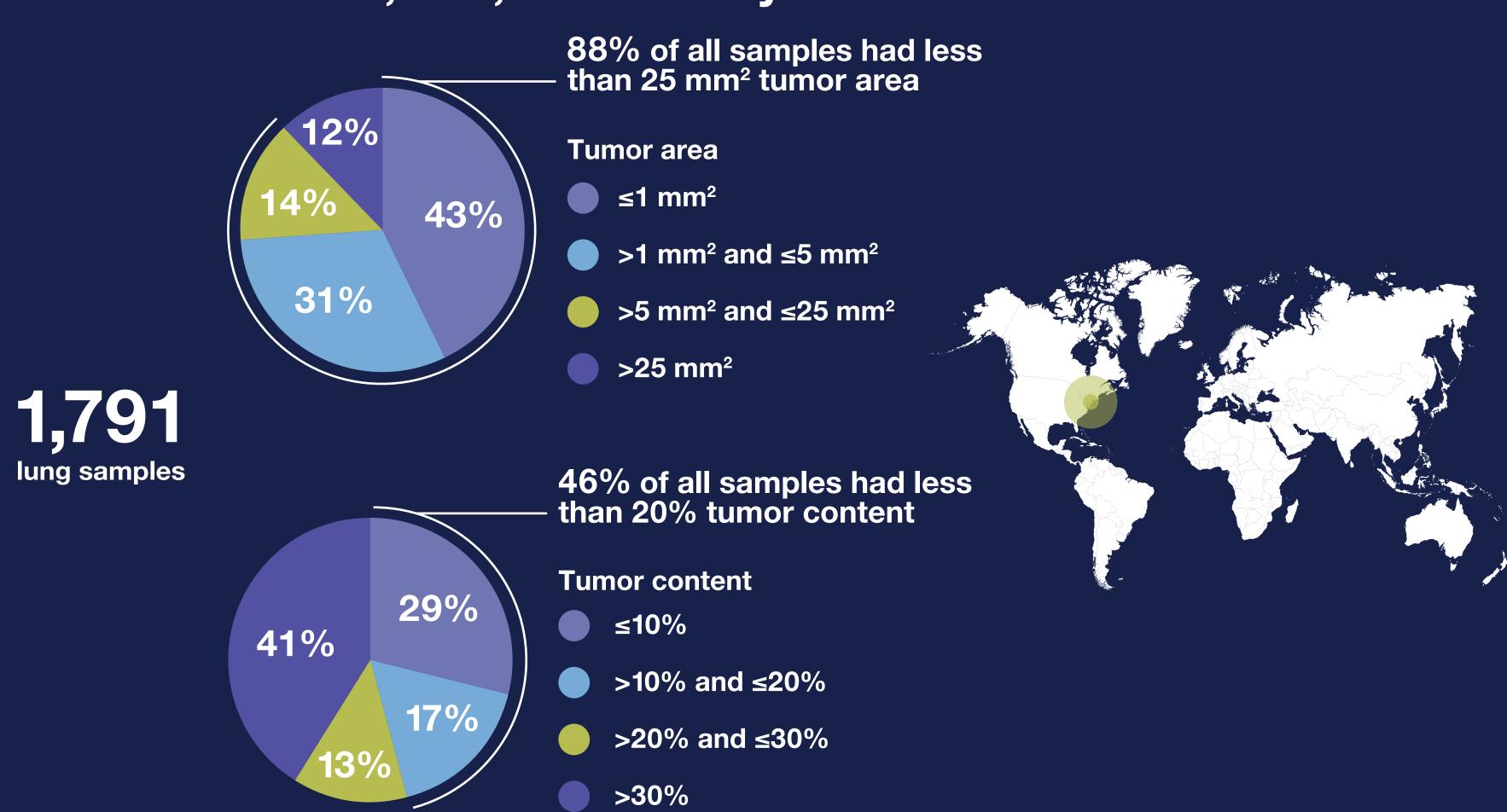
Tumor content limits some NGS-based NSCLC tests

