5.20E-13
BRSK2	2.354199485	2.719801489	7.53E-14	5.44E-13
AK5	2.022452828	3.960729447	8.23E-14	5.91E-13
EPHA8	2.42213167	-0.482075108	1.34E-13	9.40E-13
HBQ1	3.058254424	-2.360212262	1.94E-13	1.34E-12
DLL3	2.036697223	-0.709591972	2.50E-13	1.71E-12
ATP8A2	2.805192641	3.941027197	2.73E-13	1.85E-12
UGT3A1	-2.300754877	-2.195684518	2.90E-13	1.96E-12

Gene	logFC	logCPM	PValue	FDR
NKX6-1	3.539257475	-0.069017009	3.14E-13	2.11E-12
FOXB2	4.120786237	-0.339067966	3.43E-13	2.29E-12
OR2B6	2.070727347	-1.791175567	3.50E-13	2.34E-12
ZIC5	3.400800848	0.951706604	3.68E-13	2.45E-12
B3GNT6	4.168735091	3.52191008	4.20E-13	2.78E-12
FGL1	3.035621437	1.63122323	4.37E-13	2.88E-12
TFF3	2.769530436	8.238324054	8.51E-13	5.41E-12
CST2	3.537958116	4.052951673	9.02E-13	5.71E-12
FOXL2	2.386028893	1.084381767	9.59E-13	6.06E-12
TBX10	3.419608802	1.522870413	1.20E-12	7.46E-12
RHCG	-2.008813569	0.619765959	1.42E-12	8.83E-12
NLRP13	2.952695433	-1.963847664	1.51E-12	9.33E-12
ISG15	2.015582231	5.871285045	1.62E-12	9.94E-12
FEZF1	2.983525183	-2.371592675	1.62E-12	9.98E-12
UPK1B	-2.479748949	-1.685662964	1.77E-12	1.09E-11
FABP5	2.55866377	5.395196065	1.92E-12	1.18E-11
NR2E1	3.803357172	-1.451927234	2.09E-12	1.27E-11
SPINK1	4.492947788	4.716448182	2.20E-12	1.34E-11
FUT6	-2.34107223	-0.394817546	2.42E-12	1.46E-11
HOXC12	4.618237944	-0.951730916	2.59E-12	1.55E-11
OLFM4	-2.001351853	7.271508686	2.61E-12	1.57E-11
ANKRD30A	6.088697199	0.552547891	2.75E-12	1.64E-11
SPZ1	7.464030724	1.177592669	3.19E-12	1.90E-11
HOXC13	3.203398538	-1.939843545	4.23E-12	2.47E-11
CLC	-2.056516349	-3.77853227	4.31E-12	2.51E-11
RPRML	2.940731461	-1.095714471	4.65E-12	2.70E-11
OR51T1	2.54982834	-2.792011523	5.76E-12	3.32E-11
FOXI1	-2.138580221	1.090697338	6.04E-12	3.47E-11
NKAIN1	2.258465266	4.792143603	6.04E-12	3.47E-11
DNAH8	2.464627376	5.112883427	7.54E-12	4.27E-11
WFDC6	-2.255684544	-3.632961702	7.55E-12	4.28E-11
COL10A1	2.453464464	3.270292451	7.57E-12	4.29E-11
COMP	2.16226434	5.850848074	8.07E-12	4.56E-11
SPRR3	-2.650341647	-2.524440816	8.16E-12	4.61E-11
ERG	2.494207074	6.99904595	9.37E-12	5.25E-11
SSTR1	2.060786454	4.37450598	1.04E-11	5.80E-11
UGT2B4	3.221566911	2.827464057	1.08E-11	5.99E-11
IL36RN	3.03414543	-1.504655432	1.26E-11	6.97E-11
C19orf81	2.546159141	1.113739849	1.30E-11	7.16E-11
VAX1	3.961513127	-2.632789163	1.64E-11	8.92E-11
LRRTM3	-2.107441126	-1.24681776	1.91E-11	1.03E-10
FAM57B	2.031437105	-0.698387388	2.09E-11	1.13E-10
