GenOnc Liver Panel

GENOME EXPLORATIONS
A DIVISION OF COMPASS LABORATORY SERVICES LLC

GenOnc Liver Cancer Panel

Introduction

GenOnc Liver Cancer Panel is a collection of multiplexed PCR primer assays for targeted enrichment of the coding (exonic) regions of the 33 genes most commonly mutated in human liver cancer samples. Mutations in these oncogenes and tumor suppressor genes are often relevant for tumor classification, and warrant extensive investigation to enhance the understanding of carcinogenesis. Hepatocellular carcinoma (HCC), the most common form of liver cancer, has a poor prognosis and low survival rate. The second most common form of liver cancer is cholangiocarcinoma, a cancer of the bile ducts. Although these 2 forms of liver cancer have different molecular mechanisms and prognoses, there are some similarities. For example, TP53 and ß-catenin are the most common mutated genes in HCC, whereas TP53 and KRAS are the most common mutated genes in cholangiocarcinoma. There are multiple potential mutation sites in each of these genes. Therefore, sequencing analysis is an efficient method to examine a tumor sample. This panel narrows the focus to the most relevant mutated genes in liver cancer, using a variety of resources such as recent whole genome/exome sequencing studies from scientific networks including the Cancer Genome Atlas. Curated databases such as the Cancer Gene Census and COSMIC (Catalogue of Somatic Mutations in Cancer) are also used.

GenOnc Liver Cancer Panel Genes

Carcinoma:
IGF2R, ZIC3

Hepatocellular Carcinoma (HCC):
ALB, AMPH, APC, ARID1A, ARID2, ATM, AXIN1, BAZ2B, BRAF, C18orf34, CDKN2A (p16INK4), CSMD3, CTNNB1, DSE, ELMO1, ERBB2 (HER2), ERRFI1, GXYLT1, HNF1A, IGSF10, KEAP1, KRAS, MET, OTOP1, PIK3CA (p110α), SAMD9L, TP53, UBR3, USP25, WWP1, ZNF226

Cholangiocarcinoma:
AXIN1, BRAF, CTNNB1, KEAP1, KRAS, PIK3CA (p110α), TP53

Other Cancer Subtypes:
Adenoma: CTNNB1, HNF1A
Hepatoblastoma: APC, CTNNB1, TP53