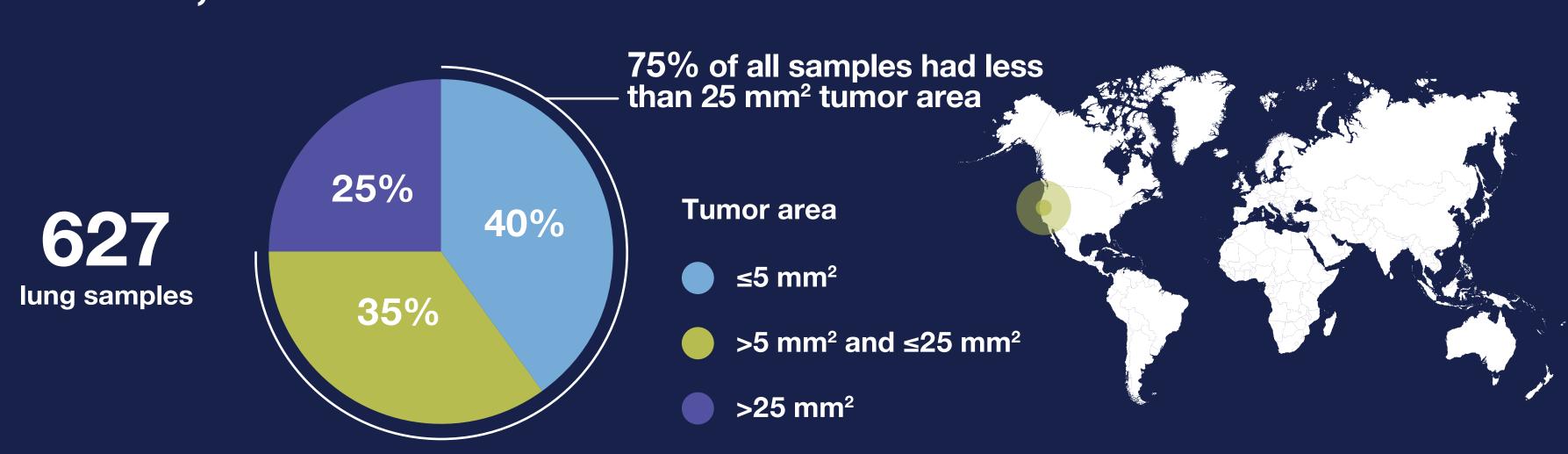
Clinical practice guidelines recommend broad genetic profiling by next-generation sequencing (NGS) for advanced non-small cell lung cancer (NSCLC) to guide first-line treatment. Yet, small biopsies and low-tumor content samples pose challenges to testing. The data below, from laboratories across the world, show how limited many of these samples are. While NGS is

generally seen as a tissue-saving method given its ability to deliver multiple biomarker results with a single sample, it is important to understand that the sample size and content requirements are not equal for all NGS-based methods. Some NGS-based methods can test smaller samples and deliver results for more patients.

