Connecting more patients to targeted therapies

Fact 1: A real-world study of more than 4,000 non-small cell lung cancer (NSCLC) patients showed only 23.6% had a tumor surface area of \geq 25 mm², the minimum requirement for hybrid capture-based next-generation sequencing (NGS). In contrast, 87.9% of the NSCLC patients were successfully tested with amplicon-based NGS [1].







of patient samples could be tested with hybrid capture-based NGS

of patient samples could be tested with amplicon-based NGS

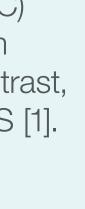
Fact 2: Approximately 60.2% of patients in western populations with advanced NSCLC have a targetable mutation [1,2].

.8% 16.3% EGFR exon t19 2.9% Other *EGFR* mutations do not have targetable 15.0% KRAS G12C mutations 10.3% Other KRAS mutations 3.8% ALK rearrangement 3.0% MET exon 14 mutations 2.6% ROS1 rearrangement 2.3% HER2 exon 20 insertion 2.1% **BRAF V600E** have targetable mutation 1.7% *RET* rearrangement 0.23% NTRK rearrangement

1. Tomlins SA et al. (2021) *JCO Precision Oncol.* 5:1312–t1324. (doi:10.1200/P0.20.00472) 2. Tan CA and Tan DSW (2022) *J Clin Oncol.* 40(6):611–625. (doi: 10.1200/JCO.21.01626)

Find out more about precision molecular profiling at oncomine.com/one-day-NGS

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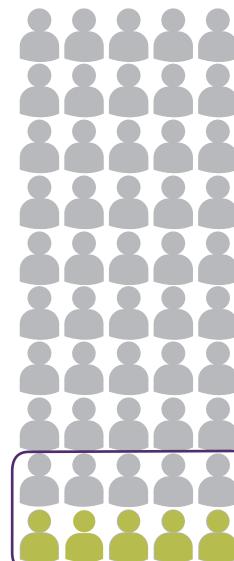


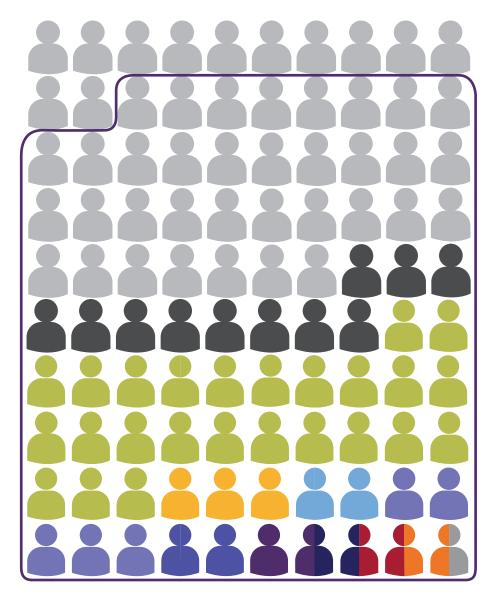




a hypothetical population of **100 NSCLC patients** Hybrid capture-based NGS Out of 100 patients ~24 patients could be tested patients could be matched to targeted therapies **Amplicon-based NGS** Out of 100 patients ~88 could be tested patients could be

Applying these facts to





Amplicon-based NGS can test more small-volume samples and potentially connect more patients to precision oncology

matched to

targeted therapies

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