maf <- read.table("input\_file.maf", header=T)

#

## use Tumor\_Sample\_Barcode instead of sample

#

colnames(maf)[1] <- "Tumor\_Sample\_Barcode"

#

## some of the "SNP" records contained INDELs.

#

maf <- maf[maf$Reference\_Allele!="-" & maf$Tumor\_Seq\_Allele2!="-",]

#

# run

#

source("SignatureAnalyzer.Broad.R")