

# Gene-based test identifies poor-prognosis colon cancers

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population of *BRAF* mutated-like *KRAS* mutants and double wild-type patients with similarly [poor prognosis](#)," the authors write. "This suggests a common biology between these tumors and provides a novel classification tool for cancers, adding prognostic and biologic information that is not captured by the mutation status alone."

Several authors disclosed financial relationships with Pfizer.

**More information:** [Abstract](#)  
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[Editorial](#)

(HealthDay) -- A sensitive and specific gene-based classifier can be used to identify *BRAF* mutant colon cancer tumors and a subpopulation of *BRAF* wild-type tumors with poor prognosis, according to a study published March 5 in the *Journal of Clinical Oncology*.

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In an effort to develop a gene expression-based classifier to identify *BRAF* mutants with high sensitivity, Vlad Popovici, M.D., of the Swiss Institute of Bioinformatics in Lausanne, and colleagues evaluated differential gene expression between *BRAF* mutant and non-*BRAF*, non-*KRAS* mutant cancers from 668 stage II and III [colon cancer](#) samples.

The researchers developed a 64 gene-based classifier which identified *BRAF* mutant tumors with 96 percent sensitivity and 86 percent specificity. A subpopulation of patients who were *BRAF* wild type (30 percent of *KRAS* mutants, 13 percent of double wild type) were found to have poor overall survival and poor survival after relapse, similar to that seen in patients with *BRAF* mutations.

"A characteristic pattern of gene expression is associated with and accurately predicts *BRAF* mutation status and, in addition, identifies a

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