

RETRACTED ARTICLE: Identification of Enzalutamide Resistance-Related circRNA-miRNA-mRNA Regulatory Networks in Patients with Prostate Cancer

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Purpose: This study aimed to identify enzalutamide resistance-related (EnzR-related) circRNAs and to characterize and validate circRNA-miRNA-mRNA ceRNA regulatory network and corresponding prognostic signature of prostate cancer patients.

Methods: We obtained circRNA expression microarray from the Gene Expression Omnibus (GEO) database and performed differential expression analysis to identify EnzR-related circRNAs using the limma package. The miRNA and mRNA expression profiling were downloaded and performed differential expression analysis, then overlapped with predicted candidates. Next, we established circRNA-miRNA-mRNA ceRNA network and PPI network utilized Cytoscape software and STRING database, respectively. In addition, univariate and Lasso Cox regression analyses were applied to generate a prognostic signature. Receiver operating characteristic (ROC) curve and Kaplan-Meier analysis were used to evaluate the reliability and sensitivity of the signature. Finally, we chose hsa_circ_0047641 to validate the feasibility of the EnzR-related ceRNA regulatory pathway using qRT-PCR, CCK8 and Transwell assays.

Results: We identified 13 EnzR-related circRNAs and constructed a ceRNA regulatory network that contained two downregulated circRNAs (has-circ-00000919 and has-circ-00000927), and two upregulated circRNAs (has-circ-0047641 and has-circ-0068697), and their sponged 6 miRNAs and 167 targeted mRNAs. Subsequently, these targeted mRNAs were performed to implement PPI analysis and to identify 10 Hub genes. Functional enrichment analysis provided new ways to seek potential biological functions. Besides, we established a prognostic signature of PCa patients based on 8 prognostic-associated mRNAs. We confirmed that the survival rates of PCa patients with high-risk subgroup were slightly lower than those with low-risk subgroup in the TCGA dataset ($p < 0.001$), and ROC curves revealed that the AUC value for prognostic signature was 0.816. Finally, the functional analysis suggested that knockdown of hsa_circ_0047641 could inhibit the progression of PCa and could reverse Enz-resistance in vitro.

Conclusion: We identified 13 EnzR-related circRNAs, and constructed and confirmed that EnzR-related circRNA-miRNA-mRNA ceRNA network and corresponding prognostic signature could be a useful prognostic biomarker and therapeutic target.

Keywords: ceRNA, circRNA, prognostic signature, prostate cancer, The Cancer Genome Atlas, Gene Expression Omnibus

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Introductions

Prostate cancer (PCa) is the most common solid malignancy in men and is the second leading tumor-associated cause of death in Western countries.¹ Androgen deprivation therapy (ADT) has become the basis treatment strategy in

patients with hormone-sensitive PCa.² However, most high-risk PCa could proceed to castration-resistant prostate cancer (CRPC)³ or metastatic PCa,⁴ which was the crucial reason for its death. Recently, discovered ADT drug enzalutamide resistance (Enz-resistance) delayed tumor development, but only sustained patient survival by 4–6 months, which could be associated with Enz-resistance after ADT.⁵ Li et al⁶ also confirmed that enzalutamide exerted its anti-PCa effects by recruiting androgens for androgen receptor (AR) and was competitively bound to the ligand-binding domain of AR. However, the precise mechanism of resistance to enzalutamide was not fully understood, but might be associated with the expression of androgen receptor splice variant-7 (AR-V7).^{7–9} Mutations such as F876L might also play a crucial role in Enz-resistance.^{10,11} It was essential to explore the mechanism of Enz-resistance further and to discover new drugs to inhibit it.

Circular RNAs (circRNAs) were a class of endogenous non-coding RNAs (ncRNAs) with covalently closed contiguous loops produced by joining the 5' and 3' ends and were resistant to exonucleases.¹² It has been reported that circRNAs were involved in various biological processes in eukaryotes,^{13,14} whose abnormal expression was closely linked to the malignancy of tumors, such as tumor proliferation, differentiation, apoptosis, or metastasis.¹⁵ Moreover, recent studies suggested that circRNAs might be involved in cancer development through the competing endogenous RNA (ceRNA) mechanism, which mediated each other at the post-transcriptional level by competitively binding to micro RNA (miRNAs).¹⁷ For example, Chen et al¹⁸ found that circRNA-GEF bound with miR-27a-3p and downregulated expression of p21, thereby suppressed the proliferation and metastasis of renal cell carcinoma. Liang et al¹⁹ found that circKDM4C inhibited breast cancer progression and attenuated doxorubicin resistance by regulating miR-348p/PBLD pathway. Similarly, circRNAs have also been reported to be involved in cell proliferation, metastasis and drug resistance. For instance, Shen et al²⁰ found that circFoxo3 inhibited PCa progression and chemoresistance to docetaxel. Wu et al²¹ reported circ17 suppressed enzalutamide resistant-related (EnzR-related) PCa progression via miRNA-181c-5p. However, studies by bioinformatics analysis to investigate the effect of circRNAs on PCa Enz-resistance were relatively rare, and the circRNA-associated ceRNA network and the prognostic value of EnzR-related circRNAs in PCa have not been fully clarified.

In the current study, based on the data downloaded from Gene Expression Omnibus (GEO) and The Cancer Genome Atlas (TCGA) database, we obtained EnzR-related circRNAs. We attempted to construct a circRNA-miRNA-mRNA ceRNA regulatory network and a protein-protein interaction (PPI) network to explore the possible biological mechanisms of EnzR-related circRNAs. Moreover, a circRNA prognostic risk-associated signature was established. We found that the prognostic signature had significantly reliable and sensitive prognostic predictive ability. Finally, we focused on hsa_circ_0047641 and performed cell functional analysis further to investigate the feasibility of the EnzR-related ceRNA regulatory pathway. Therefore, we hypothesized that the EnzR-related circRNA-miRNA-mRNA ceRNA network and corresponding prognostic signature could be an effective prognostic biomarker and therapeutic target.

Materials and Methods

Data Collection and Preparation

As shown in the flow chart (Figure 1), we downloaded two circRNA expression microarrays of PCa (GSE113153 and GSE118959) from the GEO database (<https://www.ncbi.nlm.nih.gov/geo/>). The dataset GSE113153, consisting of five Gleason score >8 PCa tissues and five corresponding Gleason <6 PCa tissues, was annotated and transformed to circRNAs expression matrixes by the circBase database (<http://circrna.org/>) using the Perl program. Similarly, the dataset GSE118959, consisting of three enzalutamide sensitive LNCap cell (LNCap-Enz-S), three high enzalutamide resistance LNCap cell (LNCap-Enz-HR) and three moderately enzalutamide resistant LNCap cell (LNCap-Enz-LR),^{22,23} was annotated and transformed, and then was sorted into Enz-S vs LNCap-Enz-HR sub-dataset and Enz-S vs LNCap-Enz-LR sub-dataset. Then, the differential expression analysis of the three circRNAs expression profiling was performed by the “limma” package in R 4.0.3 with the criteria of logFC > 1 or < -1 and p-value < 0.05. Intersection analysis was performed to determine candidate circRNAs. Subsequently, miRNA expression microarray GSE21036 was collated from the GEO database and then annotated, then performed differential expression analysis to determine differentially expressed miRNAs. The transcriptome data, downloaded from TCGA data portal (<https://portal.gdc.cancer.gov/>), were annotated, and then classified into protein-coding genes (mRNA) and long non-coding RNAs by the Ensembl human genome browser (<http://asia.ensembl.org/info/data/index>).

