

```

library(variancePartition)

## Loading required package: ggplot2

## Loading required package: limma

## Loading required package: BiocParallel

update_gene_names <- function(df){
  gene_map <- readRDS("/data/humgen/daskalakislabs/dipietro/SciencePaper/Data/RNA/Bulk/RNA_Gene_Map.RDS")

  df$genes <- rownames(df)
  df <- merge(df, gene_map, by="genes", all.x=T)
  rownames(df) <- paste0(df$symbol, "_", df$genes)
  df <- df[, -which(names(df) %in% c("genes", "symbol"))]

  return(df)
}

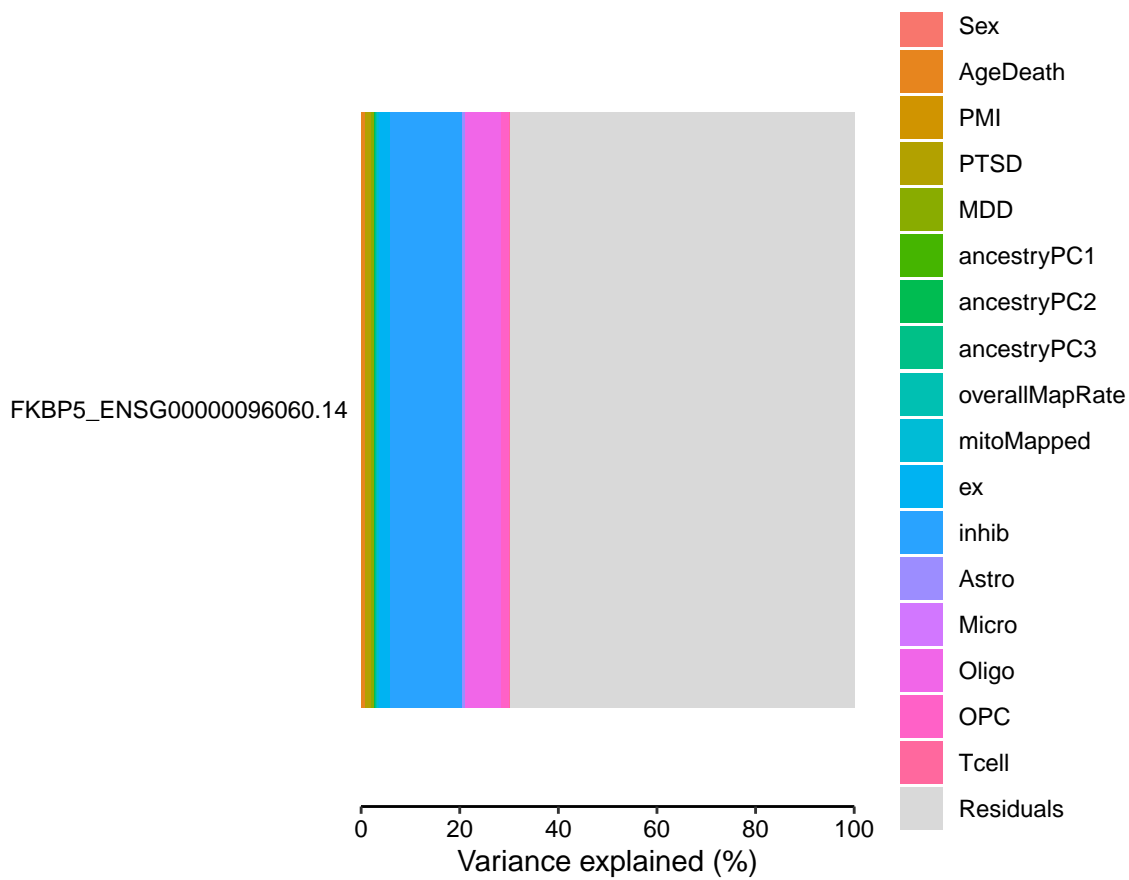
ca <- readRDS("/data/humgen/daskalakislabs/dipietro/SciencePaper/Data/RNA/VariancePartition/Genes/Finali
ca <- update_gene_names(ca)

dg <- readRDS("/data/humgen/daskalakislabs/dipietro/SciencePaper/Data/RNA/VariancePartition/Genes/Finali
dg <- update_gene_names(dg)

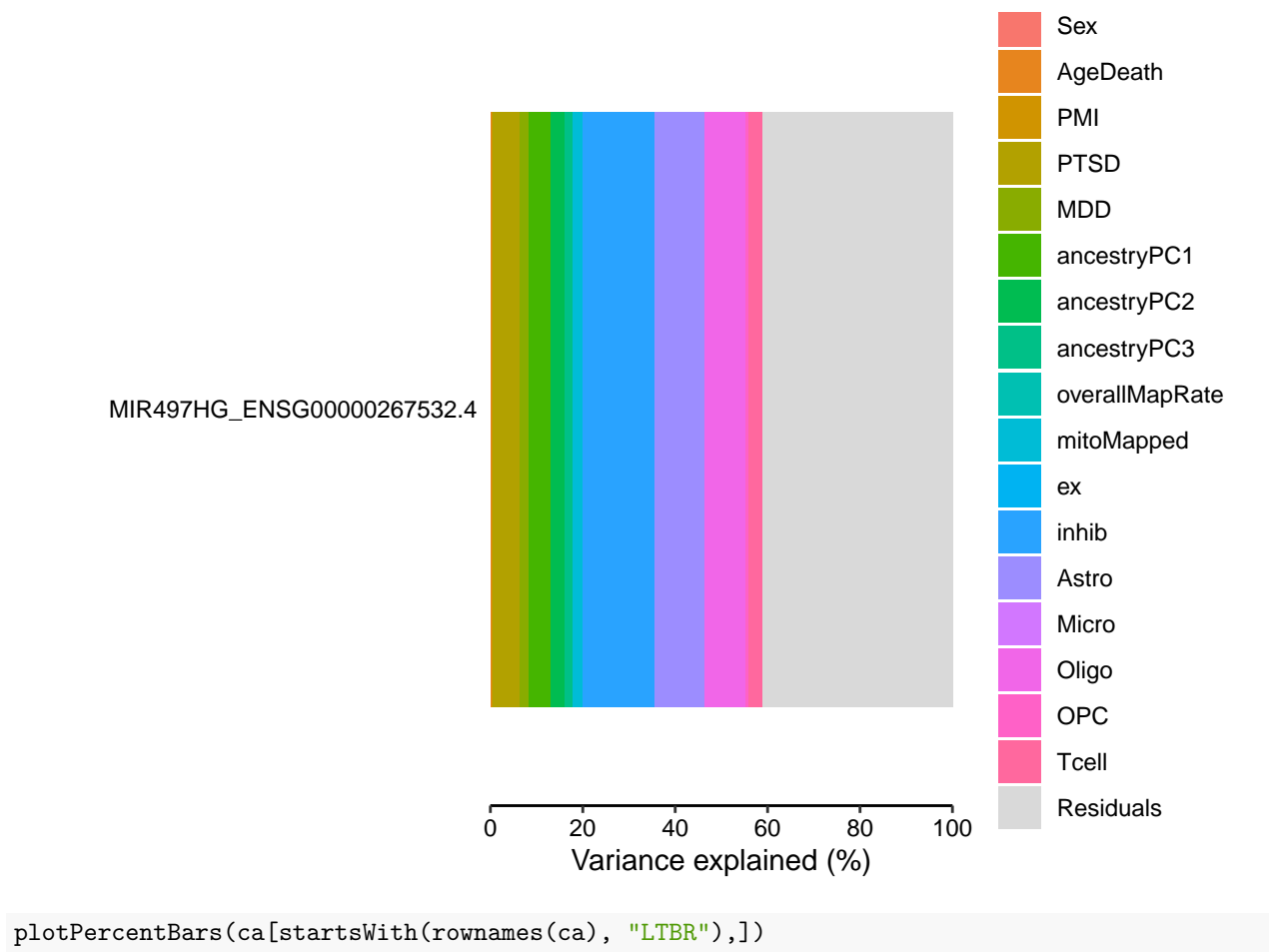
mpfc <- readRDS("/data/humgen/daskalakislabs/dipietro/SciencePaper/Data/RNA/VariancePartition/Genes/Finali
mpfc <- update_gene_names(mpfc)

#####
# Top Genes PTSD Central Amyg #
#####
# MIR497HG (FDR-)
# LTBR (FDR+)
plotPercentBars(ca[startsWith(rownames(ca), "FKBP5"),])

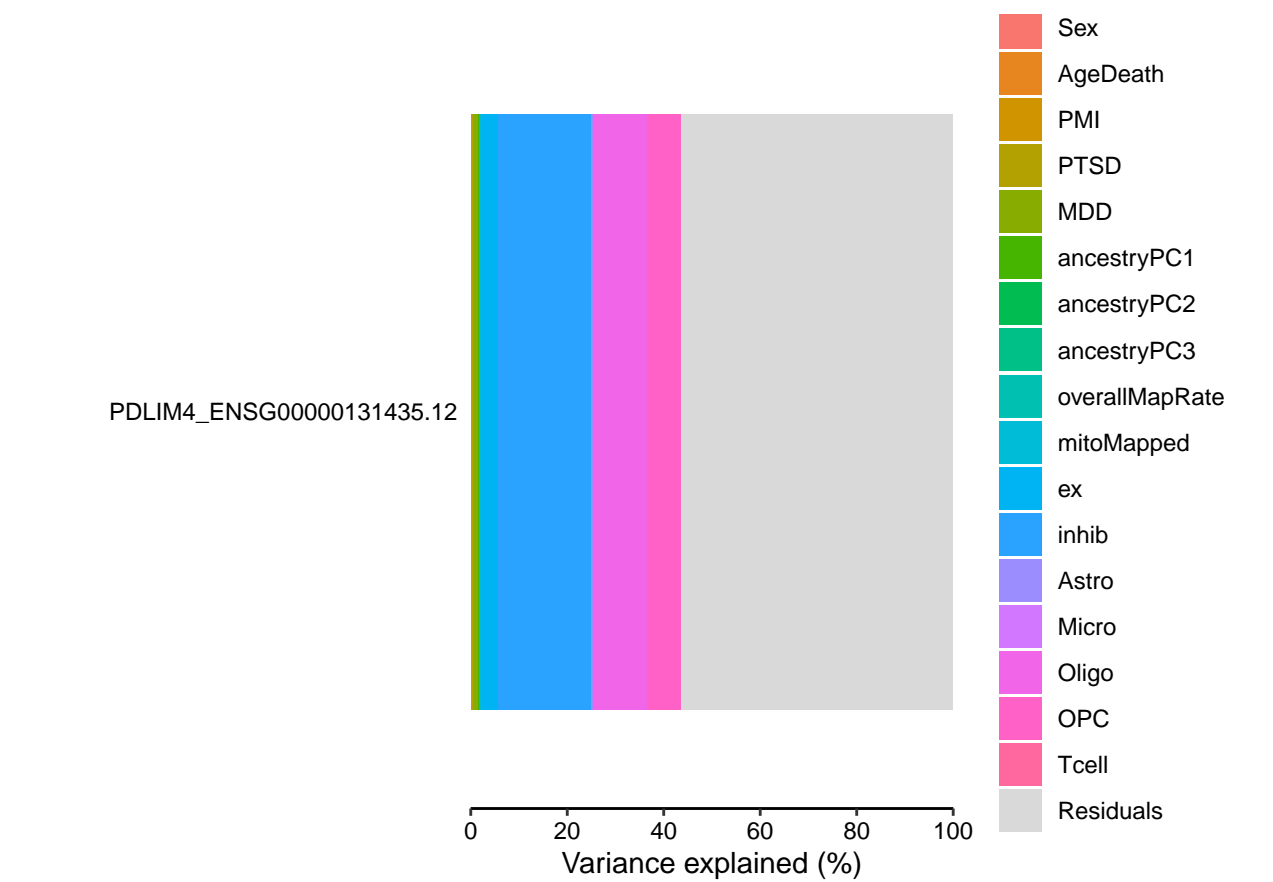
```



