

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/Pap
```

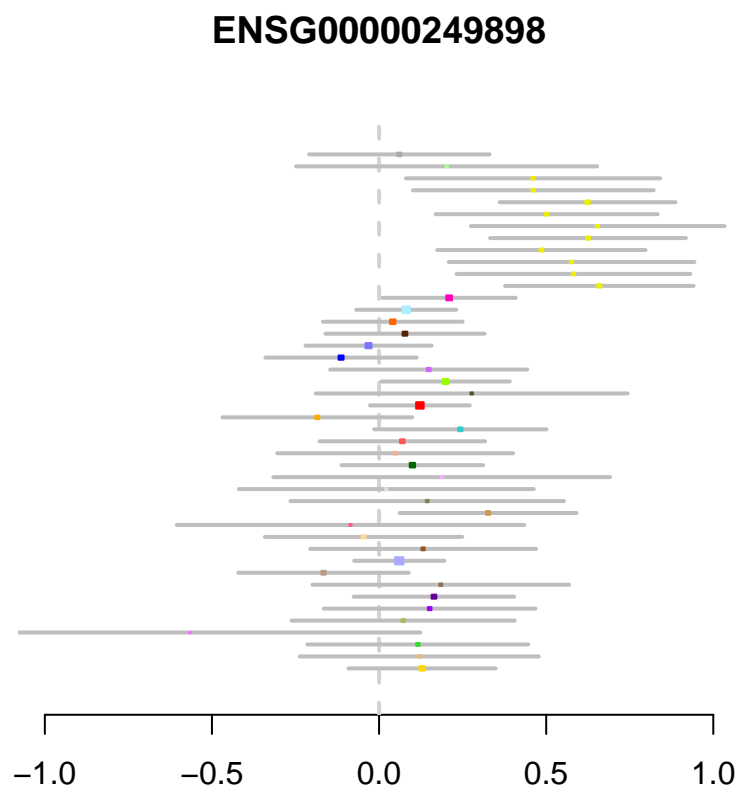
In this file, we make the metaplots demonstrating the original effects and the posterior estimates.

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

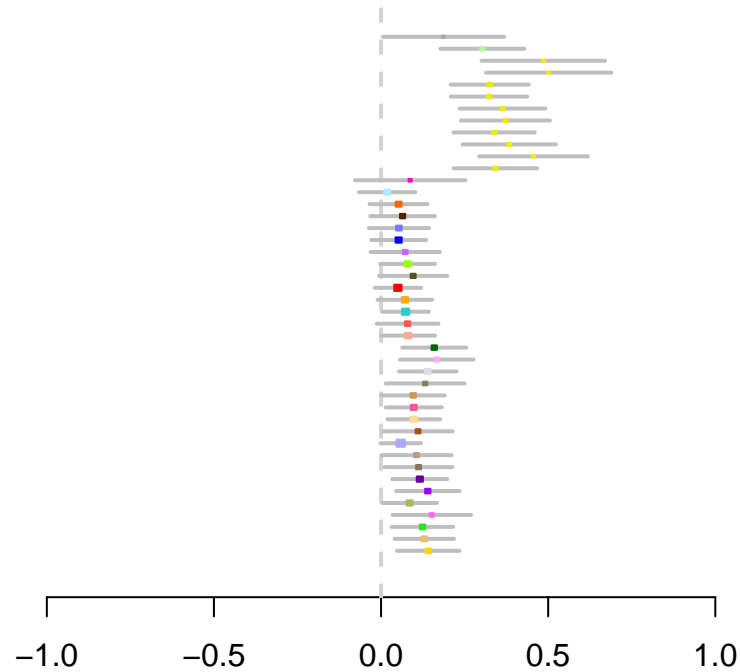
```
###
```

```
three.ex.3=which(rownames(z.stat)=="ENSG00000249898.3\_8\_6521432\_T\_C\_b37")
```

