

Integrated classifier identifies benign lung nodules

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a negative predictive value of 97, 44, and 98 percent, respectively, in distinguishing benign from malignant nodules. Performance was better with the classifier than with positron emission tomography, validated [lung](#) nodule risk models, and physician cancer probability estimates. Forty percent fewer procedures would be performed on benign nodules and 3 percent of malignant nodules would be misclassified if the integrated classifier were used to direct care.

"If used in clinical practice, invasive procedures could be reduced by diverting [benign nodules](#) to surveillance," the authors write.

Several authors disclosed financial ties to diagnostics companies, including Integrated Diagnostics, which provided funding for the study.

More information: [Abstract/Full Text Editorial](#)

(HealthDay)—An integrated plasma proteomics classifier, which integrates the relative abundance of two plasma proteins with a clinical risk prediction model, can distinguish benign from malignant lung nodules in those at low-to-intermediate risk for cancer, according to a study published in the September issue of *CHEST*.

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Gerard A. Silvestri, M.D., from the Medical University of South Carolina in Charleston, and colleagues conducted a prospective observational trial involving 685 patients with 8- to 30-mm lung nodules. The relative abundance of two plasma proteins, LG3BP and C163A, was measured using multiple reaction monitoring mass spectrometry. To identify likely benign nodules, results were integrated with a clinical risk prediction [model](#).

The researchers found that the prevalence of lung [cancer](#) was 16 percent in a subgroup of 178 patients with a clinician-assessed pretest probability of cancer \geq 50 percent. The integrated classifier demonstrated sensitivity, specificity, and

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