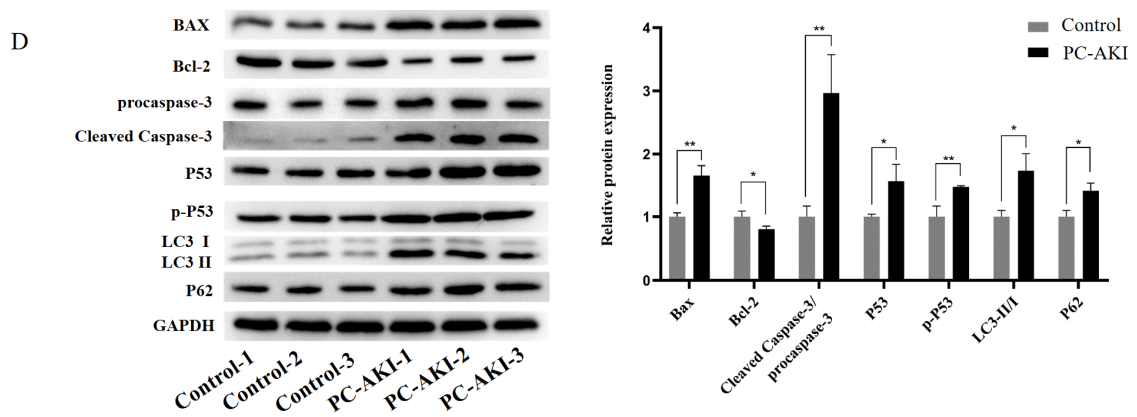
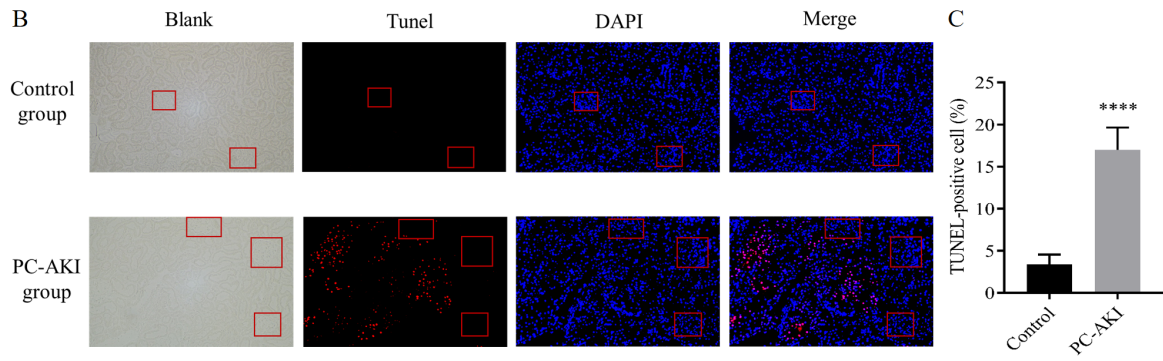
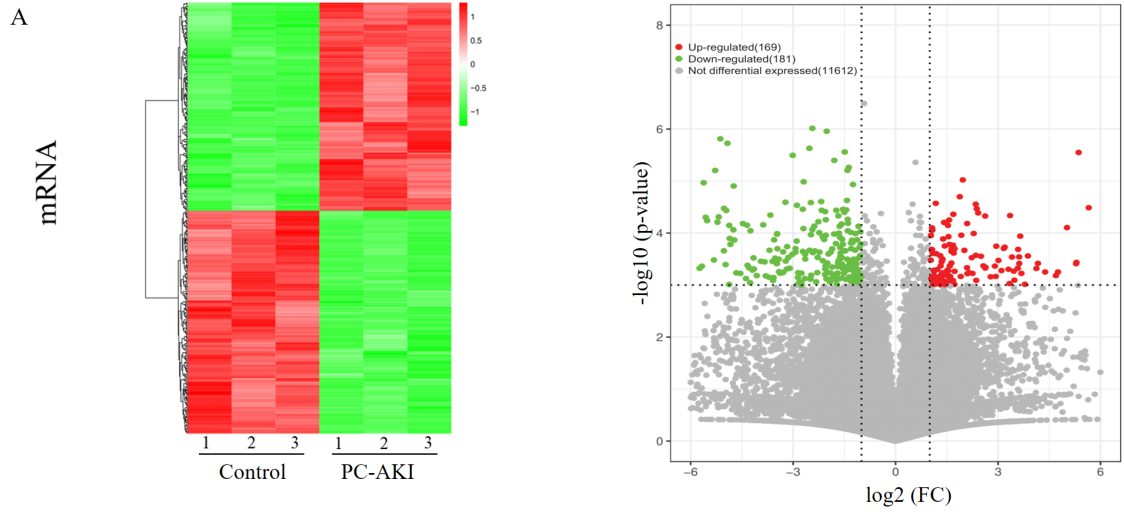
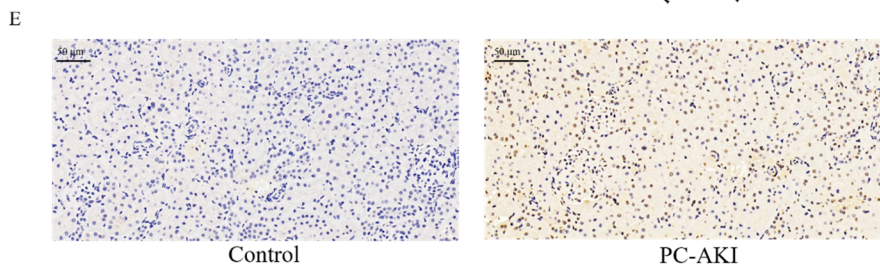
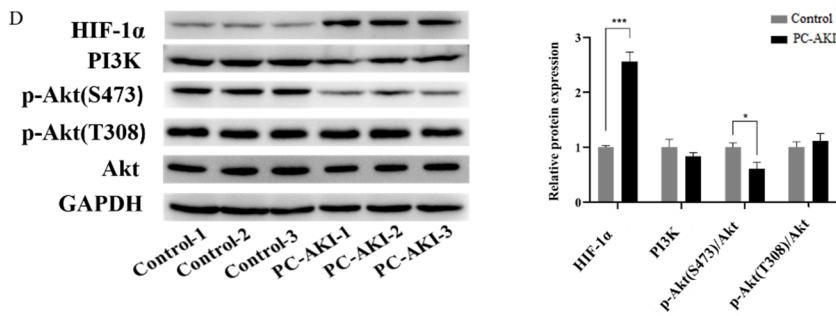
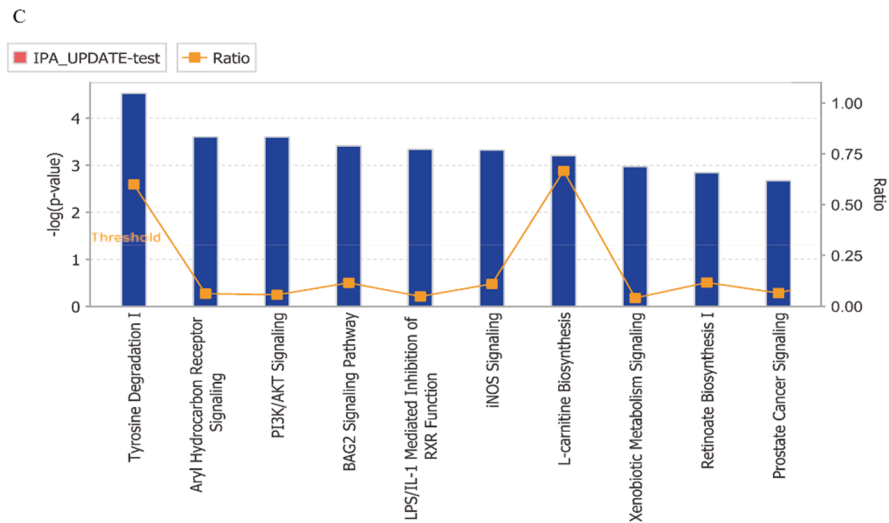
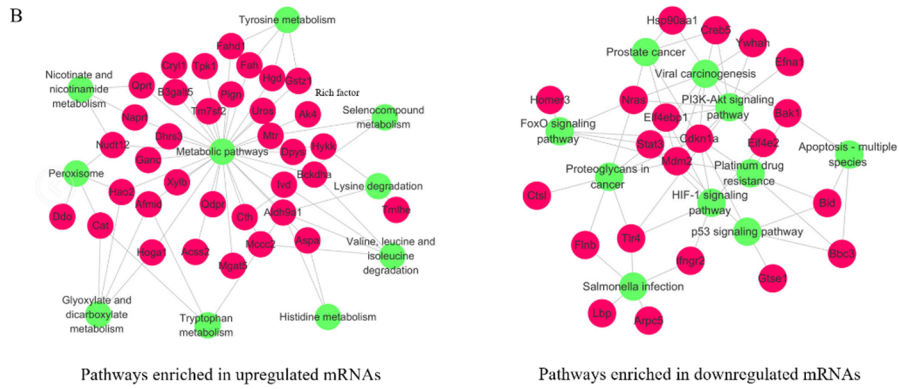
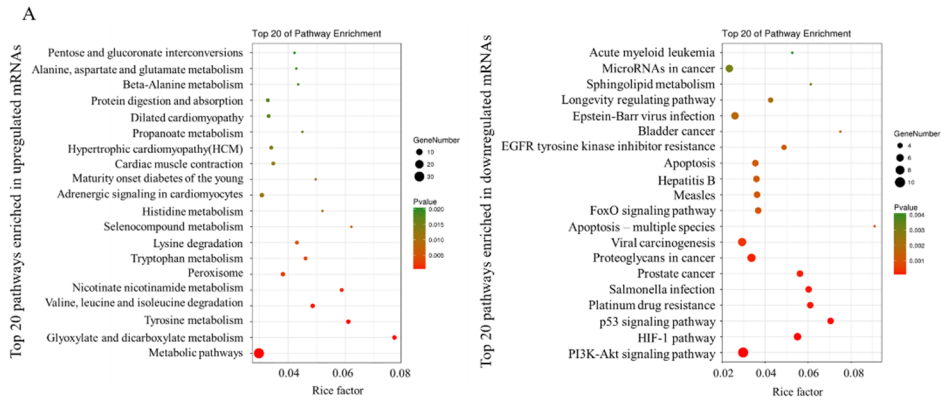


