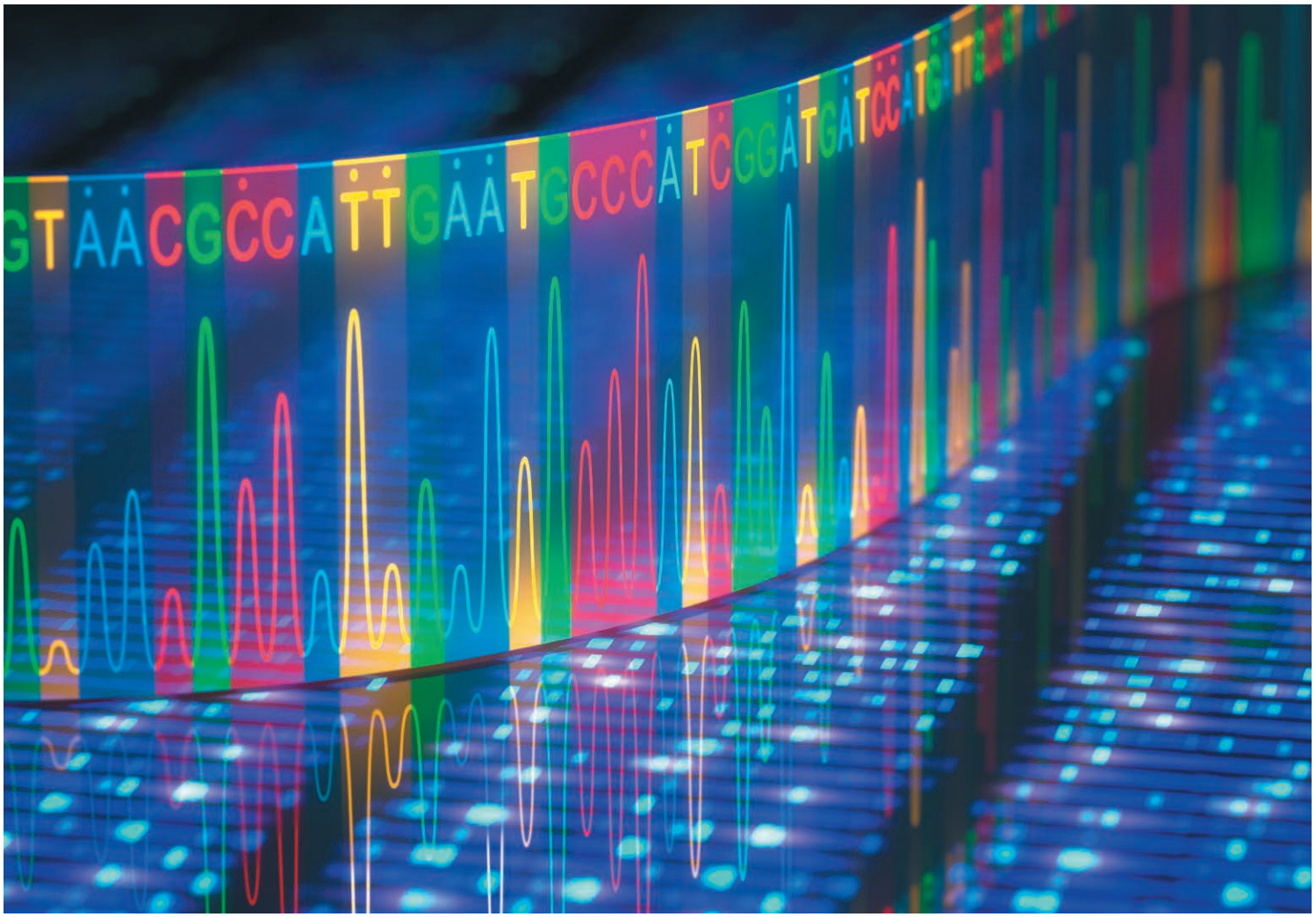

# The Promise of Precision Medicine:

# Why Equitable Access in the Treatment of Cancer Depends on Comprehensive Genomic Profiling

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1. Blueprint Medicines; 2. Health Advances

PRECISION MEDICINE now represents one of the dominant approaches for drug development in oncology. As a result, stakeholders across the cancer care continuum are under increasing pressure to identify patients with tumors harboring the associated genomic alterations or biomarkers that could be treated by the growing portfolio of targeted therapies. While stakeholders are conceptually bought into this approach, an alarming proportion of cancer patients ultimately do not receive the optimal targeted therapy for a variety of reasons.