GRIN3A	2.638844764	4.65540954	2.23E-11	1.20E-10
TUBB4A	2.469186771	2.047892023	2.36E-11	1.26E-10
ADAM29	-2.02667846	-3.775698756	2.84E-11	1.50E-10
BMP5	-2.18782084	2.684465934	4.71E-11	2.43E-10
COL2A1	3.785158888	6.15210744	4.83E-11	2.48E-10
KRT72	3.761702653	-1.981764703	5.03E-11	2.58E-10
BARX1	2.391463924	-1.658459129	5.47E-11	2.80E-10

Gene	logFC	logCPM	PValue	FDR
ROPN1L	2.092640047	-0.046359297	5.55E-11	2.83E-10
ARMC3	2.136397252	0.189599604	6.22E-11	3.16E-10
PROC	2.67020989	1.131805312	7.29E-11	3.67E-10
KCNG3	2.132031411	2.045373485	9.35E-11	4.64E-10
PCDHA1	2.795627976	0.375523362	1.20E-10	5.89E-10
UNC5A	2.709726989	3.92396467	1.24E-10	6.07E-10
SUCNR1	3.081480451	1.536548908	1.41E-10	6.85E-10
SMIM21	3.427582218	-2.986773972	1.60E-10	7.73E-10
ETV4	3.816023431	5.623026412	1.67E-10	8.03E-10
SERPINA11	2.404577025	2.545674419	1.74E-10	8.34E-10
GBX2	4.378429224	-2.072125849	1.79E-10	8.57E-10
CDC20B	4.150567923	1.534510645	1.84E-10	8.79E-10
GJA3	2.040848411	0.77159763	1.88E-10	8.94E-10
C1QTNF9B	2.025651594	0.385827111	1.89E-10	9.01E-10
SMIM23	2.240012939	-3.890952299	3.15E-10	1.46E-09
CRYGD	-2.157881056	-3.558055362	3.46E-10	1.60E-09
GRPR	2.082638062	1.422602298	4.01E-10	1.84E-09
SLC22A31	2.15465431	1.682264922	4.15E-10	1.90E-09
ZNF560	3.579830078	0.907262077	4.42E-10	2.02E-09
PTPRR	2.677564298	1.278570082	4.65E-10	2.11E-09
SFTPA2	2.026666077	6.660829826	4.67E-10	2.12E-09
HAO1	3.180714369	-0.216881708	5.37E-10	2.43E-09
CHIT1	2.124877061	3.520488959	6.25E-10	2.80E-09
DMBX1	2.075728929	-2.899045915	6.67E-10	2.98E-09
UTS2B	2.623610217	0.763054819	7.50E-10	3.33E-09
PNMA5	5.583595807	1.256206222	7.52E-10	3.33E-09
TTR	2.263010905	1.534436019	7.85E-10	3.47E-09
CER1	-2.01557727	-3.982760873	8.51E-10	3.74E-09
GMNC	2.222390659	1.731673014	9.70E-10	4.23E-09
TGM4	-2.299530484	9.058863089	1.06E-09	4.62E-09
KRT73	2.784757012	-3.396159935	1.60E-09	6.83E-09
SLC24A2	2.263093544	0.036838795	1.70E-09	7.21E-09
ANKRD30B	3.073498165	-1.41579624	1.91E-09	8.05E-09
FEZF2	5.1526634	-2.123364605	1.95E-09	8.20E-09
NKX6-3	2.059995247	-2.900165006	1.98E-09	8.34E-09
OR52I1	2.176973868	-3.001764047	2.05E-09	8.58E-09
CAMKV	2.881570973	-2.038814296	2.86E-09	1.18E-08
NOTUM	2.308455321	0.786652156	4.24E-09	1.70E-08
SFTA3	-2.106019445	-2.466203685	4.27E-09	1.71E-08
POU4F1	3.693208616	-2.095987674	4.39E-09	1.76E-08
IL1F10	2.260744127	-3.909896446	4.80E-09	1.91E-08
PBOV1	2.085675747	-2.154992386	7.36E-09	2.85E-08
