

## **A Predictor for Survival in Intermediate Grade ccRCC**

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We present a simple score to predict survival for cancer patients using an algorithm which identifies gene expression patterns at multiple time points to distinguish survivors from non-survivors. We illustrate our method using a published microarray dataset of 177 ccRCC samples with 128 intermediate Fuhrman grade tumors (grades 2, 3). At each time point when a death occurs, we identify patterns that separate patients into high/low risk survival classes. For each pattern, we compute the area under the Kaplan-Meier curve for the samples that satisfy the pattern. The average of the pattern scores for each patient defines a patient specific survival score. We find that these scores correlate very well with actual survival (c-index=72%). High/low risk class assignment based on the median of the predicted survival score is highly significant (log-rank p-value=0.0022). The median survival for the high-risk group is 23 months and for low-risk group is 163 months. High/low Fuhrman grade assignments (4 and 1) correlate well with our class assignments into high/low risk classes. However, intermediate Fuhrman grade assignments (2 and 3) do not correlate with survival class, suggesting that our classifier would outperform the Fuhrman system for intermediate grade tumors. The method is general and can be applied to any cancer type and dataset where both survival and molecular data is available.