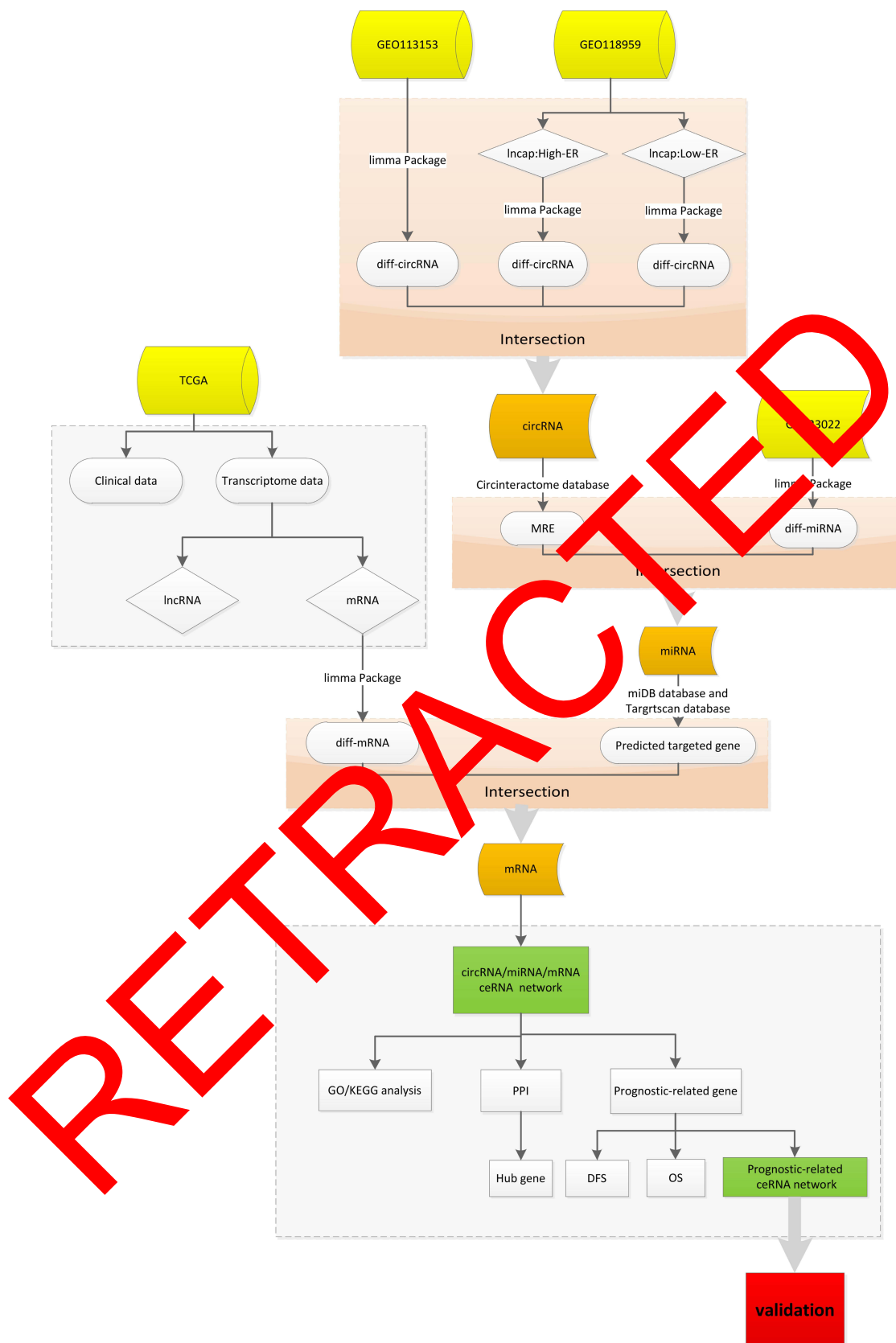


Figure 1 The flow chart of the study about constructing circRNA/miRNA/mRNA networks and validate some potential biological functions of prostate cancer.

Abbreviations: High-ER, high enzalutamide resistance; Low-ER, low enzalutamide resistance; circRNA, circular RNA; miRNA, micro RNA; mRNA, messenger RNA; diff-circRNA, differential circular RNA; GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction; OS, Overall survival; DFS, disease-free survival; MRE, miRNA-recognition elements; ceRNA, competitive endogenous RNA.

[html](#)). These mRNAs were also performed differential expression analysis using the “limma” package ($\log_{2}FC > 1$ or < -1 and p -value < 0.05). Meanwhile, corresponding clinicopathological data were downloaded from the TCGA dataset, including age, Gleason score (the most widely used prostate cancer grading system), AJCC TNM stage (The most widely used tumor-node-metastasis cancer staging system).

Prediction of miRNA Binding Sites (MRE) and miRNA Target Genes, and Constructing a circRNA-miRNA-mRNA ceRNA Regulatory Network

Circular RNA Interactome (CircInteractome) database (<https://circinteractome.nia.nih.gov/>) was utilized to predict the MREs of these candidate circRNAs. We overlapped the differentially expressed miRNAs and MRE as the candidate miRNAs. Then, the interactions between miRNAs and target mRNAs were predicted with TargetScan (<http://www.targetscan.org/>) and miRDB (<http://www.mirdb.org/miRDB/>). The differentially expressed mRNA and predicted target genes were overlapped as candidate target mRNAs for further analysis. Finally, Cytoscape software was applied to visualize the circRNA/miRNA/mRNA ceRNA regulatory networks.

Establishment of PPI Network and Identification of Hub Genes and GO/KEGG Enrichment Analysis

Those candidate target mRNAs in the ceRNA network were employed to establish a PPI network using the STRING (<https://string-db.org/>), a website that could predict interactions between functional proteins. We defined medium confidence > 0.4 as significant. Subsequently, the CytoHubba algorithm of Cytoscape was used to recognize highly interacted hub genes clustering from the PPI network. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways analysis was used to identify the function of candidate mRNAs in the ceRNA network using the “clusterProfiler package” in R software.

Construction and Verification of a circRNAs-Associated Prognostic Signature

To develop a reliable prognostic prediction model, we integrated the candidate target mRNAs expression matrix and corresponding clinical data. The univariate Cox

proportional hazards regression analysis was performed to identify prognostic-associated mRNAs in the ceRNA network. The least absolute shrinkage and selection operator (LASSO) Cox regression analysis was utilized to remove prognosis-related mRNAs that highly correlated with each other to prevent over-fitting. Then, we constructed a risk score-related signature using the expression value of these candidate prognostic genes and corresponding regression coefficients obtained from LASSO regression analysis. The format was as follows: $risk\ score = \sum_{i=1}^n coef(i) * mRNA(i)\ expression$.

We further validated the reliability and accuracy of the signature. The PCa patients were sorted into high- and low-risk subgroups based on median risk scores as the cut-off value. The receiver operating characteristic curves (ROC) and its area under the curve (AUC) values were employed to assess the specificity and sensitivity of the signature by “ROC package” in R software. The Kaplan–Meier survival curve was exploited to compare the survival outcomes of the two subgroups and candidate target mRNAs in the ceRNA network. Besides, univariate and multivariate Cox regression analyses were used to assess whether risk scores determine the prognosis of PCa patients independently of other clinical variables, including age, Gleason score, and AJCC TNM stage.

Cell Lines, Construction of Enzalutamide Resistant (Enz-Resistant) Cell Lines, Cell Culture and Oligonucleotide Transfection

The human PCa cell lines, LNCap, PC3 and DU145 cells were originally purchased from cell repository of Shanghai Institute of Life Sciences, Chinese Academy of Sciences. RPMI 1640 medium, containing 10% fetal bovine serum (FBS), penicillin (25 U/mL) and streptomycin (25 mg/mL), was used to culture these PCa cells at 37°C in a humidified 5% CO₂ environment. Generation of Enz-resistant prostate cancer LNCap cells (LNCap-EnzR) from parental LNCap cells by continuous exposure to gradually increasing enzalutamide concentrations, starting from 0.1, 1, 2 for 20 days at each concentration, and terminating with 10 μM for more than 6 months. After generation, cells were maintained with 2 μM Enzalutamide.²⁴ Small interfering RNA (siRNA) of circRNA was synthesized by GenePharma (Shanghai, China). The primer sequences of hsa_circ_0047641 used in the article were listed as follows: sense (5'-3'), CAUCAGGUUUUACCAAUUCTT; antisense (5'-3'), GAAUUGGUAACCUGAUGTT.

Lipofectamine 2000 reagent (vazyme, Nanjing, China) was applied for cell transfection according to the manufacturer's instructions.

RNA Extraction, qRT-PCR and Cellular RNA Fractionation Assays

Total RNA was isolated from PCa cells and normal prostate cells as well as LNCap-EnzR cells using Total RNA Kit I (50) (OMEGA biotech, China). Then, cDNA was synthesized using the HiScript II Q RT SuperMix (R223-01) reagent kit (vazyme, Nanjing, China). Quantitative real-time PCR (qRT-PCR) was performed using the SYBR green PCR mix (vazyme, Nanjing, China) according to the manufacturer's instructions. GAPDH was employed as the endogenous control for circRNAs. The primer sequences were listed in [Table S1](#).

Cellular fraction kit (ThermoFisher, USA) was used to isolate the nucleus and cytoplasm of PCa cells. Cells were resuspended for 10 min on ice in 500 μ L Fractionation buffer. After 500 \times g centrifugation at 4°C for 5min, the supernatant was obtained as the cytoplasmic fraction and the precipitate as the nuclear fraction of the cell was collected. Then, homogenized 2 \times lysis/binding solution with an equal volume of Fractionation buffer, respectively. The resulting mixture was then added to a collection tube and centrifuged at 8000 \times g for 1 min. Subsequently, the collection tube was purified by washing solution at 8000 \times g for 1 min at 4°C, then by washing solution at 12,000 \times g for 1 min. At last, 40–60 μ L of 95° Elution solution was added to the collection tube and the RNA was eluted by centrifugation at 12,000 \times g for 30s.