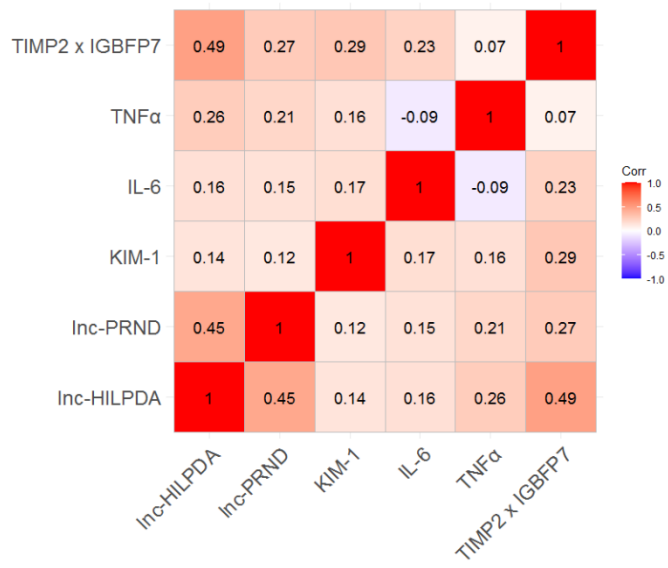
Table S1. Primer sequences and RT-qPCR conditions.