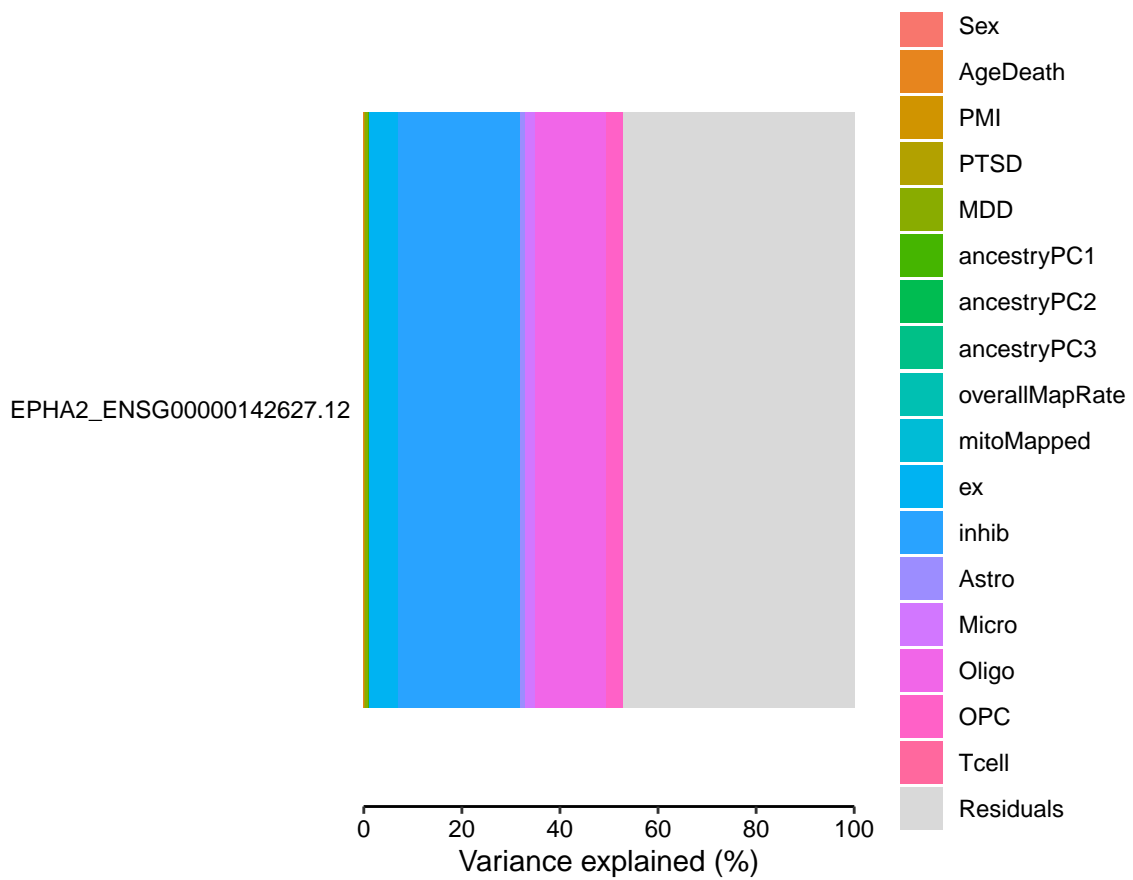
```
plotPercentBars(ca[startsWith(rownames(ca), "MIR497HG"),])
```



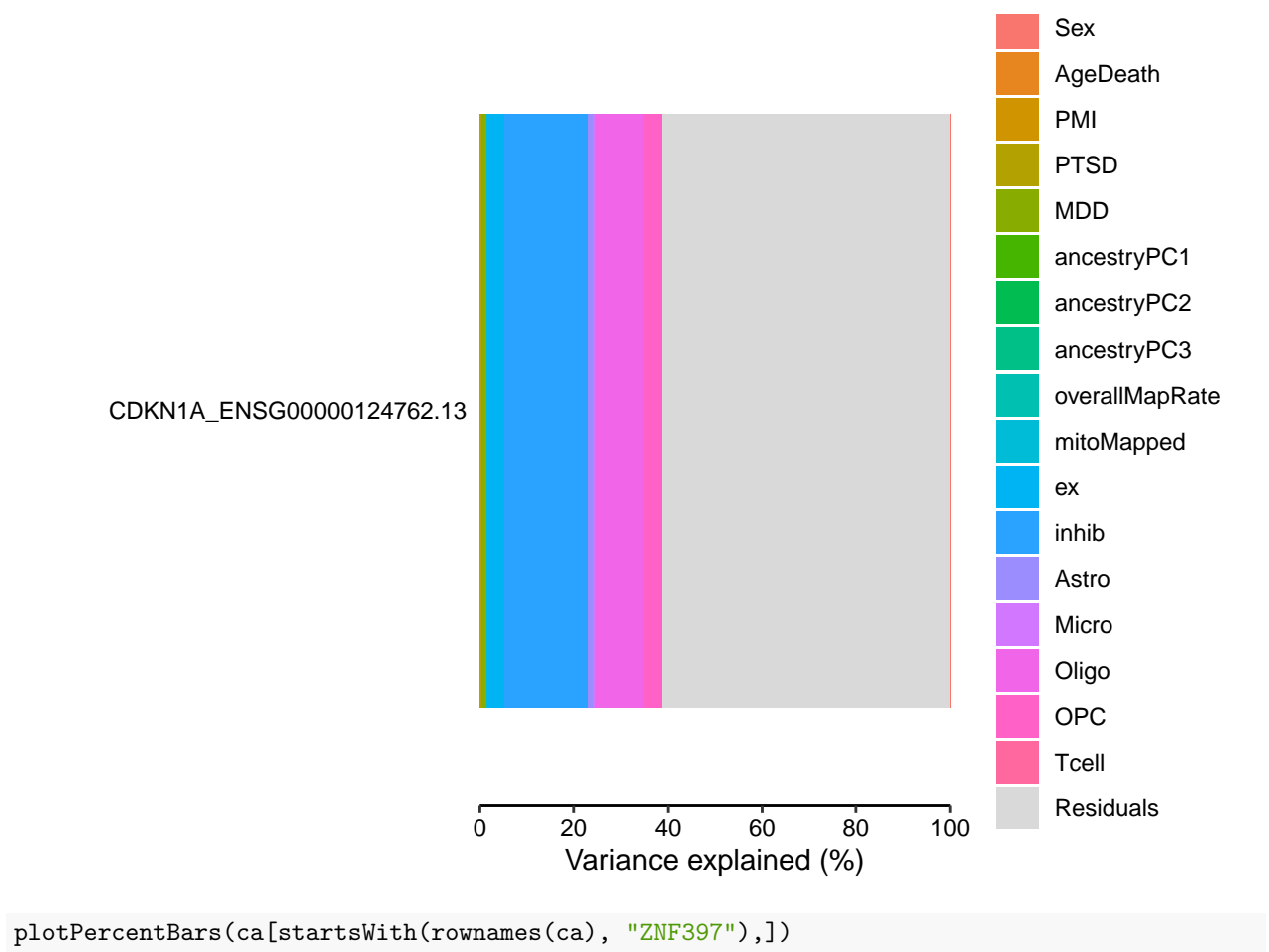


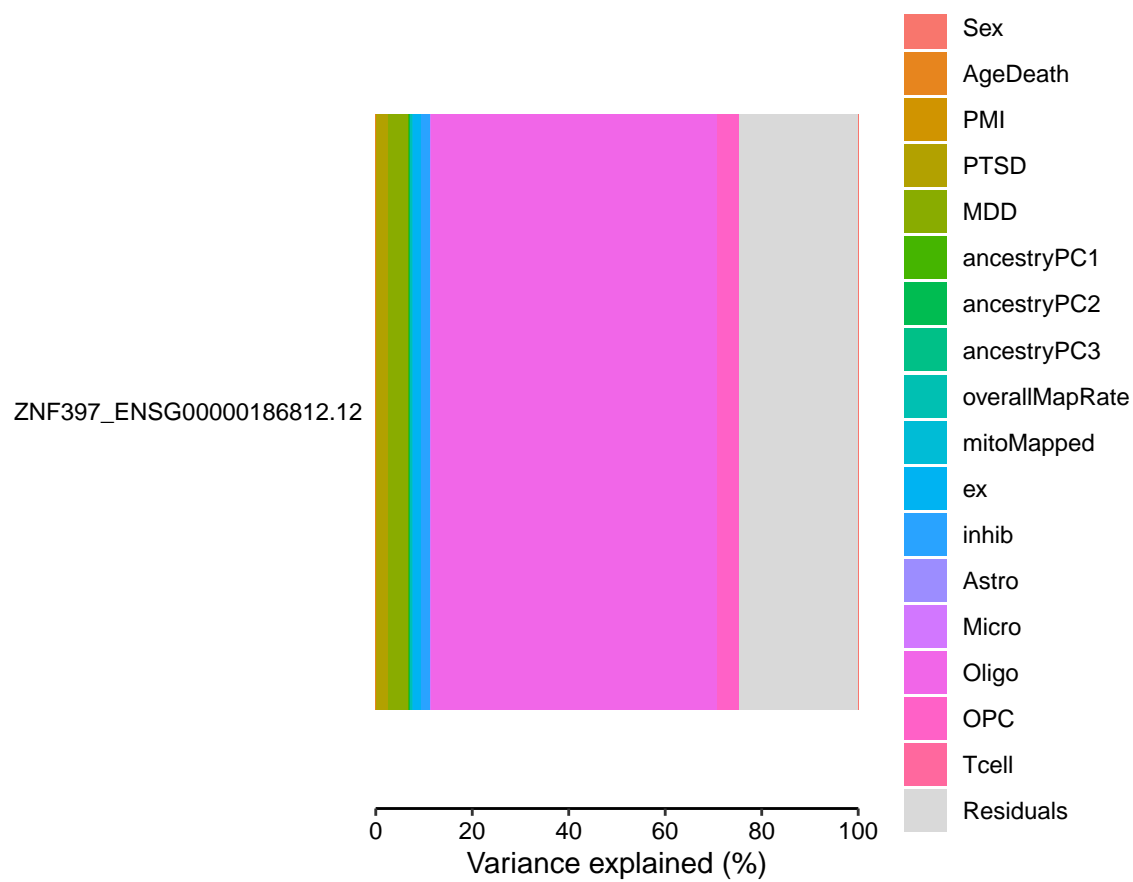


```
plotPercentBars(ca[startsWith(rownames(ca), "EPHA2"),])
```



