Supplementary material

Table S1 Triaptosis related genes (TRGs).

Table S2 LASSO coefficients;

Table S3 WGCNA-TRGs in brown module;

Table S4 WGCNA-TRGs in turquoise module;

Table S5 Upregulated and downregulated differentially expressed genes (DEGs) in **TCGA-UCEC dataset;**

Table S6 Candidate genes (CGs) by taking intersection of WGCNA-TRGs and DEGs;

Table S7 GO pathways enriched by CGs;

Table S8 KEGG pathways enriched by CGs;

Table S9 Candidate prognostic markers screen from univariate Cox model and PH test;

Table S10 Samples of high-risk and low-risk groups in TCGA-UCEC;

Table S11 Samples of high-risk and low-risk groups in validation set;

Table S12 Correlation among immune cells;

Table S13 Correlation between immune cells and prognostic markers;

Table S14-17 Pathways respectively enriched by SDF2L1, STK26, TDKH and USP18 (in order);

Table S18 Common pathways shared by prognostic markers;

Table S19 Differences between high-risk and low-risk groups in IC50 of drugs;

Table S20 Correlation between IC50 and risk scores.