Supplementary information

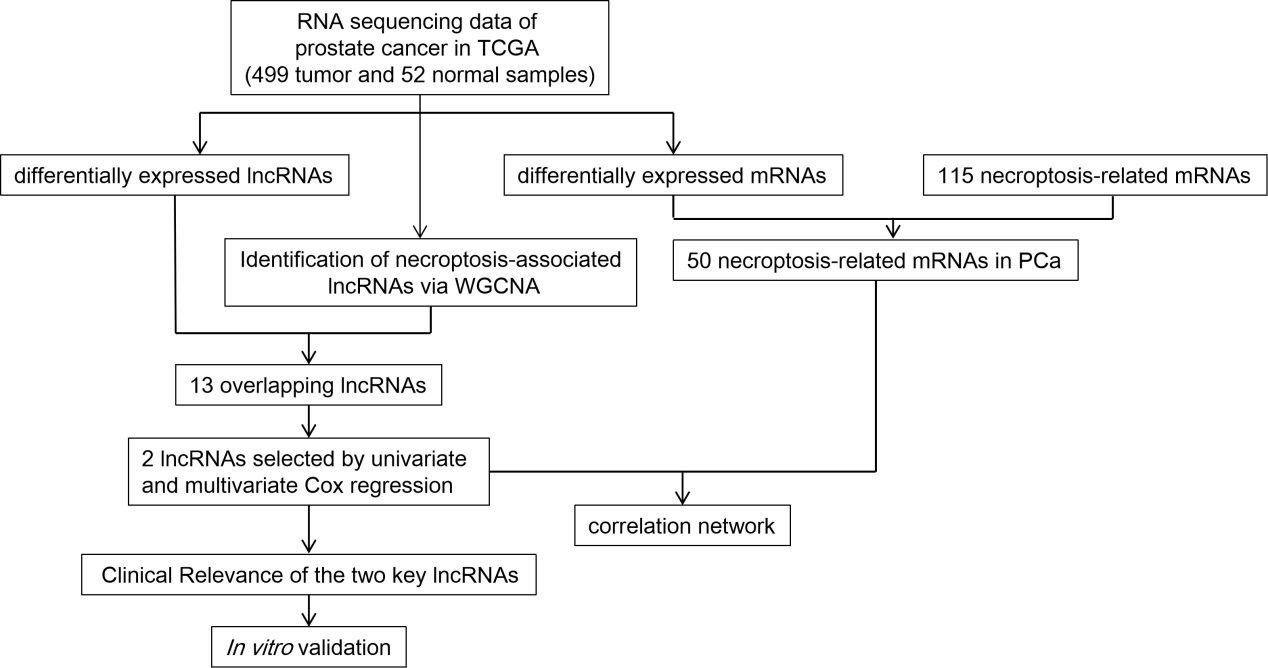


Figure S1 The flow diagram of the work. Abb: TCGA: The Cancer Genome Atlas; PCa: Prostate cancer; WGCNA: Weighted Gene Co-expression Network Analysis; lncRNA: Long non-coding RNA.

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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 μm). (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 |
| LINC00595 | 0.316756730095737 | 0.125937775562788 | 0.796701590230327 | 0.0145690375474975 |
| LINC00908 | 0.399319182740815 | 0.193470567976881 | 0.824186393683645 | 0.0130298610089711 |
| riskScore | 1.30295781595595 | 1.13194834371119 | 1.49980260105745 | 0.000227353686910414 |
| age | 1.05310487381876 | 0.95579358433835 | 1.16032362367085 | 0.295570747468548 |
| T\_merged-T3 | 3.43578449930888 | 0.643995897577091 | 18.3302644785529 | 0.148508062384383 |
| T\_merged-T4 | 10.9664709109591 | 0.845972725540981 | 142.160001865316 | 0.066950355117946 |
| N | 3.60865079499674 | 0.79899906565036 | 16.2983426640566 | 0.0952636524150151 |

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