Species	Gene symbol	Forward (5'-3')	Reverse (5'-3')	Product size (bp)	Annealing T (°C)
Human	GAPDH	TGAACGGGAAGCTCACTGG	GCTTCACCACCTTCTTGATGTC	120	59
	lnc-HILPDA	TTATGGCTATGAGATAGGTTGATC	GACAGATGTTTAGGAAGTAGGGTT	154	55
	lnc-PRND	TCCTGTCCTTCTGGGTTTG	AGCAGTGGAGGCTTTCTATG	104	55
	lnc-CDK6	GTCTTCAGGGCCAACAATACAG	TTTCTTCAAATTCAGCCAAAGC	119	59
	NEAT1	CGAGGTGCCTTTACTACAT	TGGAACCCAGAAGACAGA	181	50
	lnc-CDC42SE1	TTGTCCAAACACCAGGGAAAGAG	TCATGGTCCGGTCAATCCGTCT	159	63
Rat	GAPDH	GCCCACTAAAGGGCATCCTG	CATTGAGAGCAATGCCAGCC	111	60
	NONRATT027865 (lnc-ICE2)	CAAGACACTAAGGGTGACTACCAGA	TCTTCACAGGGAGGAGTTCAGG	110	60
	NONRATT019677 (lnc-SLC20A1)	AGCCTGTTTCAGCCTCGTTCTT	TGCGTTTGAGCGTCTGTTGTCT	153	62
	NONRATT023687 (lnc-ZDHHC18)	CCTCCAACCTGACAATAATGAAGACA	GCACAGTATCAGACTGCACAAATCCC	180	65
	NONRATT018635 (lnc-PRND)	CTCCTGAACGAATGTCCGAGTT	TGAGACAAACCAATGAGCGAGA	285	60
	NONRATG002817 (NEAT1)	ACCTTGCCTCTGGGTCATCTGG	TGCTTGCCTTGGTGAACGCTAT	245	65

