What is already known?
- The mutation profile of solid tumors can be complex. For instance, mutations in the same gene can be found in multiple types of solid tumors, and mutations in different genes can be found in tumors of the same type.\(^1\)
- The complexity can make treatment selection a challenge and can affect drug resistance.\(^1,2\)
- A universal solid tumor mutation profiling assay may assist healthcare providers in more targeted treatment selection.

What was done in this study?
- The investigators developed a mutation profiling assay for solid tumors.
- The assay included 34 cancer-associated genes that were chosen based on National Comprehensive Cancer Network (NCCN) guidelines, potential for informing therapy selection, and prevalence of somatic mutations for multiple cancer types.
- The assay used next-generation sequencing (NGS) to profile mutations in 121 consecutive, de-identified tumor specimens that were originally submitted for routine molecular testing.
  - Tumor specimens included melanoma (n=31), lung cancer (n=27), colorectal cancer (n=33), and breast cancer (n=30).
- Results of the NGS assay were compared to those of routine molecular testing.

What were the new findings in this study?
- The NGS assay detected all mutations identified by routine molecular testing (ie, no false-negative results).
- In 74% (90/121) of specimens, the NGS assay detected at least 1 mutation that was not identified by routine testing. Sixteen of these specimens harbored mutations in NCCN guideline genes.
- The assay detected mutations in 59% (20/34) of the genes included in the panel; 75% (15/20) of these genes were mutated in multiple tumor types.

What were the conclusions from the study?
- Compared with routine molecular testing, the 34-gene NGS assay demonstrated broader detection of mutations and greater sensitivity.
- This assay may provide clinically relevant results for patients with solid tumors.