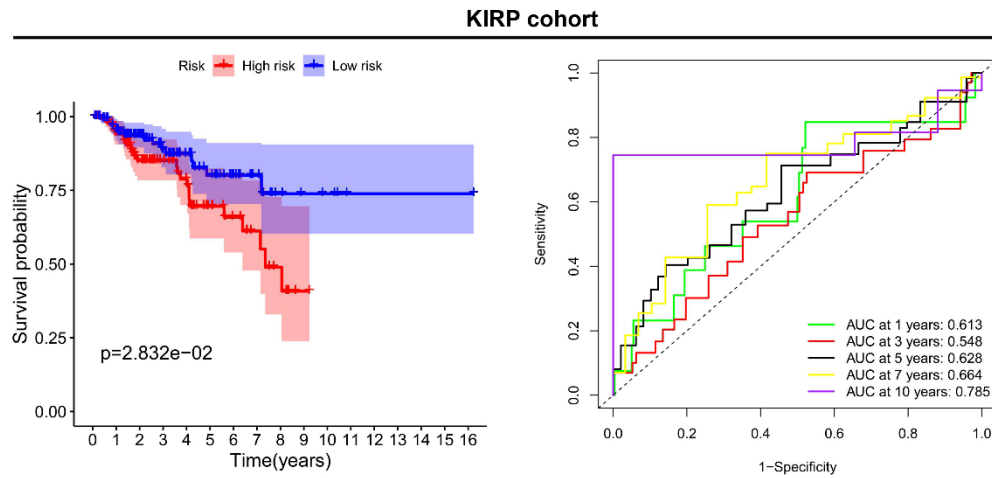


Figure S1

A



B

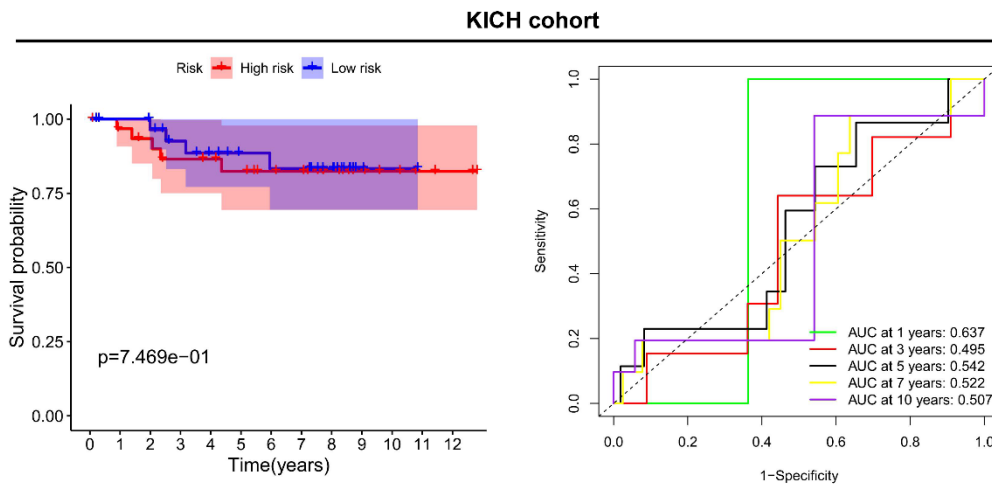


Figure S1 The prediction of KIRP and KICH cohorts by NRGs risk model.

(A) The K-M curve and time-dependent ROC curve for OS in KIRP cohort. **(B)** The K-M curve and time-dependent ROC curve for OS in KICH cohort. Abbreviations: KIRP, kidney renal papillary cell carcinoma; KICH, kidney chromophobe; NRGs, necroptosis-related genes; K-M, Kaplan-Meier; OS, overall survival.