Comprehensive genomic profiling (CGP) is a testing approach that assesses hundreds of genes in parallel including relevant cancer biomarkers, as established in guidelines and clinical trials, for therapy guidance. One of the goals of CGP is to ensure appropriate genotyping and treatment of the greatest number of patients. In this regard, we will discuss the benefits of CGP compared to single analyte testing in the setting of advanced solid tumors as related to the precision oncology patient diagnostic journey. Of perhaps equal importance, we will highlight that as CGP becomes more widely accepted in the clinic, equitable access to testing and enrollment of patients into biomarker-driven clinical trials should be incorporated into quality care planning as a critical and measurable goal.


## Part 1. Defining the Precision Oncology Patient Diagnostic Journey

The precision medicine ecosystem is increasingly adopting approaches that objectively identify and characterize each step along the journey where a patient may fall out of the process from diagnosis to prescription of a targeted therapy; we will refer to these steps at which fall out may occur as leakage points. Patients may fall out for a number of reasons, and here, we describe in detail how comprehensive genomic profiling (CGP), also referred to as next generation sequencing (NGS), broad-panel molecular profiling, genomic analysis, or a combination thereof, may be more effective than single analyte testing to resolve a greater number of leakage points along their diagnostic journey. Characterizing the various reasons behind each patient leakage point, understanding the impact of losing a patient at that point, and then objectively prioritizing solutions aimed at resolving each leakage point enables integration of testing standards that promote equitable access for all patient populations.

The diagram in **Figure 1** illustrates the patient's journey from diagnosis to biomarker identification to treatment selection. The blue icons represent the major testing-related milestones as the patient progresses on the path to treatment. The orange icons are the individual leakage points and the grey boxes highlight various factors and/or issues that contribute to the leakage point. As we will discuss, when compared to single-analyte testing, the adoption of CGP mitigates many of these issues (those highlighted in green). In the text below, we review the clinical benefit for CGP and several relevant patient leakage issues.

## Part 2. Clinical Benefit of Comprehensive Genomic Profiling and Impact on Drug Development Efforts

*The clinical utility of NGS is conceptually accepted within the US and numerous studies have demonstrated the ability of CGP to identify subsets of patients with therapeutically actionable biomarkers that would not have otherwise been detected. The identification of oncogenic drivers and resistance mechanisms across solid tumors has informed and driven drug development efforts.*

### Clinical Utility of CGP

An increasing number of clinically relevant biomarkers in different cancer types have been identified and validated in the past several years. This has encouraged researchers in academia and biopharmaceutical companies to identify novel targets and develop more precise treatment options, thus expanding the landscape of targeted therapies. Current testing and treatment guidelines in NSCLC, for example, recommend using broad molecular profiling to test for *EGFR* mutations, *ALK* rearrangements, *KRAS* mutations, *ROS1* rearrangements, *BRAF* mutations, *NTRK1/2/3* rearrangements, *MET* exon 14 skipping mutations, and *RET* rearrangements, and to test for *HER2* mutations, *NRG1* gene rearrangements and high-level *MET* amplification as emerging biomarkers to guide therapy matching for patients with metastatic disease.[1] In addition to tumor-specific biomarkers, tumor-agnostic biomarkers, such as *NTRK* gene rearrangements, Microsatellite Instability (MSI), and Tumor Mutational Burden (TMB) have been clinically validated across multiple solid tumors.[2-5]

Genomic alterations (such as mutations, amplifications, deletions, or gene rearrangements) that function as oncogenic drivers are detectable by CGP. Specifically, gene rearrangements or fusions are driver events in many solid tumors and hematologic malignancies and, when in-frame, these hybrid genes may form an oncogenic fusion protein. These are often actionable biomarkers (e.g., *RET, ALK, ROS1, NTRK1-3*) with associated targeted therapies. Fusions may be identified using various technologies, including CGP (DNA and/or RNA NGS), Fluorescence-In-Situ-Hybridization (FISH), or Polymerase Chain

