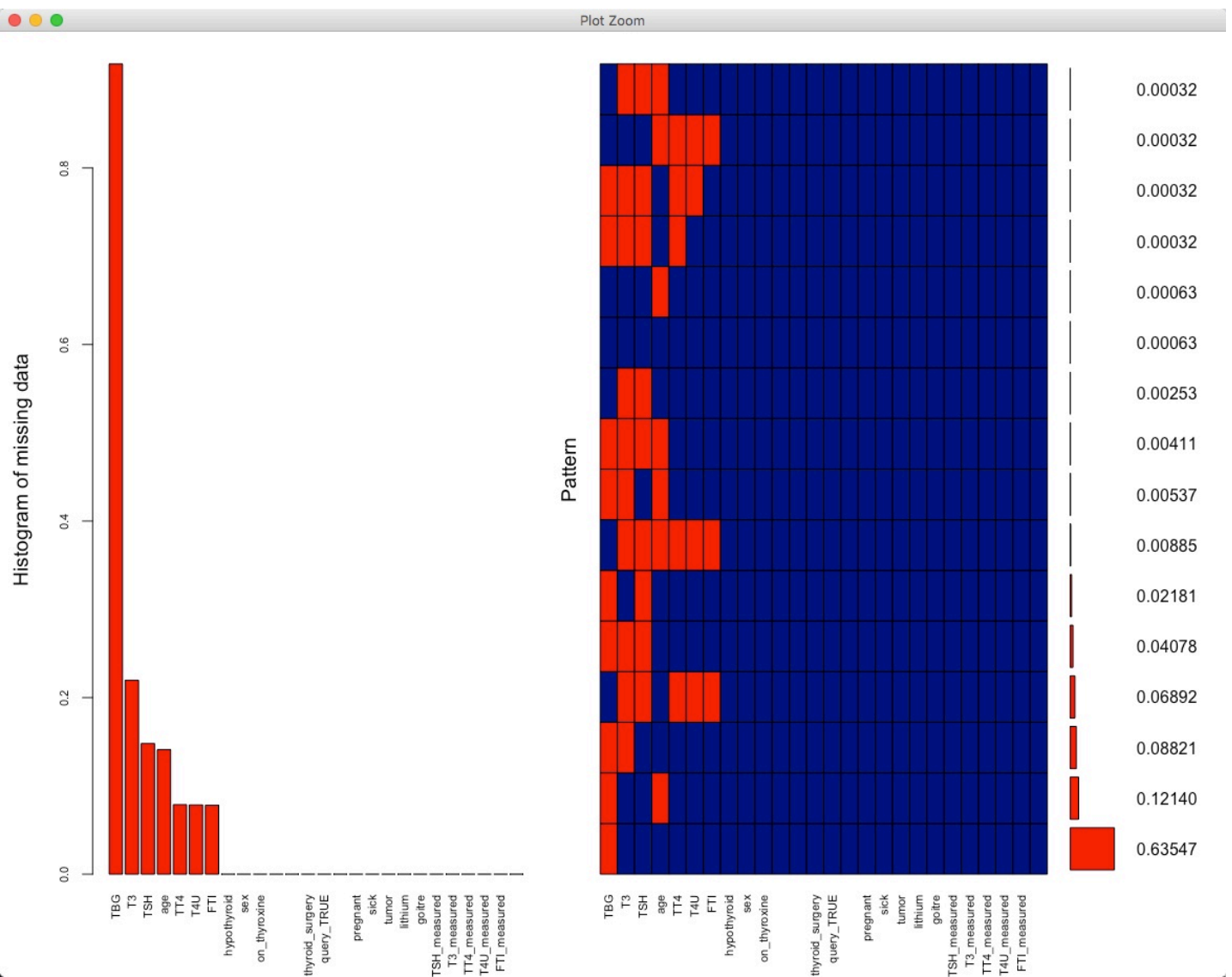
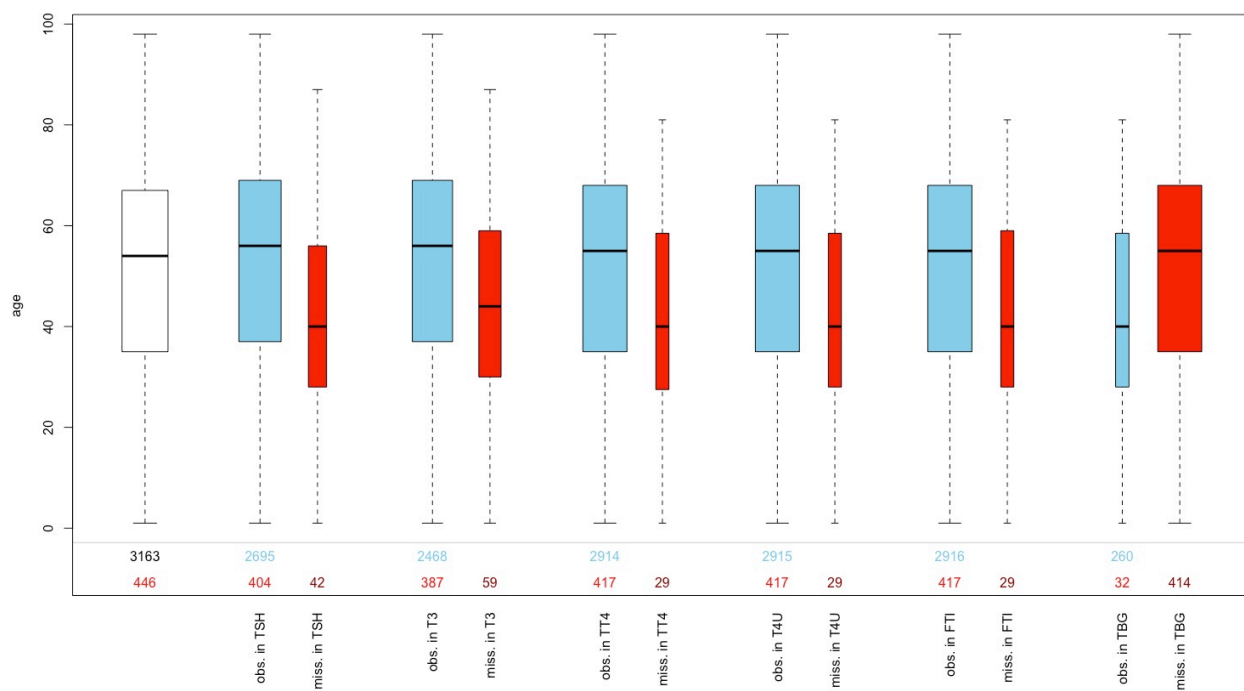
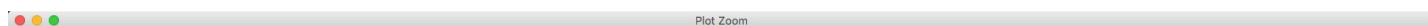
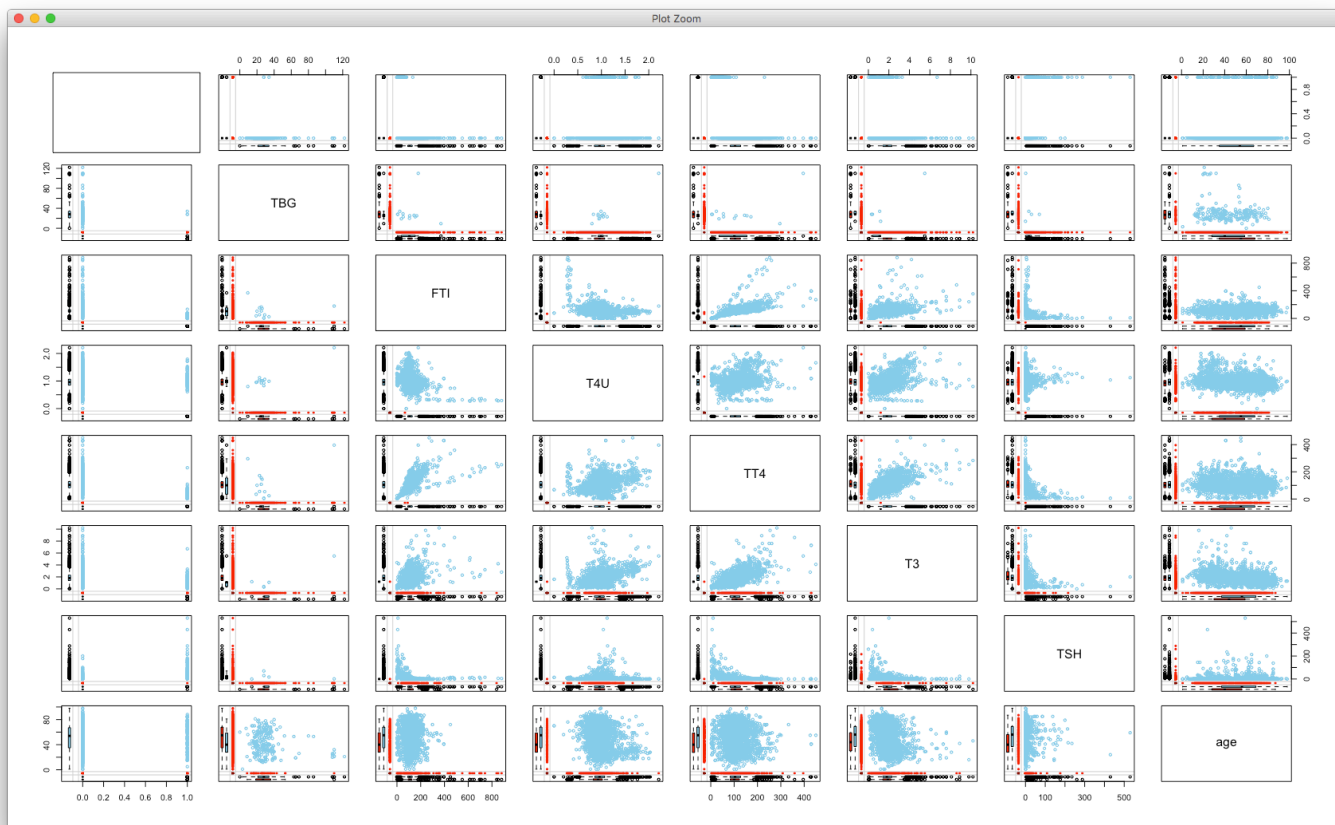
