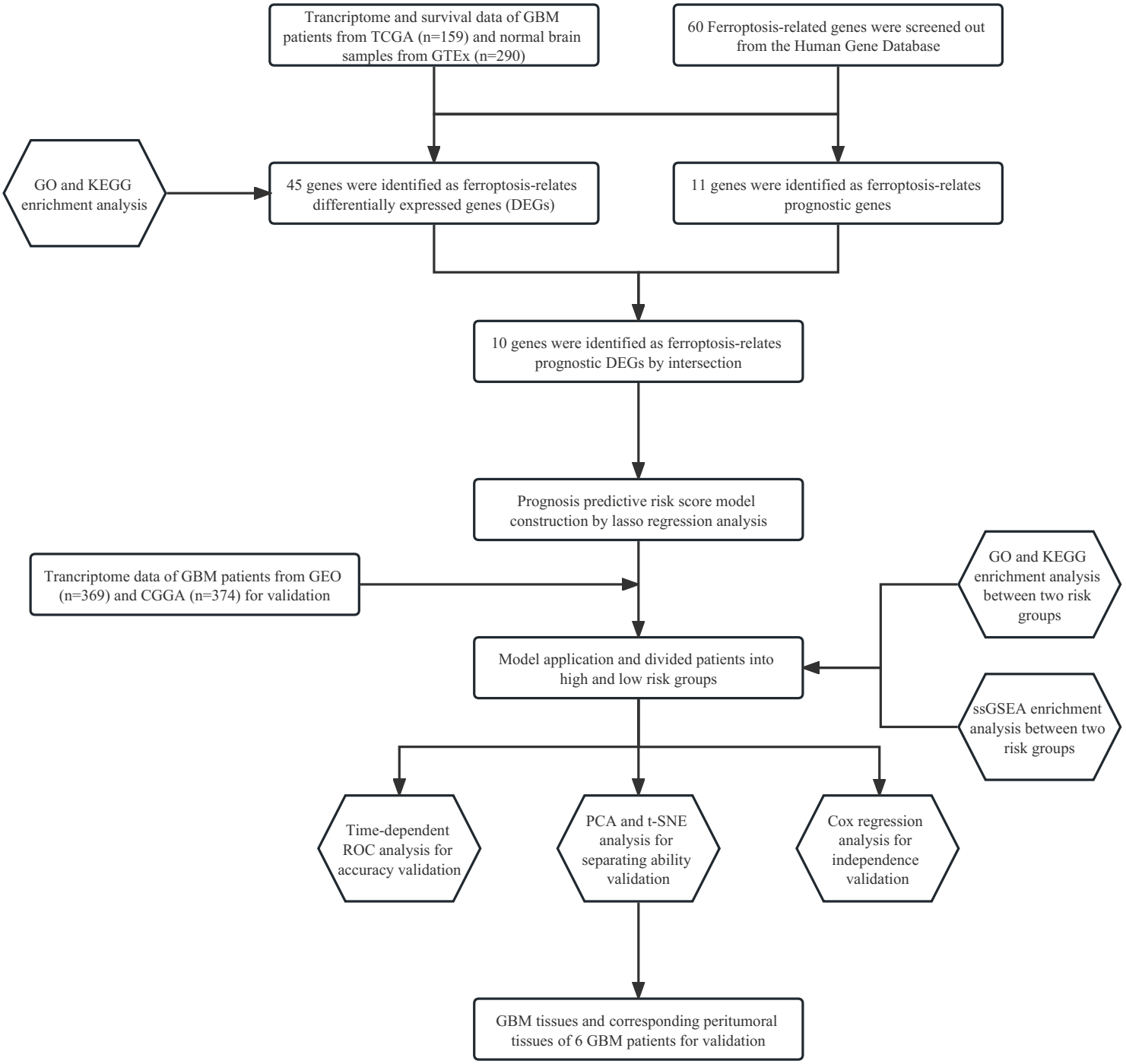
Trancriptome and survival data of GBM patients from TCGA (n=159) and normal brain samples from GTEx (n=290)
60 Ferroptosis-related genes were screened out from the Human Gene Database
GO and KEGG enrichment analysis
45 genes were identified as ferroptosis-relates differentially expressed genes (DEGs)
11 genes were identified as ferroptosis-relates prognostic genes
10 genes were identified as ferroptosis-relates prognostic DEGs by intersection
Prognosis predictive risk score model construction by lasso regression analysis
Trancriptome data of GBM patients from GEO (n=369) and CGGA (n=374) for validation
GO and KEGG enrichment analysis between two risk groups
Model application and divided patients into high and low risk groups
ssGSEA enrichment analysis between two risk groups
Time-dependent ROC analysis for accuracy validation
PCA and t-SNE analysis for separating ability validation
Cox regression analysis for independence validation
GBM tissues and corresponding peritumoral tissues of 6 GBM patients for validation