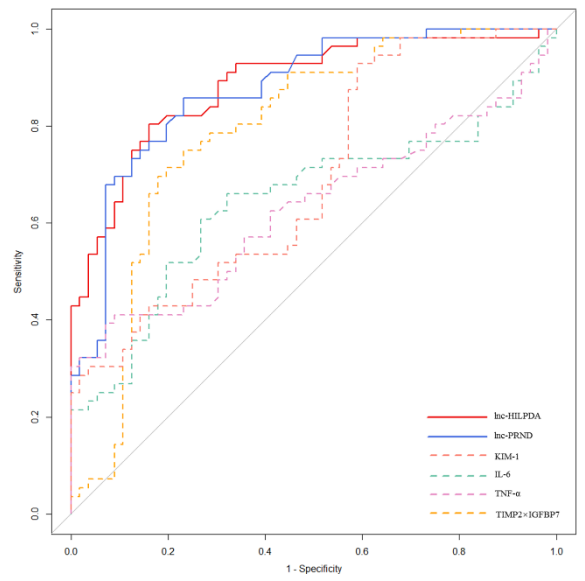
NONRATT015555 (lnc-CDC42SE1)	ATTCCGCATCCAAAGACGACAG	GCAGCAATCCTAGAGGCCAGTAAG	130	63
NONRATG017301 (lnc-CDK6)	GGCAGATGTTGGGACTTGGATT	TCACGCAGCATGTTGTGGGTAT	83	62
NONRATT029217 (lnc-VEGFA)	GCTGTGGACTTGAGTTGGGAGGAG	CCAGGGATGGGTTTGTCTGTGT	194	65
NONRATT005144 (lnc-ARL16)	TCCTGTCACTGGTTCCTGCTT	GCCTGAAACTTCTACCCTTGCTGT	243	63
NONRATT029337 (LINC01127)	CGACTCTGCGACGTGATTCCT	CGCCTCCTCTGTTCTTTCTGCT	175	63
NONRATG012854 (lnc-FRRS1)	TTGGCTCACATTCAAGTGGGCTAT	AAATCTGGCGTGGGACGTTTAG	129	63
NONRATG010899 (lnc-DND1)	GCTTTCGTGGTGCATTGTGGAT	TCACTATCTCGCTCCGGCATT	110	64
NONRATT023136 (lnc-IFNK)	CGTGAATCTGCAACATCGCTGCTC	ATGCCTCCCTCCATCGTCCTCT	175	66
NONRATG016572 (lnc-HILPDA)	TTCCCAAGAGGCAACATCAAG	CACCACCATCTCAGAGCCACAG	147	62





