

Fig. S2

Number of mutated genes on the cancer panel

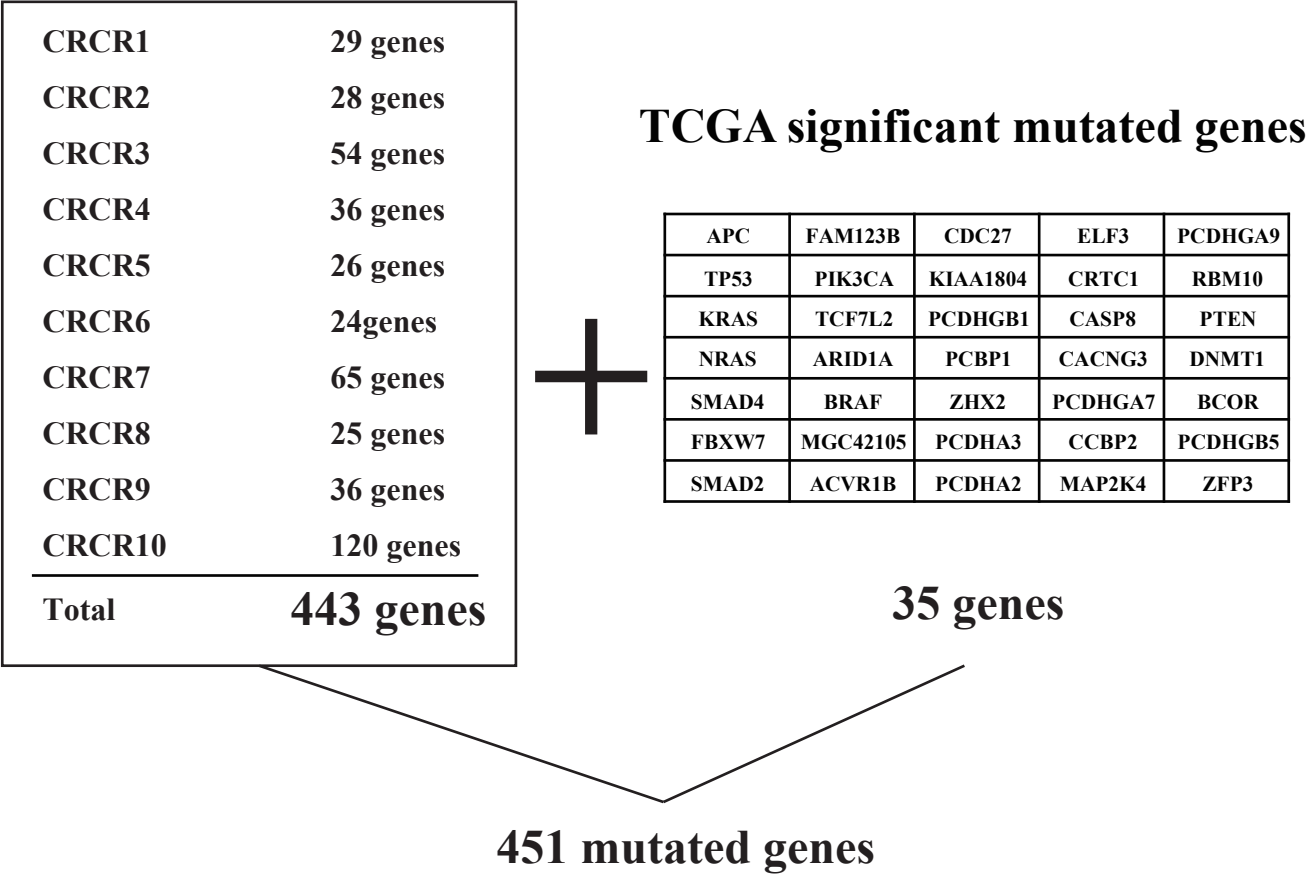


Fig. S2: The number of genes on the customized cancer panel.
We selected 443 commonly mutated genes between 10 primary sites and ten recurrent (metastatic) sites to establish a cancer panel for target resequencing. In addition, we added 35 established significant mutated genes from TCGA to the bottom of the customized cancer panel to avoid missed ctDNA detection. Eventually, we selected 451 genes for the bespoke cancer panel.