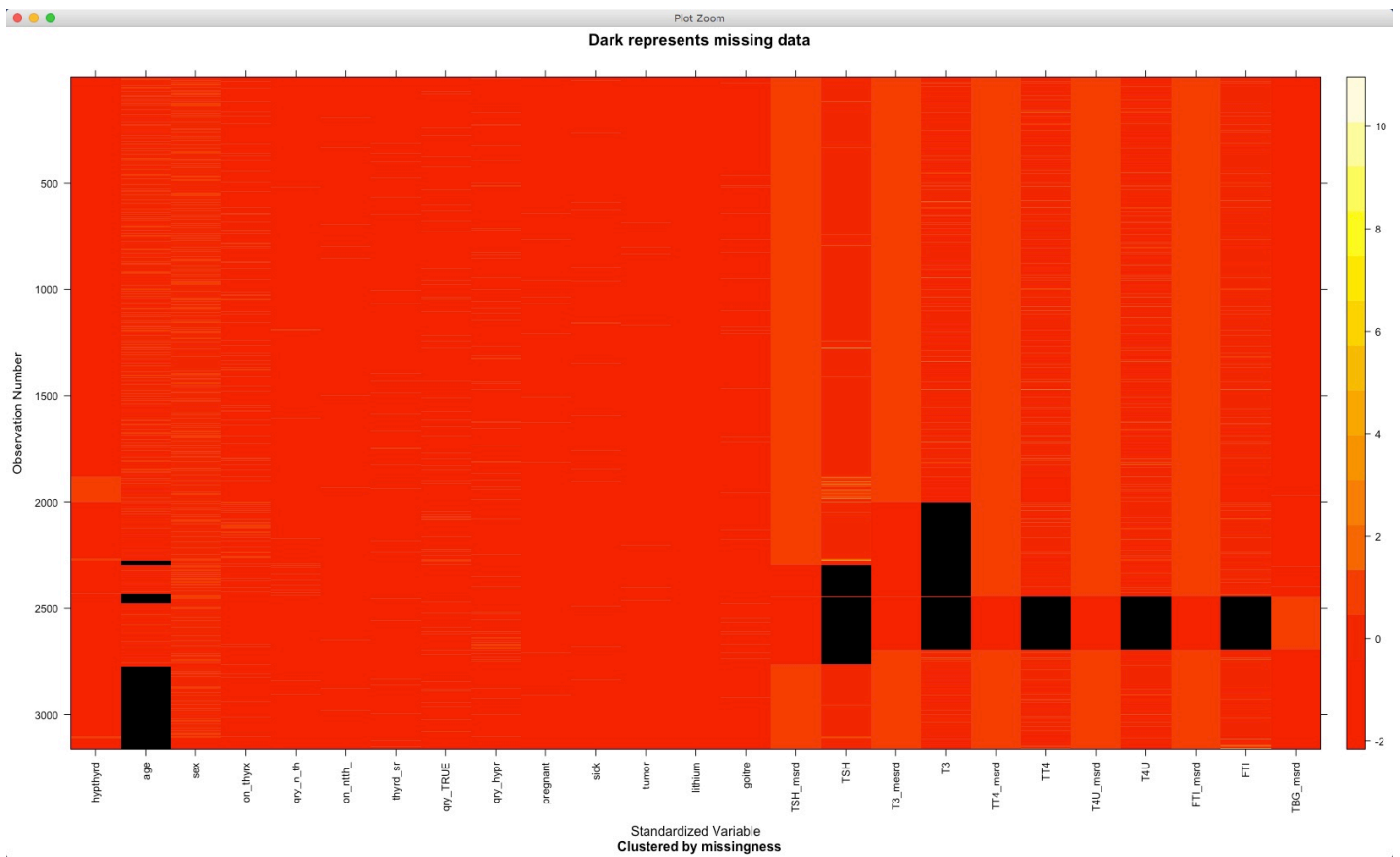


hypothyroid

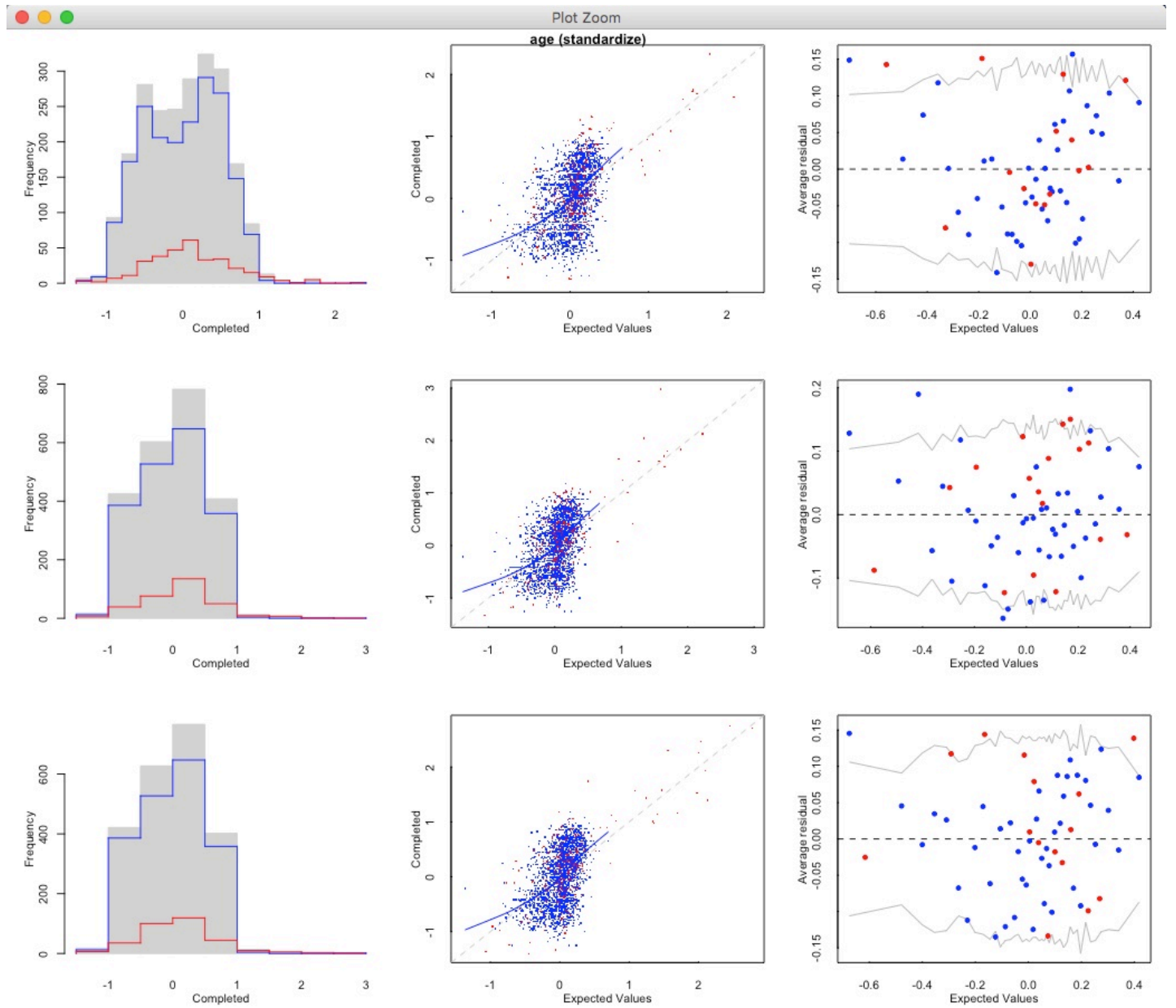
```
1 dat <- read.csv("Data/hypothyroid_1109.csv")
2
