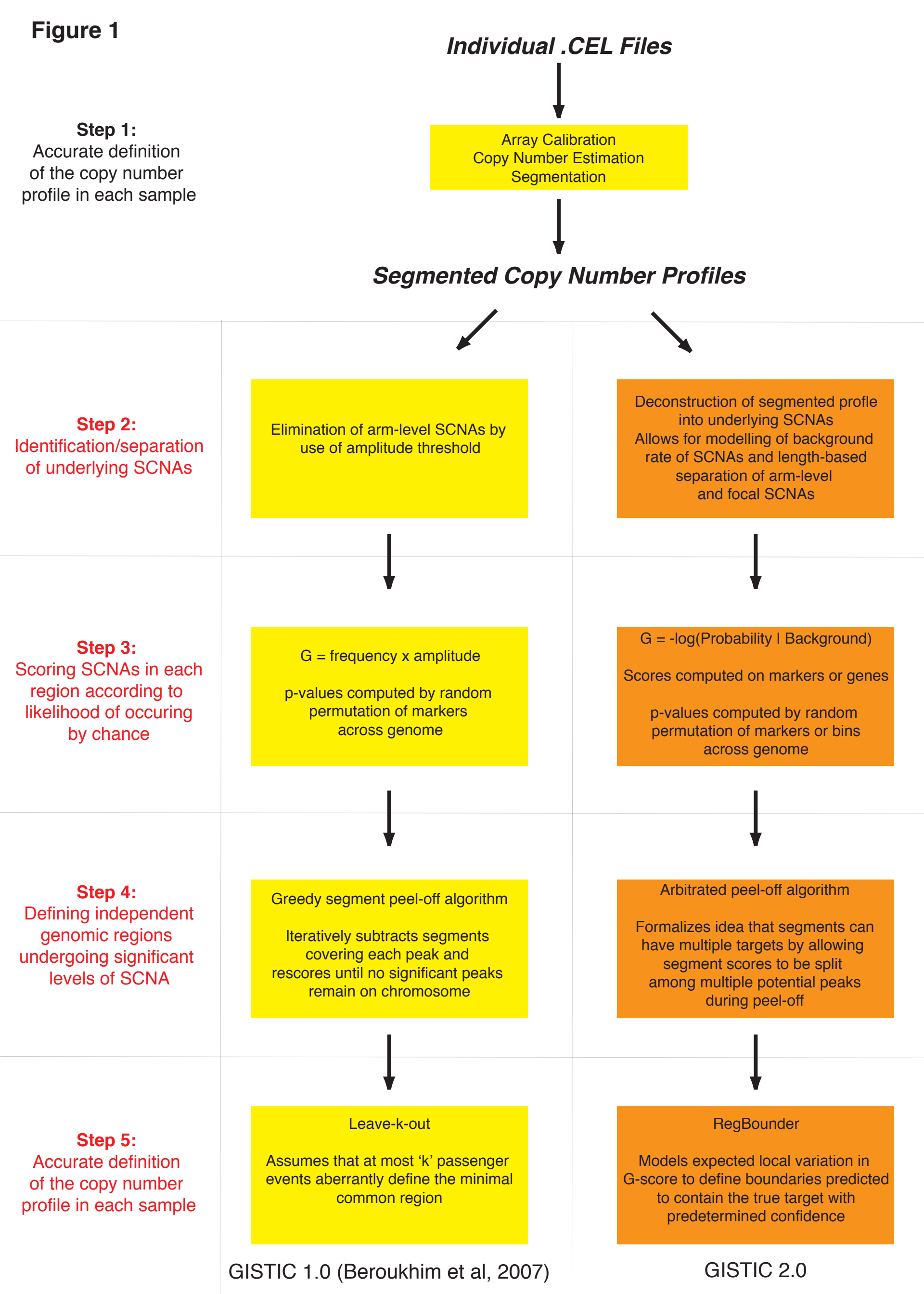
