

The difference and prognosis analysis of AIM2 in pan-cancer.

Exploring the expression of AIM2 in pan-cancer based on CCLE database.

TCGA database combined with GTEX database to analyze the differential expression of AIM2 in tumor tissue and normal tissue.

Using univariate COX regression analysis to explore the prognosis of AIM2 in pan-cancer based on TCGA database.

Multivariate COX regression analysis for prognostic analysis of BLCA, ACC, UVM, COAD, SKCM.

Comprehensive analysis of AIM2 in SKCM.

Differences and clinicopathological characteristics of AIM2 in SKCM.

Prognostic analysis of AIM2 in SKCM.

Functional enrichment analysis:GO,KEGG, GSEA,.

Immune correlation analysis.

AIM2-related genes in SKCM.

Based on the TCGA-SKCM and GSE65904 data sets, AIM2-related genes (correlation coefficient > 0.6) were screened

Single factor COXUI analysis of AIM2 and 15 strongly correlated genes.

Based on the TCGA SKCM dataset, Lasso regression analysis was performed on these 16 genes to construct a risk signature.

Validation of the constructed model on the GSE65904 dataset.