Figure4

This is using the matrix of correlated residuals

```
library('knitr')

library('rmeta')
```

```
## Loading required package: grid
#knitr::opts_chunk$set(cache = TRUE,collapse = TRUE,comment = "#",
#                        fig.path = "figures/Figure3.Rmd",fig.align = "center",
#                        fig.width = 8,fig.height = 6,fig.path = #"/Users/sarahurbut/Dropbox/PaperEdits/P
```

**In this file, we make the metaplots demonstrating the original effects and the posterior estimates.**

Our first example is MCPH1: original estimates and then posteriors:

```
###
three.ex.3=which(rownames(z.stat)=="ENSG00000249898.3_8_6521432_T_C_b37")
newfunc.2(three.ex.3)
```



```
whole.blood.spec=which(rowSums(pm.beta.norm[,-44]<0.5)==43&(rowSums(lfsr[,1:44]<0.05)>=40))
```
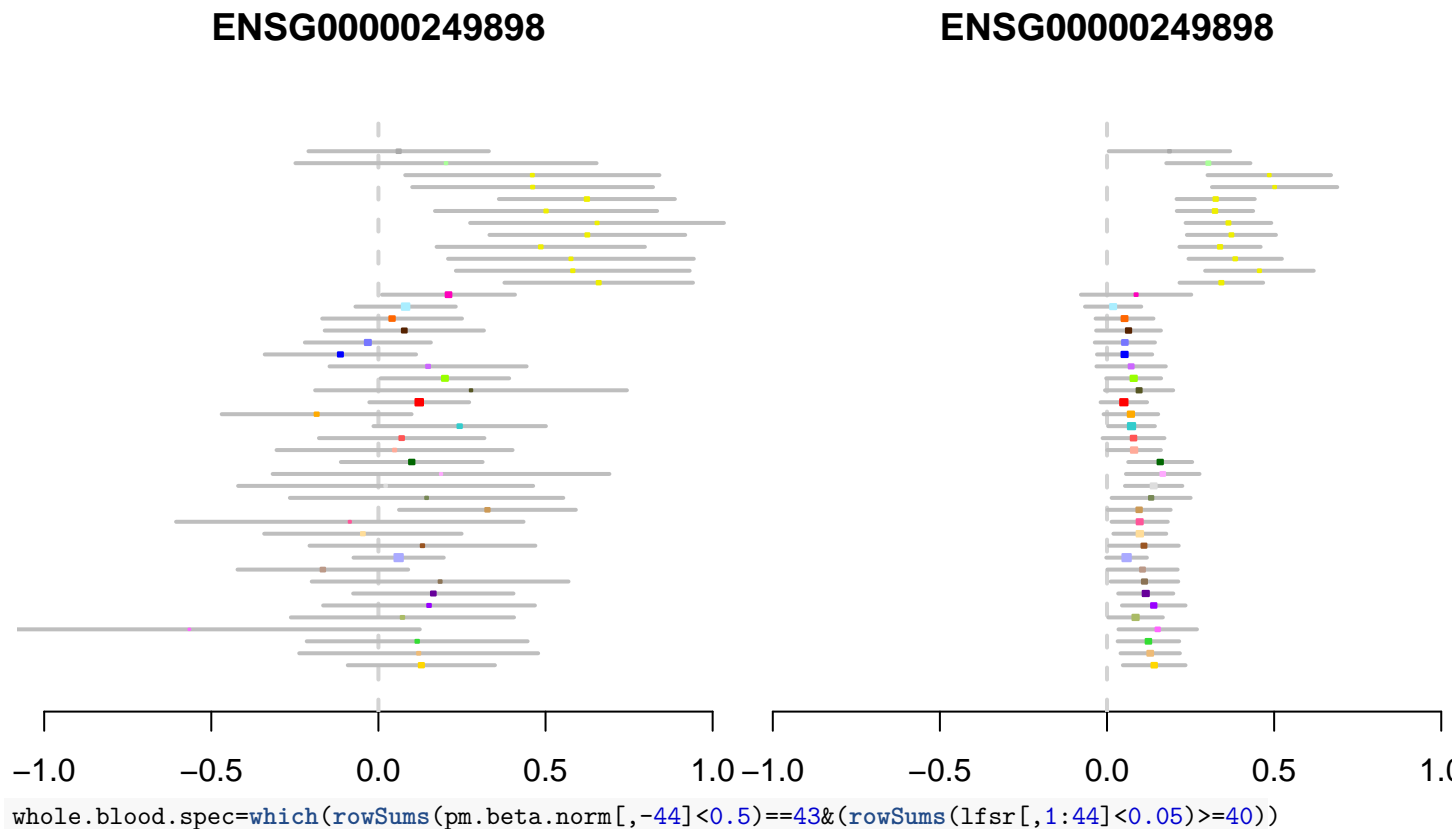
FLJ13114

```
###
five.ex=which(rownames(z.stat)=="ENSG00000120029.8_10_103924251_G_A_b37")
testes.spec=which(rowSums(pm.beta.norm[,-40]<0.5)==43&(rowSums(lfsr[,1:44]<0.05)>=40))[1:10]

newfunc.2(five.ex)
```

