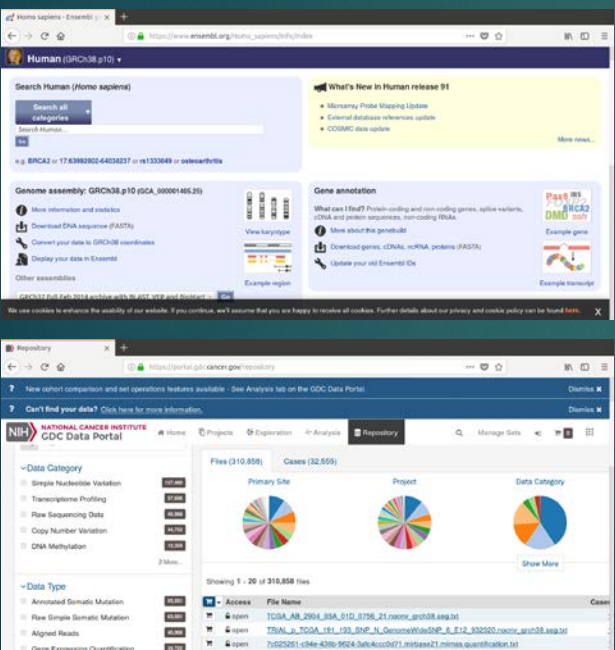




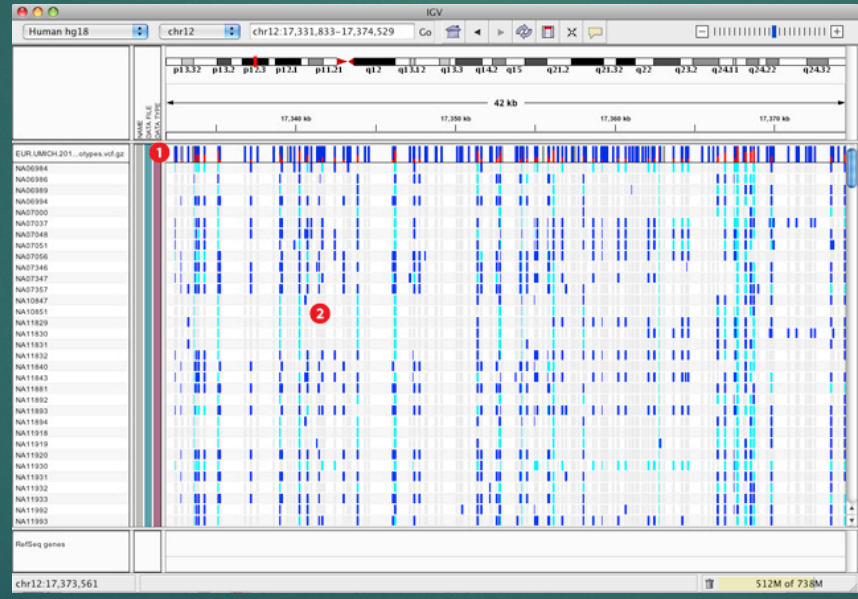
Data Collection

The first step is to collect the data. Data can be gathered yourself or taken from an existing source. One source of data that is useful for cancer treatment is the National Cancer Institute's Genomic Data Commons Data Portal, which has a repository of genomes taken from cancer tumors.



Data Input

Mutations, or variant bases, are identified by workflow software. Workflow software generates a Variant Call Format file (VCF). VCF is used in bioinformatics for storing gene sequence variations.



Data Output & Communication

iCAGES is a software that identifies cancer driver genes/variants and optimal drug treatments. It inputs VCF files specific to patient's tumor mutations. Then, it outputs the best candidate drug to treat the patient.