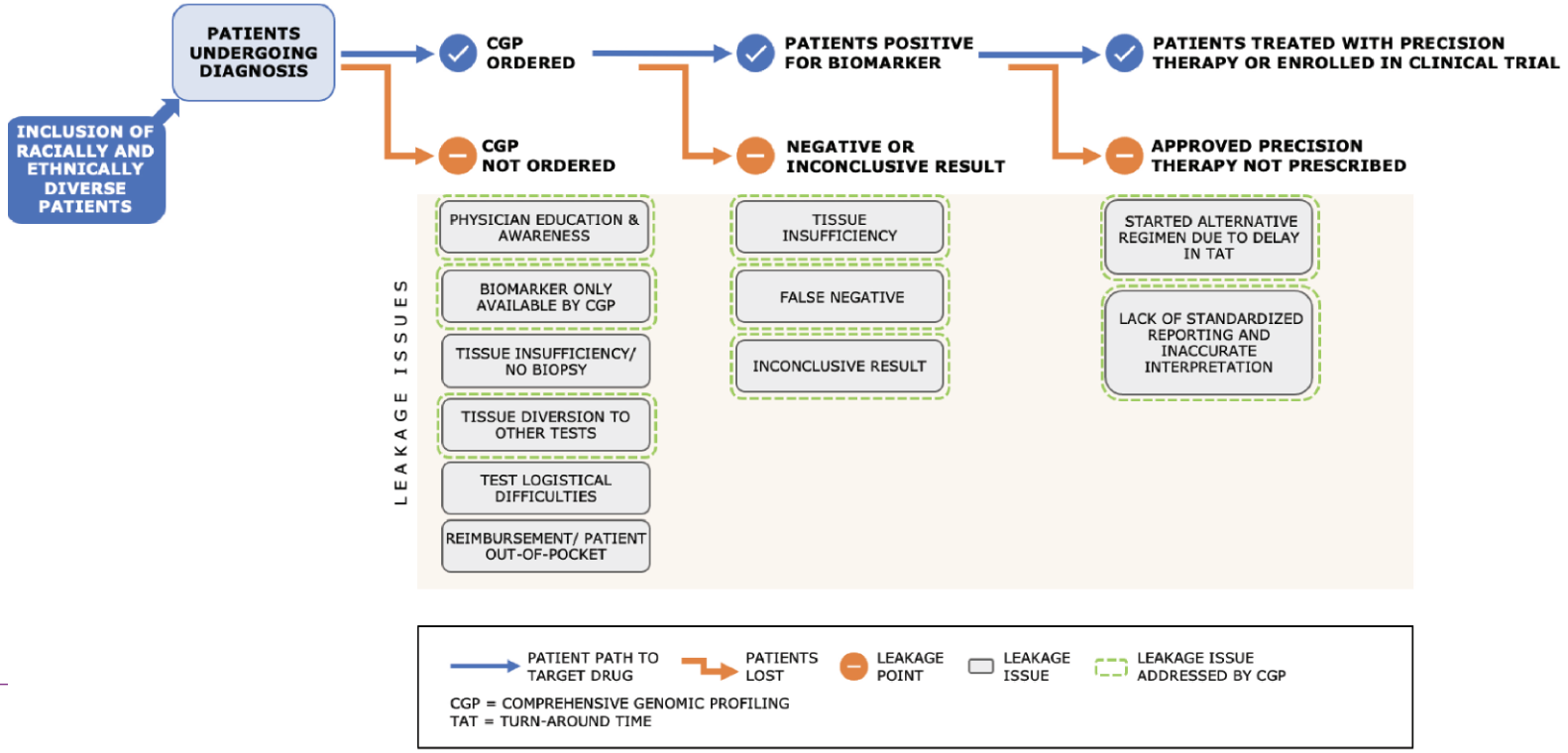



**Figure 1:** Precision Oncology Patient Diagnostic Journey

Reaction (PCR). However, studies have shown that fusion events may be missed using single gene methodologies such as FISH, and even DNA NGS, often due to non-canonical breakpoints in the non-coding regions of the genes.[6-8]

The most comprehensive method to detect all clinically relevant fusions is by DNA and RNA NGS. For example, in a study of 2,522 patients with lung adenocarcinoma sequenced using DNA-only NGS, 1933 (77%) of tumors were positive for at least one driver alteration. Among the 232 negative samples, 36 (15.5%) samples were positive for an oncogenic driver by RNA sequencing, including 27 in-frame fusions (*ROS1* [n=10], *NRG1* [n=5], *ALK* [n=4], *RET* [n=3], *NTRK3* [n=2], *BRAF/FGFR2/NTRK2* [n=1 each]) and 6 *MET* exon 14 skipping mutations.[8]

Additionally, CGP may be useful in patients with cancer of unknown primary to identify potentially actionable biomarkers and to aid in classifying the tumor site of origin.[9,10] Importantly, multiple studies have demonstrated that patients who are treated with biomarker-matched targeted therapy have improved outcomes compared to those treated with unmatched therapy.[11-13] For example, a clinicogenomic analysis of 4064 patients with NSCLC showed a significant improvement in overall survival for patients treated with matched targeted therapy.[14] Such clinically meaningful findings highlight the need for, and importance of prioritizing comprehensive NGS assays versus single analyte testing that may not be designed to capture all actionable events.

