Background

Esophageal carcinoma (EC) is a common cancer with a high mortality. The identification of gene expression signatures for the tumor microenvironment in EC is necessary to predict prognosis and guide treatment selection. This is the first study examining the immune and metabolic gene signatures of EC for prognosis prediction and for constructing a prediction model using transcriptional data.

Methods

Differential expression analysis was used to compare the transcriptomic data associated with immunity and metabolism from The Cancer Genome Atlas dataset between 10 normal and 162 EC patient samples. Differentially expressed genes (DEGs) related to prognosis were screened by univariate Cox regression. Subtype clusters were identified and the characteristics were analyzed. Multivariate Cox and LASSO regression were used to establish and validate a risk score (RS) prediction model for EC.

Results

12 prognosis-related genes were obtained through one-way Cox analysis based on the immune and metabolic genes. Patients were categorized into 3 subtypes by He and Spearman unsupervised clustering. KM survival analysis identified significant prognostic differences (P = 0.0016) (Figure 2).

In the training set, 7 genes were identified to be significantly associated with prognosis by one-way Cox regression (P < 0.05, KM < 0.05). A prognostic model consisting of six genes including STC2, APLN, GPER1, FMO1, SNRPB, and FABP3 was constructed by multifactorial COX regression analysis (Figure 3).

Based on median risk score, the training set was divided into high- and low-risk groups. Patients with a low risk score had significantly higher OS (P < 0.001). The ROC curves were used to calculate the 1-, 3-, and 5-year AUC values, which were 0.862, 0.769, and 0.818, respectively, showing a certain predictive accuracy (Figure 4).

Similar predictive performance is validated in the testing and external validation sets (Figure 5-6).

Conclusion

Immune- and metabolism-related genes were significantly correlated with the prognosis of EC patients. A prognostic model constructed with six DEGs had good prediction efficiency. These findings may help the clinical diagnosis and treatment of EC patients and provide a new perspective to explore the molecular mechanisms of EC.