

## Spotlight

By Caroline Seydel

### **Molecular profile can give patients thumbs-up or thumbs-down**

Schulte *et al.*

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Neuroblastoma, one of the most common childhood tumors, is clinically heterogeneous. Sometimes, tumors disappear on their own; other times, even intensive therapy can't save the patient. To help predict whether a tumor is favorable or unfavorable, Schulte *et al.* analyzed microRNAs from many different neuroblastomas. They found that microRNA expression can predict patient outcome.

MicroRNAs (miRNAs), small non-coding RNAs, grab onto mRNAs and prevent translation, thereby regulating protein expression. Predicting neuroblastoma outcome using mRNA expression profiles has been successful, suggesting that miRNA expression profiles might also provide a useful predictive tool. Schulte *et al.* analyzed miRNA expression in 69 patients from the German Neuroblastoma Trial. They applied a classification algorithm called SVM (support vector machines) and found that it could predict disease recurrence with high accuracy based on the miRNA profile. The researchers then successfully used a second technique, called CASPAR, to predict overall survival and thus they separated the patients into two groups based on whether or not they suffered a relapse.

Amplification of the oncogene *MYCN*, the team found, correlated with downregulated miRNA, corroborating the notion that *MYCN* status plays an important role in tumor biology and eventual outcome. Also, high levels of the protein TrkA correlates with favorable outcome, and so the researchers looked at how miRNA expression patterns vary with TrkA expression. They found TrkA expression associated with upregulation of miRNAs was associated with a favorable outcome, and downregulation of miRNAs heralded poor outcome. Analyzing miRNA signatures may be a valuable tool for predicting patient outcome and prove useful in the clinical setting.