# Week 3 Assignment: Gene Mutation Analysis (Liver Hepatocellular Carcinoma)

Dataset Selected: TCGA Liver Hepatocellular Carcinoma (Firehose Legacy)  
Number of Patients: 377  
Number of Samples: 379

## Selected Gene: TP53

TP53 is the most frequently mutated gene in this liver cancer dataset, with mutations found in 118 samples. This corresponds to a frequency of approximately 30.8%. TP53 is a tumor suppressor gene that helps regulate cell division by keeping cells from growing and dividing too fast or in an uncontrolled way.

## Type of Mutation Identified

The most common mutations in TP53 are missense mutations. These result in a single amino acid change in the p53 protein, often disrupting its ability to bind DNA and control cell cycle progression. Such changes can impair the tumor-suppressive functions of the protein.

## Amino Acid Change and Functional Impact

An example of an amino acid change in TP53 is R249S (arginine to serine at codon 249). This change is known to be highly impactful because it disrupts the DNA-binding domain of p53. According to the dataset, such mutations are predicted to be deleterious or damaging, potentially leading to loss of normal function.

## Summary

TP53 mutation (especially missense mutations like R249S) plays a significant role in the pathogenesis of hepatocellular carcinoma. Its high frequency highlights its importance as a diagnostic or therapeutic target in precision oncology.