Figures

Figure 1: Boxplots including raw data for two selected SNPs and phenotypes of the Bogalusa Heart Study.

Figure 2: QQ- and Manhattan-plot for the phenotype waist circumference in the Bogalusa Heart Study.

Tables

Additional Files

The R code

The data set `tg` contains the subject-specific diastolic blood pressure data and the related genotype level, see Table 5.

PLEASE INCLUDE TABLE 5 about here

```r
medrs12607553<- tapply(tg$dbp, tg$rs12607553, median) # group-specific medians
medrs12607553V< - medrs12607553[as.integer(tg$rs12607553)] # median for each subject
tg$tdbp<- abs(tg$dbp-medrs12607553) # Levene transformation

library(multcomp)

lrs12607553< - lm(tdbp~rs12607553, data=tg) # fit one-way ANOVA linear model
summary(glht(lrs12607553, linfct=mcp(rs12607553 = "AVE"), test=adjusted(maxpts=2500000, abseps=1e-10)))$test$Pvalues # MCT-average
summary(glht(lrs12607553, linfct=mcp(rs12607553 = "Tukey"), test=adjusted(maxpts=2500000, abseps=1e-10)))$test$Pvalues # MCT pairs
```