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ABOUT THE COVER

Current cancer taxonomy is based on the organ and tissue origin of tumors (histopathology), which can potentially be reflected by gene expression as well. This makes it possible to establish equivalency between histopathology and molecular pathology by transcriptome expression. Guo and colleagues report seven distinct gene expression profiles corresponding to seven major cancer types with high within-type and generally low between-type correlation. The described algorithm can be a foundation for the development of future cancer diagnostics. Color bars at the top and to the left denote cancer types. For details, see article by Guo and colleagues on page 4619.

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The Journal of Cancer Research (1916–1930) | The American Journal of Cancer (1931–1940)

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