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Validation of a 5-gene signature for predicting outcomes in early-stage NSCLC patients

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Background: Early-stage non-small cell lung cancer(NSCLC) present high rates of recurrence, even undergoing curative treatment such as surgery and/or adjuvant chemotherapy(ACT). Specific criteria lack to define a therapeutic approach that offers the maximum survival benefit for prognosis improvement. Aim: To validate a 5-gene signature to predict prognosis in early-stage NSCLC patients. **Methods:** Surgically resected patients(n=138) were retrospectively included. RNA was isolated from formalin-fixed paraffin-embedded samples to evaluate the expression of *DUSP6*, *ERBB3*, *LCK*, *MMD*, and *STAT1* by Elements XT custom panel(NanoString technologies). Patients were stratified as low-risk(favorable outcome) and (unfavorable outcome), and overall(OS) and event-free survival(EFS) were assessed. Receiver operating characteristic(ROC) curves were measured for 12, 24, and 36 months of survival to evaluate the accuracy of the predictive model. **Results:** The 5-gene panel stratified patients(n=138) as low- and high-risk. High expression of was associated with better OS(HR=0.64;p=0.001 and HR=0.68;p=0.003, respectively). However, the expression of *LCK*, *MMD* and *STAT1* was not associated with survival. High-risk patients presented unfavorable outcomes for OS(HR=3.19;p<0.001) and EFS(HR=2.17;p=0.005).Moreover, the model showed good accuracy(AUC(t=12):0.72;AUC(t=24):0.73;and AUC(t=12):0.73) for discriminating survival status. **Conclusion:** The 5-gene panel successfully stratifies low- and high-risk patients, and may be a promising tool for predicting outcomes in early-stage NSCLC patients.