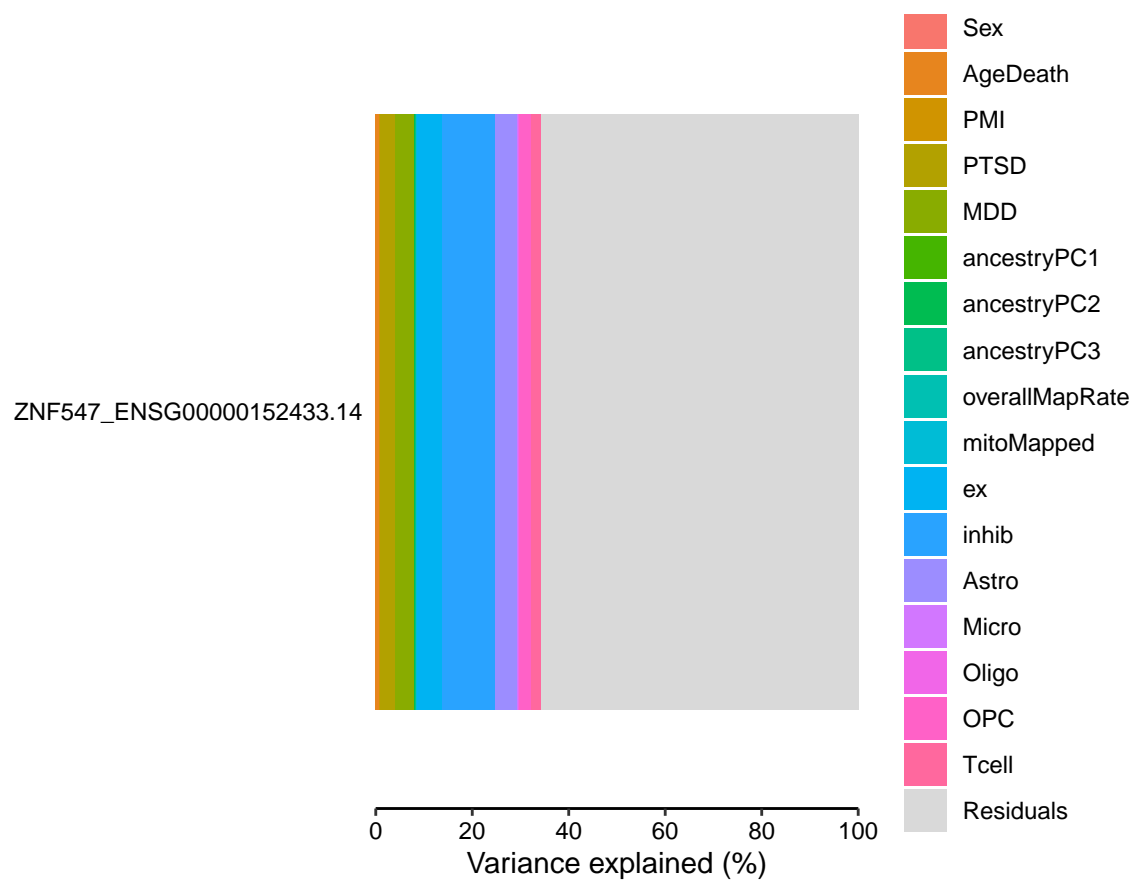
```
plotPercentBars(ca[startsWith(rownames(ca), "CDKN1A"),])
```



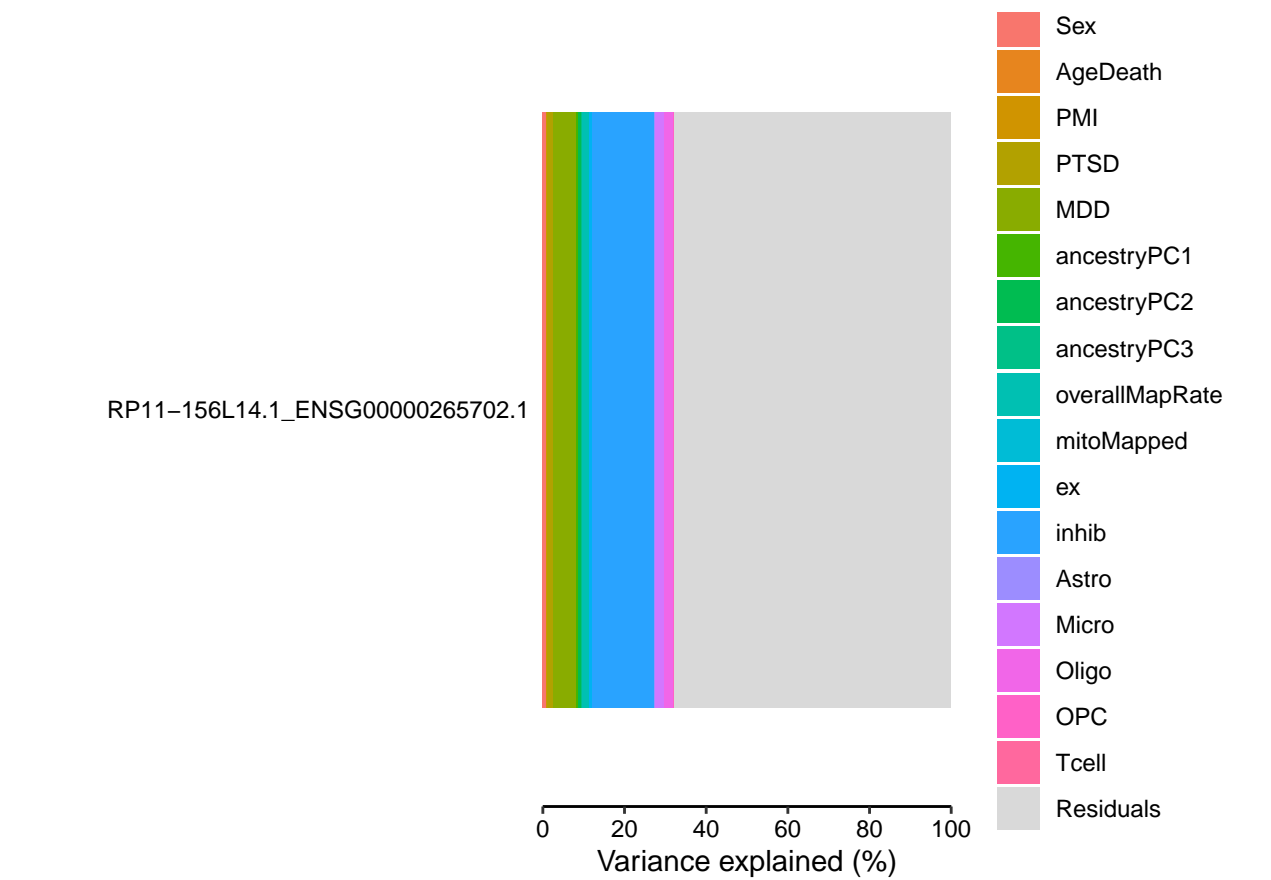


```
plotPercentBars(ca[startsWith(rownames(ca), "ZNF547"),])
```

