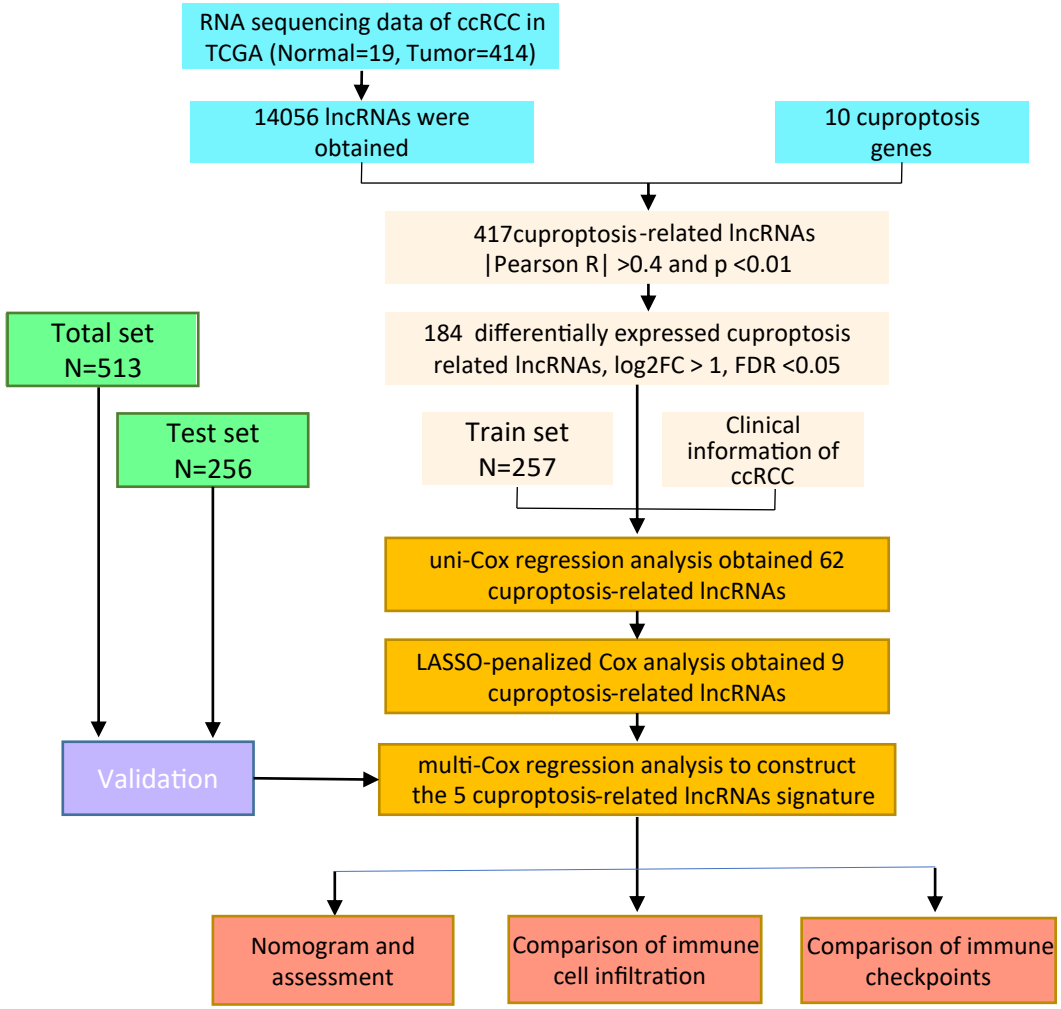
RNA sequencing data of ccRCC in TCGA (Normal=19, Tumor=414)
14056 lncRNAs were obtained
10 cuproptosis genes
417cuproptosis-related lncRNAs |Pearson R| >0.4 and p <0.01
184 differentially expressed cuproptosis related lncRNAs, log2FC > 1, FDR <0.05
Total set N=513
Test set N=256
Train set N=257
Clinical information of ccRCC
uni-Cox regression analysis obtained 62 cuproptosis-related lncRNAs
LASSO-penalized Cox analysis obtained 9 cuproptosis-related lncRNAs
Validation
multi-Cox regression analysis to construct the 5 cuproptosis-related lncRNAs signature
Nomogram and assessment
Comparison of immune cell infiltration
Comparison of immune checkpoints