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 Jersey

- **Method 1**: 20% minimum, 30% optimum tumor content
- **Method 2**: 10% minimum tumor content

#### Tumor area
- ≤1 mm²
- >1 mm² and ≤5 mm²
- >5 mm² and ≤25 mm²
- >25 mm²

#### Potential impact of different sample requirements on patients

- **Sarah Cannon Molecular Diagnostic Laboratory, London**
  - 32% of all samples had less than 20% tumor content
  - 12% of samples can be tested
  - n = 2,796 lung samples

- **Life Lab, California**
  - 75% of all samples had less than 25 mm² tumor area
  - 40% of samples can be tested
  - n = 627 lung samples

### Sample requirements can differ greatly from one test to the next

- **Method 1** requires a minimum of 20% tumor content and a surface area of 25 mm² or 10 slides required, while **Method 2** requires only a 10% minimum tumor content and no minimum surface area requirement.

### Potential impact of different sample requirements on patients

- **Method 1** can test 12% of samples, while **Method 2** can test 100% of samples.

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.