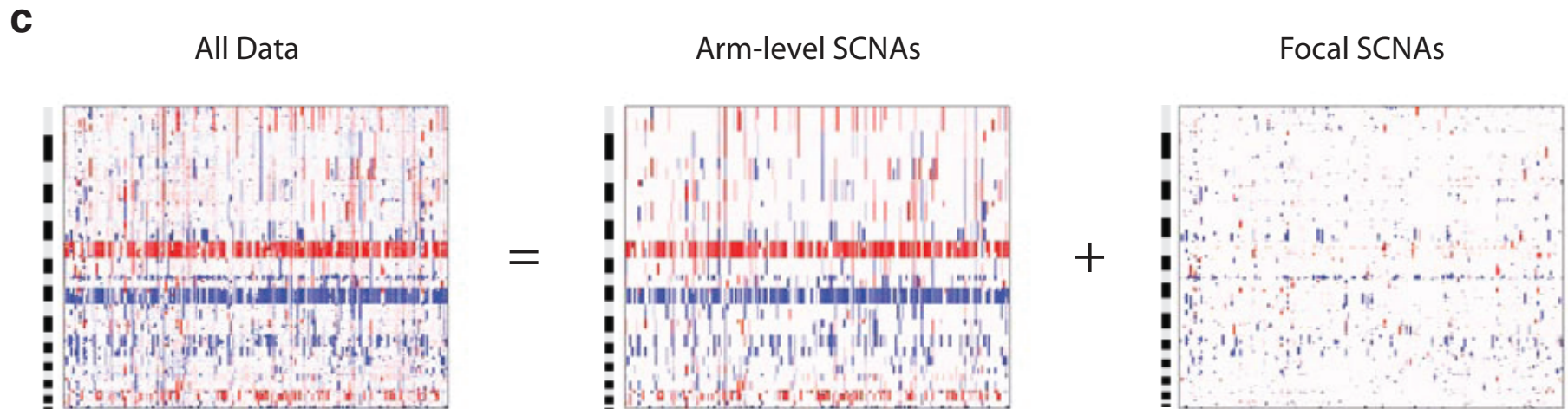
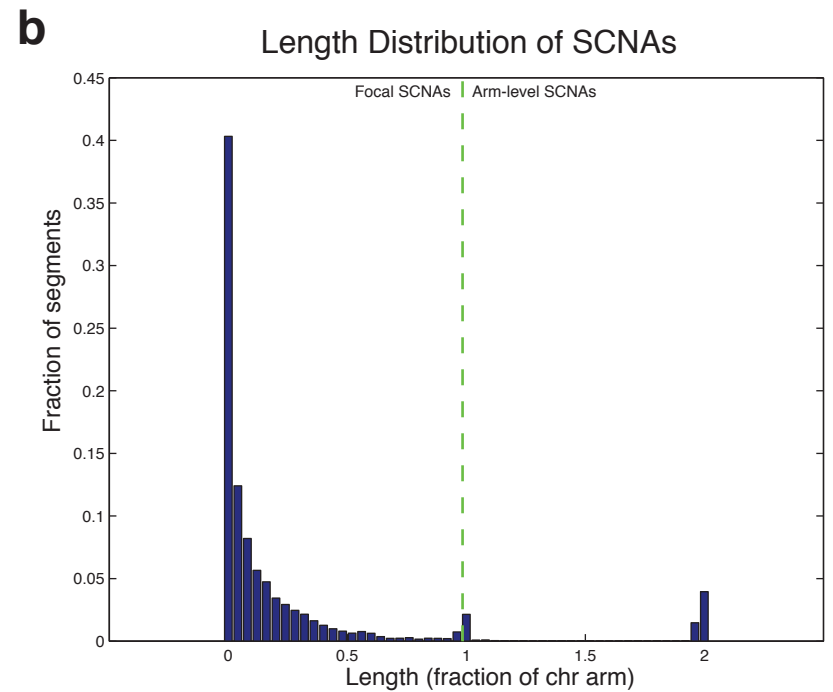