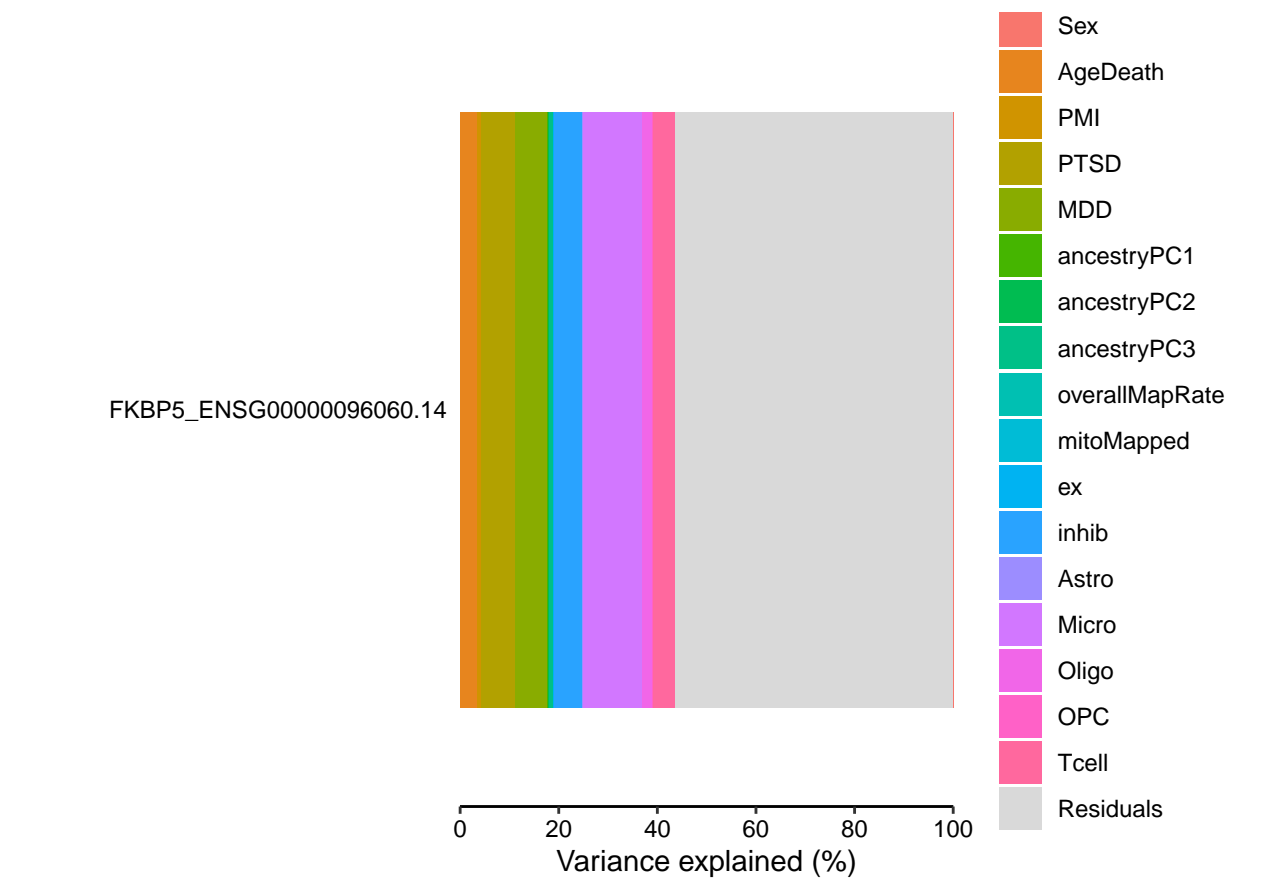




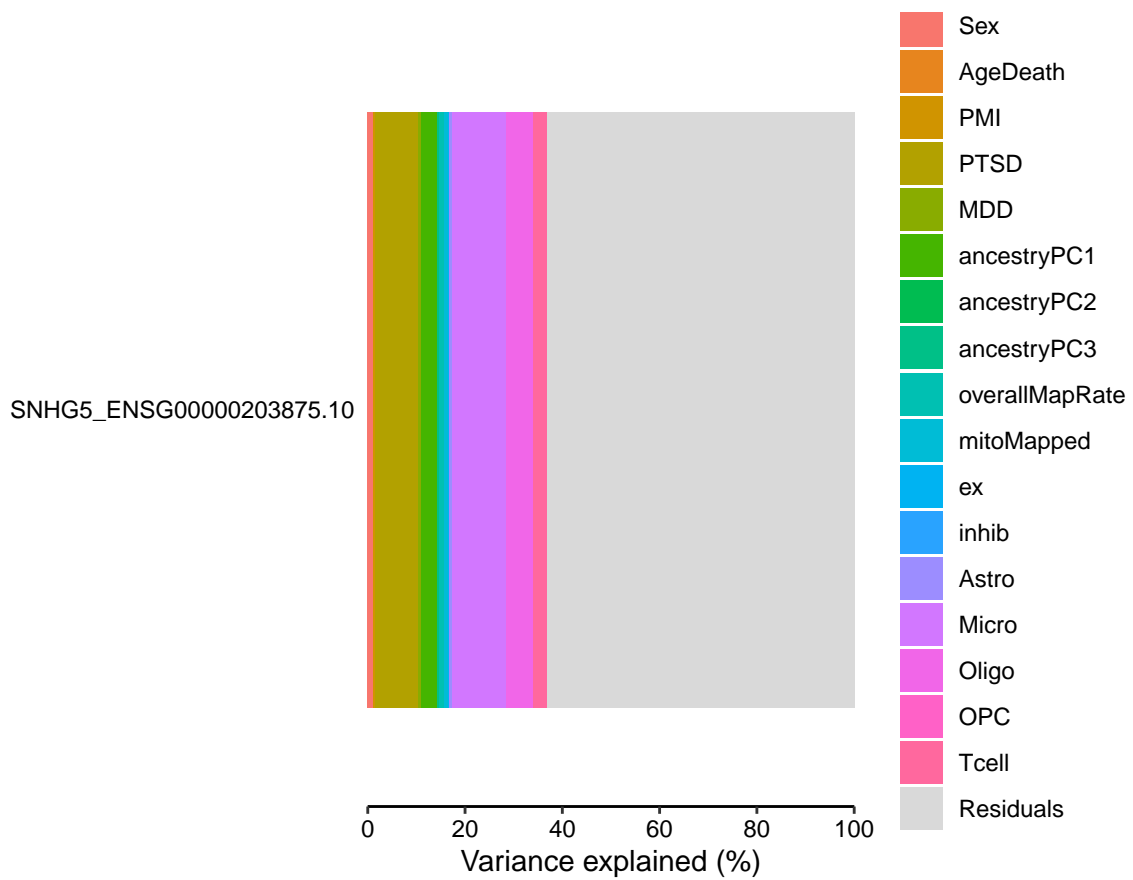
```
plotPercentBars(ca[startsWith(rownames(ca), "RP11-156L14.1"),])
```



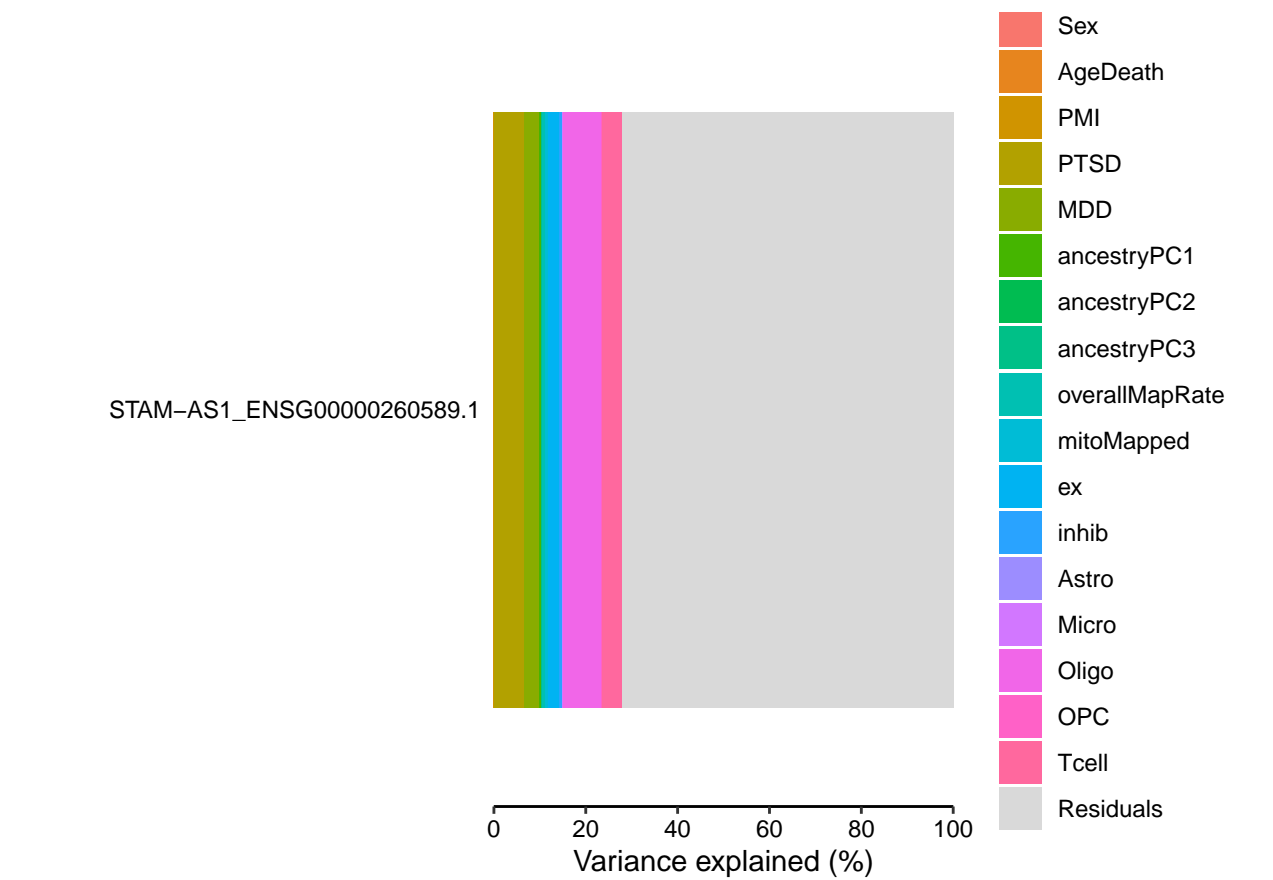
```
#####
# Top Genes PTSD DG #
#####
# SNHG5 (nom+)
# STAM-AS1 (nom-)
plotPercentBars(dg[startsWith(rownames(dg), "FKBP5"),])
```



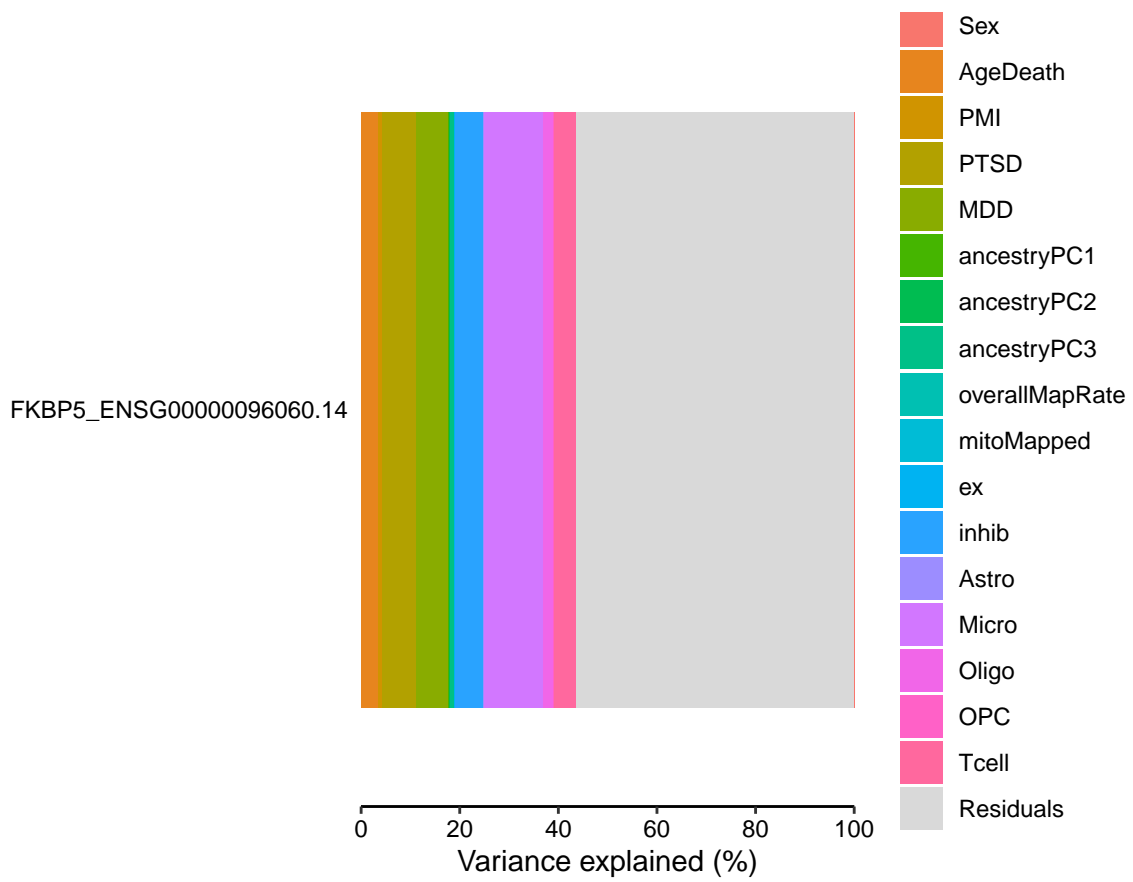
```
plotPercentBars(dg[startsWith(rownames(dg), "SNHG5"),])
```



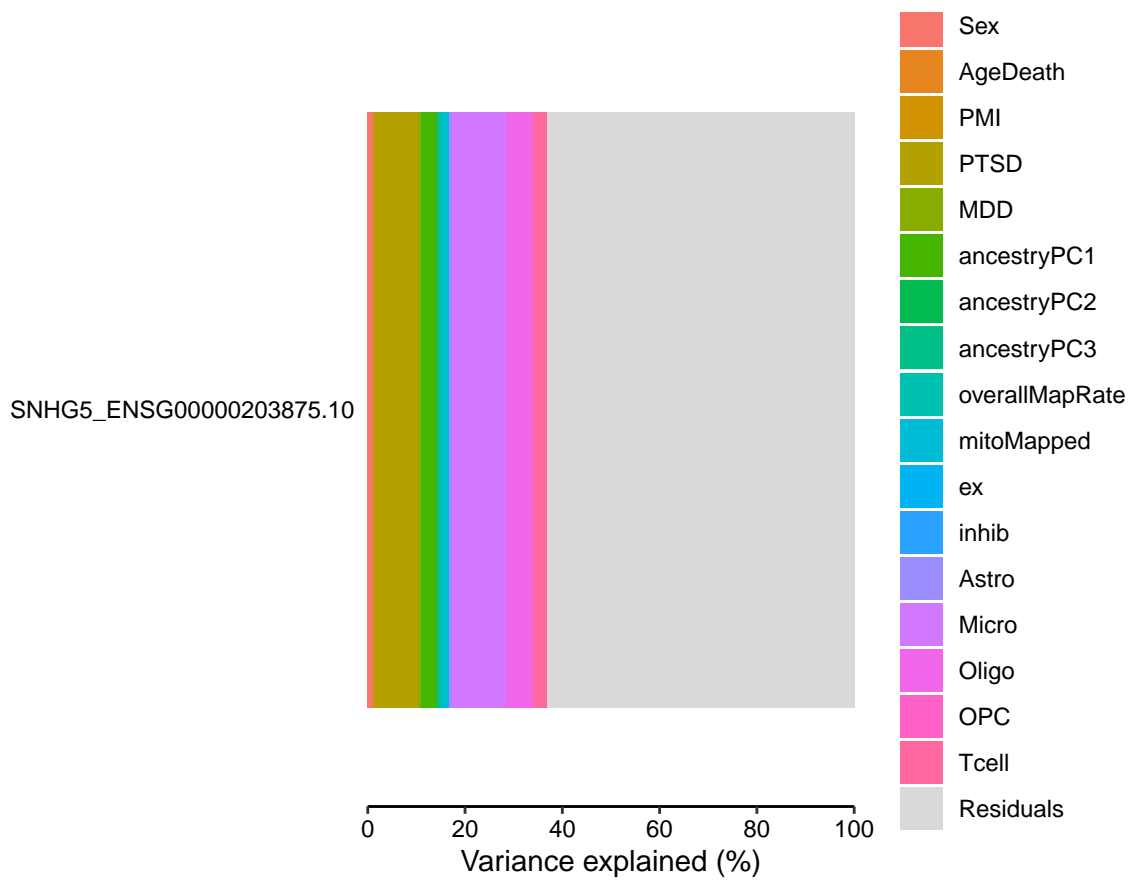
```
plotPercentBars(dg[startsWith(rownames(dg), "STAM-AS1"),])
```