ENSG00000120029   **ENSG00000120029**
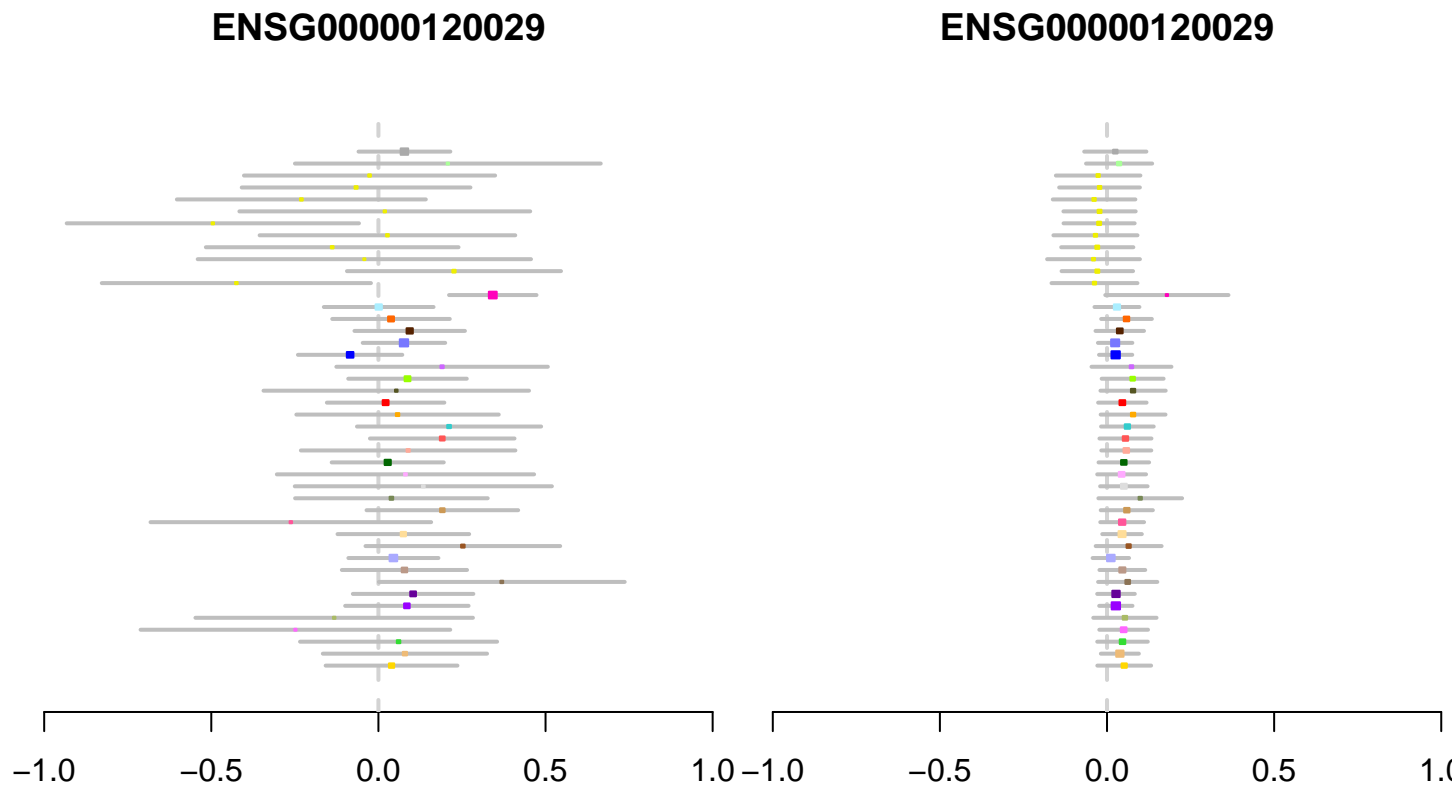
RALBP1

```
###
wholebloodfour=(which(rownames(z.stat)=="ENSG00000017797.7_18_9488704_C_T_b37"))
newfunc.2(wholebloodfour)
```

ENSG00000017797   **ENSG00000017797**