## This script generates oncoplot/oncoprint from the Annovar output of SNVs/INDELs of specified genes

library(maftools)

### Load the package or install if not present

if (!require("RColorBrewer")) {

install.packages("RColorBrewer")

library(RColorBrewer)

}

#################

# Read maf file

# read.maf reads MAF files, summerizes it in various ways and stores it as an MAF object

################

#read ESCC maf file for LAML

laml = read.maf(“input\_file.txt”)

#Read FAB classification of ESCC data;

laml.fab.anno = read.delim('ESCC\_laml\_fab\_annotation.txt', sep = '\t')

head(laml.fab.anno)

#########################################

# changing colors and adding annotations

########################################

#Changing colors for variant classifications (You can use any colors, here in this example we will use a color palette from RColorBrewer)

#col = RColorBrewer::brewer.pal(n = 8, name = 'Paired')

col = RColorBrewer::brewer.pal(n = 8, name = 'Set1')

names(col) = c('Multi\_Hit', 'Missense\_Mutation', 'Nonsense\_Mutation', 'Frame\_Shift\_Del','Frame\_Shift\_Ins',

'In\_Frame\_Ins', 'Splice\_Site', 'In\_Frame\_Del')

#Color coding for FAB classification; try getAnnotations(x = laml) to see available annotations.

fabcolors = RColorBrewer::brewer.pal(n = 2,name = 'Spectral')

names(fabcolors) = c("Non-responder", "Responder")

fabcolors = list(FAB\_classification = fabcolors)

###############

# Oncoprint

##############

oncoplot(maf = laml, top = 20, showTumorSampleBarcodes = TRUE, drawColBar = TRUE, colors = col, writeMatrix = TRUE, fontSize = 0.7, SampleNamefontSize = 1, legendFontSize = 1.2, sepwd\_genes = 0.5, sepwd\_samples = 0.25, borderCol = "white")