Cell Proliferation Assays

Cell Counting Kit-8 and X-Cell Kit (X-Cell Technology, Nanjing, China) was used to evaluate the cell proliferation according to the manufacturer's instructions. In short, the transfected cells were seeded into 96-well plates at a density of 1000 cells per well, respectively. After incubation overnight, 10 μ L of CCK-8 solution was added to each well on days 1, 2, 3 and 4, then incubated for another 3 h at 37 °C, the absorbance values at 450 nm absorption wavelength were measured using a microtiter plate reader (Bio-Rad, Hercules, CA, USA).

Transwell Migration and Matrigel Invasion Assays

Cell migration and invasion assays were carried out in a 24-well Transwell chamber (BD, USA). The transfected

cells were digested, centrifuged and resuspended in an FBS-free medium and adjusted the density to 1×10^6 cells/mL. Then, 100 μ L (1×10^5 cells) of the cell suspension was added to the upper chamber (Invasion assay required 0.5 mg/mL matrigel to pre-coat the upper chamber and incubated for 1 h), and 600 μ L of complete medium was added to the lower chamber. Based on the different migration abilities of PCa cells, these cells were incubated for 8–24h. Subsequently, Transwell chambers were washed with PBS, fixed in methanol, stained with crystal violet, and photographed under a light microscope.

Statistical Analysis

The statistical analysis was carried out in R software (version 4.0.3). The R programming language (Version 5.30.2) was used for data processing. A P-value <0.05 was regarded as statistically significant.

Results

Differentially Expressed circRNAs, miRNAs, and mRNAs in Prostate Cancer Patients Based on GEO and TCGA Database

Compared high Gleason score with low Gleason score prostate cancer tissues, a total of 1903 differentially expressed circRNAs were identified from GSE113153 dataset of PCa tissues, including 1017 upregulated circRNAs and 886 downregulated circRNAs ([Figure 2A](#)). The GSE118959 dataset was downloaded and divided into two sub-datasets. One compared LNCap-Enz-HR with LNCap-Enz-S cell; a total of 339 differentially expressed circRNAs were identified, including 113 up-regulated circRNAs and 226 down-regulated circRNAs ([Figure 2B](#)). The other compared LNCap-Enz-LR with LNCap-Enz-S cell, a total of 90 differentially expressed circRNAs were identified, including 30 up-regulated circRNAs and 60 downregulated circRNAs ([Figure 2C](#)). Then, intersection analysis was performed and a total of 13 EnzR-related circRNAs were identified, including 4 upregulated circRNAs ([Figure 2D](#)) and 9 downregulated circRNAs ([Figure 2E](#)). The basic characteristics of these circRNAs are described in [Table 1](#).

Compared with normal prostate tissues, a total of 184 differentially expressed miRNAs were identified from GSE21036 dataset, including 95 upregulated miRNAs and 89 downregulated miRNAs ([Figure 3A](#)). Subsequently, the CircInteractome database was utilized to predict miRNAs that interacted with 13 EnzR-related

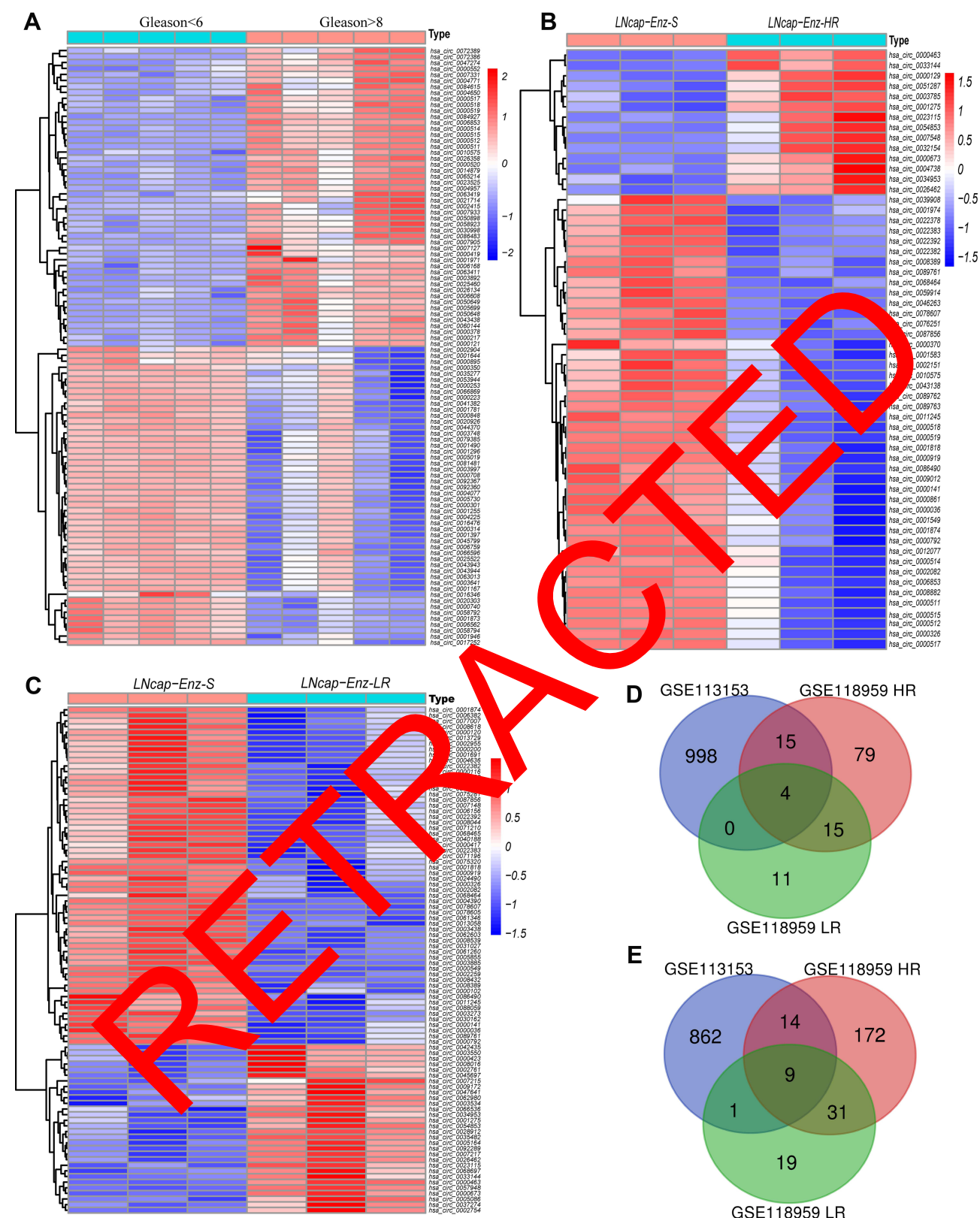


Figure 2 The heatmaps and Venn Diagrams showed the differential circRNAs in prostate cancer (PCa). **(A)** Heatmaps of the differentially expressed circRNAs comparing Gleason>8 with Gleason<6 in GSE113153. **(B)** Heatmaps of the differentially expressed circRNAs comparing enzalutamide-sensitive LNCap cell with high enzalutamide resistant LNCap cell in GSE118959. **(C)** Heatmaps of the differentially expressed circRNAs comparing enzalutamide-sensitive LNCap cell with moderately enzalutamide resistant LNCap cell in GSE118959. Venn Diagrams showing the overlap of significantly upregulated **(D)** and downregulated **(E)** circRNAs between GSE113153 and GSE118959.

Abbreviations: LNCap-Enz-HR, high enzalutamide resistant LNCap cell; LNCap-Enz-LR, moderately enzalutamide resistant LNCap cell; LNCap-Enz-S, enzalutamide-sensitive LNCap cell.

Table I The Basic Characteristics of Enzalutamide Resistance-Related circRNAs

circRNA ID	Position	Strand	Genomic Length	Spliced Length	Transcript	Gene Symbol	Regulation
hsa_circ_0023115	chr11:67351934-67352712	+	778	299	NM_000852	GSTP1	Up
hsa_circ_0068697	chr3:196846280-196869639	-	23,359	749	NM_004087	DLG1	Up
hsa_circ_0047641	chr18:46783379-46798673	-	15,294	335	NM_017653	DYM	Up
hsa_circ_0033144	chr14:99723807-99724176	-	369	369	NM_138576	BCL11B	Up
hsa_circ_0000919	chr19:19760861-19761115	-	254	254	NM_020410	ATP13A1	Down
hsa_circ_0000141	chr1:156220621-156220731	-	110	110	NM_015327	SMG5	Down
hsa_circ_0062603	chr22:24698162-24765288	+	67,126	3124	NM_015330	SPECC1L	Down
hsa_circ_0001818	chr8:103299660-103300494	-	834	244	NM_015902	UBR5	Down
hsa_circ_0003438	chr16:70294946-70296427	-	1481	293	NM_001605	AA	Down
hsa_circ_0031027	chr13:114164552-114193822	+	29,270	652	NM_017905	MCO3	Down
hsa_circ_0000792	chr17:56409123-56409324	-	201	201	NR_038411	LOC100506775	Down
hsa_circ_0001874	chr9:95500310-95500614	-	304	304	NM_00100008	E2F2	Down
hsa_circ_0000036	chr1:28199932-28200152	+	220	220	NM_0011055	CLDN3	Down

circRNAs, named MRE, and a total of 210 miRNAs were identified. After intersecting with the differentially expressed miRNAs, a total of 18 miRNAs were identified (Figure 3D). Similarly, 2472 differentially expressed mRNAs were identified by analyzing transcriptome profiling data of PCa patients from TCGA database, including 1016 upregulated mRNAs and 1456 downregulated mRNAs (Figure 3B and C). Besides, TargetScan and miRDB database were applied to predict targeting mRNAs that interacted with 18 miRNAs, and 386 mRNAs were identified. Next, we acquired 167 mRNAs by overlapping the differentially expressed mRNAs and predicted mRNAs (Figure 3E).