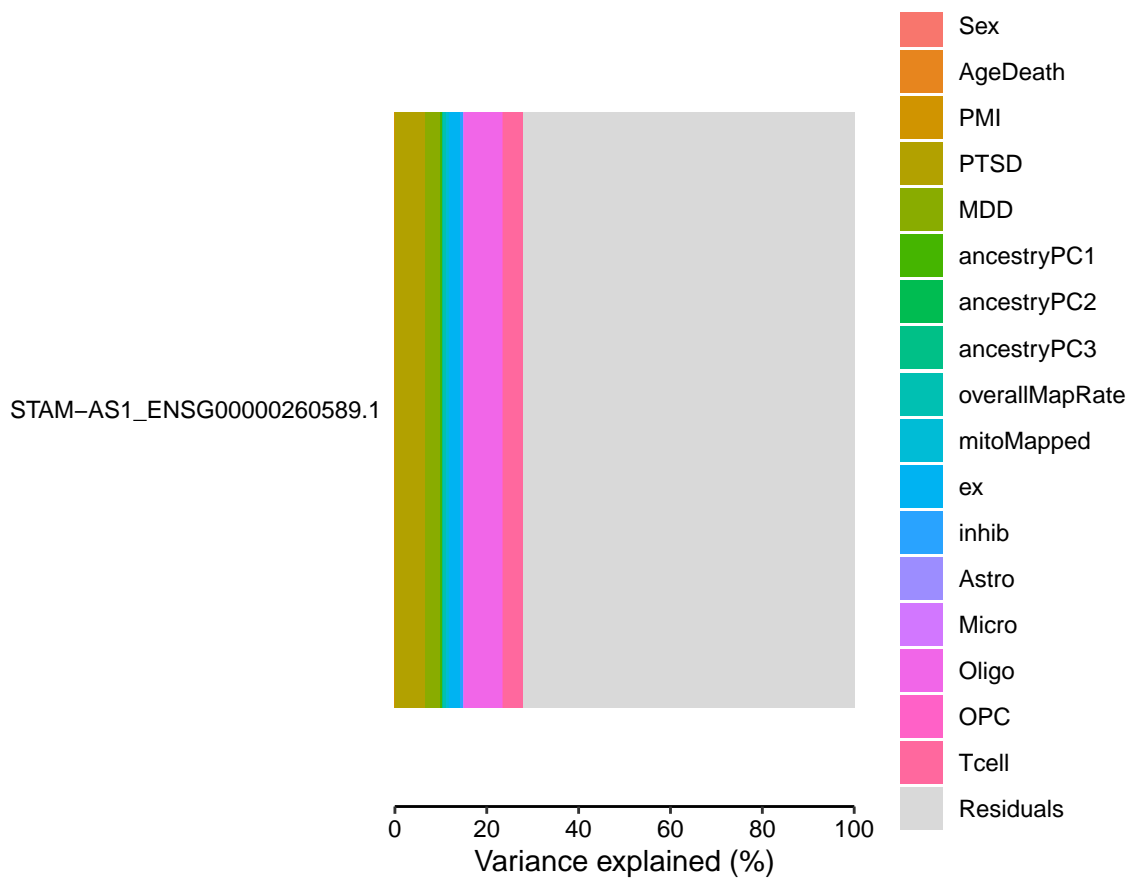
```
#####
# Top Genes MDD DG #
#####
# CLU (FDR+)
# TMBIM6 (FDR+)
# UBE2H (FDR+)
# THBS3 (FDR-)
# ZNF814 (FDR-)
# MPPED2 (FDR-)
plotPercentBars(dg[startsWith(rownames(dg), "FKBP5"),])
```



```
plotPercentBars(dg[startsWith(rownames(dg), "SNHG5"),])
```



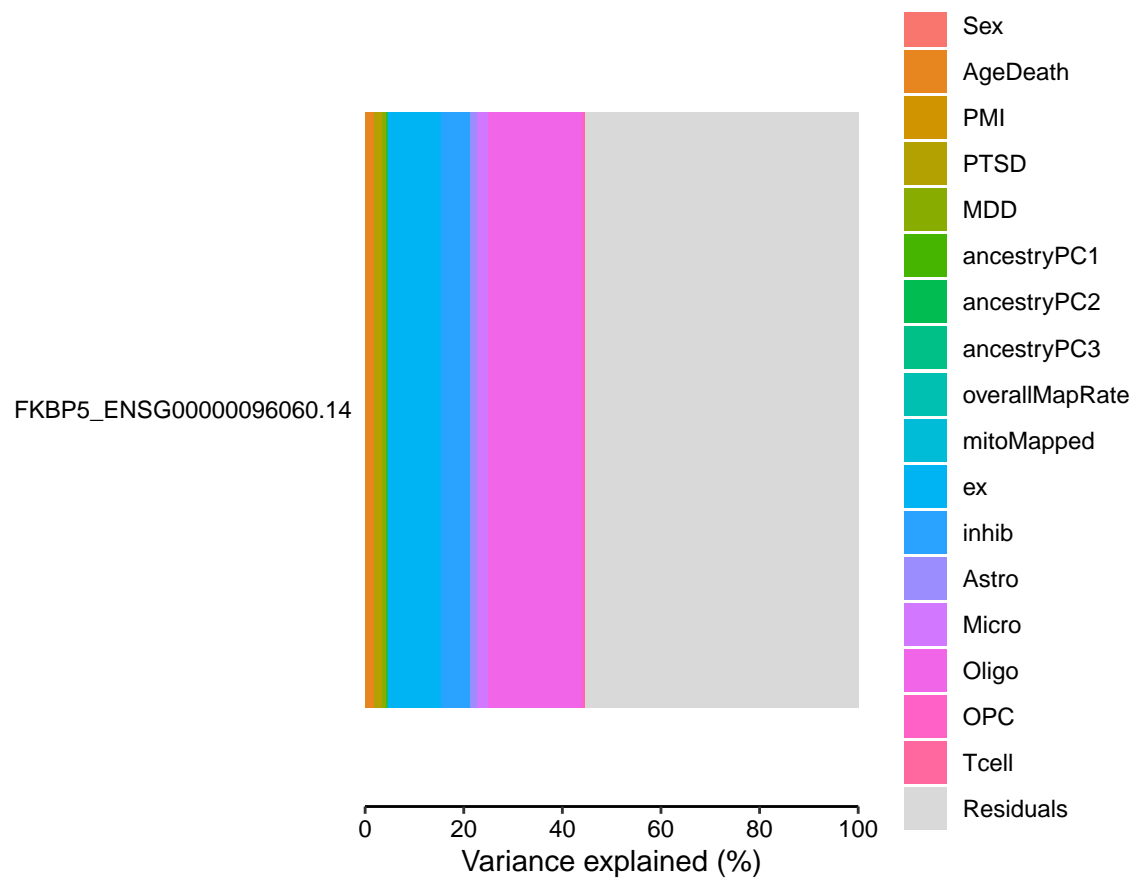
```
plotPercentBars(dg[startsWith(rownames(dg), "STAM-AS1"),])
```



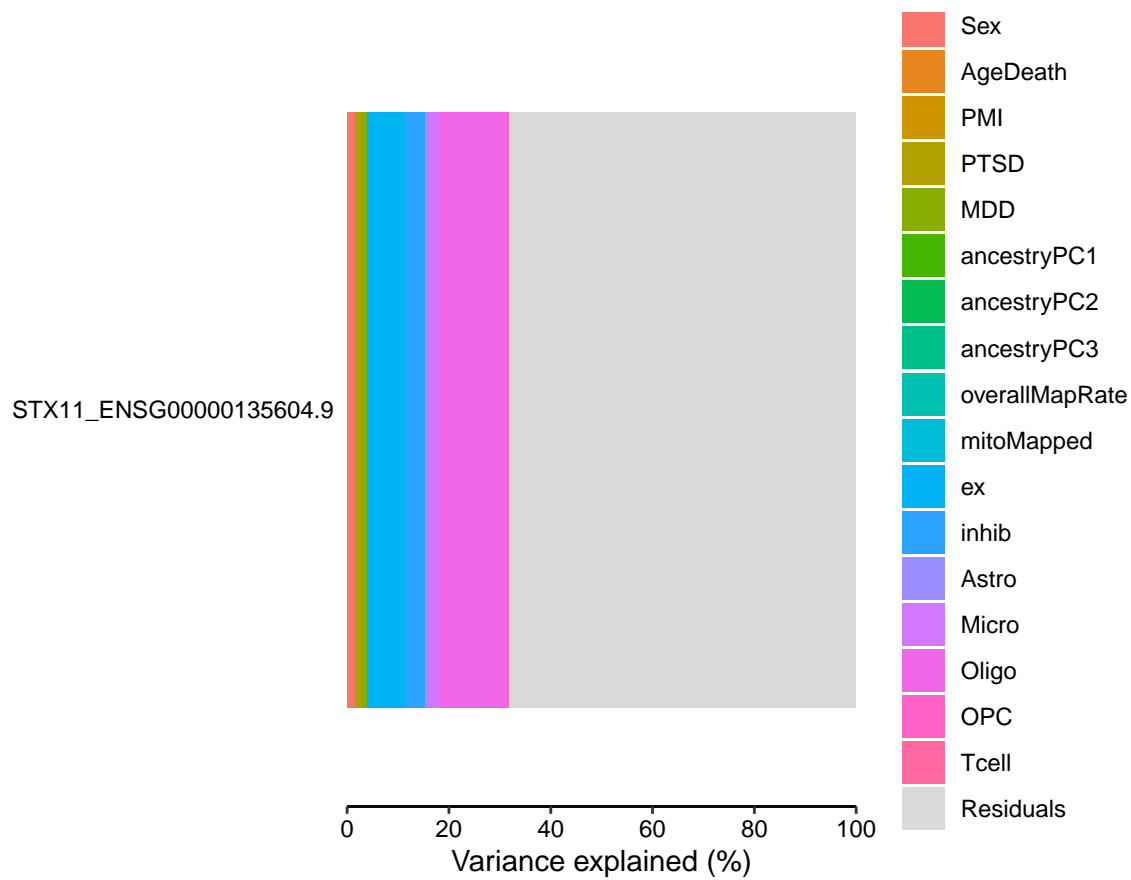
```
#####
# Top Genes PTSD mPFC #
#####
# STX11 (FDR+)
# RP11-413N10.3 (FDR-)
# CEBPB (FDR+)
# VASP (FDR+)
# STX3 (FDR-)
# SNX18P7 (FDR-)
```

```
plotPercentBars(mpfcs[startsWith(rownames(mpfcs), "FKBP5"),])
```