Additional patient management implications for this type of NGS testing on patient's tumors may need to be considered, including identification of hereditary cancer variants in cancer predisposition genes. In a study at Memorial Sloan Kettering using the MSK-IMPACT panel utilizing a paired tumor and germline sequencing approach, 1040 patients with advanced cancer consented to secondary germline analysis of 76 cancer predisposition genes. Pathogenic hereditary cancer variants were detected in 182 patients (17.5%); 101 of these patients would not have been eligible for hereditary testing based on published clinical guidelines at that time.[15]

## Targeted Therapy Resistance and Drug Development

Although targeted therapies provide clinical benefit in tumors harboring matched biomarkers, tumor evolution and the development of resistance mechanisms are inevitable. Acquired resistance mechanisms may develop as "on-" or "off-" target, based on whether they occur in the target gene or in another oncogenic bypass pathway in the tumor. Examples of disease states in which this is especially relevant are *EGFR*-mutated and *ALK* fusion-positive metastatic NSCLC (mNSCLC).[16] For example, current standard of care for *EGFR*-mutated mNSCLC patients is osimertinib, a third-generation EGFR tyrosine kinase inhibitor (TKI) that was developed to combat the EGFR T790M on-target resistance mutation that develops in response to treatment with earlier generation EGFR TKIs in approximately half of patients.[16]

Emerging data from clinical trials utilizing osimertinib in the first- and second-line setting and retrospective institutional datasets have shown the development of both on- and off-target acquired resistance mechanisms to osimertinib.[17-18] The most common on-target mechanism is the EGFR C797S mutation that prevents binding of osimertinib to the EGFR kinase domain. Off-target resistance mechanisms, such as acquired *MET* amplification, oncogenic gene fusions, and histologic transformation have also been observed.[19-20]

Drug development efforts include combating the EGFR C797S resistance mutation with next generation EGFR TKIs and combination therapy strategies, such as EGFR + MET TKIs.[21-23] Similarly, in the *ALK* fusion-positive mNSCLC space, newer-generation ALK TKIs have been developed to combat on-target *ALK* mutations, such as ALK L1196M, that develops in response to treatment with crizotinib, a first-generation ALK inhibitor, and G1202R or I1171N/S/T, that develops in response to treatment with second-generation inhibitors, such as alectinib, ceritinib, and brigatinib; these newer agents have been shown to improve outcomes.[16,24]

Histologic transformation is also a known resistance mechanism to targeted therapy, such as

EGFR TKIs, in NSCLC and is typically identified histologically on a tumor biopsy at the time of progression.[16] Recent data suggests transformation may be associated with inactivating alterations in *TP53* and *RB1*.[25] In *EGFR*-mutated NSCLC, concurrent *TP53* mutations are associated with worse prognosis and inferior response to EGFR TKI therapy.[26-29] Similarly, in KRAS-mutated NSCLC, *STK11* and/or *KEAP1* mutations may be associated with inferior response to immune checkpoint inhibitors.[30] Identification of these alterations in a patient's pre-treatment biopsy may predict the presence of pre-existing subclones within the tumor that drive resistance to targeted therapies and help stratify patients that may benefit from therapy escalation. As additional primary and acquired resistance biomarkers are discovered, CGP may serve as an efficient, time-saving and cost-effective methodology to decipher the genomic landscape of the patient's tumor and best assign appropriate therapy.

Thus, CGP addresses the key challenge of probing for the appropriate biomarker(s) effectively. The spectrum-based nature of these tests implies that physicians can simply order the test, while casting a wide net, instead of fishing for the right, often rare, biomarker in a large pool. The wider adoption of CGP will enable physicians to overcome barriers in the diagnostic process and amplify efforts to include as many patients as possible in the treatment journey, getting us closer to the target of personalized medicine for all who may benefit.

## Part 3. The Case for Comprehensive Genomic Profiling vs Single Analyte Tests: Challenges Yet to be Fully Addressed

### Physician Education and Awareness Challenges

*When relying on single analyte tests, clinicians, particularly those managing multiple tumor types, may not comprehensively test for the growing list of actionable tumor-specific or tumor-agnostic biomarkers due to a lack awareness, or the perception (and often reality) that many of these biomarkers occur rarely. Adoption of CGP largely overcomes this challenge.*

For a significant proportion of cancer patients, physicians are commonly successful in identifying an actionable biomarker and associated targeted or precision therapy.[12,31] However, the expanding dataset of clinically actionable but increasingly rare cancer biomarkers (e.g., MSI-H, *NTRK1-3* fusions) make it more challenging for physicians to provide equally effective diagnosis to all different genotypes of cancer. Further compounding this reality for physicians are a lack of critical infrastructure elements such as test reporting standardization, clinical decision support tools, genetic counseling and ongoing education, which increases the likelihood that patients' tumors will not be tested for the appropriate biomarkers and thus are unable to proceed on the path of personalized treatment.[32]

> *"Thus, CGP addresses the key challenge of probing for the appropriate biomarker(s) effectively. The spectrum-based nature of these tests implies that physicians can simply order the test, while casting a wide net, instead of fishing for the right, often rare, biomarker in a large pool."*

### Tissue Insufficiency and Diversion to Single Analyte Tests

*When ordering multiple sequential single analyte tests, tissue may be exhausted before completing all recommended biomarker tests leading to an incomplete result. CGP may provide a more tissue-efficient process when there are several biomarkers of interest.*

In traditional biomarker testing paradigms, multiple single analyte tests are conducted in an iterative fashion. In NSCLC, for example, this may mean prioritizing more common biomarkers (e.g., PD-L1 and *EGFR*), resulting in a lack of tissue for the remainder of the recommended, often rarer, biomarkers if the initial testing is negative.[1] Depending on the tissue available, quality of the sample, and the number of individual tests, CGP may be a more tissue-efficient means of assessing all clinically relevant biomarkers.