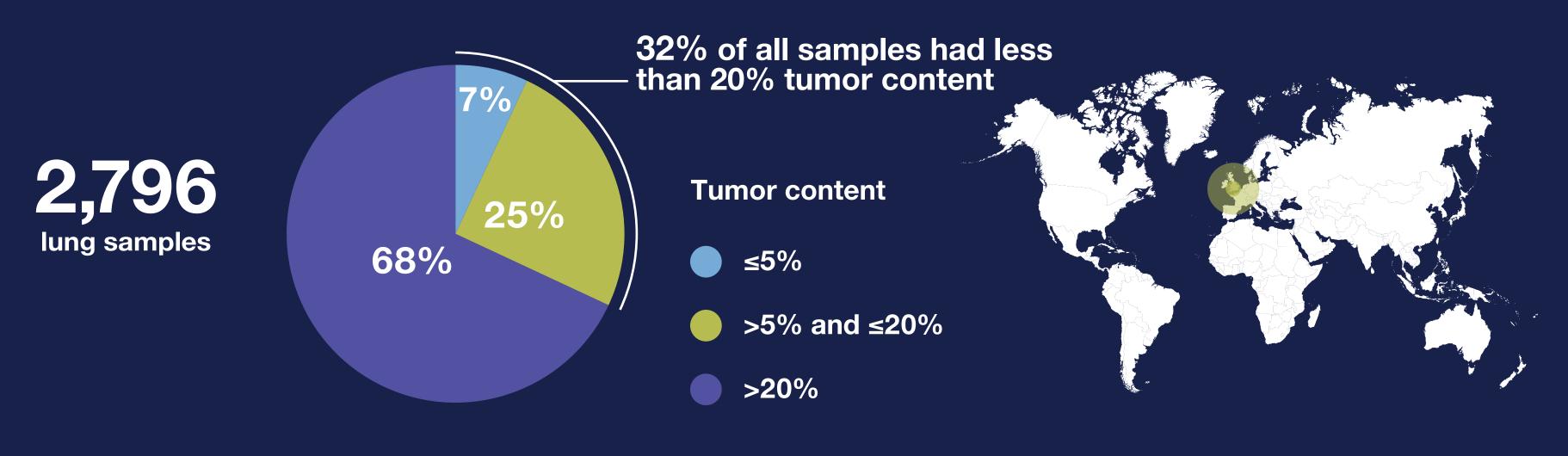
Cancer Genetics, Inc., New Jersey¹



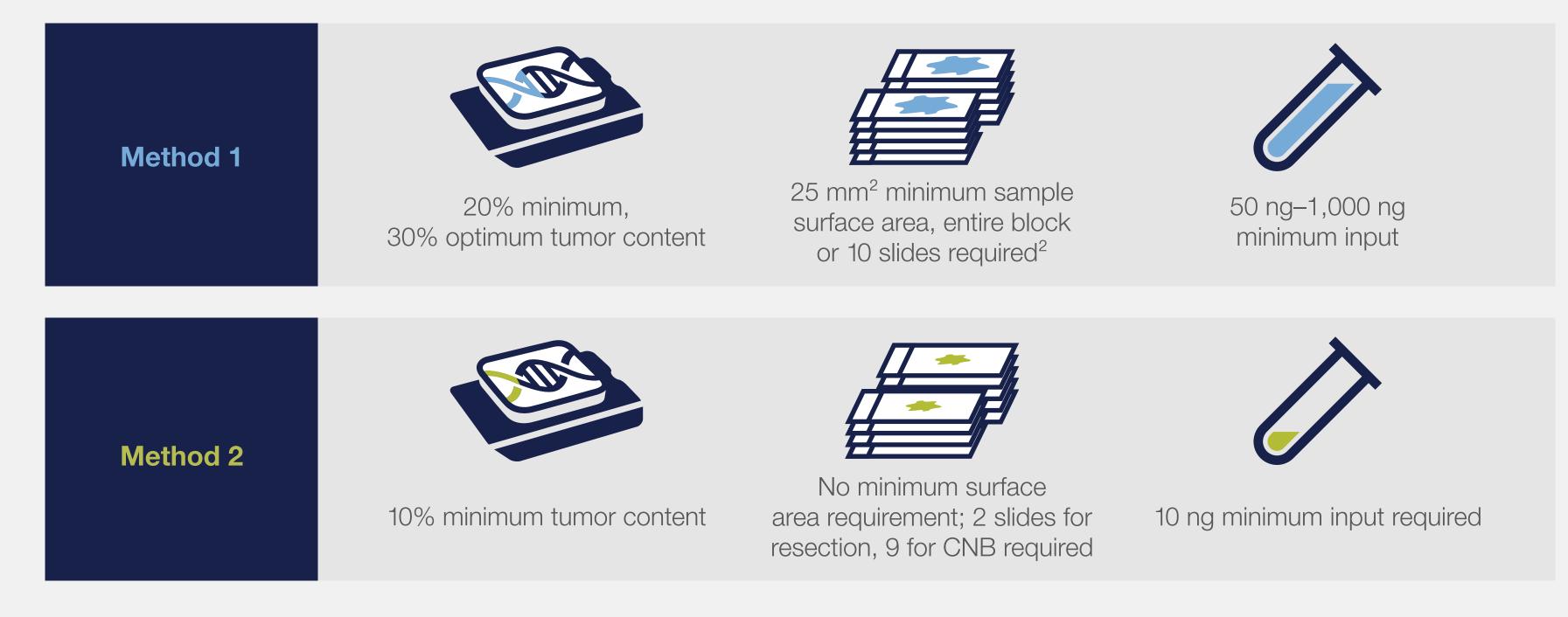
Life Lab, California²



Sarah Cannon Molecular Diagnostic Laboratory, London³



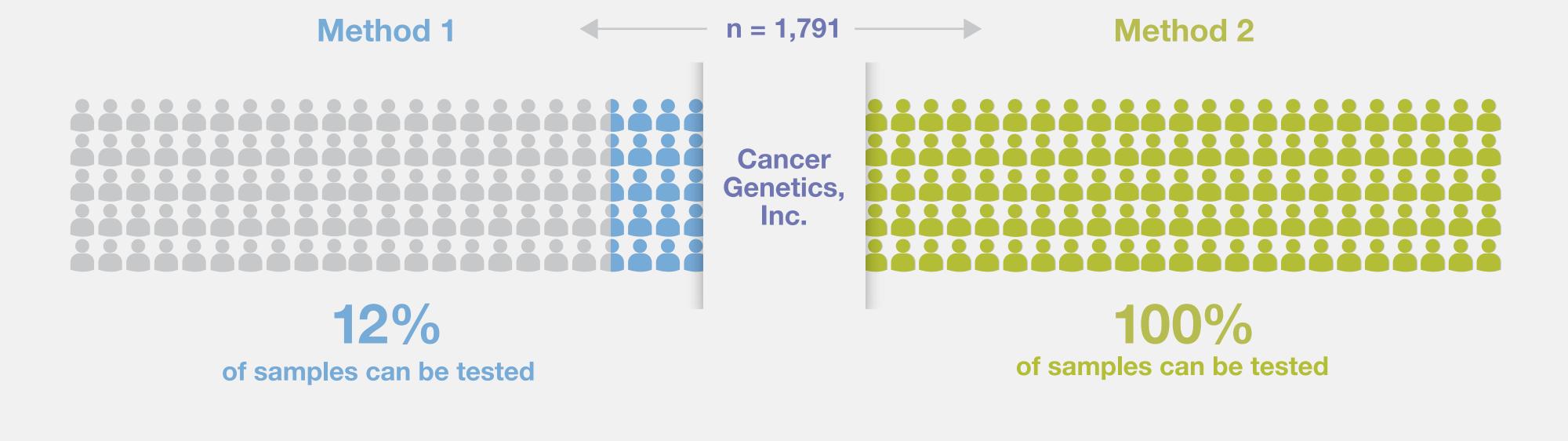
Sample requirements can differ greatly from one test to the next



NGS-based testing input requirements are typically expressed as X ng of nucleic acid, and can differ significantly between different NGS-based tests. The figures below explain the practical implications of these different requirements in terms of tissue, tumor area, and

content. Even if similar numbers of slides are required for both tests, the tumor area and percent tumor content required are significantly higher for Method 1, in order for testing to be successful.

Potential impact of different sample requirements on patients



The difference in the ability of each method to accommodate small samples can have a direct impact on patients' outcomes. Based on the tumor area alone, only 215 out of 1,791 patient samples submitted to Cancer Genetics, Inc. could be tested using Method 1, while all 1,791 samples could be tested using Method 2.

References 1. NGS to take top spot as cancer biomarker testing broadens. *CAP TODAY*, June 2018

2. Life Lab Internal Audit data on file