

The Cancer Genome Atlas Pilot Project
Stanford University School of Medicine
Data Descriptions

Platform: Illumina Infinium 550K SNP Array

Segmented Data

We will provide summary tables of CNVs discovered for each sample based on our segmentation software. Each line of summary will contain the sample ID, the beginning and ending SNPs of the CNV, their positions, gene(s) affected, and the estimated nature of variation (deletion, loss of heterozygosity, or amplification, etc).