

Supplementary Figure 1

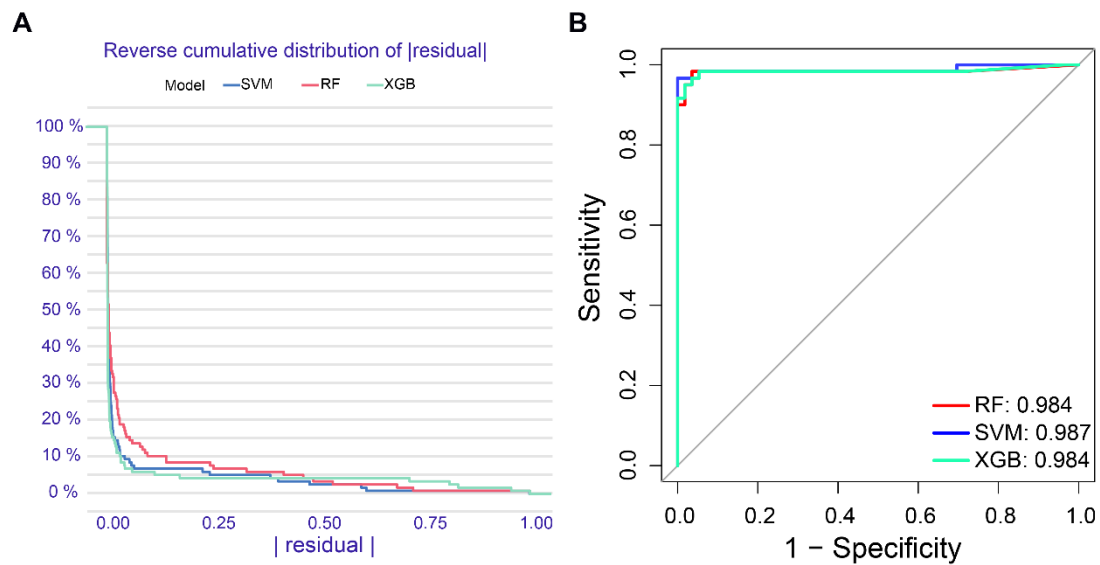


Figure S1. Three machine learning models in human renal ischemia-reperfusion injury dataset. **(A)** Reverse cumulative distribution of the residual and **(B)** Receiver Operating Characteristic curves of the SVM (Support Vector Machine), RF (Random Forest) and XGB (Extreme Gradient Boosting) machine learning models.

Supplementary Figure 2

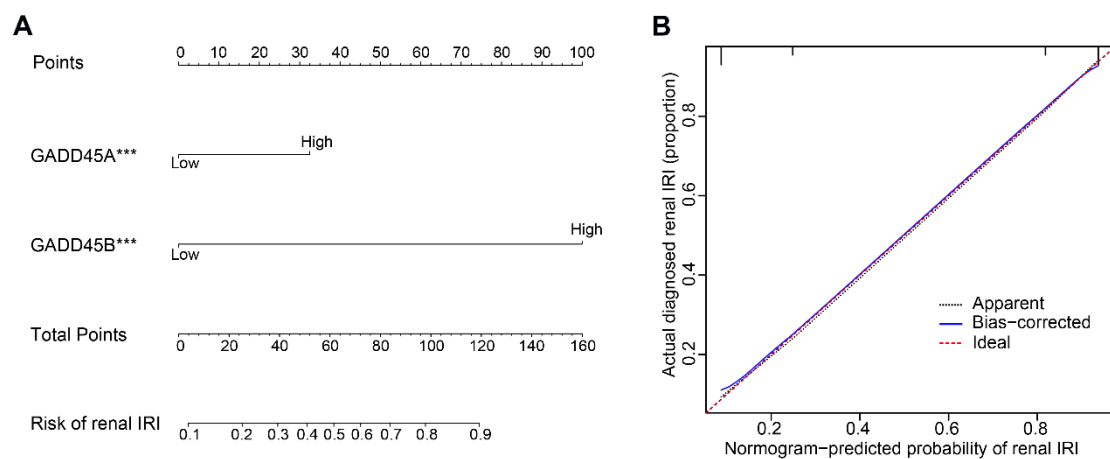


Figure S2. The predictive nomogram and calibration curve in human renal ischemia-reperfusion injury dataset. **(A)** The nomogram of *GADD45A* and *GADD45B* low-/high-gene expression score in the GSE43974 dataset (training cohort). **(B)** Nomogram calibration curve in the training cohort. *GADD45A* (Growth Arrest and DNA Damage Inducible protein 45 alpha); *GADD45B* (Growth Arrest and DNA Damage Inducible protein 45 beta). *** $p < 0.001$.