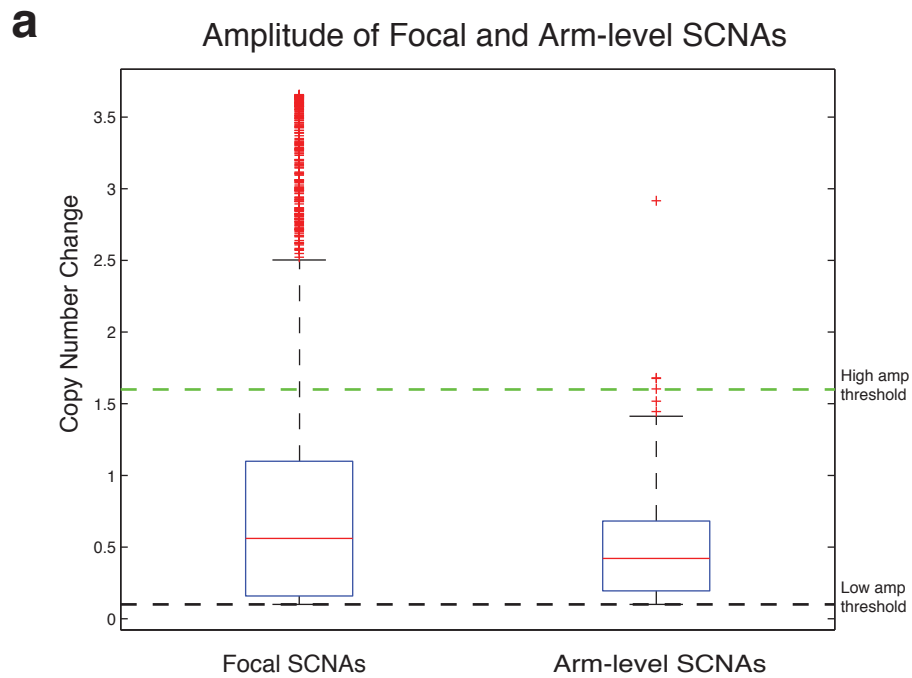