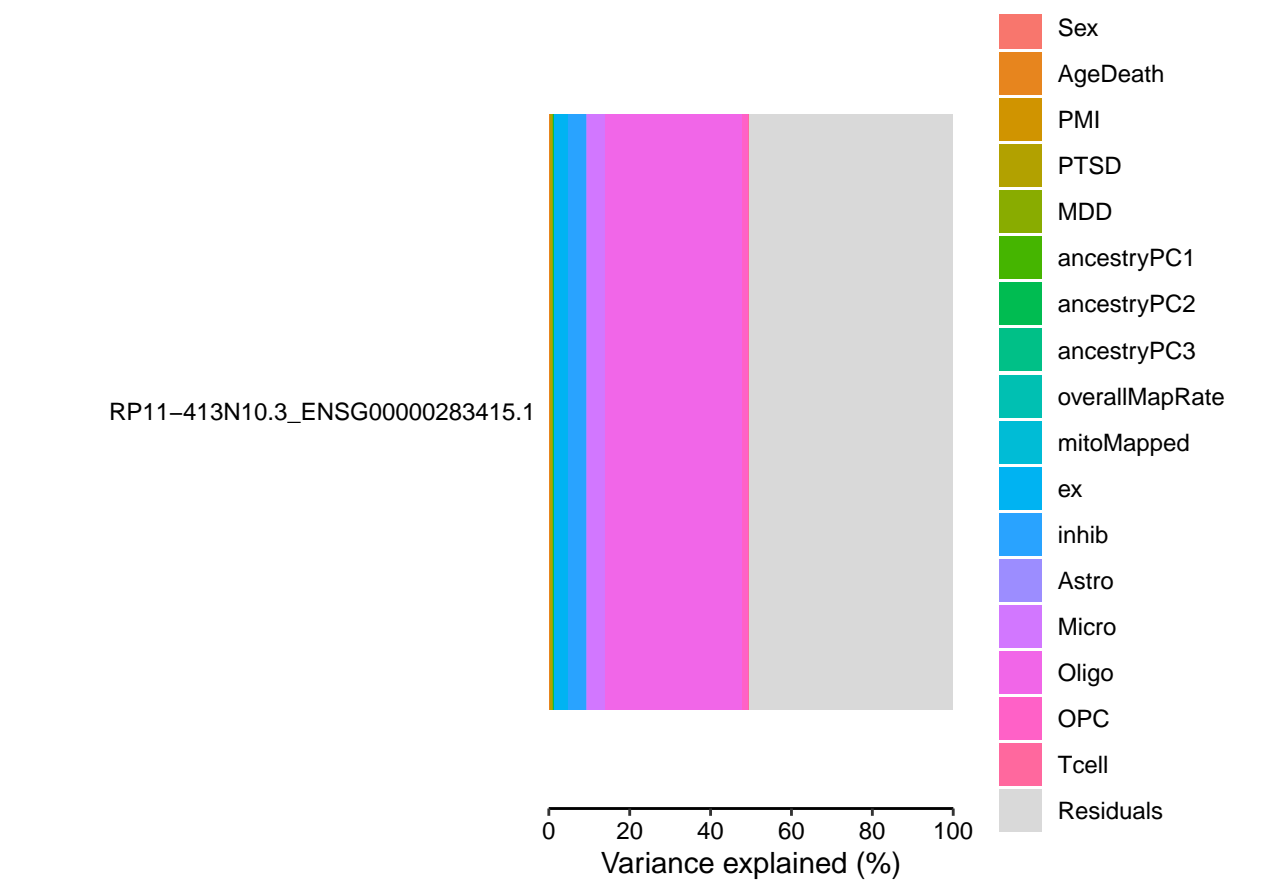




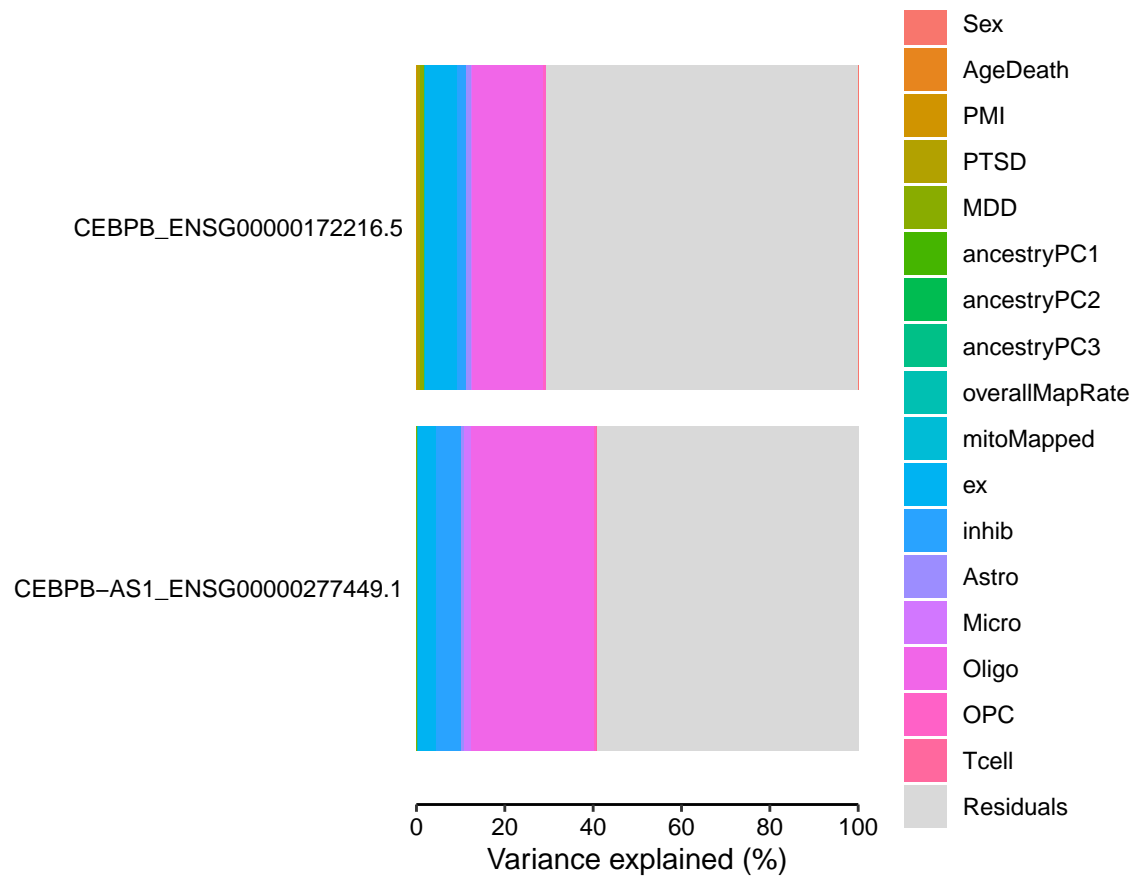
```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "STX11"),])
```



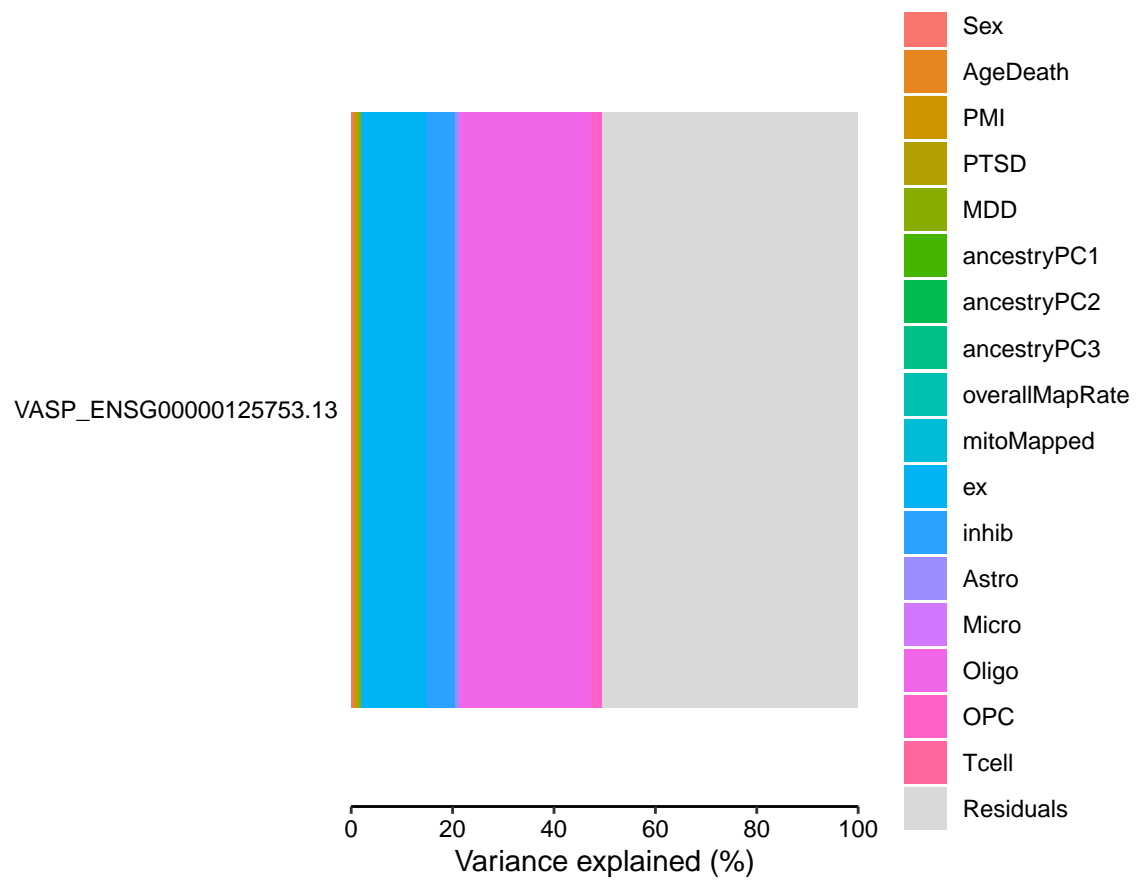
```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "RP11-413N10.3"),])
```



