```r
#This R script makes a Circlize graph from 3 sources (gene density,
tRNA scan, infernal) for all 18 chromosomes
library(circlize)

#set colors
#18 colors
col = c('#E41A1C', '#A73C52', '#6B5F88', '#3780B3', '#3F918C',
'#47A266',
        '#53A651', '#6D8470', '#87638F', '#A5548D', '#C96555',
'#ED761C',
        '#FF9508', '#FFC11A', '#FFEE2C', '#EBDA30', '#CC9F2C',
'#AD6428')

#get phoenix cytoband read in
#18 chrom
cyto.info<-read.table("Data/Phoenix_Chr_BedFile_18chr.txt", header =
FALSE, sep = "\t")
head(cyto.info)

#name index of chromosomes (chro no's using)
#18chrom
index<-paste("chr",1:18,sep="")
print(index)

#start ideogram with chrom index and cytoband
circos.par("track.height" = 0.1)
#increase gap size for labels
circos.par(gap.after=3)

#start plotting
pdf(file = "3sources_full_18chrom_50KB.pdf")
#initialize plot with tickmarks
circos.initializeWithIdeogram(cytoband = cyto.info, chromosome.index =
c(index), plotType = c("axis", "labels"))

####gene density#####

#read in genome GFF BED
bed_genome<-read.table("Data/BED_FILES/genome_bed_full.bed", header =
FALSE, sep = "\t")
head(bed_genome)

#add track labels
circos.text(sector.index="chr1",track.index =
1,get.cell.meta.data("cell.xlim")-
mean(get.cell.meta.data("cell.xlim"))/2,
            get.cell.meta.data("cell.ylim")-
max(get.cell.meta.data("cell.ylim"))/.7, labels = "A",facing =
"clockwise",
            niceFacing = TRUE, adj = c(0,0),cex = 0.5)
```

```
#make genome density plot
circos.genomicDensity(bed_genome, window.size = 50000, col =
c("#FF000080"), track.height = 0.1)
######################

####tRNA scan#######

#Label
circos.text(sector.index="chr1",track.index =
2,get.cell.meta.data("cell.xlim")-
mean(get.cell.meta.data("cell.xlim"))/3,

get.cell.meta.data("cell.ylim")-1.2*max(get.cell.meta.data("cell.ylim"
)), labels = "B",facing = "clockwise",
            niceFacing = TRUE, adj = c(0,0),cex = 0.5)

#tRNA track
bed_trna<-read<-read.table("Data/BED_FILES/tRNA_bed_full_50KB.bed",
header = FALSE, sep = "\t")
head(bed_trna)
circos.genomicTrackPlotRegion(bed_trna, bg.border = "black", ylim =
c(0, 1), panel.fun = function(region, value, ...) {
  i = get.cell.meta.data("sector.numeric.index")
  circos.genomicLines(region, value, border = "black", type = "h",
baseline = 0, col = col[i])
}, track.height = 0.1)
#########################

#######Infernal########
#infernal track loop
infernal_bed_list<-
c("infernal_tRNA_full.bed","infernal_snoR71_full.bed","infernal_snoR11
4_full.bed","infernal_5S_rRNA_full.bed")
for (i in infernal_bed_list) {
  bed_inf<-read.table(paste("Data/BED_FILES/",i,sep=""), header =
FALSE, sep = "\t")
  circos.genomicTrackPlotRegion(bed_inf, bg.border = "black", ylim =
c(0, 1), panel.fun = function(region, value, ...) {
    j = get.cell.meta.data("sector.numeric.index")
    circos.genomicLines(region, value, border = "black", type = "h",
baseline = 0, col = col[j])
  }, track.height = 0.1)
}
#####################


dev.off()
```