Figure 1



# Figure 2

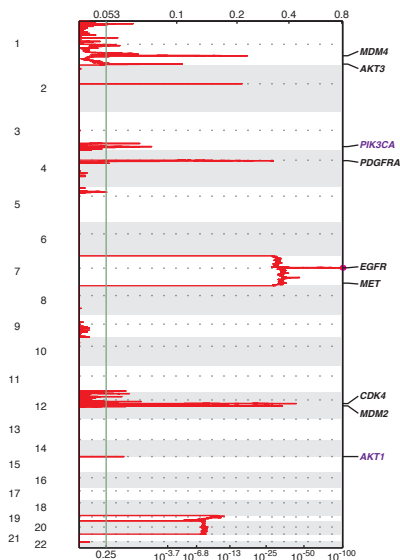


# Figure 3

**a**

All Data  
Low Amplitude Threshold

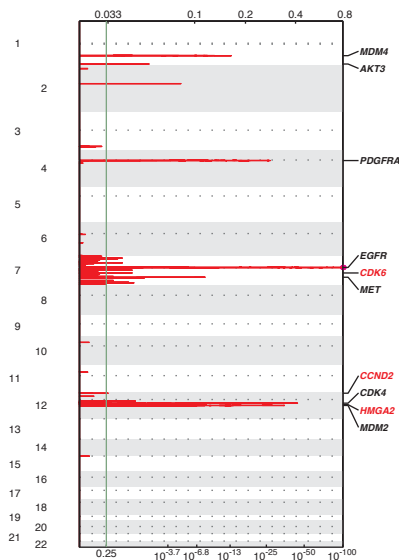
Amplifications



27 Amplified Regions

**b**

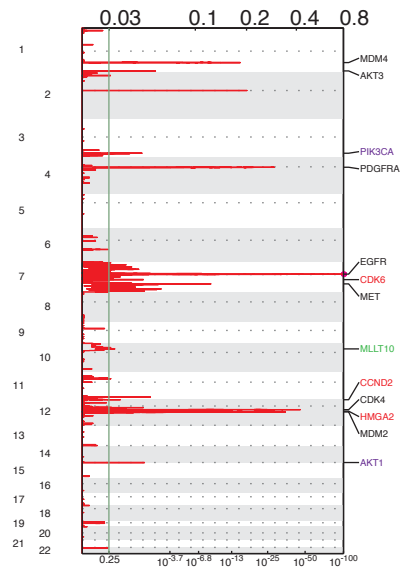
All Data  
High Amplitude Threshold



41 Amplified Regions

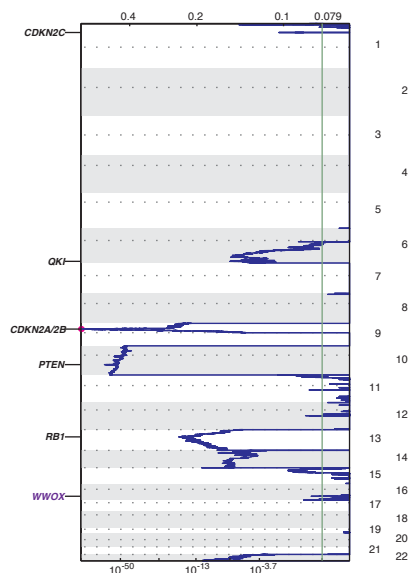