Construction of an EnzR-Related circRNA-miRNA-mRNA ceRNA Regulatory Network and PPI Network in PCa and Functional Enrichment Analysis

To clarify how EnzR-related circRNAs regulate targeting mRNAs expression by sponging miRNAs in PCa, we constructed a circRNA-miRNA-mRNA ceRNA network based on the above intersection results. We performed PPI analysis using the STRING database to explore its biological functions. We constructed an EnzR-related ceRNA regulatory network that contained two downregulated circRNAs (has-circ-00000919 and has-circ-0000036) and two upregulated circRNAs (has-circ-0047641 and has-circ-0068697), as well as their sponged 6 miRNAs and 167 targeted mRNAs, to explore the potential biological function of EnzR-related

circRNA (Figure 4A). Subsequently, these 167 targeted mRNAs were performed to implement PPI analysis (Figure 4B). The interaction nodes of the top 30 targeted mRNAs were displayed in the PPI network, with TTK, RRM2, CDCA8 having the most connecting nodes (Figure 4C). In addition, given the importance of Hub genes in the PPI network, we obtained the top 10 Hub genes (CDCA8, MCM10, TTK, RRM2, CDCA5, CEP55, CENPF, HJURP, E2F2, FOXM1) using the CytoHubba plugin of Cytoscape software, which unveiled the critical roles in PCa (Figure 4D).

Next, to investigate the potential biological functions and signaling pathways involved in molecular heterogeneity, GO enrichment analysis and KEGG pathway analysis of 167 targeted mRNAs were implemented in the network. GO enrichment results revealed that a total of 389, 45, and 33 GO terms were enriched in the biological process, cellular component and molecular function, respectively ($p < 0.05$). The top 5 GO terms for biological processes were forebrain development, urogenital system development, kidney development, renal system development, regulation of membrane potential (Figure 4E); the top 5 GO terms for cellular components were neuron to neuron synapse, postsynaptic density, asymmetric synapse, postsynaptic specialization, glutamatergic synapse (Figure 4F); and the top 5 GO terms for molecular functions were metal ion transmembrane transporter activity, channel activity, passive transmembrane transporter activity, monovalent inorganic cation transmembrane transporter activity, sodium ion

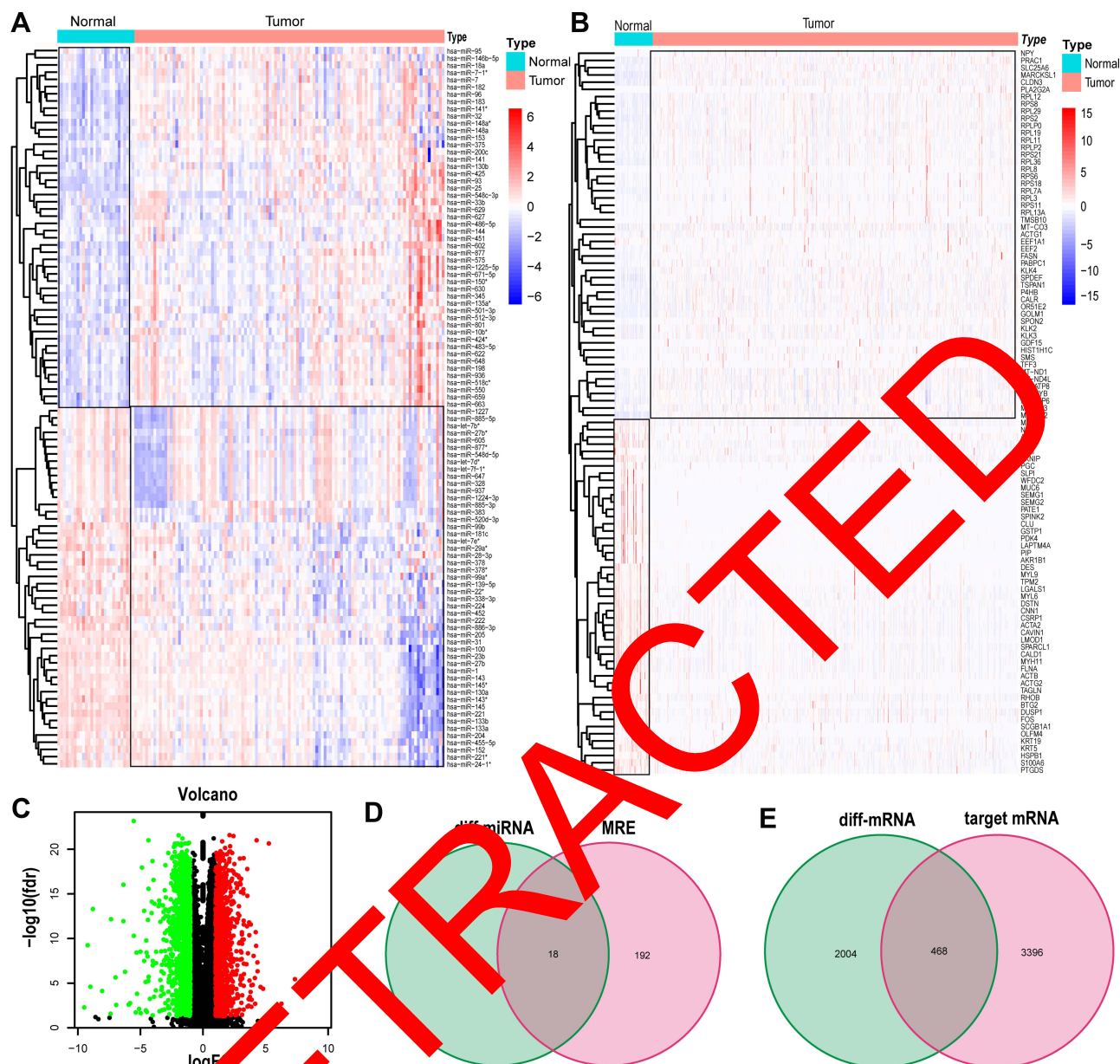


Figure 3 (A) Heatmaps of the differentially expressed miRNAs comparing normal tissue with tumor tissue in GSE21036. (B and C) Heatmaps and volcano of the differentially expressed mRNAs identified from TC database using the limma R package ($|\log_2(\text{fold-change})| > 1$, $P < 0.05$ and $\text{FDR} < 0.05$). (D) Venn Diagrams showing the overlap of miRNA between differentially expressed miRNAs and miRNA-recognition elements (MRE). (E) Venn Diagrams showing the overlap of mRNAs between differentially expressed mRNAs and predicted target genes.

Abbreviations: miRNA, micro RNA; mRNA, messenger RNA; diff-miRNA, differential micro RNA; MRE, miRNA-recognition elements.

transmembrane transporter activity (Figure 4G). KEGG analysis revealed that there were 21 enriched signaling pathways, of which the top 5 were Calcium signaling pathway, cGMP-PKG signaling pathway, Axon guidance, Salivary secretion, Pancreatic secretion (Figure 4H). These results offered us new ways to investigate the potential biological functions of EnzR-related circRNAs in PCa.

