

## ***CFL1* Expression Levels as a Prognostic and Drug Resistance Marker in Non-small Cell Lung Cancer**

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Non-small-cell lung cancer is the major determinant of cancer mortality worldwide. Our previous data suggest that *CFL1* gene is a potential biomarker candidate. The aim of this research was to experimentally and clinically validate the role of *CFL1* gene as a prognostic and drug resistance marker in NSCLC. Using meta-analysis of a databank of NSCLC biopsies containing gene expression data and clinical and pathologic information from a cohort of 111 patients, we generated Kaplan–Meier mortality curves by clustering patients according to *CFL1* gene expression levels and NSCLC stage grouping. We found that patients with high *CFL1* gene expression levels had a significant lower survival rate. *Hoc* analysis showed a high sensitivity and specificity for *CFL1* gene as a prognostic biomarker in stages IA, IB and IIA/B. Others 40 genes were tested and none of them were significant. Immunohistochemistry analysis showed increased *CFL1* gene product immunocontent in tumor biopsies. Using human NSCLC cell lines (H460, HOP92, H23, A549, H226, EKVX) with different degree of *CFL1* gene expression level, we found that high mRNA levels and protein immunocontent were correlated with tumor invasiveness, determined using an invasive chamber system. Moreover, we found that high *CFL1* expression is significantly correlated with resistance (increased drug GI50 value) against alkylating agents. Our results demonstrate that *CFL1* gene is a potent biomarker to predict NSCLC patient outcome and could be used as a NSCLC biomarker with high sensitivity and specificity.

Keywords: *CFL1* gene; NSCLC; biomarker

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