Despite the improvement of tissue efficiency that CGP provides compared to single analyte testing, at times there remains a challenge in successful completion of CGP due to insufficient quantity and quality of tissue. Potential solutions to mitigate this issue are discussed in additional detail in Part 4.

### Biomarker Only Available by CGP

*Some novel biomarkers and signatures may not be available as single analyte tests – TMB is an early example and others may emerge in the future.*

During a patient's diagnosis-treatment journey, a few useful diagnostic and prognostic indicators may not be available with traditional single analyte tests. Recently, tumor mutational burden (TMB), an indirect measure of tumor-derived neoantigens, has emerged as a promising biomarker for stratification of patients undergoing immune checkpoint inhibitor therapy. Clinicians are increasingly finding that tumor mutational burden (TMB) may play a role in prescribing immunotherapies, particularly the checkpoint inhibitors.[5,33-37] TMB is only assessed when NGS or whole-exome sequencing is performed. In one study across diverse tumors, patients with high TMB versus patients with intermediate or low TMB had a higher response rate (58% vs. 20%; $p = .0001$) and longer median progression-free survival (12.8 vs. 3.3 months; $p < .0001$).[34] Another work described a strong linear correlation between TMB and objective response rate across 27 tumor subtypes enrolled in clinical trials and treated with anti–PD-1 or anti–PD-L1 monotherapy.[35] Of note, these trials did not select for patients based on PD-L1 expression. These studies advocate for the increasing importance of CGP testing in evaluating tumor mutational burden and predicting response to immunotherapy in combination with other immuno-oncology biomarkers.

### False Negatives and Inconclusive Results

*There are numerous examples where CGP offers superior sensitivity and/or specificity. A single analyte test may inadvertently miss a rare fusion partner, for example.*

CGP (including DNA and RNA NGS) has been shown to be more sensitive as compared to FISH in detecting gene fusions in solid tumors, such as NSCLC (discussed above). Additionally, the use case for detecting microsatellite instability (MSI) status in cancer patients is another example that highlights the improved capabilities of DNA NGS.[38] With multiple FDA-approved drugs for patients with microsatellite instability high (MSI-H) tumors, identifying such patients early in the treatment journey is critical.[4] NGS-based approaches have the concurrent capability to interrogate thousands of microsatellite loci as compared to 5-7 loci that are detected by PCR (a test specifically developed for patients with colorectal cancer).[38,39] The additional benefit of NGS in this setting, like TMB described above, is that the same test utilized to identify genomic biomarkers in individual genes is also utilized for MSI and TMB, potentially saving tissue and reducing cost, and providing broader applicability across advanced solid tumors.

### Started Alternative Regimen Due to Delay in Turn-Around-Time (TAT)

*In the case of sequential single analyte tests, a patient's disease might progress requiring initiation of treatment prior to the reporting out of biomarker status. This can result in a missed opportunity for a targeted therapy to be used at the appropriate time.*

The sequential nature and the cumulative slow speed of single analyte biomarker testing often proves to be time consuming. In many cases, the patient's worsening condition may not allow the treating physician to exercise the flexibility of waiting for the entire duration of the sequence of tests. With limited insights into the genomic profile of the patient's cancer, the physician may initiate therapy with the most suitable, biomarker-agnostic treatment option available at that time point.

Due to the comprehensive and potentially time and tissue-efficient nature, use of CGP in upfront clinical settings allows physicians to develop more accurate and timely treatment plans for advanced cancer patients.

Some stakeholders believe that CGP itself is time consuming and may delay treatment initiation. Increasingly however, thought leaders maintain that if CGP is ordered earlier in the process, many delays may be mitigated. Other factors that may help to improve turn-around time (TAT) are ensuring availability of high quality and quantity of tissue and collaboration among medical oncology, pathology, and tissue collectors (e.g., surgeon, pulmonologist, interventional radiologist). Involvement of the pulmonologist in the NGS testing process for patients diagnosed with NSCLC has been demonstrated to reduce TAT for testing and time to treatment initiation.[40,41]

### Targeted Therapy Only Available in Clinical Trials

*With the discovery and validation of novel targets, relevant agents in development may only be available through enrollment into a clinical study. Access to appropriate testing to qualify for many of these studies may be limited without the assistance of CGP to identify rare targets for enrollment.*

The number of genomic alterations being assessed is a fundamental difference between single analyte tests and CGP. With an expanding list of FDA-approved targeted therapy options and biomarker-driven clinical trials, performing broad-based CGP on a patient's tumor may increase potential treatment options.