Development of an EnzR-Related circRNAs Prognostic Risk-Associated Signature and Establishment of Corresponding Prognostic-Associated ceRNA Regulatory Subnetwork

To develop a new prognostic biomarker for PCa patients, we constructed an EnzR-related circRNA prognostic

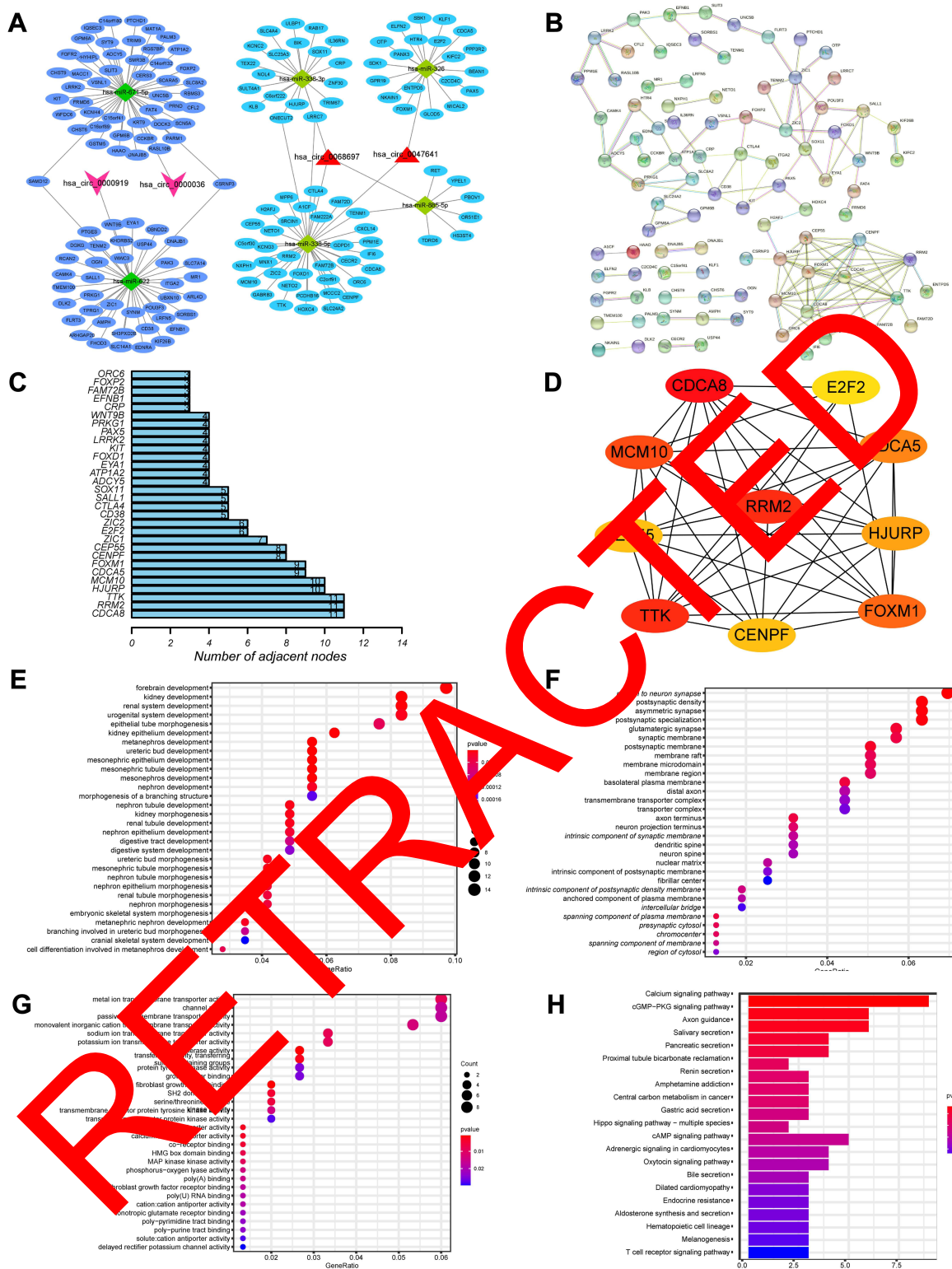


Figure 4 Construction of circRNA-miRNA-mRNA ceRNA networks and protein-protein interaction (PPI) network, as well as functional enrichment analysis of target genes. **(A)** The circRNA-miRNA-mRNA ceRNA network displayed 2 downregulated circRNAs (has-circ-00000919 and has-circ-0000036) and 2 upregulated circRNAs (has-circ-0047641 and has-circ-0068697) and their sponged miRNAs and targeted mRNAs. **(B)** PPI network of target genes. **(C)** Bar chart showed the number of connecting nodes of target mRNAs in the PPI network. **(D)** PPI network of the top 10 hub genes obtained from CytoHubba plugin of Cytoscape. Bubble diagram of Gene Ontology (GO) analysis of targeted genes revealed the enriched biological processes, cell components, and molecular functions. **(E)** Bar chart of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of targeted genes revealed the enriched signaling pathways.

Abbreviation: ceRNA, competitive endogenous RNA.

signature. Univariate Cox proportional hazards regression analysis of expression of the 167 mRNAs in the ceRNA regulatory network was performed. Expressions of 21 mRNAs (FOXN1, MCM10, SLC23A3, RRM2, E2F2, ZIC2, TEX22, ULBP1, HJURP, CERS3, CDCA8, SOX11, NXPH1, TTK, OTP, FAM72B, ORC6, A1CF, CDCA5, HS3ST4, DOCK3) were proved to be significantly linked to the prognosis of PCa patients. LASSO Cox analysis was adopted to filter out these mRNAs highly interrelated to prevent over-fitting (Figure 5A and B), and 8 prognostic-associated mRNAs and coefficients of each were identified (Figure 5C), which were utilized to establish a prognostic model. The formula was generated as follows: risk score = $1.57079 * SLC23A3 + 0.031395 * RRM2 + 0.50525 * ZIC2 + 1.39005 * CERS3 + 0.65839 * NXPH1 + 3.79846 * OTP + 0.16715 * HS3ST4 + 0.78409 * DOCK3$. In addition, the prognostic-associated circRNA-miRNA-mRNA ceRNA subnetworks were established, as shown in Figure 5D, contained 1 downregulated circRNAs (has-circ-0000036) and 2 upregulated circRNAs (has-circ-0047641 and has-circ-0068697) and their sponged 5 miRNAs and 8 targeted mRNAs.

To determine the reliability and sensitivity of the prognostic risk-related signature, the PCa patient datasets in TCGA database were allocated to low- and high-risk subgroups based on the median value of risk score. ROC curves revealed that the AUC value for prognostic signature was 0.816 (Figure 5E). Moreover, the AUC value

for 1-, 3-, and 5-year predictive accuracy in PCa patients in TCGA dataset. (F) ROC curves and their AUC value represented 1-, 3-, and 5-year predictive accuracy in PCa patients in TCGA dataset. (G) Kaplan-Meier survival curves of PCa patients showed that the high-risk group had worse survival rates than the low-risk group in TCGA dataset. (H) The risk score distribution chart showed the distribution of high-risk and low-risk PCa patients; the scatter plot showed the correlation between survival outcomes and the risk score of PCa patients. The heatmap showed 8 prognostic-related mRNAs expression profiles in the high-risk and low-risk groups in PCa patients in TCGA dataset. (I) The univariate Cox regression analysis showed that risk score and clinicopathological features, included Gleason score and AJCC T stage, were prognostic-related variables. (J) The multivariate Cox regression analysis showed risk scores were independent prognostic factors. (K) Multivariate ROC curves showing high predictive sensitivity and specificity of risk score (AUC=0.985).