```
newfunc.2(three.ex.3)
```



ENSG00000249898



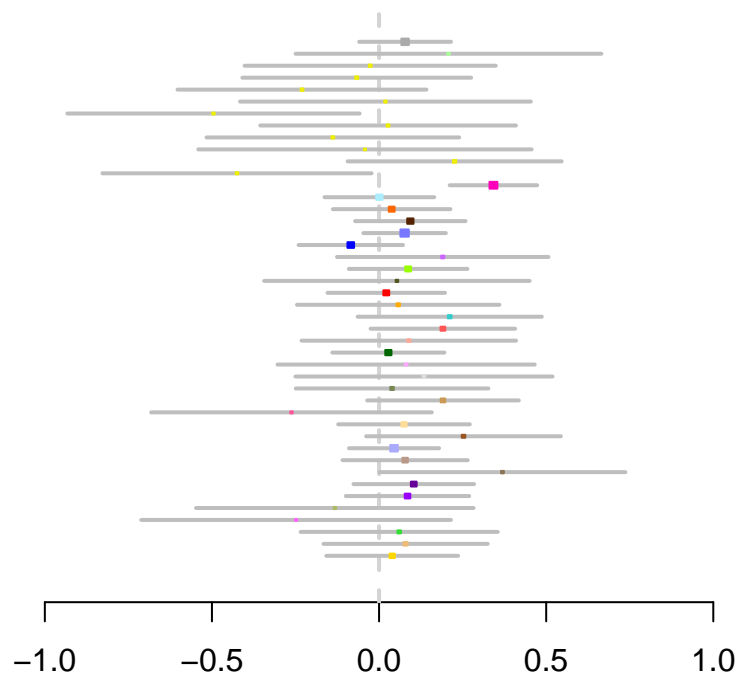
```
whole.blood.spec=which(rowSums(pm.beta.norm[, -44] < 0.5) == 43 & (rowSums(lfsr[, 1:44] < 0.05) >= 40))
```

FLJ13114

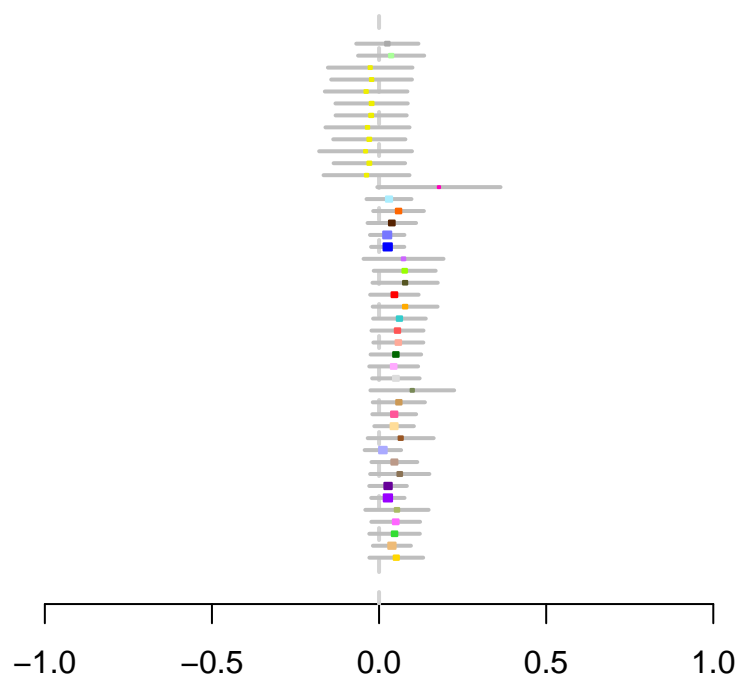
```
###
five.ex=which(rownames(z.stat) == "ENSG00000120029.8_10_103924251_G_A_b37")
testes.spec=which(rowSums(pm.beta.norm[, -40] < 0.5) == 43 & (rowSums(lfsr[, 1:44] < 0.05) >= 40)) [1:10]

newfunc.2(five.ex)
```

ENSG00000120029



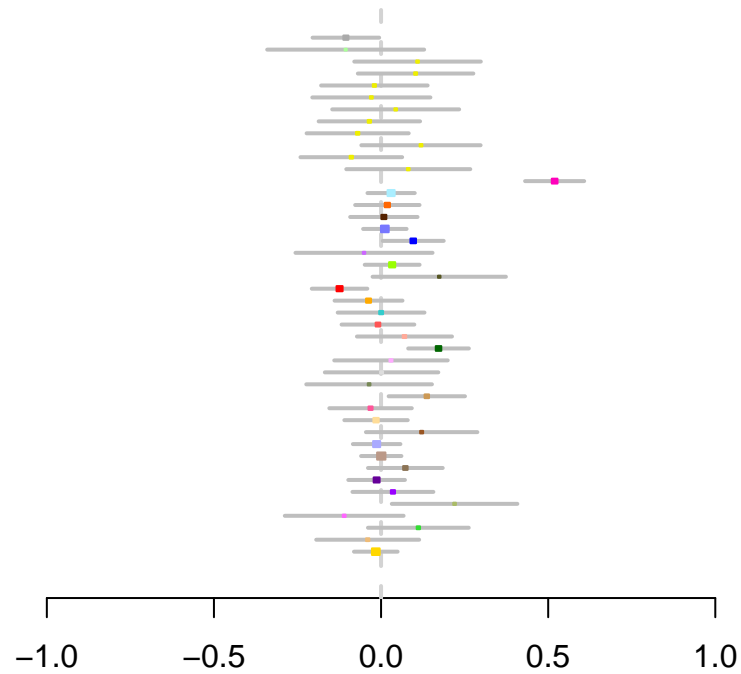
ENSG00000120029



RALBP1

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

ENSG00000017797



ENSG00000017797