**c**

Focal Data  
Low Amplitude Threshold

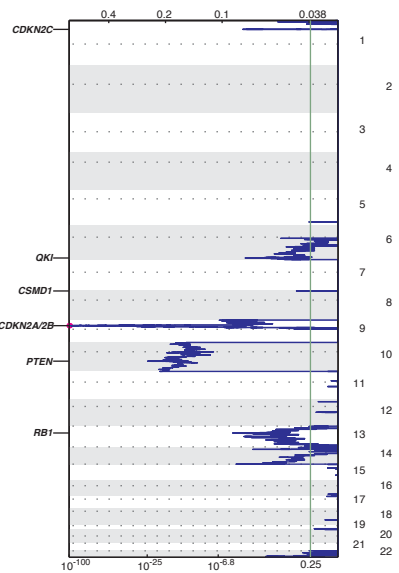


55 Amplified Regions

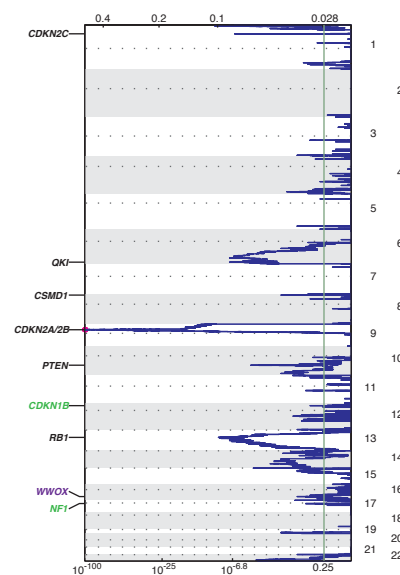
Deletions



15 Deleted Regions



31 Deleted Regions

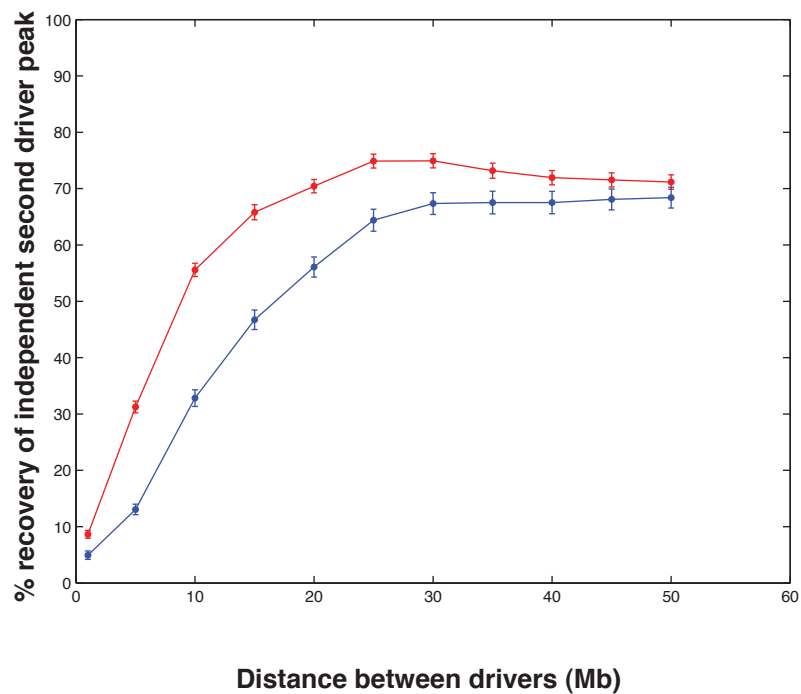


36 Deleted Regions

# Figure 4

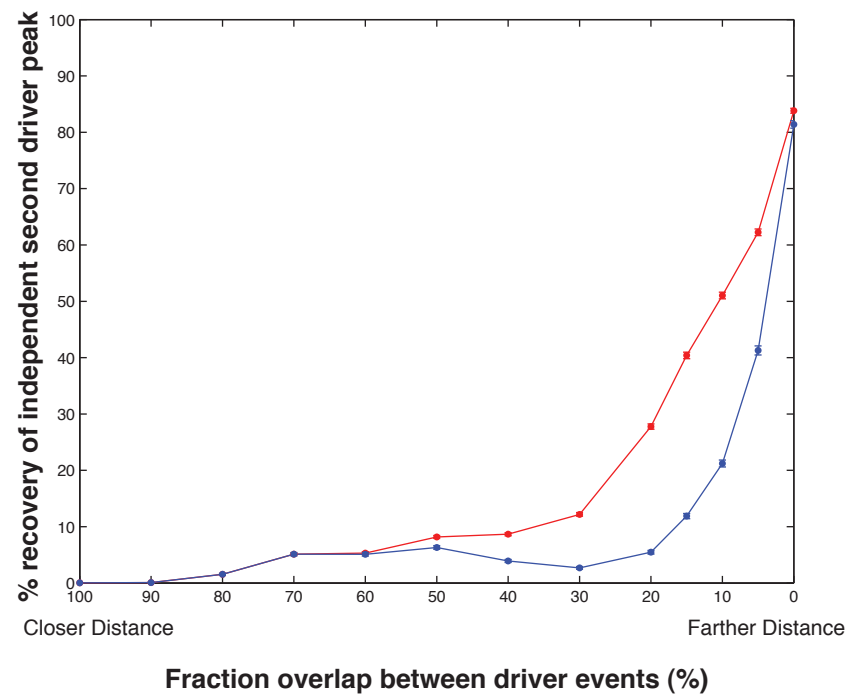