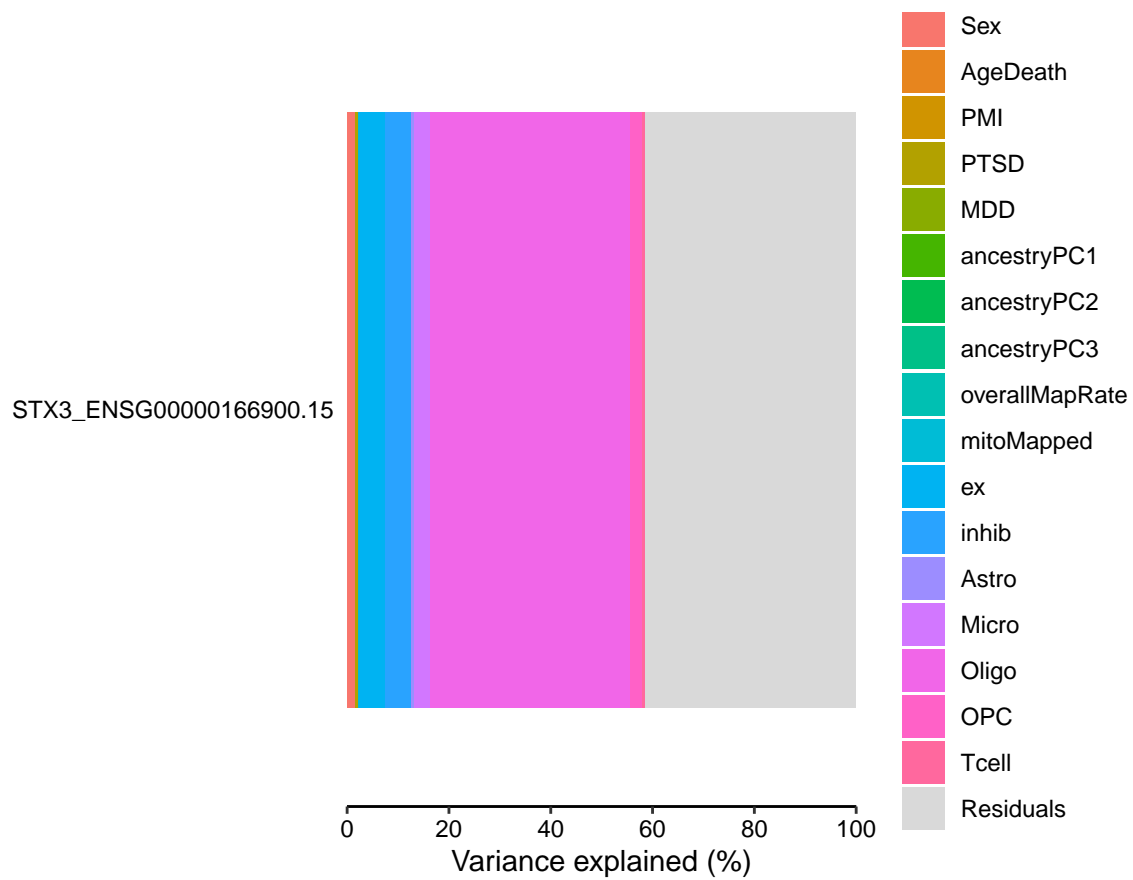
```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "CEBPB"),])
```



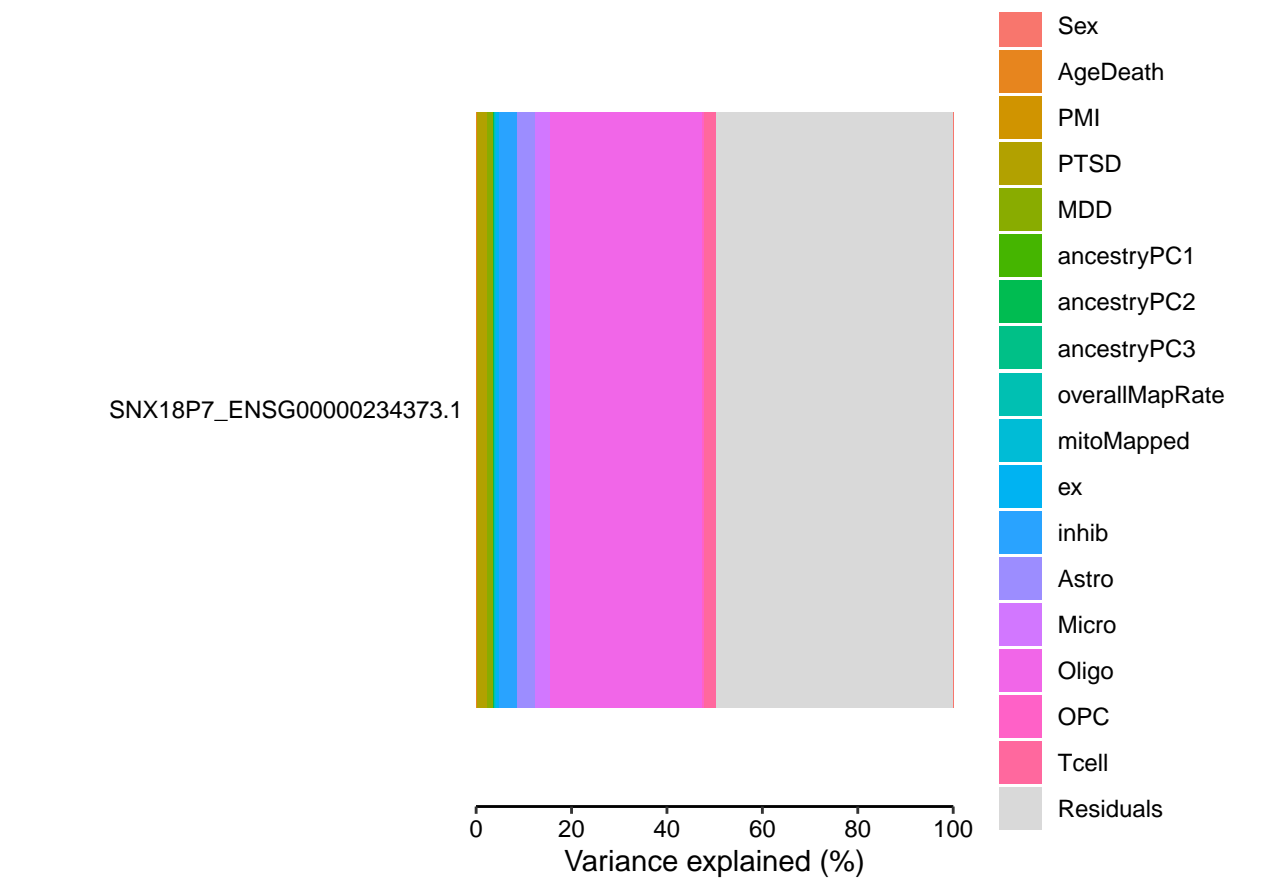
```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "VASP"),])
```



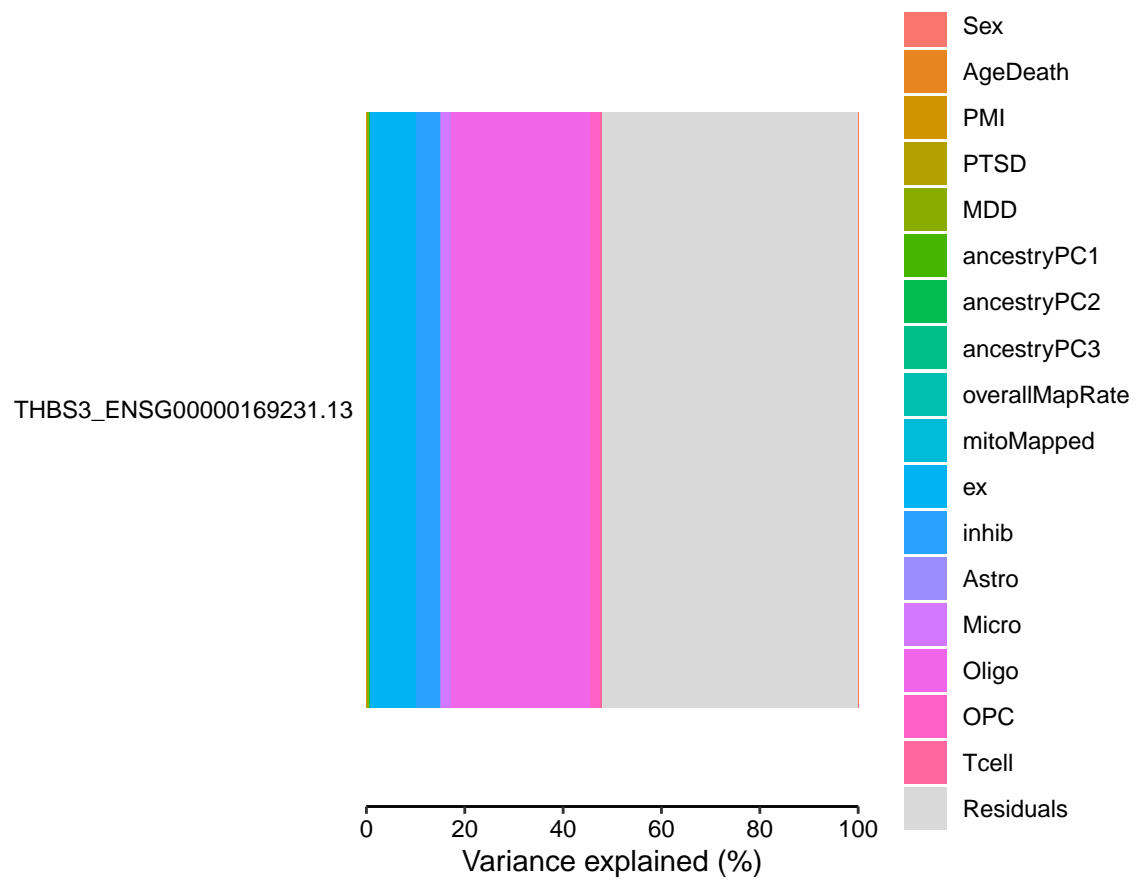
```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "STX3"),])
```



```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "SNX18P7"),])
```

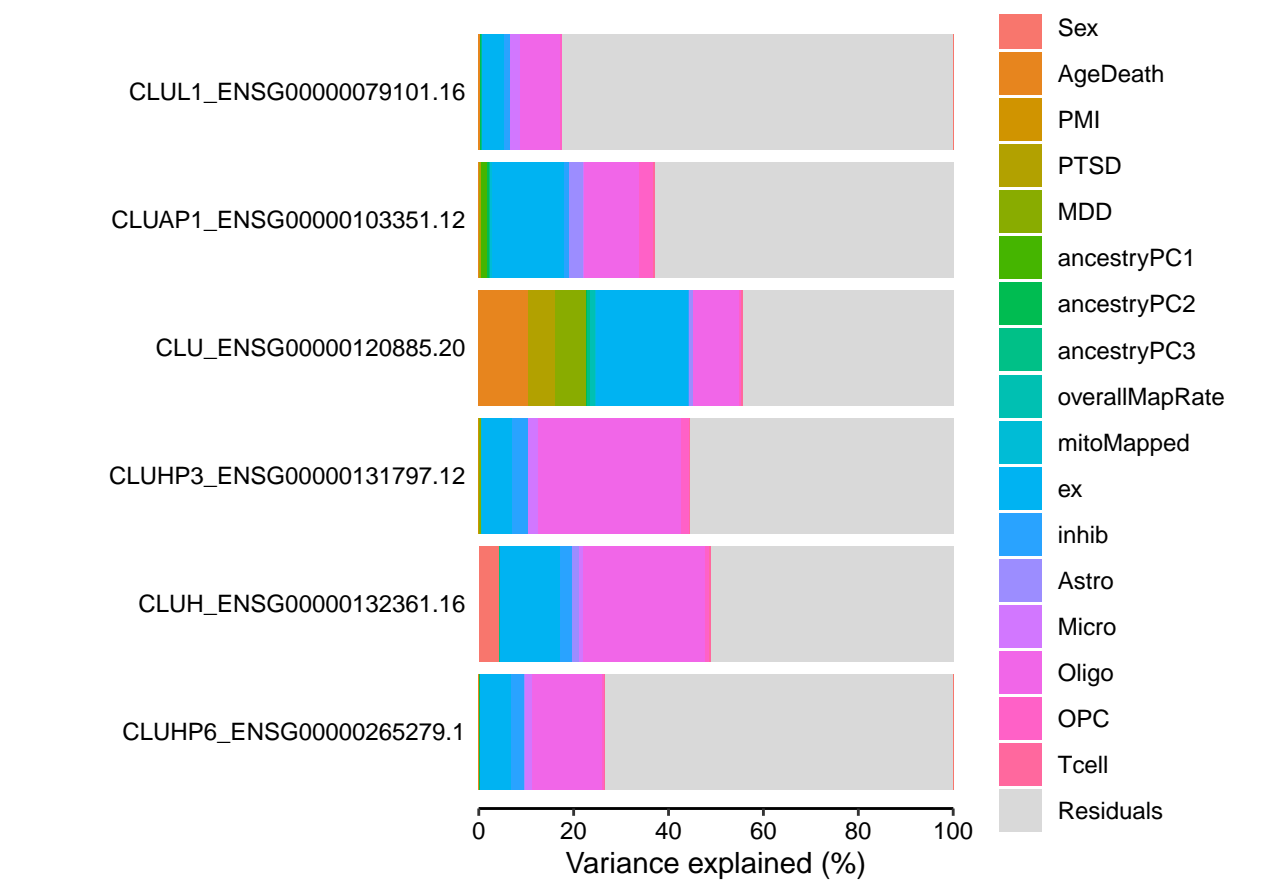


```
#####
# Top Genes MDD mPFC #
#####
# THBS3 (FDR-)
# CLU (FDR+)
# ZNF814 (FDR-)
# TMBIM6 (FDR+)
# MPPED2 (FDR-)
# UBE2H (FDR+)
plotPercentBars(mpfc[startsWith(rownames(mpfc), "THBS3"),])
```