Supplementary Figure 3

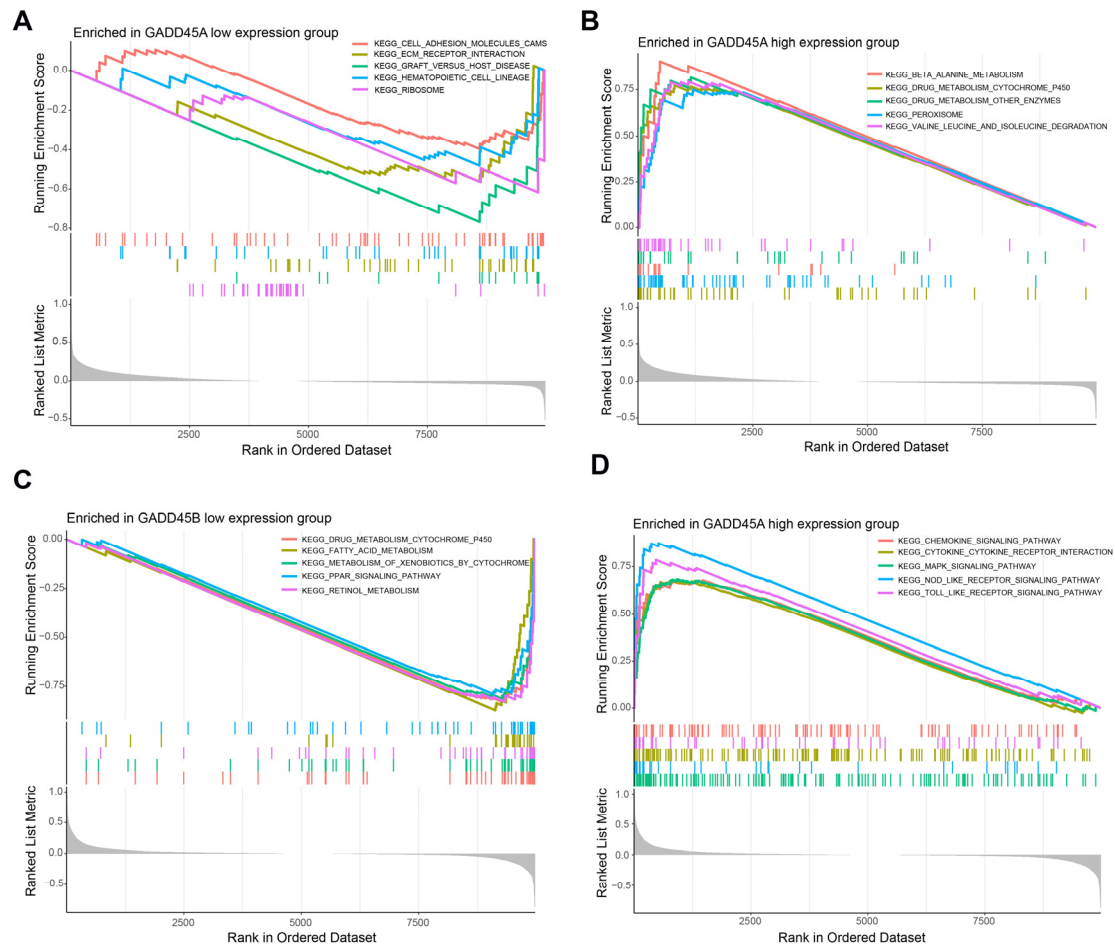


Figure S3. Gene set enrichment analysis (GSEA) of low/high *GADD45A* and *GADD45B* expression in human renal ischemia-reperfusion injury. (A) The Kyoto Encyclopedia of Genes and Genomes (KEGG)-enriched low-*GADD45A* gene sets using the GSEA method. (B) The KEGG-enriched high-*GADD45A* gene sets using the GSEA method. (C) The KEGG-enriched low-*GADD45B* gene sets using GSEA method. (D) The KEGG-enriched high-*GADD45B* gene sets using the GSEA method.