DIO1	2.26987907	0.891743028	7.38E-09	2.86E-08
NETO1	3.568491117	0.942120675	8.02E-09	3.10E-08
PPP3R2	2.570526002	-2.677368344	8.10E-09	3.12E-08
HNF1A	2.906394479	0.190866031	8.41E-09	3.24E-08
OR51A7	2.638046472	-3.56624315	9.38E-09	3.59E-08
GSTA3	2.806870513	-1.42037873	9.39E-09	3.59E-08
AC011604.2	2.143482743	-3.108314603	9.51E-09	3.64E-08

Gene	logFC	logCPM	PValue	FDR
SMR3A	-2.635771323	-4.144131086	1.06E-08	4.01E-08
PANX3	2.326305366	-3.160277377	1.42E-08	5.32E-08
POTEB3	3.730685749	-3.713452026	1.60E-08	5.94E-08
APOA2	6.084002355	-0.989674056	1.65E-08	6.13E-08
HMX1	3.620329015	-2.282249925	1.71E-08	6.34E-08
KLK14	2.199159846	2.763344004	1.74E-08	6.44E-08
TEX19	2.109864247	-3.789954315	1.75E-08	6.48E-08
FOXB1	2.548534069	-3.326675239	1.83E-08	6.77E-08
OR2T4	-2.107781427	-4.107614379	1.95E-08	7.16E-08
DEFA6	8.471273836	1.646111486	2.42E-08	8.78E-08
HIST2H2AA3	2.438596056	-2.699403297	2.65E-08	9.60E-08
CPN1	3.764667337	-3.646951466	2.86E-08	1.03E-07
SHD	2.349865496	-1.643837394	3.07E-08	1.10E-07
SLC17A4	3.661486856	0.041233394	3.45E-08	1.23E-07
AFP	2.561513116	-1.819167591	3.62E-08	1.29E-07
A1CF	2.968271138	-0.721602281	3.74E-08	1.33E-07
CENPVL3	2.108254917	-3.236233695	3.84E-08	1.36E-07
DEFA5	9.398510106	3.364489602	3.89E-08	1.38E-07
ADAM2	2.268866369	1.975249434	3.95E-08	1.40E-07
OR51F2	2.001274564	-3.505887555	4.08E-08	1.44E-07
VIL1	2.44441479	-1.715247996	4.27E-08	1.51E-07
GC	5.399505393	0.791302383	4.74E-08	1.66E-07
GLP1R	2.638173244	0.005120757	5.23E-08	1.82E-07
HABP2	2.053307035	-0.144814994	6.05E-08	2.08E-07
AMBN	5.985888716	-2.328310244	6.27E-08	2.16E-07
HELT	2.793749673	-3.373803166	7.89E-08	2.68E-07
ETV1	2.242859964	5.823683585	8.08E-08	2.74E-07
CGA	3.095258408	2.341413952	1.05E-07	3.52E-07
SCGB2A2	4.164296891	-2.821900282	1.26E-07	4.18E-07
NXPH1	2.742113092	-2.408586056	1.51E-07	4.94E-07
PAX1	2.566319949	0.613275567	1.56E-07	5.11E-07
FOXG1	4.413970069	-2.305401919	1.66E-07	5.40E-07
KRT75	2.558006156	-1.069230467	1.66E-07	5.41E-07
CD5L	3.99795932	-2.274198075	1.96E-07	6.32E-07
INSM2	2.764301541	-2.31599136	1.97E-07	6.34E-07
TM4SF20	2.812654396	-2.785614732	2.06E-07	6.62E-07
SLCO1B7	2.01296759	-3.7612757	2.07E-07	6.65E-07
DYTN	3.239601987	-0.530752709	2.16E-07	6.93E-07
POTEC	3.432674516	-3.289200505	2.22E-07	7.11E-07
NAA11	2.650446317	-2.486862885	2.26E-07	7.21E-07
MYH13	2.066063048	-2.482864861	2.50E-07	7.92E-07
CDHR4	2.337589644	-0.649813964	2.54E-07	8.03E-07
AKAP14	2.517486668	-2.274812756	2.62E-07	8.29E-07