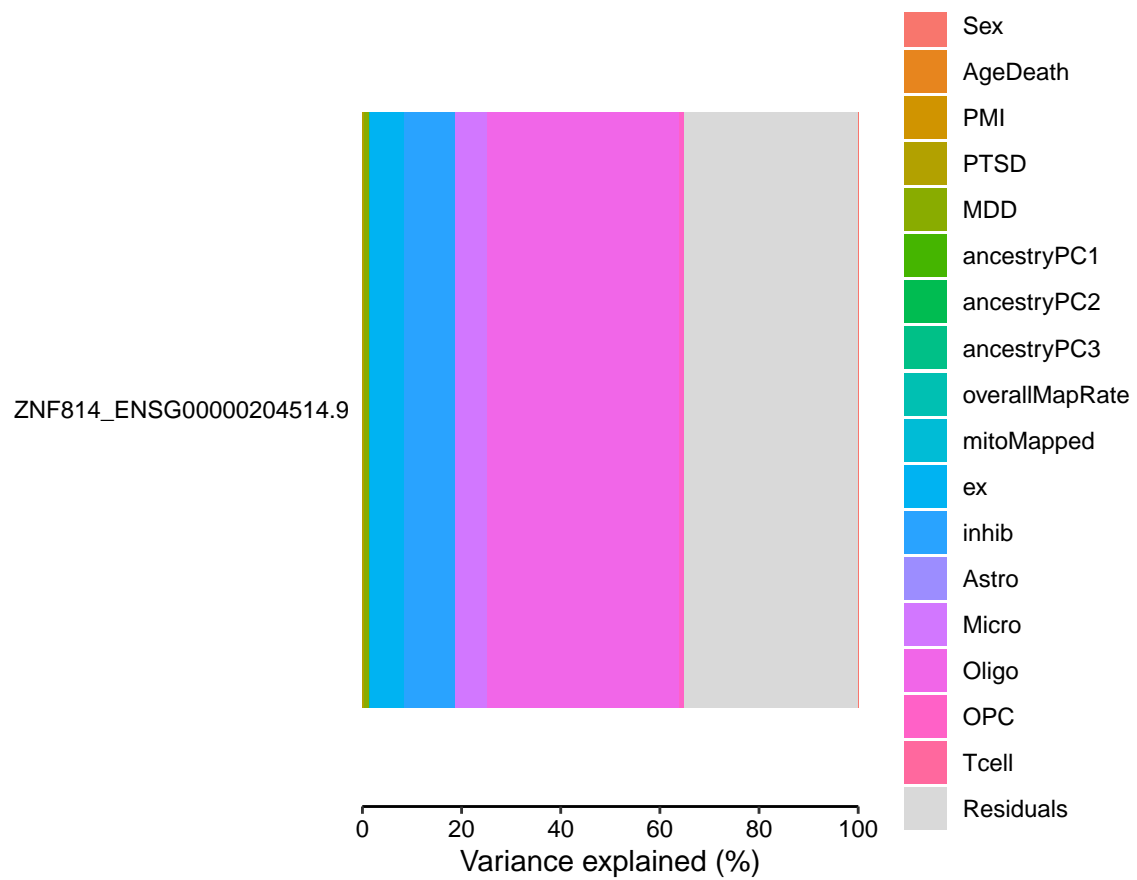


```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "CLU"),])
```

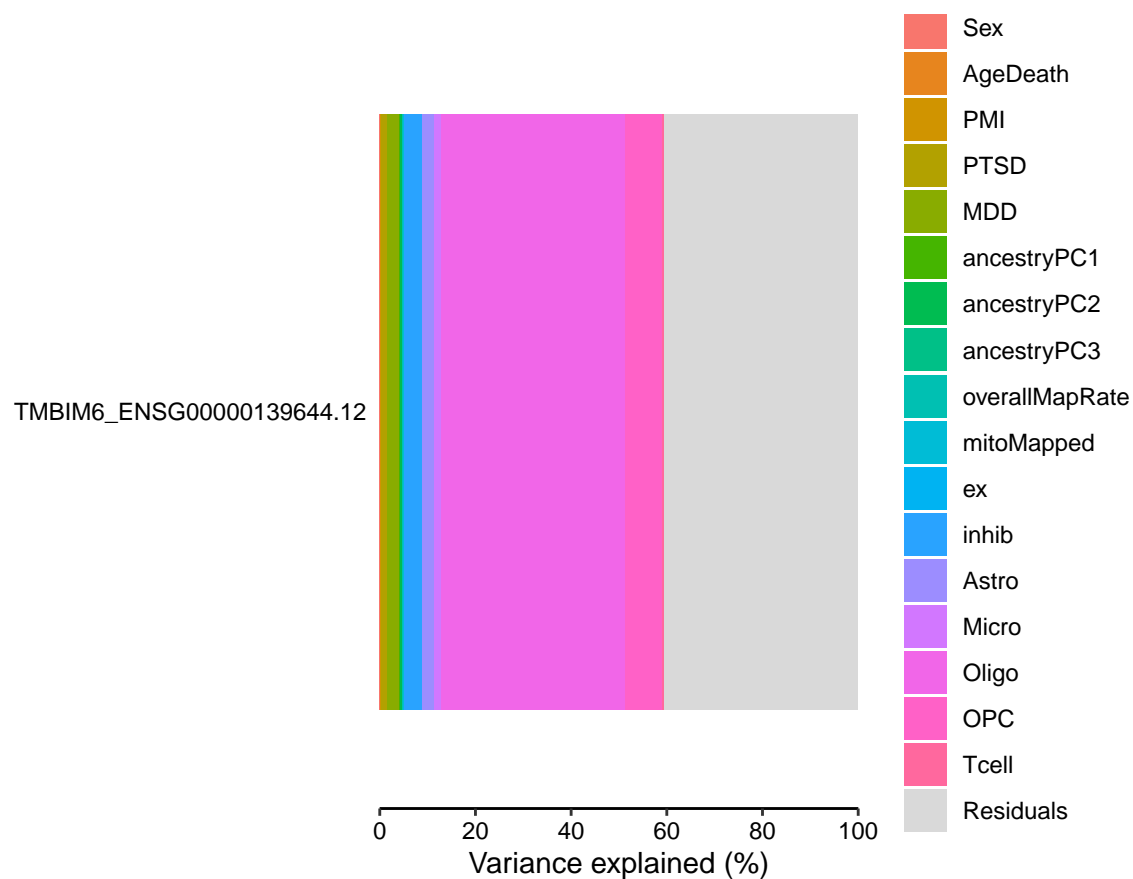




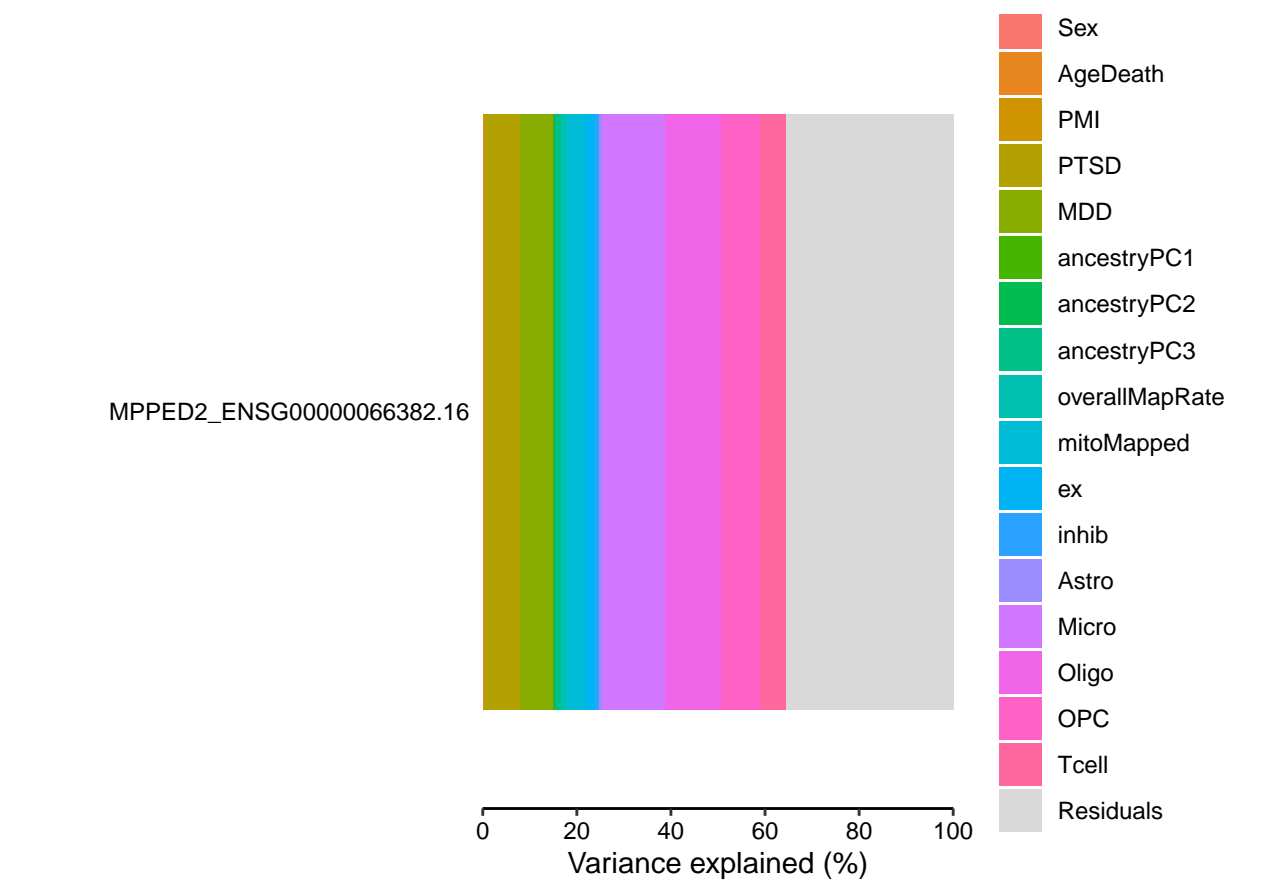
```
plotPercentBars(mpfcr[startsWith(rownames(mpfcr), "ZNF814"),])
```



```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "TMBIM6"),])
```



```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "MPPED2"),])
```



```
plotPercentBars(mpfc[startsWith(rownames(mpfc), "UBE2H"),])
```