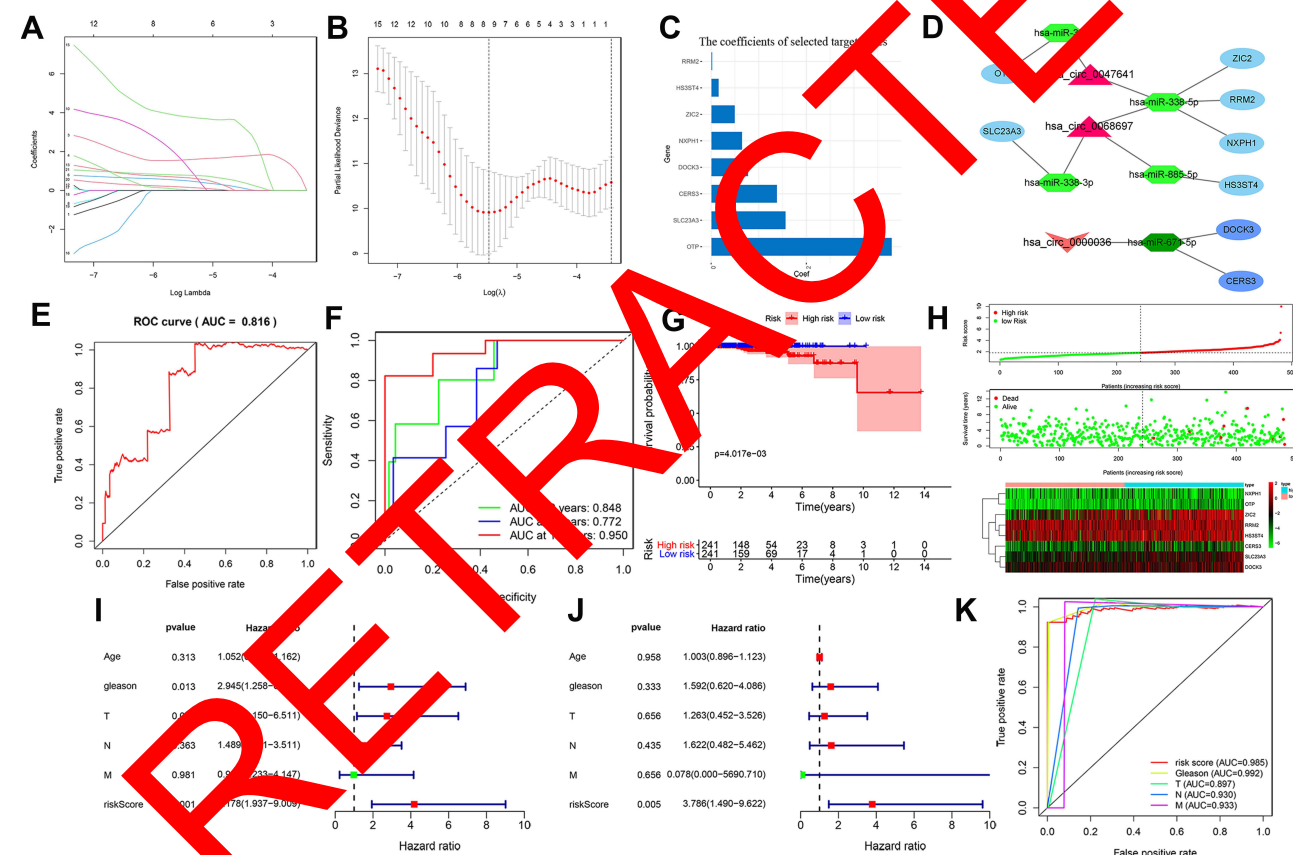


Figure 5 Construction and evaluation of an ER-related circRNAs prognostic signature and establishment of corresponding prognostic-associated ceRNA regulatory subnetwork. The least absolute shrinkage and selection operator (LASSO) Cox regression analysis was utilized to prevent over-fitting after univariate Cox regression analysis. Lasso coefficient values (A) and vertical dashed lines (B) were estimated at the best log value (lambda). (C) Bar chart revealed the lasso coefficient profiles of prognosis-related mRNAs, which were applied to construct the prognostic signature. (D) The prognostic-associated ceRNA subnetworks were established, contained 1 downregulated circRNAs (has-circ-0000036) and 2 upregulated circRNAs (has-circ-0047641 and has-circ-0068697) and their sponged miRNAs and targeted mRNAs. (E) Receiver operating characteristic (ROC) curves and its AUC value for the prognostic signature of prostate cancer (PCa) patients in TCGA dataset. (F) ROC curves and their AUC value represented 1-, 3-, and 5-year predictive accuracy in PCa patients in TCGA dataset. (G) Kaplan-Meier survival curves of PCa patients showed that the high-risk group had worse survival rates than the low-risk group in TCGA dataset. (H) The risk score distribution chart showed the distribution of high-risk and low-risk PCa patients; the scatter plot showed the correlation between survival outcomes and the risk score of PCa patients. The heatmap showed 8 prognostic-related mRNAs expression profiles in the high-risk and low-risk groups in PCa patients in TCGA dataset. (I) The univariate Cox regression analysis showed that risk score and clinicopathological features, included Gleason score and AJCC T stage, were prognostic-related variables. (J) The multivariate Cox regression analysis showed risk scores were independent prognostic factors. (K) Multivariate ROC curves showing high predictive sensitivity and specificity of risk score (AUC=0.985).

Abbreviations: ceRNA, competitive endogenous RNA; ER-related circRNAs, enzalutamide resistance-related circular RNAs; AUC, area under the curve.

referring to 3-,5-,10 years of survival outcomes were 0.848, 0.772 and 0.950, respectively (Figure 5F), indicating that the prognostic signature harbored a promising potential to predict prognosis for PCa patients. Kaplan–Meier survival curves were implemented and shown that the survival rates of PCa patients with a high-risk subgroup were slightly lower than those with low-risk subgroup in the TCGA dataset ($p < 0.001$) (Figure 5G). Besides, the scatter plot showed that high-risk score PCa patients had poorer survival rates than low-risk score subgroup; the risk Score distribution plot depicted that the high-risk subgroup had higher risk scores than the low-risk subgroup; furthermore, the heatmap showed significant differences in the expression profiles of 8 prognosis-related target mRNAs between the high-risk and low-risk subgroups (Figure 5H). To estimate the clinical value of the prognostic signature, we integrated the risk scores from prognostic signature and clinicopathological characteristics, including age, Gleason score and TNM stage. The univariate (Figure 5I) and multivariate Cox regression analysis (Figure 5J) were performed and confirmed that risk score was independent prognostic factors (HR:3.786, 95% CI: 1.490–9.622, $p < 0.01$). Subsequently, the multivariate ROC curve revealed that the AUC value for risk score was 0.985 (Figure 5K). Overall, the prognostic risk-related signature we developed had significant reliability and sensitivity in predicting the prognosis of PCa patients.

Exploration of Survival Outcomes of the 8 mRNAs Involved in Prognostic Signature and Validation of Expression Profiles of Prognostic-Associated ceRNA Regulatory Subnetwork

Subsequently, to elaborate the prognostic values of the 8 target mRNAs involved in the EnzR-related ceRNA regulatory network, the mRNAs were assigned to low- and high-expression subgroups based on the median value of the expression levels of PCa patients in TCGA database, and Kaplan–Meier survival analysis was performed. The results revealed high expression of RRM2 and SLC23A3 were linked to poor OS and DFS ($p < 0.05$) (Figure 6).

We further analyzed the differential expression of circRNA, miRNA, mRNA in prognostic-associated ceRNA subnetwork in normal and tumor tissues. We found that EnzR-related hsa_circ-0047641 and hsa_circ-0068697 were downregulated in tumor tissues compared

with normal tissues, whereas hsa_circ-0000036 was upregulated in tumor tissues (Figure 7A). By intersecting the Hub gene with prognosis-related genes and the Hub gene with target genes in the prognostic signature, we found that RRM2 played an essential role in PCa (Figure 8A and B). Therefore, we focused on the hsa_circ_0047641/hsa_miR338-5p/RRM2 ceRNA regulatory subnetwork. We found that the expression of hsa_miR338-5p was downregulated while RRM2 was upregulated in PCa (Figure 7B and C)

Identification and Characterization of hsa_circ_0047641 in PCa

To further demonstrate the feasibility of the EnzR-related ceRNA regulatory pathway, we focused on hsa_circ_0047641 and performed functional analysis. We first confirmed the expression level of hsa_circ_0047641 in normal prostate cells (RPW-1) and different PCa cell lines (LNCap, PC3, DU145). The results indicated that the expression level of hsa_circ_0047641 was significantly increased in PCa cell lines compared with normal prostate cells (Figure 8C). Furthermore, the expression levels of androgen-dependent LNCap cells were significantly lower than those of androgen-independent PC3 and DU145 cells, which suggested that hsa_circ_0047641 contributed to the formation of CRPC. Meanwhile, cellular RNA fractionation assays illustrated that hsa_circ_0047641 was mainly located in the cytoplasm (Figure 8D), which suggested that hsa_circ_0047641 could produce pathophysiological effects through the ceRNA pathway. To further investigate the biological functions of hsa_circ_0047641 in PCa, small interfering RNAs (siRNAs) were constructed and transfected into the LNCap and DU145 cell lines. qRT-PCR was performed to examine the transfection effect (Figure 8E). CCK8 assays showed that hsa_circ_0047641 knockdown could suppress cell proliferation of PCa cells (Figure 8F). Consistently, Transwell analysis demonstrated that hsa_circ_0047641 knockdown inhibited migration and invasion capabilities in PCa cells (Figure 8G). Besides, we constructed Enz-resistance LNCap cells and performed cell proliferation assays. The results showed knockdown of hsa_circ_0047641 inhibited the proliferation of Enz-resistance prostate cancer cells (Figure 8H and I). In summary, these findings suggested that knockdown of hsa_circ_0047641 could inhibit the progression of PCa cells and could reverse Enz-resistance in vitro.