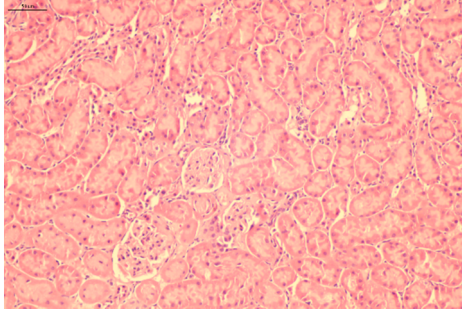


A

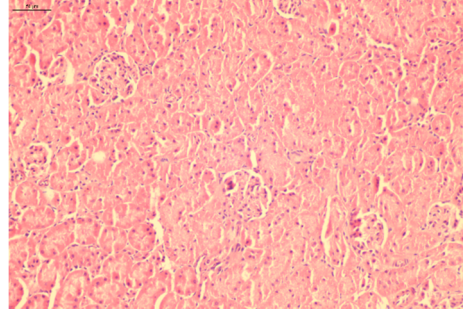


B

A

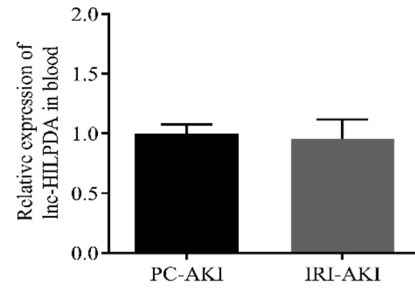
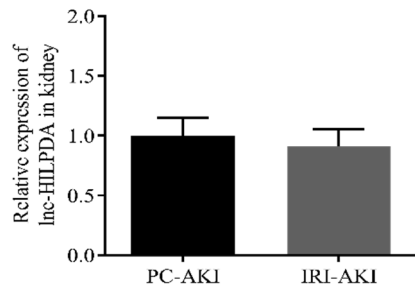


Control

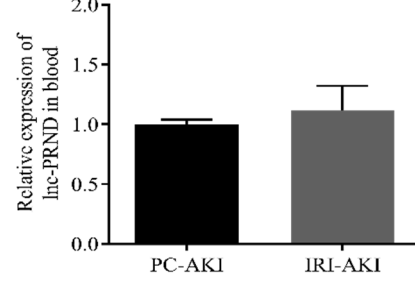
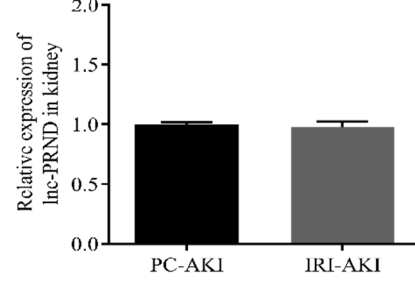


IRI-AKI

B



C



Supplementary Figure Legends

Figure S1 GO analysis and experimental validation of apoptosis and autophagy functions in PC-AKI. (A) Heat map and volcano plot of significantly differentially expressed mRNAs in PC-AKI rat kidney tissues, as determined by RNA sequencing ($|\log_2(\text{fold change vs. control})| > 1$ and $P < 0.001$). (B) TUNEL analysis of kidney tissue from PC-AKI rats and controls. Red frames indicate the glomeruli. (C) Quantitative analysis of TUNEL-positive cells. (D) Expression of apoptosis and autophagy markers in kidney tissues, as determined by western blot analysis. The measurement data are expressed as the means \pm SD. *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$, ****: $P < 0.0001$.

Figure S2 Pathway analysis and experimental validation of PI3K/Akt, P53, and HIF-1 pathway enrichment in PC-AKI. (A) Top 20 pathway enrichment scores determined by KEGG pathway analysis of upregulated and downregulated mRNAs. (B) Pathway interaction networks in PC-AKI. The green nodes indicate the pathways predicted by KEGG pathway analysis. The red nodes indicate the shared differentially expressed genes connecting different pathways. (C) Top 10 pathway determined by IPA analysis of differentially expressed mRNAs. (D) Expression of markers in the PI3K/Akt and HIF-1 pathways in kidney tissues evaluated by western blot analysis. The measurement data are expressed as the means \pm SD. (E) Immunohistochemical analysis of HIF-1 in kidney tissues. *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$.

Figure S3 Correlations analysis between two lnc-RNAs and other validated biomarkers. (A) Spearman's correlation analysis between lnc-HILPDA, lnc-PRND and the other previous validated AKI biomarkers. Red indicates positive correlations while blue indicates negative. The numerical value represents the correlation coefficients. (B) ROC curve of lnc-HILPDA, lnc-PRND and the other biomarkers for discrimination between PC-AKI and non-AKI group.

Figure S4 Evaluation of the diagnosis value of lnc-HILPDA and lnc-PRND to distinguish PC-AKI with other kinds of AKI. (A) Representative pathological changes during IRI-AKI in rat kidney tissues (haematoxylin-eosin (HE) staining: 40 \times , scale bar = 50 μm). (B and C) Expression level of lnc-HILPDA and lnc-PRND in kidney tissue (B) and blood (C) of PC-AKI rats and IRI-AKI rats.