Specifically in the context of clinical trials, several prominent basket or umbrella trials are currently enrolling patients based on matched genomic alterations. These studies include the NCI-MATCH (NCT02465060), ASCO TAPUR (NCT02693535), and Sarah Cannon's MyPathway (see, e.g., NCT02091141). Enrollment on these studies almost exclusively relies on CGP, which allows for the greatest possibility of accessing the available study agents, especially for tumors harboring rare genomic events. Analysis of these results and evaluation of the tumor genomic profile versus the therapeutic response will inform future research and discovery efforts. It is likely that the next iteration of basket studies will look at combination therapies with improved matching and will account for the unique genomic profiles of each tumor when assigning the "basket" or treatment arm.

> *"Due to the comprehensive and potentially time and tissue-efficient nature, use of CGP in upfront clinical settings allows physicians to develop more accurate and timely treatment plans for advanced cancer patients."*

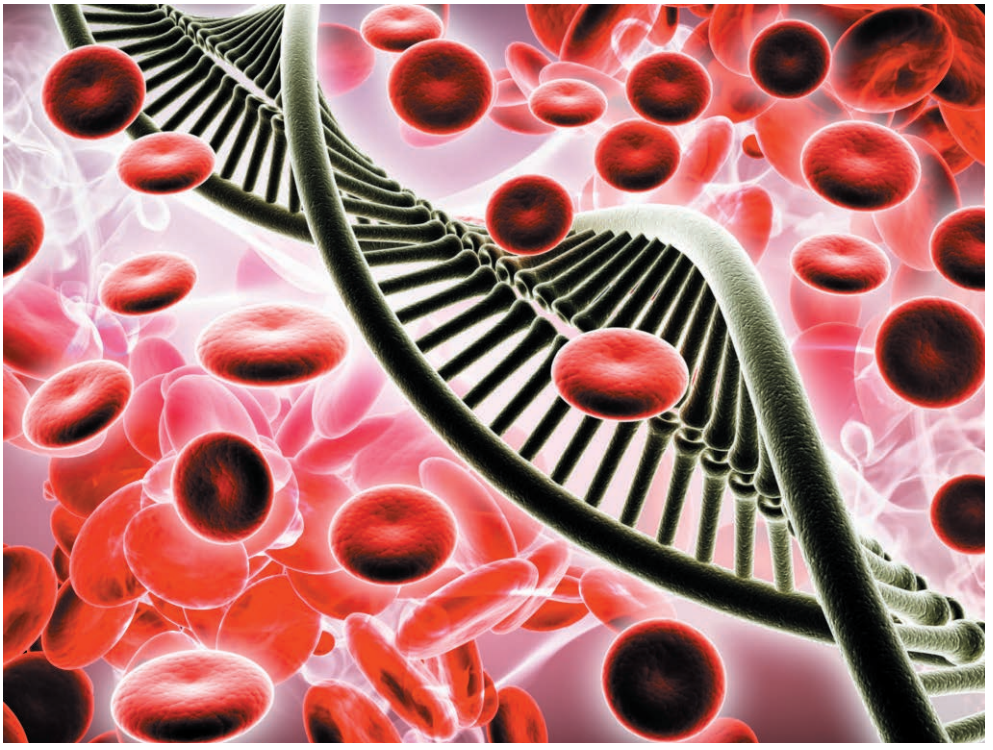
## Part 4. Liquid Biopsy: A Powerful Tool in Combination with Tissue-Based CGP

*While CGP in solid tumors offers a multitude of advantages over single analyte testing, this technology alone may not address all the potential challenges involved in a typical precision oncology patient diagnostic journey. The use of liquid biopsy, particularly in the resistance setting, is a rapidly evolving diagnostic tool that represents a strong complement to traditional tissue-based CGP.*

In the real-world clinical setting, insufficient quantity and/or quality of tissue leading to limited amplifiable nucleic acid, often due to small biopsies continues to remain a challenge to the successful completion of CGP (see Part 3).[42-44] Many patient-related and clinical factors, including the functional status of the patient, accessibility of the tumor, bleeding, and pneumothorax during biopsy, contribute to this tissue acquisition challenge. In the IASLC global survey on molecular testing in lung cancer conducted in 2018, for example, the main reasons for failure to obtain a molecular diagnosis reported were insufficient tumor cells (93% of respondents) and inadequate tissue quality (55%).[44] Potentially limited by the availability of adequate tumor samples, a significant portion of lung cancer patients do not receive comprehensive biomarker testing for all recommended biomarkers.[45,46]