Figure S2

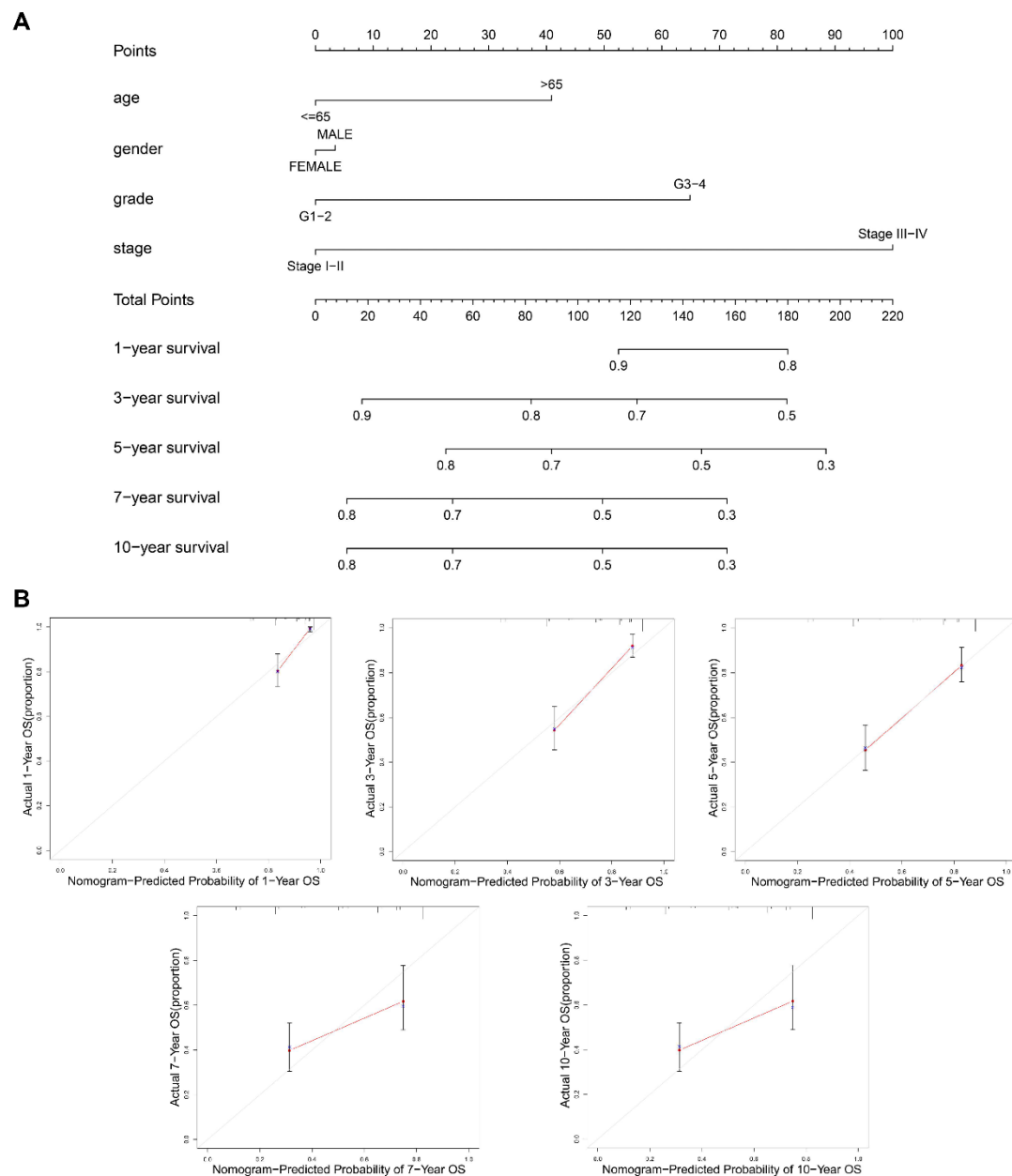
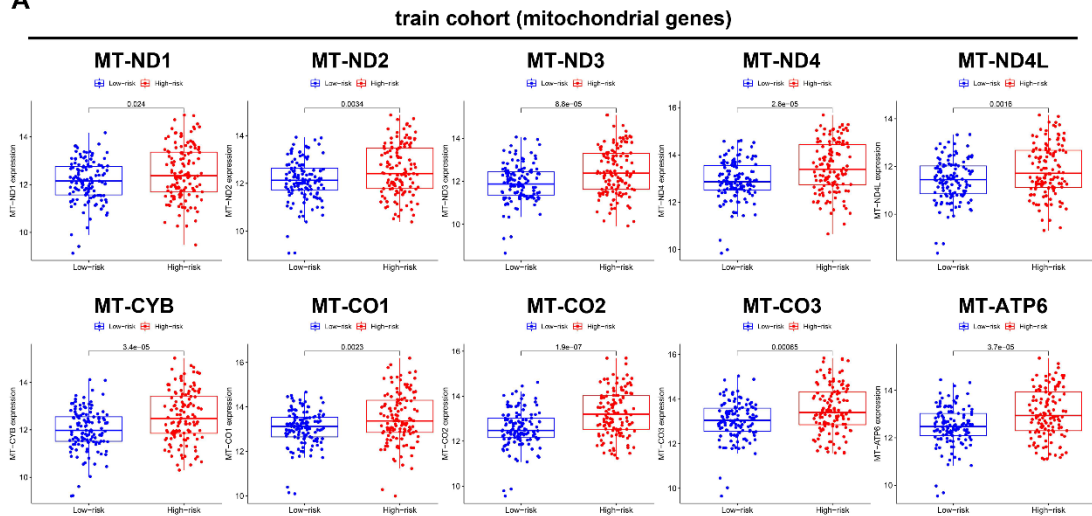