**a**

## Sensitivity vs. Driver Distance



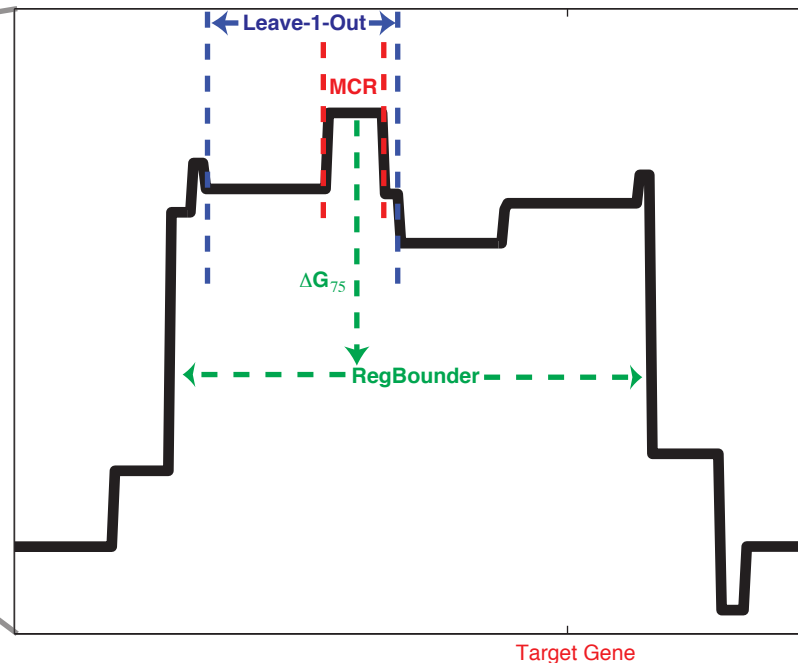
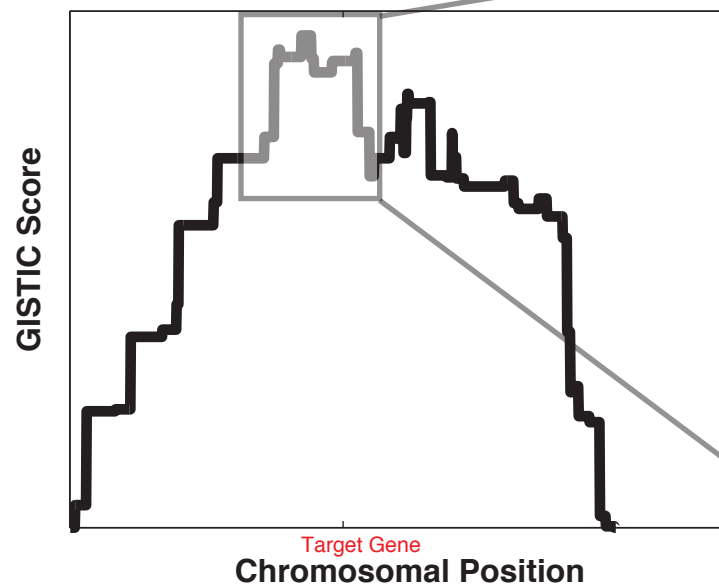
**b**

## Sensitivity vs. Driver SCNA Overlap



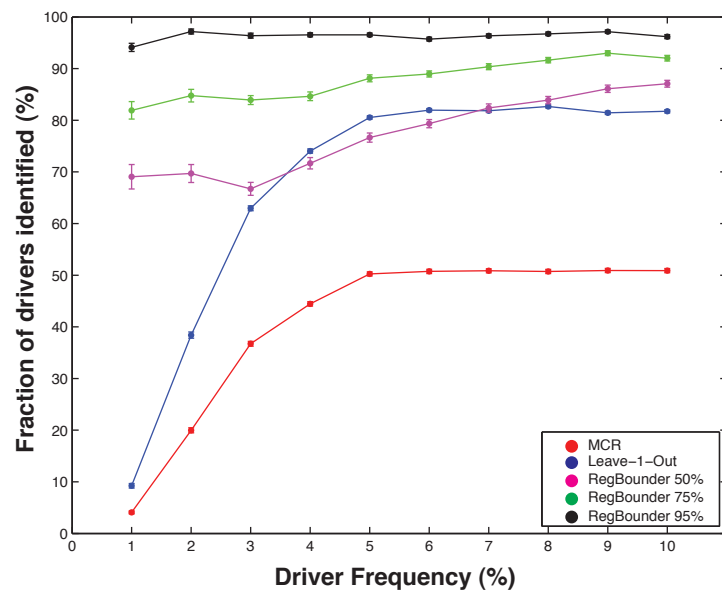
# Figure 5

**a**



**b**

Driver Recall as Function of Driver Frequency  
(n = 500 samples)



**c**

Driver Recall as Function of Sample Size  
(5% driver frequency)