S100A7A	-2.151656547	-4.15011295	2.68E-07	8.45E-07
CACNA1I	2.167388874	-0.161792924	2.78E-07	8.76E-07
MAGEA12	4.253847274	-1.629199508	2.83E-07	8.91E-07
MS4A15	2.679036167	-1.548974492	3.54E-07	1.10E-06
C6orf10	2.932100927	-1.675723134	3.67E-07	1.14E-06
7BBX	2.218935272	-1.371954365	4.27F-07	1.31F-06
	107 3 5 2 1 2	2.07 275 1305		2.012 00

Gene	logFC	logCPM	PValue	FDR
NWD2	2.691936171	-1.688128902	5.21E-07	1.58E-06
APOBEC4	2.432607195	-2.444614927	5.34E-07	1.62E-06
DRGX	5.581607276	-0.548299892	5.36E-07	1.62E-06
CAPSL	2.141430537	-0.478931097	5.42E-07	1.64E-06
SNTN	2.12725837	-0.315435664	5.66E-07	1.70E-06
KNG1	2.617105398	-2.091853619	6.24E-07	1.87E-06
PRSS48	3.821948787	-2.662238738	6.31E-07	1.89E-06
WDR38	2.180078528	-0.64579903	7.41E-07	2.20E-06
SCN1A	3.512060368	-0.40236363	8.22E-07	2.43E-06
PNLIP	2.328354606	-1.788983069	9.04E-07	2.65E-06
CST1	2.792052996	5.564777783	9.11E-07	2.68E-06
AHSG	3.199438746	-2.773945144	1.06E-06	3.08E-06
CRYBA4	2.772621752	-1.320349749	1.06E-06	3.08E-06
IAPP	3.324462289	-0.773721066	1.07E-06	3.11E-06
ZNF716	3.052270573	-4.06518223	1.16E-06	3.35E-06
LIPF	6.326103	2.912495858	1.35E-06	3.87E-06
SERPINA6	2.943682115	-1.793361739	1.43E-06	4.10E-06
IRS4	2.223425105	-0.100658114	1.47E-06	4.21E-06
MAGEA4	6.312010735	-1.437186342	1.48E-06	4.22E-06
MAGEA8	2.386730522	-2.00924606	2.03E-06	5.70E-06
APOC3	4.606628396	-2.654273715	2.09E-06	5.86E-06
ZIC3	2.575224827	-0.857692039	2.48E-06	6.86E-06
FGB	4.323384685	-0.115174883	2.96E-06	8.13E-06
UGT1A3	2.37472128	0.542246428	3.02E-06	8.29E-06
UGT1A1	3.262526158	-1.071235534	3.03E-06	8.30E-06
MAGEA1	4.69097688	-1.863592199	3.13E-06	8.56E-06
HRG	3.137868897	-3.339954046	3.64E-06	9.89E-06
PRAME	2.341567845	0.717925667	3.89E-06	1.05E-05
SCRT2	3.638442309	-3.636567385	3.91E-06	1.06E-05
CHAT	3.19066275	-1.980217619	4.36E-06	1.17E-05
GAPDHS	2.418577557	-3.713135428	4.53E-06	1.21E-05
BARHL1	3.015059095	-3.539516674	4.66E-06	1.25E-05
C8B	2.984778011	-4.131577497	5.40E-06	1.43E-05
C1orf158	2.231593922	-2.248366293	5.60E-06	1.48E-05
TUBA4B	2.083283692	-1.021407683	5.88E-06	1.55E-05
TAC3	2.369711799	-1.769799158	6.35E-06	1.67E-05
DCAF4L2	4.181333285	-3.336994371	6.42E-06	1.68E-05
MAGEA11	-2.334344997	-4.12452691	6.47E-06	1.70E-05
OOSP2	3.211424198	-4.128101138	6.88E-06	1.80E-05
CALML5	2.96302721	-0.373435971	6.97E-06	1.82E-05
CELA3B	2.509137069	-3.052407547	7.67E-06	1.99E-05
FGF3	3.877010188	-3.428917251	7.80E-06	2.02E-05