Figure S2. The construction of a nomogram for predicting survival.

(A) A nomogram including only clinicopathological features was constructed to predict 1/3/5/7/10-year OS. (B) The calibration plots for predicting 1/3/5/7/10-year OS based on the NRGs nomogram.

Figure S3

A



B

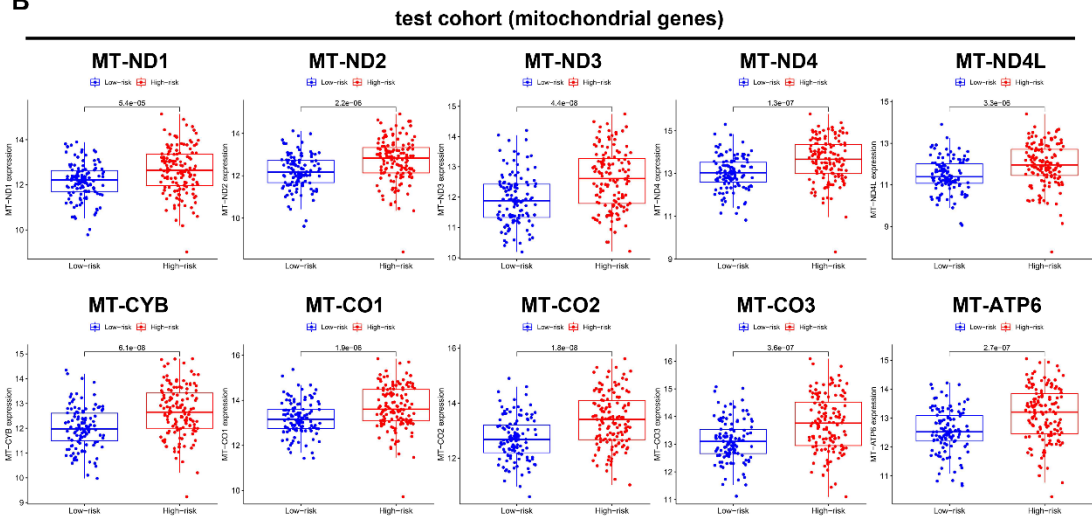


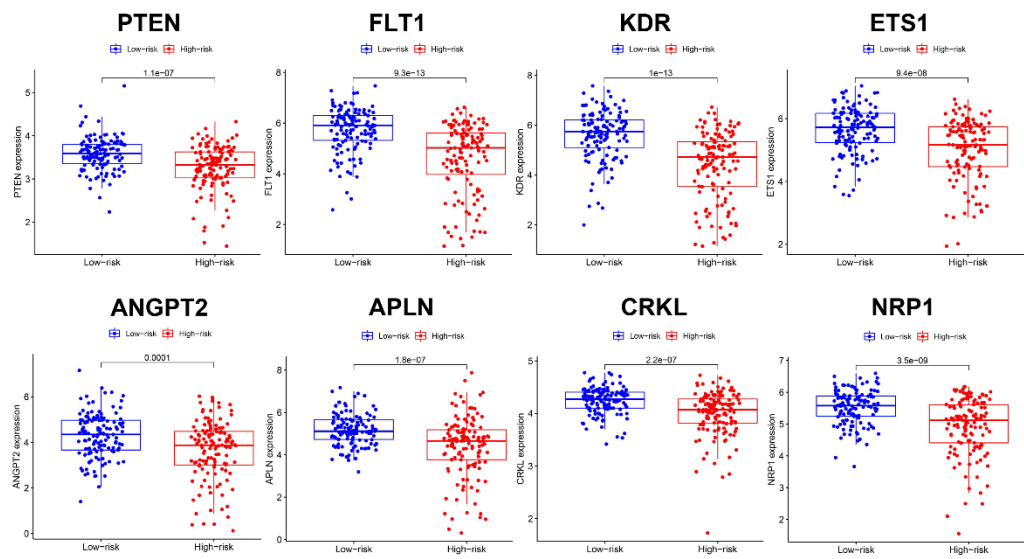
Figure S3. The comparison of mitochondrial gene expressions.

The expressions of mitochondrial genes, including MT-ND1, MT-ND2, MT-ND3, MT-ND4, MT-ND4L, MT-CYB, MT-CO1, MT-CO2, MT-CO3, and