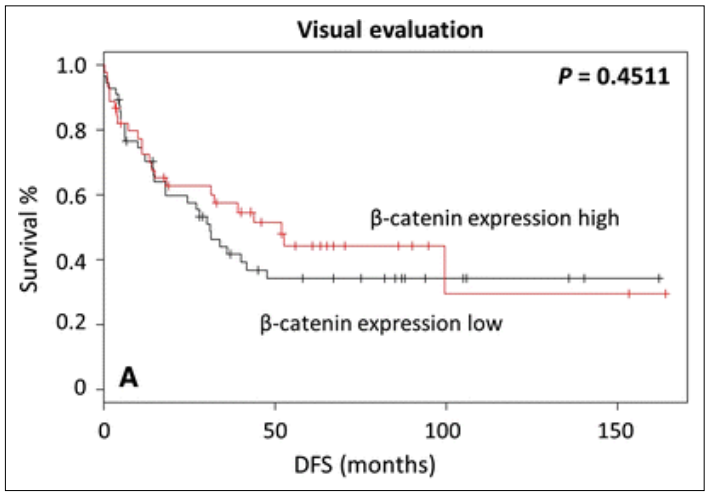
DEFINIENS®
the tissue phenomics company

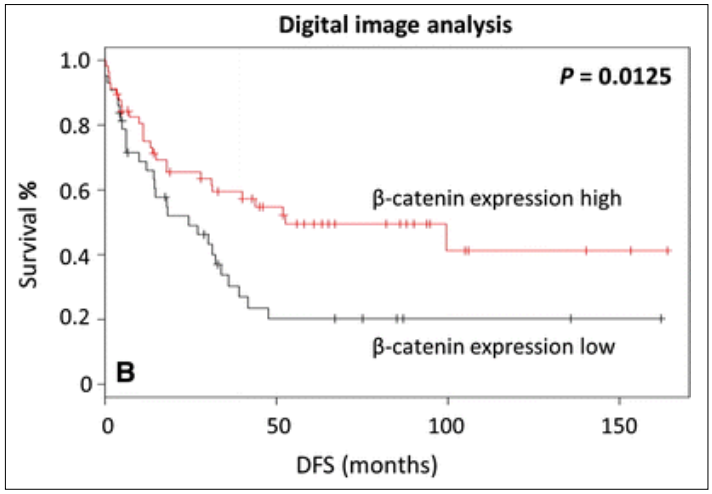
Identification of a More Accurate Scoring System to Stratify Patients

By quantifying all tissue features and their relationships in context, statistical methods can be used to identify the most relevant and accurate scoring system. The aim of this study was to compare routine manual scoring of five biomarkers in esophageal adenocarcinomas to digital image analysis. By using Definiens technology, the scoring system was improved and the authors concluded that digital image analysis was superior to visual scoring.

Survival analysis example:
β-catenin expression in esophageal adenocarcinomas



A) disease-free survival using visual evaluation



B) disease-free survival using image analysis

Study Synopsis

- Researchers compared the expression levels of five membrane-binding proteins (HER2, EGFR, pEGFR, β-catenin, and E-cadherin) measured by manual qualitative scoring and digital image analysis using Definiens technology on 153 esophageal cancers.
- All biomarkers were assessed for their ability to predict disease-free and overall survival.
- The digital image analysis approach identified cut points for four biomarkers (HER2, pEGFR, β-catenin, and E-cadherin) with a significant prognostic value in disease-free and overall survival. Previous manual attempts failed to identify a significant cut point.
- Additionally, the digital image analysis approach improved the prediction of prognosis of EGFR in esophageal cancer.

Benefits

- Definiens technology significantly improves the sensitivity and standardization of IHC evaluation.
- By quantifying all tissue features and their relationships in context, a more accurate scoring systems was identified.

Implications

- With the possibility to measure different tissue features, Definiens enables the discovery of meaningful signatures for prognosis in different indications.
- Definiens technology has great potential as a diagnostic support tool by providing more accurate scoring systems.

Additional Information

Feuchtinger et al.; Histochem Cell Biol. 2015 Jan; 143(1):1-9