In situations where the tissue sample is limited, liquid biopsy, in this case testing of the circulating cell-free DNA in the patient's plasma, may be an effective tool to understand the genomic landscape of the patient's cancer. Although tumor tissue testing is still viewed as the gold standard, liquid biopsy offers a convenient, minimally invasive option to aid in the diagnosis and treatment selection process and may provide a more global profile of the heterogenic genomic landscape of both primary and metastatic lesions.[47-50]

Additionally, the shorter TAT using liquid biopsy has been shown to decrease time to biomarker test result and treatment initiation.[41] Importantly, similar clinical outcomes have been described with liquid biopsy-based guided genotyping and treatment compared with standard tissue-based methods.[51-53] Moreover, the identification of potentially actionable biomarkers may be improved if both tissue CGP and liquid biopsy methods are





used complementarily. For example, the addition of liquid biopsy testing to routine management of advanced NSCLC increased detection of targetable alterations and improved delivery of targeted therapy.[41,50]

Liquid biopsy is, however, associated with several limitations. These include lower test sensitivity compared with tissue-based biomarker testing leading to false negative results, the potential for misinterpretation of results leading to false positives, challenges in detecting certain types of gene fusions or splice variant alterations, and the detection of germline variants that may be misclassified as somatic.[48,54,55] Several factors, including lower tumor burden and extent of disease, or slowly proliferating tumors, may limit tumor DNA shedding; limited circulating tumor DNA contributes to false negative results.[56-58]

Due to these limitations, tissue-based CGP is recommended when liquid biopsy results are negative to confirm biomarker status.[1,48] One emerging strategy that has been utilized in NSCLC to optimize comprehensive biomarker testing may be a liquid biopsy-first approach followed by reflex tissue CGP testing in cases where the liquid biopsy is biomarker-negative, especially in patients where there is insufficient tissue or lack of access to upfront tissue testing. This approach may counteract treatment delays for patients, especially while potential diagnosis and treatment delays have been intensified by the COVID-19 pandemic. Overall, the balanced and thoughtful use of an integrated liquid biopsy plus tissue CGP diagnostic protocol has potential to help genotype and effectively treat more patients in a personalized manner.

*"In this analysis, Caucasian and Asian patients were overrepresented in precision oncology clinical trials with ratios of 1.35 and 1.46 respectively, while African American, Hispanic, and American Indian/Alaska Native were under-represented with ratios of 0.49, 0.24 and 0.43 respectively."*

## Part 5. Addressing Health Disparities Across the Precision Oncology Patient Diagnostic Journey

With advances in CGP to identify actionable oncogenic drivers and targeted therapies, another important issue to address is access to both testing and targeted therapies for racially and ethnically diverse patient populations in the real-world setting. A large-scale cross-sectional study of 93 precision oncology clinical trials that reported racial/ethnic demographics of patients across lung, breast, prostate and colorectal cancer, identified racial and ethnic disparities among patients who participated in these trials, relative to the racial diversity in the US population (Caucasian, Asian, African American, Hispanic and American Indian/Alaska Native populations).[59]

In this analysis, Caucasian and Asian patients were overrepresented in precision oncology clinical trials with ratios of 1.35 and 1.46 respectively, while African American, Hispanic, and American Indian/Alaska Native were under-represented with ratios of 0.49, 0.24 and 0.43 respectively.[59]

In addition, TCGA's pan-cancer analysis identified differences in chromosomal instability between European Americans and African Americans across different cancer types; the frequencies of *TP53* mutations and *CCNE1* gene amplification were significantly higher in African American patients in cancer types with higher chromosomal instability.[60] In some of the most common cancers with dedicated efforts to develop precision therapies, such as *EGFR*-mutated NSCLC[61] and HR-positive/HER2-negative breast

cancer[62], underlying genomic differences have been uncovered in racially diverse patient populations. Including racially diverse patient populations in clinical trial enrollment and earlier phases of drug development may also provide robust and valuable insights into the biological differences and potentially variable responses to treatment in diverse populations.

With the increasing number of precision therapies and clinical trials, efforts should be made to have representation of diverse patients in clinical trials comparable to the real-world. To address these disparities, FDA issued a draft guidance in April 2022 for industry to include plans in their clinical trials to improve the enrollment of diverse and underrepresented patient populations across the US.

