

## Supplementary information

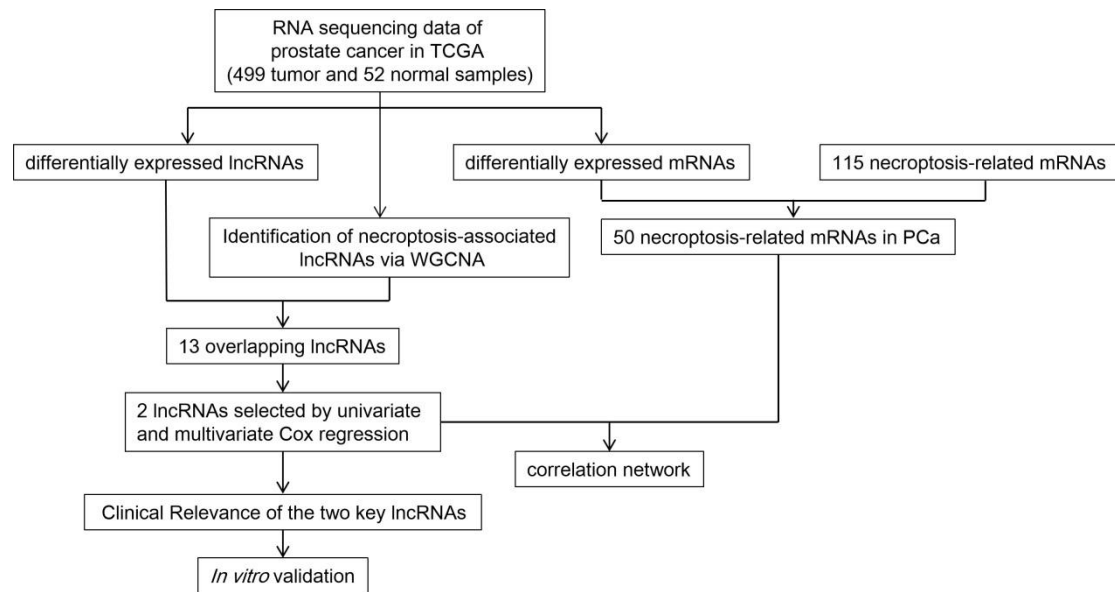


Figure S1 The flow diagram of the work. Abb: TCGA: The Cancer Genome Atlas; PCa: Prostate cancer; WGCNA: Weighted Gene Co-expression Network Analysis; lncRNA: Long non-coding RNA.