AKR1C4	2.494703252	-3.934584544	8.50E-06	2.19E-05
SULT1C3	2.186968852	-1.355115719	1.01E-05	2.57E-05
GPR52	2.388393967	-3.786669653	1.09E-05	2.77E-05
FAM92B	2.05640783	-1.500495388	1.13E-05	2.87E-05
OR5B2	2.609194338	-3.807269643	1.20E-05	3.03E-05
FAM216B	2.374779824	-0.518608291	1.23E-05	3.11E-05
CA6	2.513401867	-2.76088127	1.31E-05	3.29E-05

Gene	logFC	logCPM	PValue	FDR
CTAG2	4.925601332	-0.782603962	1.32E-05	3.31E-05
 TAS2R38	2.622407082	-3.630778383	1.34E-05	3.36E-05
 GLRA3	3.223686569	-0.188435203	1.51E-05	3.75E-05
 GUCA2A	3.562863475	-2.288541517	1.72E-05	4.24E-05
 LHX3	2.215818134	-4.129011745	1.75E-05	4.30E-05
 TMEM212	2.577624226	-3.145400789	1.88E-05	4.61E-05
 UCN3	2.272500127	-1.200540549	2.21E-05	5.37E-05
 MAGEC1	4.686921382	-1.392116181	2.23E-05	5.41E-05
 CT45A10	4.045321429	-3.548760894	2.50E-05	6.03E-05
 AL035425.2	2.735879316	-3.680989103	2.58E-05	6.19E-05
 CLCA1	3.776638394	-1.530223149	2.64E-05	6.33E-05
 PDE6H	2.153226877	-3.916344045	2.81E-05	6.71E-05
 KRTAP13-2	2.243103436	0.468205823	2.93E-05	6.99E-05
 COX7B2	4.741214645	-1.121111491	2.99E-05	7.10E-05
 MAGEA3	4.054216829	-1.757379075	3.30E-05	7.81E-05
 MAGEA6	4.274899658	-1.956846537	3.38E-05	7.99E-05
 IQCM	2.579364621	-4.047403881	3.50E-05	8.25E-05
 LYPD8	2.256064736	-1.241702493	3.54E-05	8.34E-05
 NKX2-5	2.801832118	-2.378705948	3.87E-05	9.07E-05
 REG3A	3.736515651	-3.332085299	4.10E-05	9.56E-05
 IGFBP1	2.14975531	-3.545161931	4.49E-05	0.000104171
 MC4R	3.25596124	-2.085215369	4.57E-05	0.000105886
 АРОН	3.130989094	-0.333603889	4.69E-05	0.00010841
 PRSS56	3.770792623	-1.397434252	4.82E-05	0.000111245
 FMR1NB	2.403293682	-3.119019324	5.25E-05	0.000120751
 CARD18	3.618460498	-3.641480606	5.95E-05	0.000135585
 C6orf15	3.15734794	-3.509243731	6.39E-05	0.000144602
 ABCC12	2.447749702	-0.858545305	6.48E-05	0.00014656
 SLC6A18	3.381785529	-2.97339517	6.57E-05	0.000148554
 IFNK	2.684220062	-3.827516977	6.73E-05	0.000151888
 TRIM49	3.177581725	-3.476981911	7.20E-05	0.00016148
 PRB1	3.326542308	-3.729099839	7.35E-05	0.000164634
 TMEM207	2.647209716	-4.101090504	7.69E-05	0.000171776
 INSL6	2.073304179	-2.965377473	8.41E-05	0.000186712
 OBP2B	2.109540767	-1.09806609	8.91E-05	0.000197245
 SOX3	2.572786664	-2.593667145	9.58E-05	0.000210846
 PIH1D3	2.051029477	-3.248873998	0.000111697	0.000243629
 OR52E8	2.720510067	-3.728113618	0.000130226	0.000281198
 IBSP	2.064740445	-2.938509758	0.000152455	0.000325344