MT-ATP6, were significantly higher in the high-risk group both in **(A)** train cohort and **(B)** test cohort.

Figure S4

A

train cohort (angiogenesis-related genes)



B

test cohort (angiogenesis-related genes)

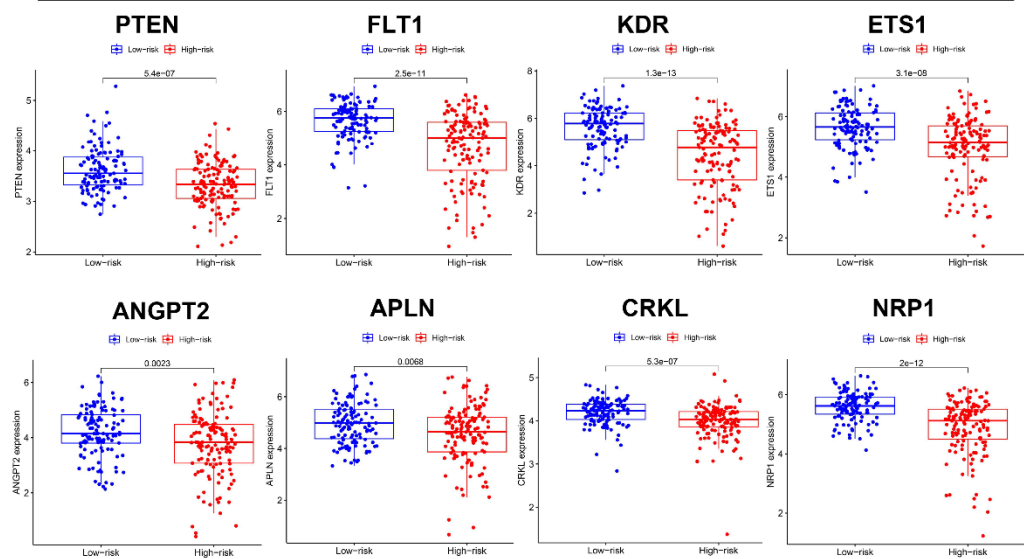


Figure S4. The comparison of angiogenesis-related gene expressions.

The expressions of angiogenesis-related genes, including PTEN, FLT1, KDR, ETS1, ANGPT2, APLN, CRKL, and NRP1, were significantly lower in the high-risk group both in (A) train cohort and (B) test cohort.