At the very core of precision therapy drug development is the identification of actionable targets representative across society to fuel enrollment into oncology clinical trials. A recent study by multiple academic centers showed that in NSCLC, frequency of actionable molecular targets such as *EGFR* and *KRAS* mutations were not significantly different between Caucasian and African American lung adenocarcinoma patient populations.[63] Yet, a recent study reported disparities in both biomarker testing and clinical trial enrollment in lung, breast and colorectal cancers.[64] Another recent study showed that, while racially diverse patients are willing to participate in oncology clinical trials, the biggest barrier is the access to clinical trials where they receive care.[65] American Society of Clinical Oncology (ASCO) and Association of Community Cancer Centers (ACCC) have pin-pointed additional barriers for participation of patients from diverse racial and ethnic backgrounds in cancer clinical trials and have identified strategies for higher trial participation and retention.[66,67]

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Therefore, there is a need to identify and enroll patients from under-represented communities where they are being treated, by bringing precision medicine clinical trials into the community. In recognition of these barriers in community participation in cancer trials, National Cancer Institute (NCI) and NCI-designated Centers of Excellence have published the gaps and recommendations for community outreach, education and engagement at NCI-designated cancer centers and the encompassing "catchment areas" to aid with prevention, detection and diagnosis, and treatment of community patients.[68,69] We support and champion continued initiatives as detailed above, to include racially and ethnically diverse patient populations upfront into the pool of patients undergoing cancer diagnosis and CGP, potentially leading to treatment with an FDA-approved precision therapy or enrollment into an ongoing clinical trial (blue box, **Figure 1**)

## Part 6. Equitable Access to Precision Medicine in the Treatment of Cancer is in Scope: Call to Action

Quality testing in the diagnosis and treatment of cancer is currently not equitable for all patients, particularly with regard to race, ethnicity, geography and socioeconomic status. New approaches to expand the footprint of precision oncology to improve health outcomes, reduce cost, and optimize healthcare resource utilization in cancer patients are needed.[70]

The promise of precision medicine will be realized when all patients have access to guideline-recommended, timely, comprehensive, and accurate testing utilized to inform therapeutic decisions. Now more than ever, this promise is in scope as diverse stakeholders



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across the precision medicine ecosystem are working together in the achievement of common goals. Advocacy, policy, and professional organizations – for example, LUNGevity Foundation, The Personalized Medicine Coalition (PMC) and Association of Community Cancer Centers (ACCC) – are developing evidence for clinical utility of CGP as well as stakeholder specific tools focused on education of patients and the cancer care team. In recent years new coalitions such as From Testing to Targeted Treatment (FT3), Access to Comprehensive Genomic Profiling (ACGP, see Q&A with Maude Champagne in this issue), and Precision Cancer Consortium (PCC) are combining expertise and resources for greater reach through targeted high-impact programs.

While equitable access to quality testing for all patients is the current goal, success will eventually be measured by the ubiquitous empowerment of all patients and providers communicating to develop biomarker-informed treatment plans together, bolstered by inclusive evidence, and ultimately improving and extending life. JoPM

## Sunitha Rangaraju, PhD

Sunitha, in her current role as Principal Medical Science Liaison at Blueprint Medicines, collaborates with key opinion leaders/healthcare providers from academia and community, towards addressing the unmet medical needs of patients with cancer and rare diseases, using a precision medicine approach. Throughout her 17 years of Biomedical Sciences and Biotech Industry experience, Sunitha has always been passionate about working on therapeutic pathways that could be targeted to address underlying disease, using a combination of genomics and drug discovery efforts. Sunitha serves as a bridge between scientists, clinicians, and the healthcare ecosystem, towards continuously innovating and addressing precision therapy needs of underserved patient populations.

## Elissa Quinn

Elissa works in partnership with leaders across academia, professional societies, advocacy, and national labs to shape policy and improve patient access to personalized medicine. With more than 20 years of industry experience in cancer and rare disease, Elissa's unique understanding of the interplay between diagnostics and therapeutics has established her as a trusted ally within the precision medicine ecosystem. In her role at Blueprint Medicines, Elissa leads programs addressing barriers to adoption and integration of personalized medicine tools and genomically guided patient care.

## Gary Gustavsen

Gary Gustavsen joined Health Advances in 2005 and currently leads its Precision Medicine Practice. A noted writer and workshop leader in the field of companion diagnostics and precision medicine, his work focuses on commercialization strategy, indication prioritization, pricing and reimbursement strategy, health economics, and business development opportunities for both diagnostic and therapeutic clients.

## Alison Nagle, PhD

Alison (Ali) is currently a Senior Medical Science Liaison at Blueprint Medicines. She completed her PhD training at the University of Pittsburgh School of Medicine in 2018 with a focus in breast cancer biology and precision medicine and has spent 4.5 years in US Medical Affairs in the oncology diagnostics and targeted therapy drug development space. Ali has a passion for improving education surrounding the use of comprehensive genomic profiling for advanced cancer patients to increase access to appropriate and timely biomarker testing and associated targeted therapies.

## Himanshu Singh, PhD

Himanshu Singh holds a Ph.D. in Biomedical Engineering from the National University of Singapore and has 8+ years of extensive research and consulting experience with academic and industrial partners from Singapore, the UK, and the USA. With >15 research publications, Himanshu has led numerous international collaborative studies from developing innovative diagnostic technologies to studying disease pathophysiology in cancer patients.


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