



Precision Medicine for Cancer Patients

NGS Solid Tumor Profiling

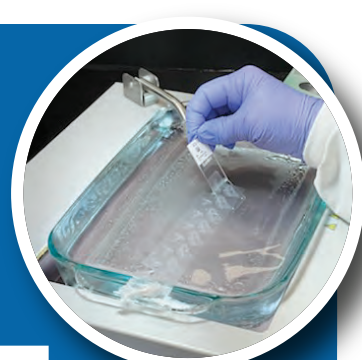
NGS Solid Tumor Profiling is a targeted next-generation sequencing test that assesses DNA and RNA in solid tumors. Through identification of specific DNA/RNA mutations, NGS is able to provide important clinical information such as available therapies and clinical trials that can be used to create a customized treatment plan for patients.

How Does NGS Profiling Work?



Step 1: Tumor Resection

Tissue from the patient's tumor is collected by the clinician. The tissue sample is given to HNL Lab Medicine's Histology department for processing.



NGS Test is ordered by the doctor

Step 2: Slide & Block Creation

The tumor tissue is used to create a formalin fixed paraffin embedded (FFPE) block from which slides are created and H&E stained. A pathologist reviews the stained slides to determine tumor cell type. FFPE blocks are stored for further testing.



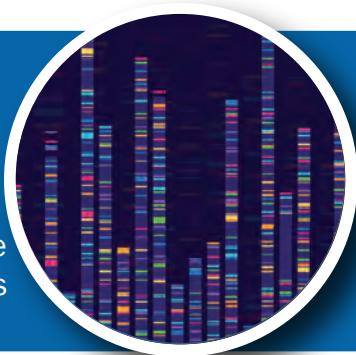
Step 3: Preparing the Sample for Extraction

Prior to extraction of DNA and RNA, a pathologist determines tumor cell percentage and identifies the tumor cell location which correlates with the location within the FFPE block. The block is dissected to retrieve tumor tissue for NGS testing in the Molecular department.



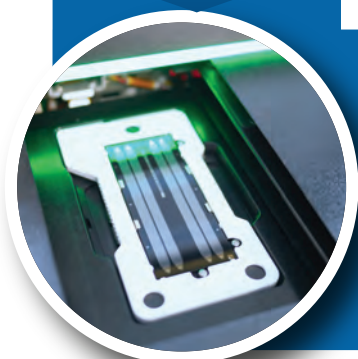
Step 5: NGS Libraries Are Prepared

Copies are made of selected regions in the DNA/RNA that are associated with cancer. This amplification of the DNA/RNA fragments creates libraries that are used for sequencing.



Step 4: DNA & RNA Extraction

The Molecular department uses the dissected tumor tissue from the FFPE block for DNA & RNA extraction.



Step 6: Sequencing the Libraries

The libraries are placed on a next-generation sequencing system which reveals the exact sequence of nucleotides (A, T, G, C) in the fragments. The sequenced fragments are matched to the human genome sequence to determine if mutations are present in the selected regions. Mutations in these regions are associated with the onset of cancer.



Note:

Mutations that are uncommon or not present in Cancer databases are analyzed by prediction tools to see if these mutations are predicted to be harmful or not.

Step 7: Bioinformatics

Analysis of the identified mutations includes filtering out, or removing, common mutations that are seen in the normal healthy population. Cancer databases are used to identify any mutations in different types of cancers that are present.



Step 8: Identify Treatment Options

The final list of mutations are used to search databases for available clinical therapies and clinical trials. Treatment is designed specifically for the mutations found in the patient specimen and tumor type customizing the treatment to the patient.



Interested in Implementing NGS Solid Tumor Profiling?

Contact us, we would be happy to answer any questions you might have.
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