 CRX	2.116262219	-2.812440876	0.000155787	0.000332099
 RAX	2.56782095	-2.046630028	0.000161204	0.000342911
 SLC6A19	2.216142084	2.683437613	0.000161511	0.000343482
 SLCO6A1	3.116278974	-4.027389676	0.000171515	0.000363202
 FGF4	3.429130493	-3.126190388	0.000186328	0.000392617
 VPREB1	3.522957645	-3.50589044	0.000189054	0.000397891
 PRDM9	3.406136372	-3.227166206	0.000197076	0.000413366
 LGALS16	3.375273982	-3.96329701	0.000210268	0.000439385
CSAG1	2.447454631	-1.666596873	0.000211937	0.000442615
 FGA	3.556112828	-1.177897264	0.000231462	0.000480249

Gene	logFC	logCPM	PValue	FDR
TM4SF5	2.007153954	-3.706723742	0.000236151	0.000489409
 BARHL2	2.496114201	-3.403339289	0.000325784	0.000661897
GIF	2.108620219	-3.831577628	0.000351243	0.000709509
OR1N2	3.286097731	-2.80552916	0.000522382	0.001028372
LIN28B	2.080144856	-3.937283675	0.000578444	0.001130644
OTOP1	2.945283928	-3.891057771	0.000579885	0.001132841
SLC18A3	2.169664988	-1.026690515	0.000704233	0.001358103
APCS	2.769781173	-3.531743743	0.000885631	0.001680557
SP9	2.005599586	-2.921939416	0.000947647	0.00178931
PRB4	2.598407211	-4.012142174	0.00097319	0.001834634
CYP2C9	2.028397643	-4.040000218	0.0011091	0.002073755
TMPRSS11B	3.351520815	-2.537086097	0.001404034	0.002581258
TPTE	2.586293693	-3.849215013	0.001431842	0.002628596
DSCR8	2.143606791	-3.733115111	0.001984814	0.003563974
UGT1A10	2.29302094	-1.689729261	0.002529475	0.004471915
HTN3	2.485178564	-4.015732583	0.002830284	0.00496153
OR2T10	2.159593297	-2.004107925	0.003677882	0.0063374
FGG	2.324040335	-2.102893311	0.004863442	0.008221775
MT4	2.334444629	-3.227723792	0.005440693	0.009120681
 INS	2.330844774	-3.828167758	0.00568305	0.009495118



Supplementary Figure 1. Differentially expressed mRNAs in prostate cancer. The horizontal axis shows sample names in TCGA. The right vertical axis means the mRNA names. Downregulated genes are green and upregulated genes are red.



Supplementary Figure 2. Differentially expressed lncRNAs in prostate cancer. The horizontal axis shows sample names in TCGA. The right vertical axis means the lncRNA names. Downregulated genes are green and upregulated genes are red.



Supplementary Figure 3. Differentially expressed miRNAs in prostate cancer. The horizontal axis shows sample names in TCGA. The right vertical axis means the miRNA names. Downregulated genes are green and upregulated genes are red.

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