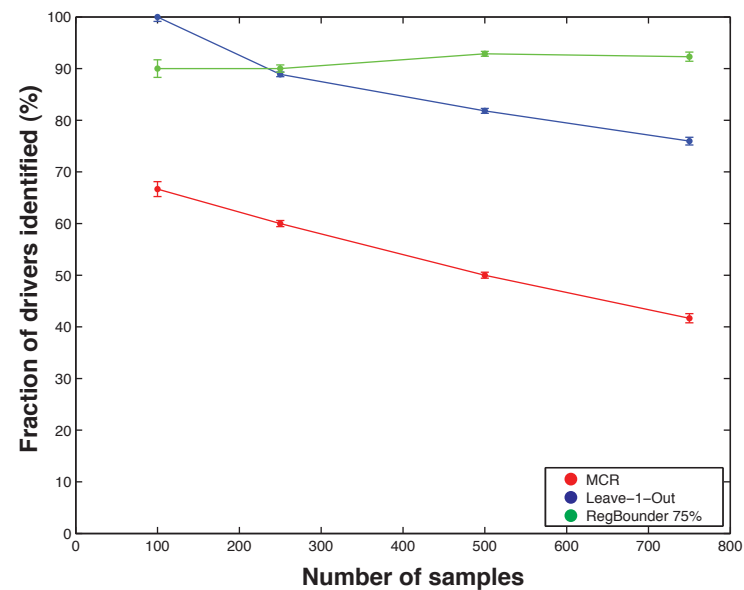
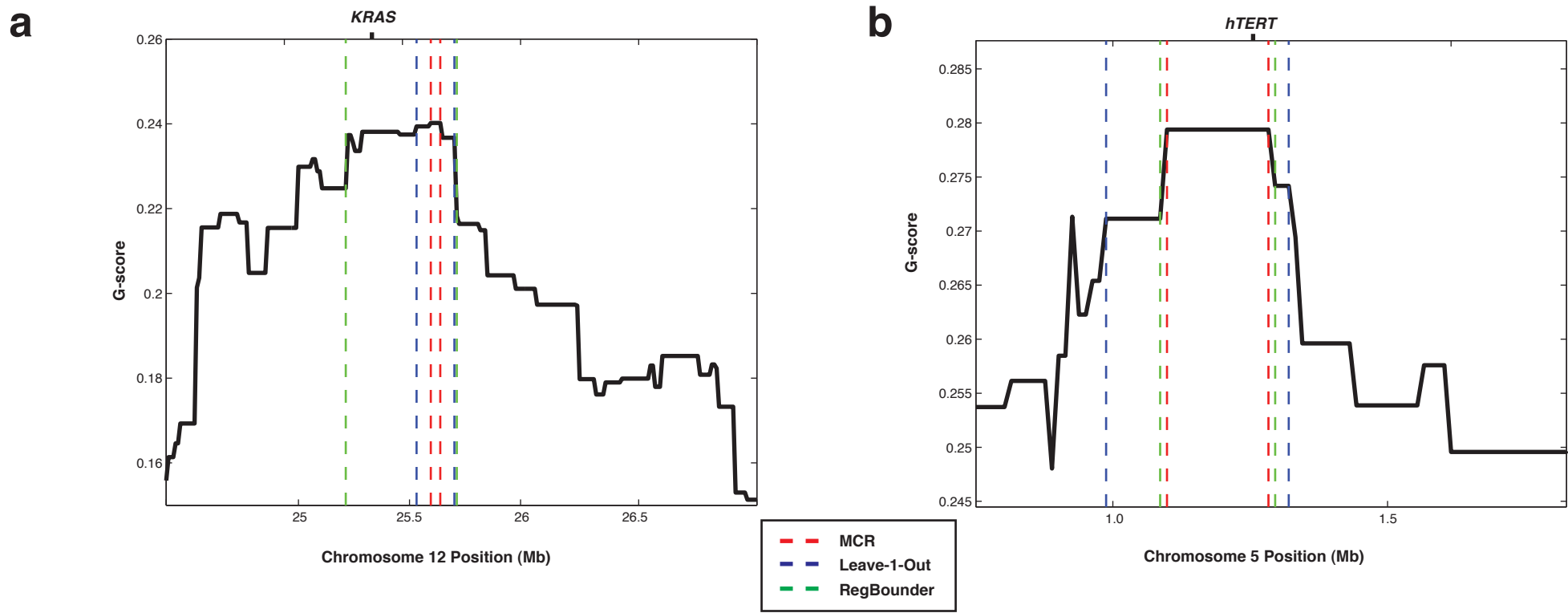