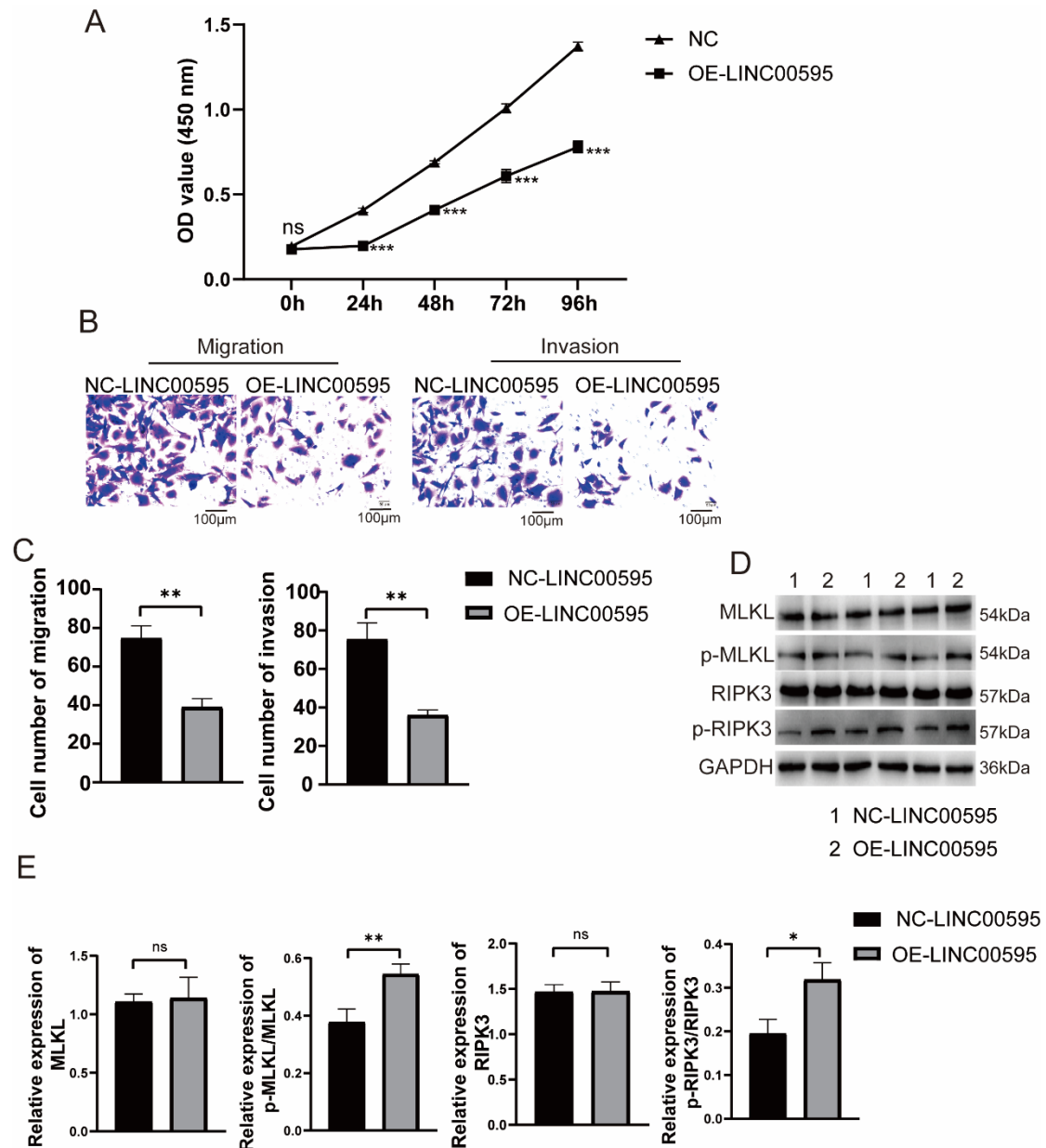


Figure S2 Functional validation of LINC00595 in DU145 cells. (A) CCK-8 assay demonstrating inhibited proliferation of DU145 cells after LINC00595 overexpression (OE-LINC00595) compared to controls ( $p < 0.05$ ). (B and C) Transwell assays showing reduced migration and invasion of DU145 cells in the OE-LINC00595 group ( $p < 0.05$ ; scale bar: 100  $\mu$ m). (D and E) Western blot analysis revealing reveals increased phosphorylation of RIPK3 (p-RIPK3) and MLKL (p-MLKL) in OE-LINC00595-transfected DU145 cells, indicating enhanced necroptosis. ns: no significant,  $*p < 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ .

Table S1 Univariate Cox Regression Analysis of the prognostic value of risk score.

Variable	HR	Lower_CI	Upper_CI	p_value
<b>LINC00595</b>	0.316756730095	0.125937775562	0.796701590230	0.014569037547497
	737	788	327	5
<b>LINC00908</b>	0.399319182740	0.193470567976	0.824186393683	0.013029861008971
	815	881	645	1
<b>riskScore</b>	1.302957815955	1.1319483437111	1.499802601057	0.000227353686910
	95	9	45	414
<b>age</b>	1.053104873818	0.955793584338	1.160323623670	0.295570747468548
	76	35	85	
<b>T_merged-</b>	3.435784499308	0.643995897577	18.33026447855	0.148508062384383
<b>T3</b>	88	091	29	
<b>T_merged-</b>	10.96647091095	0.845972725540	142.1600018653	0.066950355117946
<b>T4</b>	91	981	16	
<b>N</b>	3.608650794996	0.798999065650	16.29834266405	0.095263652415015
	74	36	66	1

Abb: HR: Hazard Ratio; CI: Confidence Interval.