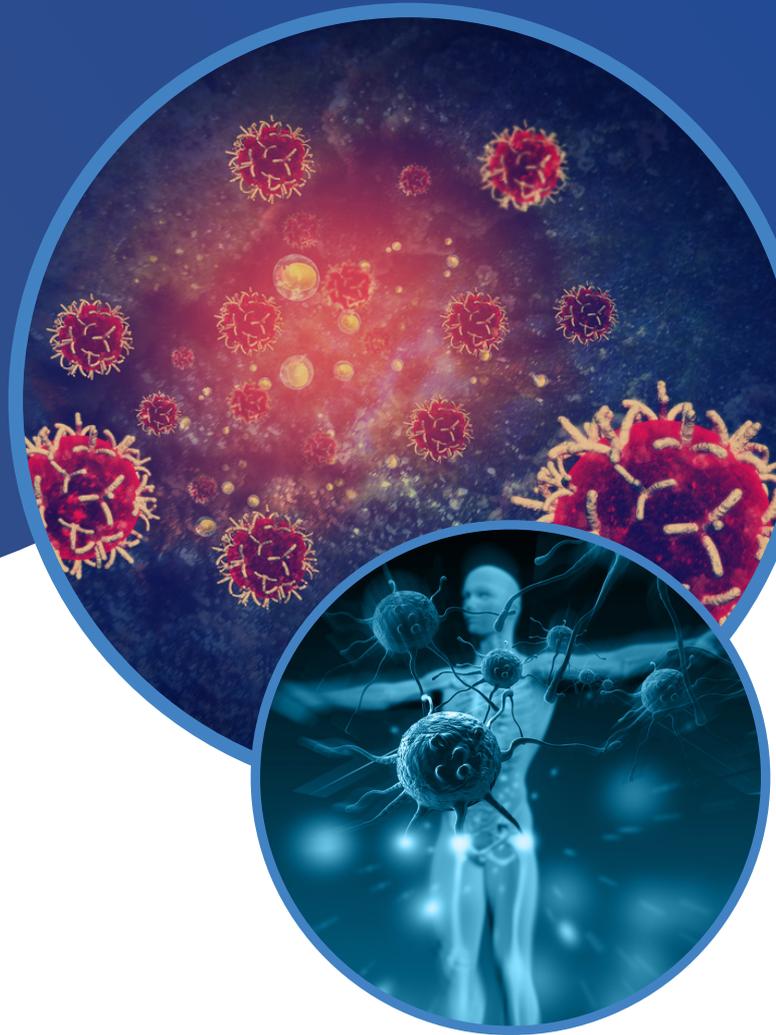


Uncovering Mutations in Tumor DNA

& providing clinically actionable data
for choice of the most optimal
treatment



COMPREHENSIVE CANCER PANEL

Next-generation sequencing (NGS) has significantly improved the understanding of various cancers and targeted treatment of cancer. Major advantage of NGS is the ability to assay multiple genomic variants from different genes (also known as panels) at the same time from limited amounts of clinical samples.

Comprehensive Cancer Panel examines **409 tumour suppressor genes and oncogenes frequently mutated in cancer**. Our test covers over **15500 COSMIC (Catalogue of Somatic Mutations in Cancer)** mutation targets across cancer driver genes, drug targets, signalling cascades, apoptosis, DNA repair, transcription regulators, inflammatory response, and growth factor genes in a single assay.

This test helps your oncologist in determination of personalized therapy and prognosis assessment.

WHAT ARE THE ADVANTAGES COMPREHENSIVE CANCER PANEL?

- Different individuals with the same cancer can respond differently to the same therapy and detecting genomic alterations gives a more complete picture of the cancer. Therefore, this test helps your oncologist in determination of personalized therapy best suited to your case or design a tailored treatment for each patient and prognosis assessment based on genomic profile.

- Our panels are Internally validated as a reliable and are cost-effective tool for detecting mutations, in a range of genes linked to reaction or resistance to targeted therapies.
- Prognosis and recovery planning for patients with solid tumours, both at the onset and as the disease progresses or recurrence.
- The panel can detect SNVs and Short-Indels with as little as a 5% mutant allele frequency, in genes of high prognostic and therapeutic significance like MET, ALK, TP53, APC, and PTEN.

WHO NEEDS THIS TEST?

Treating oncologists may refer patients to develop treatment strategies that target, specific tumour genome mutations, allow follow up of disease and understand the appropriateness of future second line treatments