Figure 6

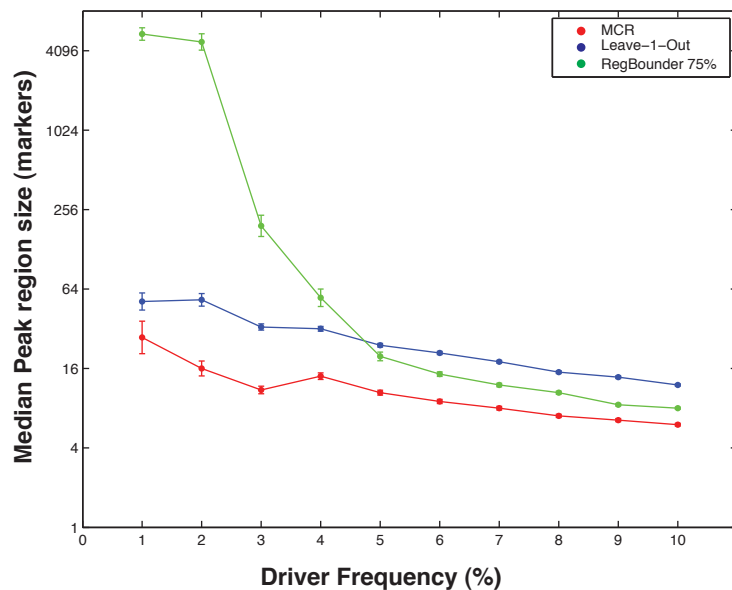
RegBouncer vs. MCR and Leave-1-Out  
on Lung Adenocarcinoma Samples



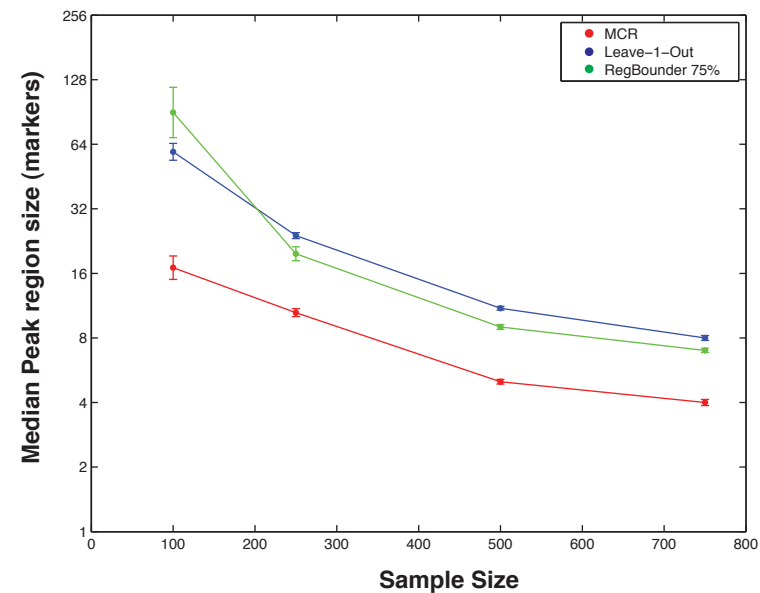
# Figure 7

**a**

## Peak Region Size As Function of Driver Frequency (n = 500 samples)

**b**

## Peak Region Size As Function of Sample Size (5% Driver Frequency)

**c**

## RegBounder vs. Theoretically Optimal Peak Region (n = 500 samples)