3 library(Hmisc)
4 describe(dat)
5
6 library(mice)
7 md.pattern(dat)
8 # md.pairs(dat)
9 flux(dat)
10 fluxplot(dat)
11
12 library(VIM)
13 aggr_plot <- aggr(dat, col=c('navyblue','red'), numbers=TRUE, sortVars=TRUE, labels=names(data), cex.axis=.7, gap=3, ylab=c("Histogram of missing data", "Pattern"))
```

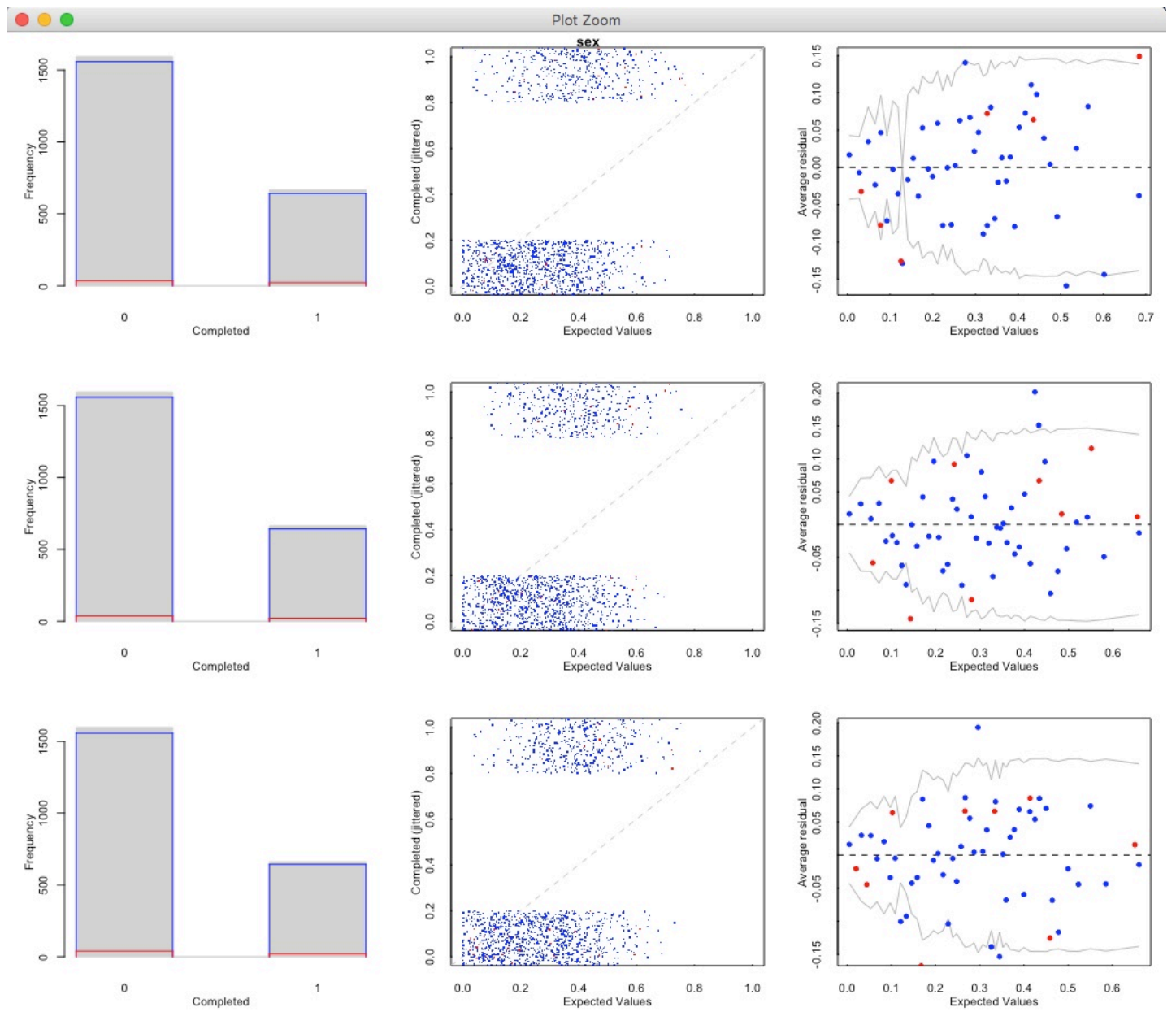


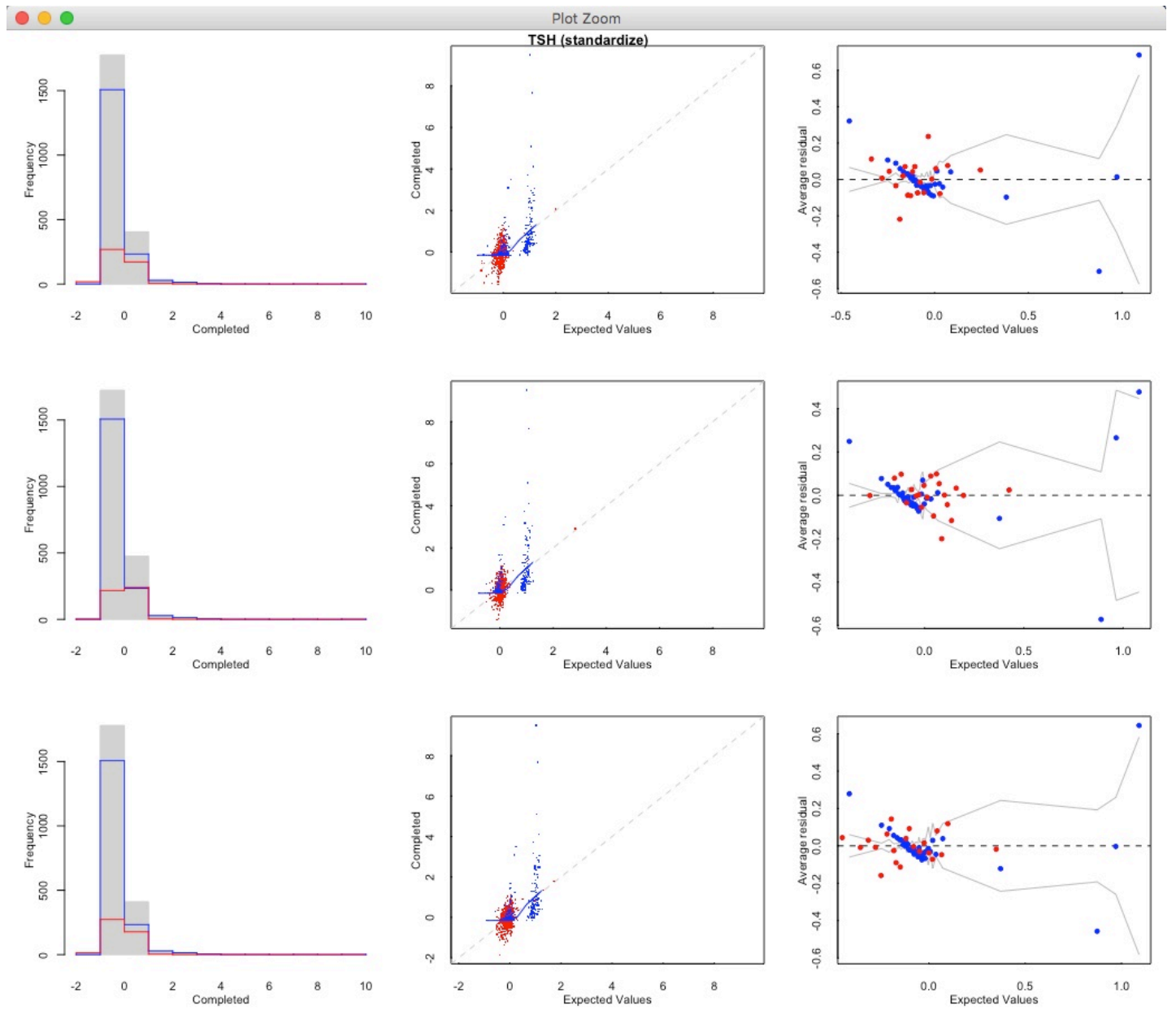


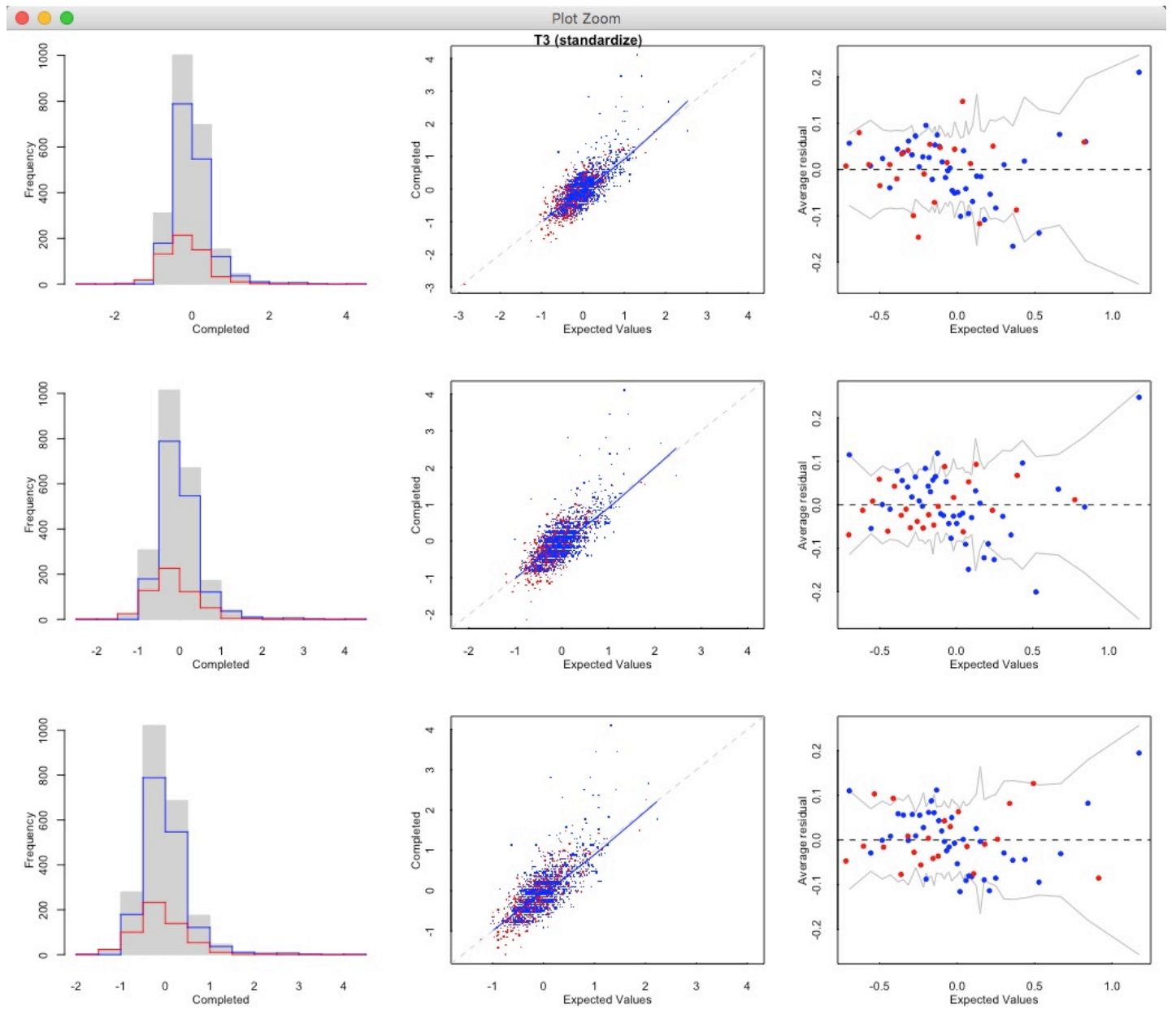


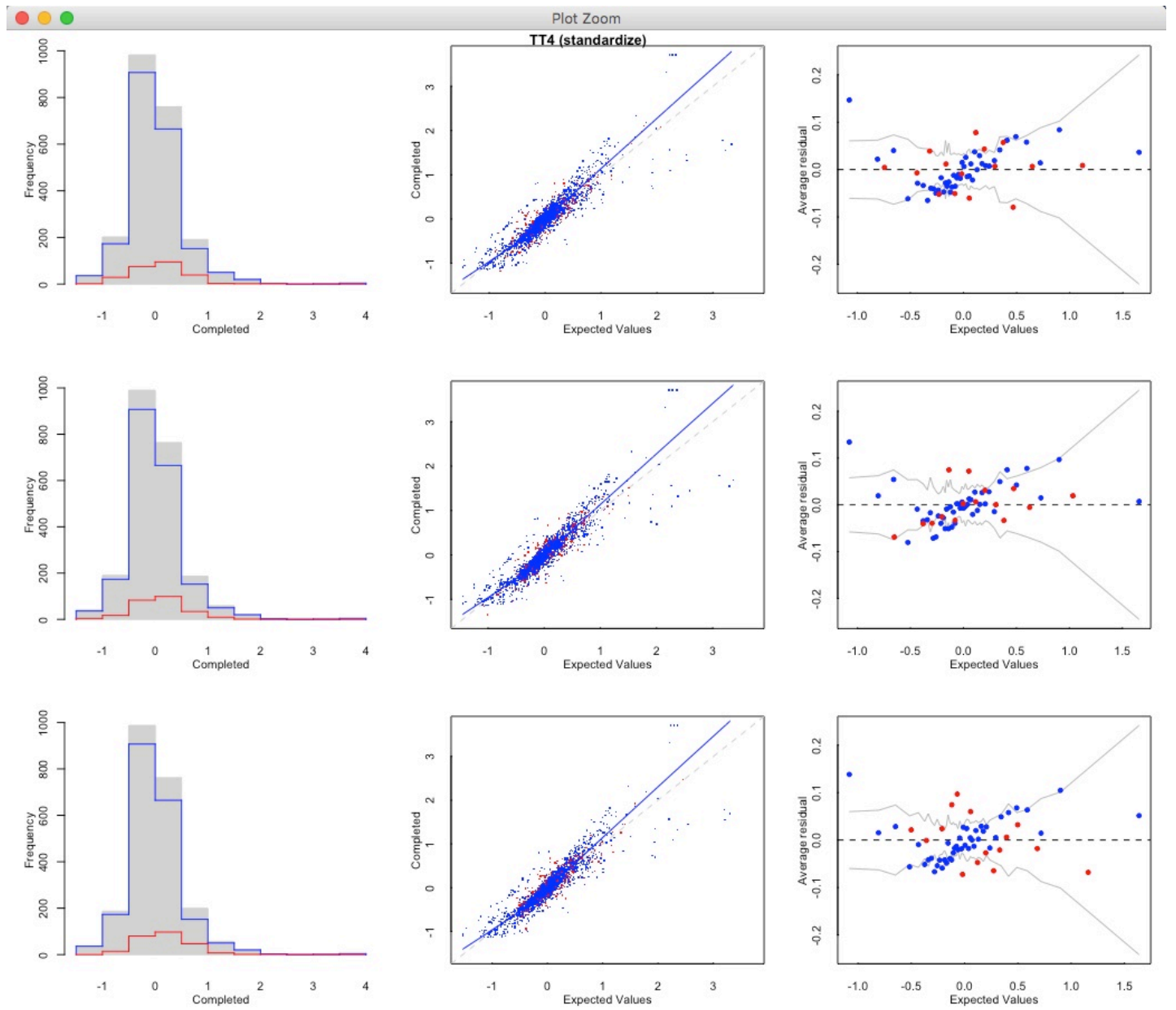