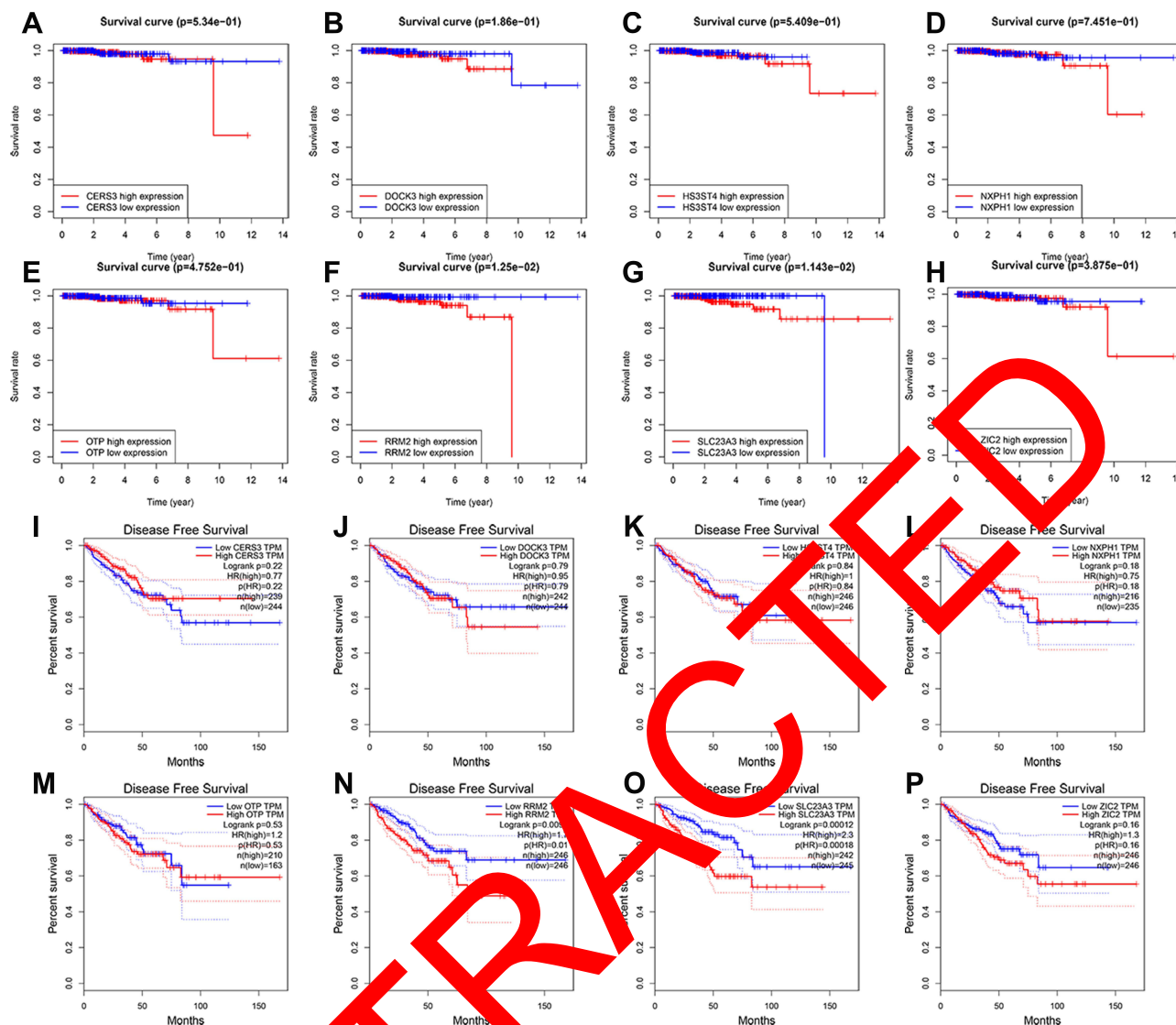


Figure 6 Kaplan-Meier (K-M) survival analysis of the 8 target genes in prognostic signatures for patients with prostate cancer (PCa) in TCGA database and GEPIA database. The K-M survival curves showed there was no significant difference in overall survival (OS) in the high expression of CERS3 (A), DOCK3 (B), HS3ST4 (C), NXPH1 (D), OTP (E), ZIC2 (H) compared to its low expression in TCGA database. The K-M survival curves showed high expression of RRM2 (F) and SLC23A3 (G) had worse overall survival (OS) than its low expression in TCGA database ($p < 0.05$). The K-M survival curves showed there was no significant difference in disease-free survival (DFS) in the high expression of CERS3 (I), DOCK3 (J), HS3ST4 (K), NXPH1 (L), OTP (M), ZIC2 (P) compared to its low expression in GEPIA database. The K-M survival curves showed high expression of RRM2 (N) and SLC23A3 (O) had worse DFS than its low expression in the GEPIA database ($p < 0.05$).

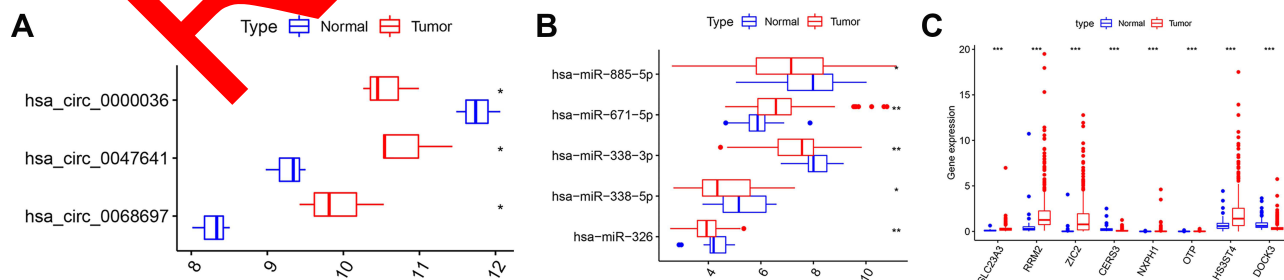


Figure 7 Differential expression of circRNA, miRNA, mRNA in prognostic-related ceRNA subnetwork in normal and tumor tissues. (A) Box plot showed the differential expression of circRNAs in normal and tumor tissues in GSE113153 dataset. (B) Box plot showed the differential expression of miRNAs in normal and tumor tissues in GSE21036 dataset. (C) Box plot showed the differential expression of mRNAs in normal and tumor tissues in TACA database. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. **Abbreviations:** circRNA, circular RNA; miRNA, micro RNA; mRNA, messenger RNA; ceRNA, competitive endogenous RNA.

