

Code Editor

```
9 install.packages("gProfiler")
10 install.packages("tidyverse")
11 install.packages("ggpubr")
12 library(GenomicRanges)
13 options(stringsAsFactors = F)
14 setwd("~/work") # This is the path to the working directory.
15 credSNP = read.delim("Supplementary_Table_8_Jansen.txt", header=T)
16 credSNP = credSNP[credSNP$Credible.Causal=="Yes", ]
17
18 credranges = GRanges(credSNP$Chr, IRanges(credSNP$bp, credSNP$bp), rsid=cr
19 save(credranges, file="AD_credibleSNP.rda")
20
```

Environment History Connections

Global Environment

datMeta	345 obs. of 10 variables
datProbes	17085 obs. of 5 variables
exon	324422 obs. of 4 variables
exonranges	Large GRanges (324422 elements)
genome	16767 obs. of 2 variables
geneAnno1	57317 obs. of 8 variables
hic	149097 obs. of 5 variables

R Console

```
~/work/
v4 CTX Prenatal 5.803337
v7 CTX Prenatal 5.810975
v9 CTX Prenatal 5.827192
v11 CTX Prenatal 5.883260
v12 CTX Prenatal 5.980518
v13 CTX Prenatal 5.827781
> ggplot(dat,aes(x=Unit, y=Expr, fill=Unit, alpha=Unit)) + ylab("Normalized expr
ession") + geom_boxplot(outlier.size = NA) + ggtitle("Brain Expression") + xlab
("") + scale_alpha_manual(values=c(0.2, 1)) + theme_classic() + theme(legend.pos
ition="na")
>
>
```

Type codes here