```
1 library(mi)
2 mdf <- missing_data.frame(dat)
3 show(mdf)
4 summary(mdf)
5 image(mdf)
6 hist(mdf)
7 options(mc.cores=8)
8 imp <- mi(mdf,n.chains=8)
9 show(imp)
10 round(mipply(imp, mean, to.matrix = TRUE), 3)
11 Rhats(imp)
12 imp <- mi(imp, n.iter = 5)
13 plot(imp)
14 image(imp)
```

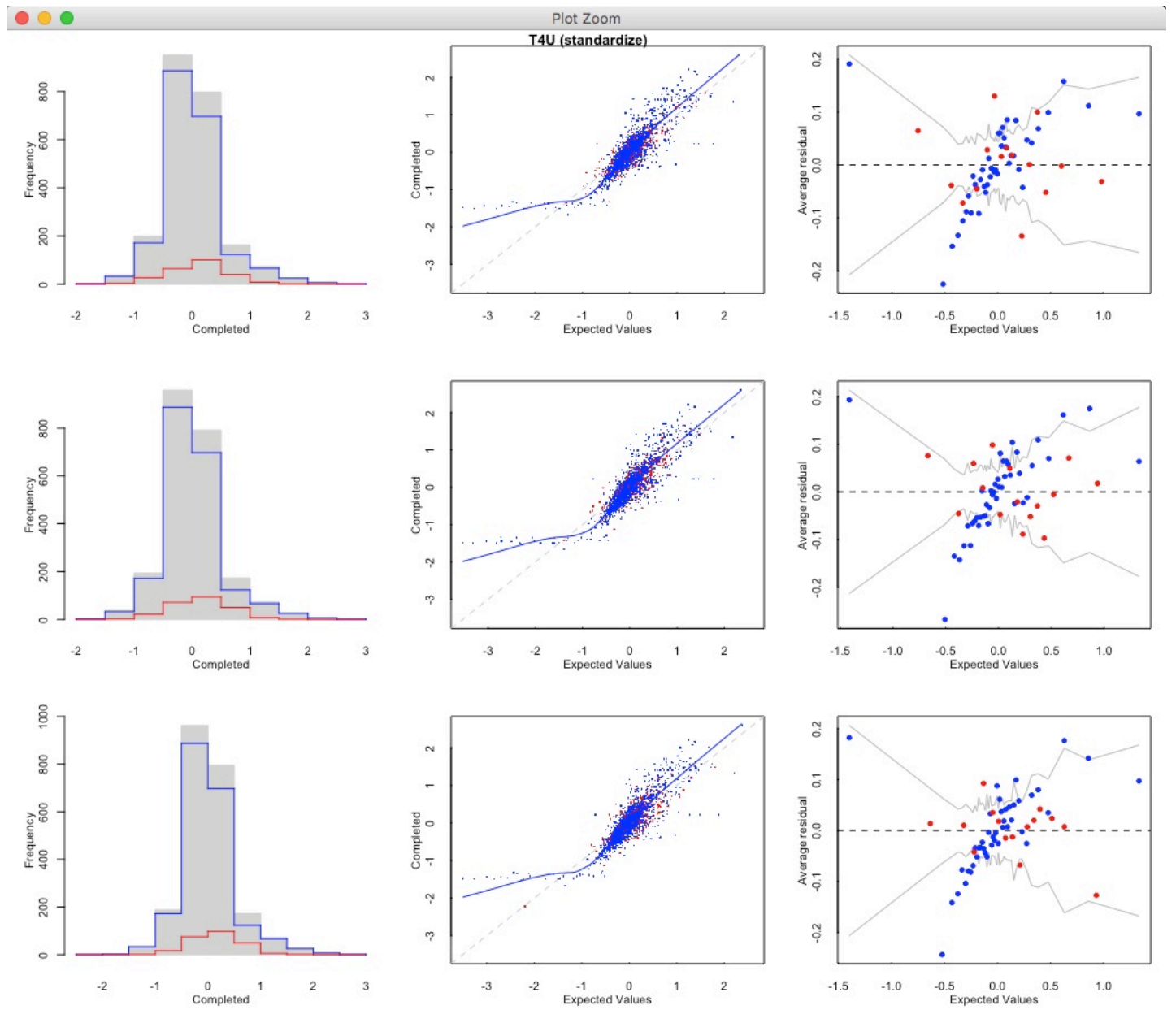


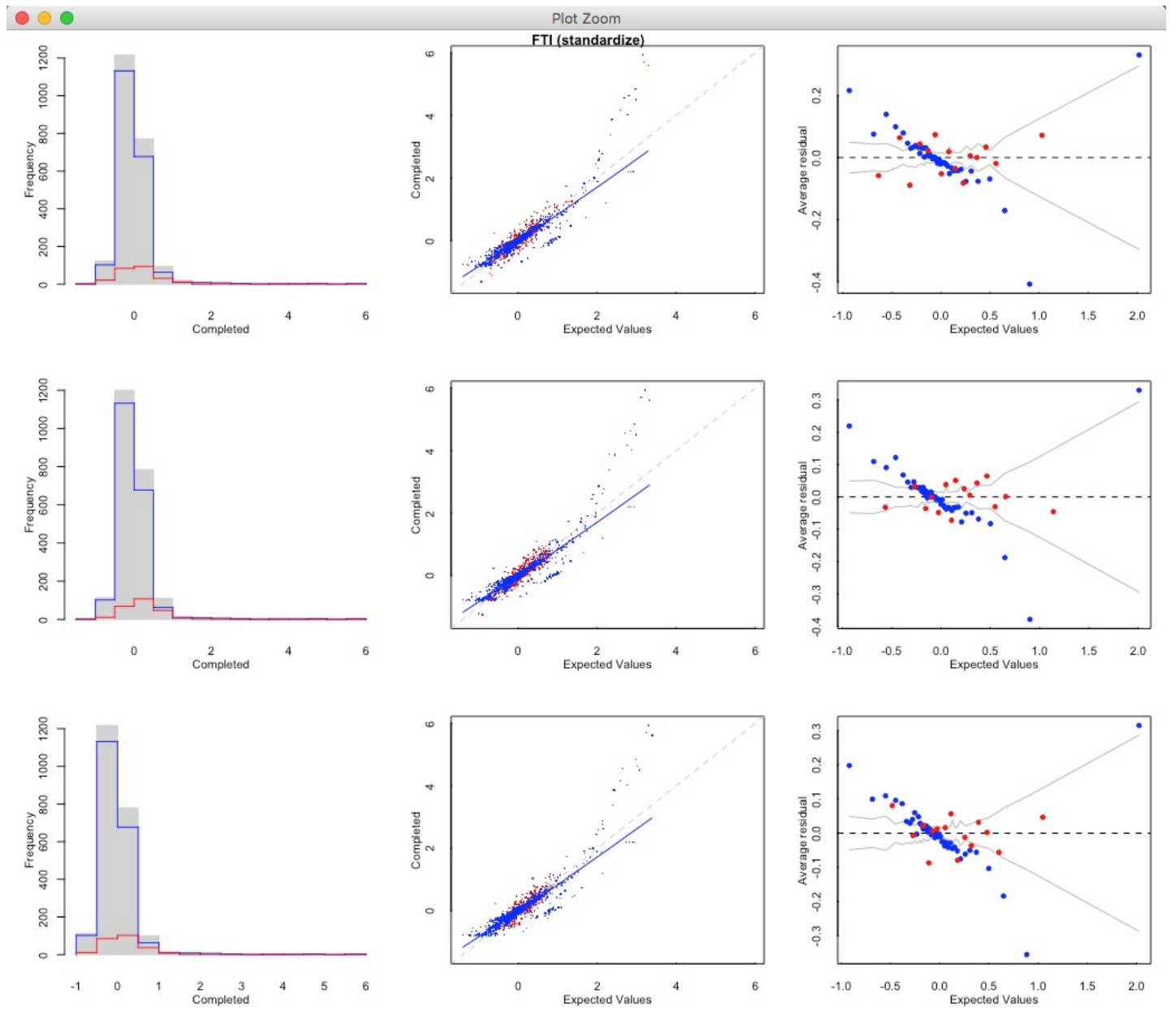




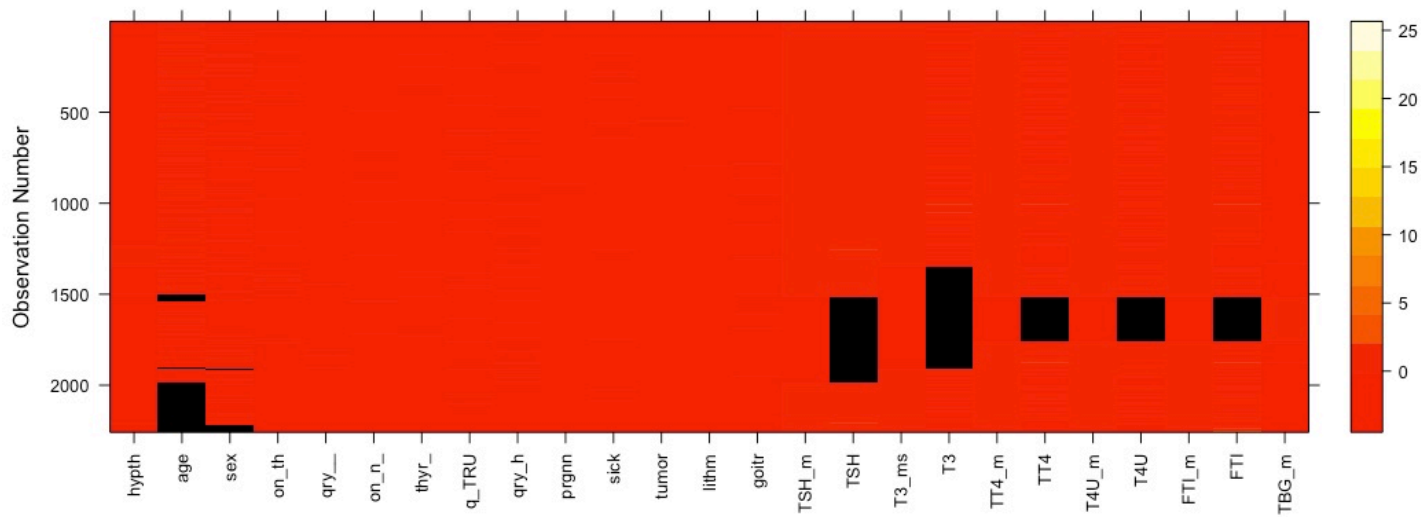








Original data



Average completed data