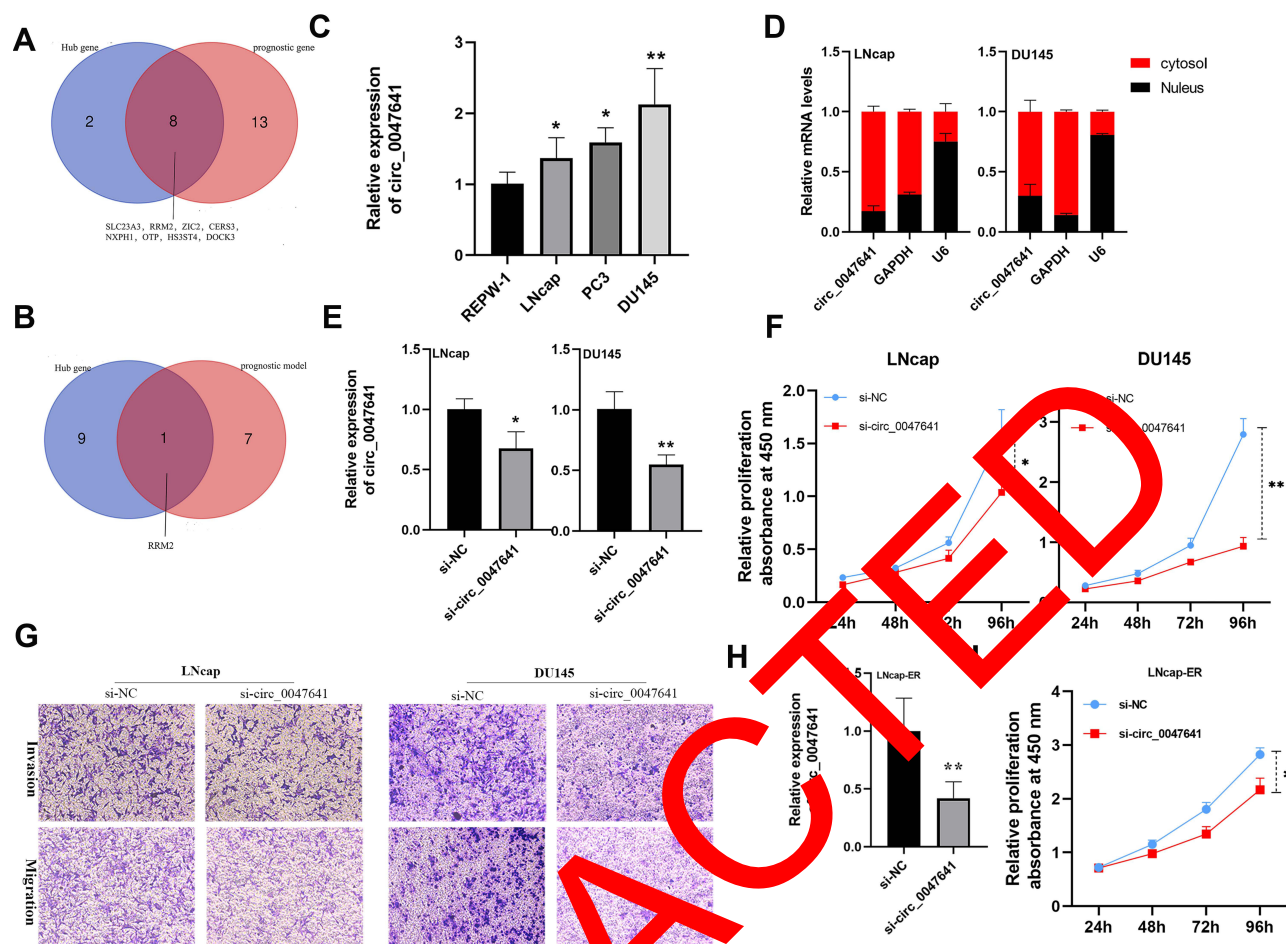


Figure 8 Identification and characterization of hsa_circ_0047641 in prostate cancer (PCa). (A) Venn Diagrams showing the overlap of Hub genes and prognosis-related target genes. (B) Venn Diagrams showing the overlap of Hub genes and target genes in prognostic signature. (C) qRT-PCR was performed to examine the expression levels of hsa_circ_0047641 in normal prostate cells (REPW-1) and different cell lines (LNCap, PC3, DU145). (D) The cellular distribution of hsa_circ_0047641 was analyzed by cellular RNA fractionation assays and qRT-PCR in LNCap and DU145 cells. U6 was being used as a nucleus marker and GAPDH as a cytosol marker. (E) qRT-PCR was used to detect the expression level of hsa_circ_0047641 in LNCap and DU145 cells after treatment with si-circ_0047641 or si-NC. (F) CCK-8 assays showed that silencing circ_0047641 suppressed the proliferation of LNCap and DU145 cells. (G) Transwell migration and invasion assays showed that silencing circ_0047641 suppressed the migration and invasion capabilities of PCa cells. (H) qRT-PCR was used to detect the expression level of hsa_circ_0047641 in enzalutamide resistance LNCap (LNCap-EnzR) cells after treatment with si-circ_0047641 or si-NC. (I) CCK-8 assays showed that silencing circ_0047641 suppressed the proliferation of LNCap-EnzR cells. * $p < 0.05$, ** $p < 0.01$.

Abbreviations: si-circ_0047641, siRNA against circ_0047641. si-NC, siRNA for negative control

Discussions

PCa is one of the most prevalent male malignancies worldwide.¹ ADT has become the mainstream treatment strategy in patients with hormone-sensitive PCa, but anti-androgen drug resistance, such as Enz-resistance, inevitably emerged. circRNAs were involved in a range of biological processes in eukaryotes partly via the ceRNA mechanism.^{25,26} However, EnzR-related circRNA ceRNA regulatory network has rarely been studied. In our present study, we constructed a circRNA-miRNA-mRNA ceRNA regulatory network and PPI network based on the data from GEO and TCGA database to explore the possible biological mechanisms and established a circRNA prognostic risk-associated signature, which was validated as a reliable and

stable prognostic biomarker. Furthermore, we chose hsa_circ_0047641 and performed functional analysis to investigate the feasibility of the EnzR-related ceRNA regulatory pathway. Firstly, expression datasets of circRNAs, miRNAs, mRNAs were obtained from GEO and TCGA database, then differentially expression analysis and online database predictive analysis were performed. Intersection analysis was applied and screened candidate circRNAs, miRNAs, mRNAs for the development of circRNA-miRNA-mRNA ceRNA regulatory networks. Then, a PPI network was established to determine its biological functions, and the Hub genes were explored. Meanwhile, GO and KEGG enrichment analysis was implemented to confirm the vital biological functions and downstream

pathways of these target genes in the ceRNA regulatory network. In addition, we integrated the target mRNAs expression matrix and corresponding clinical data. The univariate Cox proportional hazards regression analysis was undertaken and identified 21 prognostic-associated mRNAs in the ceRNA regulatory network. LASSO Cox regression analysis was utilized to prevent over-fitting and ultimately, 8 candidate mRNA and corresponding regression coefficients were screened and constructed the prognostic risk score model. Subsequently, we performed ROC analysis and Kaplan–Meier survival analysis to evaluate the predictive ability of the prognostic signature. The result showed that this model had accurate and stable prognostic predictive ability. Besides, we focused on hsa_circ_0047641 and performed functional analysis. The result suggested that hsa_circ_0047641 could promote the progression of PCa and could reverse enzalutamide resistance for PCa. Collectively, our results indicated that circ-related ceRNA regulatory network and corresponding prognostic signature could be a promising and useful predictive tool and therapeutic target for PCa.

CircRNA was a novel family of endogenous non-coding RNA, which was believed to be the result of “splicing mistakes” in the 1970s.^{12,27} Whereas with the advancement of high-throughput sequencing technology and bioinformatics, it has been found that circRNAs were involved in many biological processes in eukaryotes,^{28,29} and accumulating evidence has demonstrated that the development of cancer was often accompanied by abnormal expression of circRNAs.^{30–32} In the current study, we intersected the differentially expressed circRNAs profiles and identified 13 circRNAs, which were associated with Enz-resistance in patients with CRPC. We chose hsa_circ_0047641 to validate and found that knock-down of circ_0047641 could inhibit PCa proliferation, metastasis and reversed Enz-resistance, which provided new treatment strategies for PCa, especially for ADT drug resistance. It has been reported that circRNAs could sponge the corresponding MRE and played a critical role in regulating gene expression through ceRNA regulatory mechanisms.³³ We established a circRNAs-related ceRNA regulatory network to explore the potential roles of these EnzR-related circRNAs, and discovered its possible molecular mechanism via GO and KEGG analyses. Besides, we constructed a prognostic signature that was validated to have a high predictive value compared to previous predictive models. In short, this suggested that the ceRNA regulatory network and the prognostic signature had the

potential to become a new molecular marker and therapeutic target.

To confirm our findings through basic experiments and clinical trials was essential. By intersecting analysis, RRM2 was confirmed to play an essential role in PCa. In the planning step, the focus was on the role of RRM2 and hsa_circ_0047641/hsa_miR338-5p/RRM2 ceRNA regulatory subnetwork. We found hsa_circ_0047641 to be up-regulated in PCa and to promote tumor progression and reversed Enz-resistance. Bhatia et al³⁴ stated that epigenetic silencing of miRNA-338-5p drove PCa progression. Moreover, RRM2, a DNA repair gene, acted as an oncogene in PCa cells and could be transcriptionally inactivated by FOXM1, whose overexpression promoted the proliferation and metastases of PCa.³⁵ It suggested that hsa_circ_0047641 could sponge hsa_miR338-5p to regulate the expression of RRM2, which affected the progression of PCa. Our results provided evidence of the EnzR-related ceRNA regulatory mechanism of PCa.

However, our study also had some downfalls. Firstly, our study was based on a variety of bioinformatics algorithms and web databases, some of which contained only small samples. It could lead to biased results or even incorrect conclusions. Second, we were failed to find proper external data to assess the reliability of the prognostic model. Reasonable external data and clinical data should be collected for further in-depth studies to verify the reliability and sensitivity of the prognostic features. Finally, we only selected one circRNA to verify its molecular function. The other 12 EnzR-related circRNAs should be studied in depth to discover their regulatory mechanisms except for miRNA “sponges”, including RBP sponge, transcription activator, or inhibitor and some circRNA can even exert their function by encoding polypeptides or proteins, which has been reported in other cancers.^{36–38} In the next step, we will select other algorithms to validate our findings further. Meanwhile, we will select a large number of experiments, such as luciferase reporter assay, RNA IP assay, to validate the accuracy of the ceRNA pathways in PCa cell lines and clinical samples.

To conclude, in the current study, we identified 13 EnzR-related circRNAs, and constructed circRNA-miRNA-mRNA ceRNA regulatory networks to explore their possible biological mechanisms. Besides, PPI network analysis was constructed and GO and KEGG functional enrichment analysis was performed, which provided us with new ways to search for potential functions of

mRNAs in the ceRNA regulatory network. Moreover, we established a circRNA prognostic risk-associated signature and found that the prognostic signature had significantly reliable and sensitive prognostic predictive ability. Finally, we chose hsa_circ_0047641 further to investigate the feasibility of the EnzR-related ceRNA regulatory pathway. In short, we confirmed EnzR-related circRNA-miRNA-mRNA ceRNA regulatory network and corresponding prognostic signature had the potential to be a useful prognostic biomarker and therapeutic target.

Abbreviations

PCa, prostate cancer; GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas; circRNA, circular RNA; miRNA, micro RNA; mRNA, messenger RNA; ROC, receiver operating characteristic; AR, androgen receptor; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; AUC, area under the curve; PPI, protein-protein interaction; OS, Overall survival; DFS, disease-free survival; HR, Hazard ratios; AJCC, American Joint Committee on Cancer; MRE, miRNA-recognition elements; LASSO, Least absolute shrinkage and selection operator; ceRNA, competitive endogenous RNA; RRM2, ribonucleotide reductase small subunit M2.

Research Involving Human Participants and/or Animals

This article does not contain any studies with human participants or animals performed by any of the authors.

Data Sharing Statement

The datasets used and analyzed during the study are available from the corresponding author on reasonable request.

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Author Contributions

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work.

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Disclosure

The authors report no conflict of interest.

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