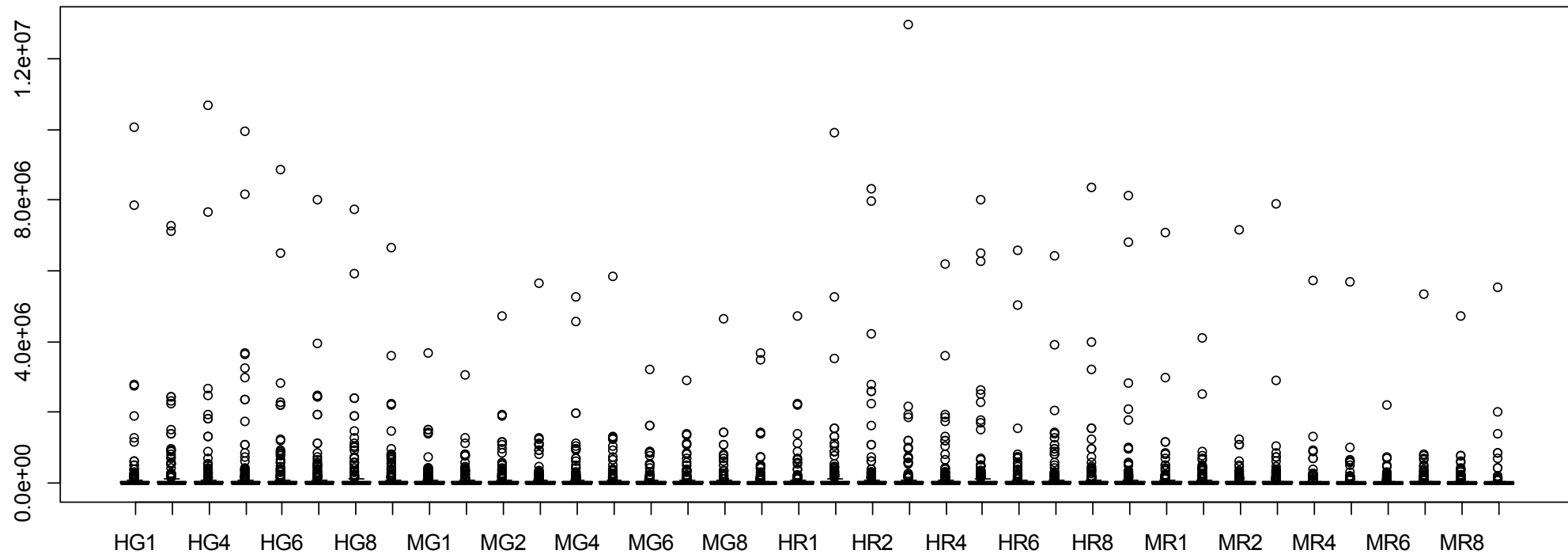# Processing and Visualization of Metabolomics Data Using R

Log transformation

Normalization and scaling
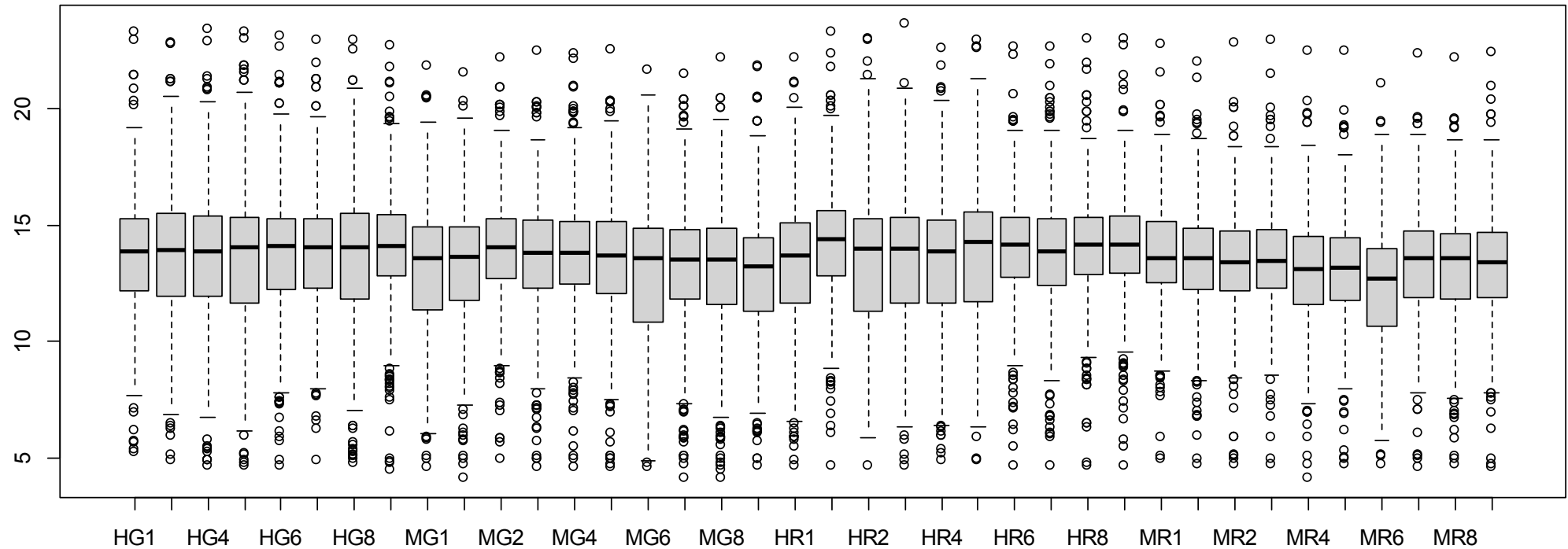
Raw Data

```
dat1 <- read.csv("xcmsresults.csv", header=T, row.names=1)
boxplot(dat1)
```
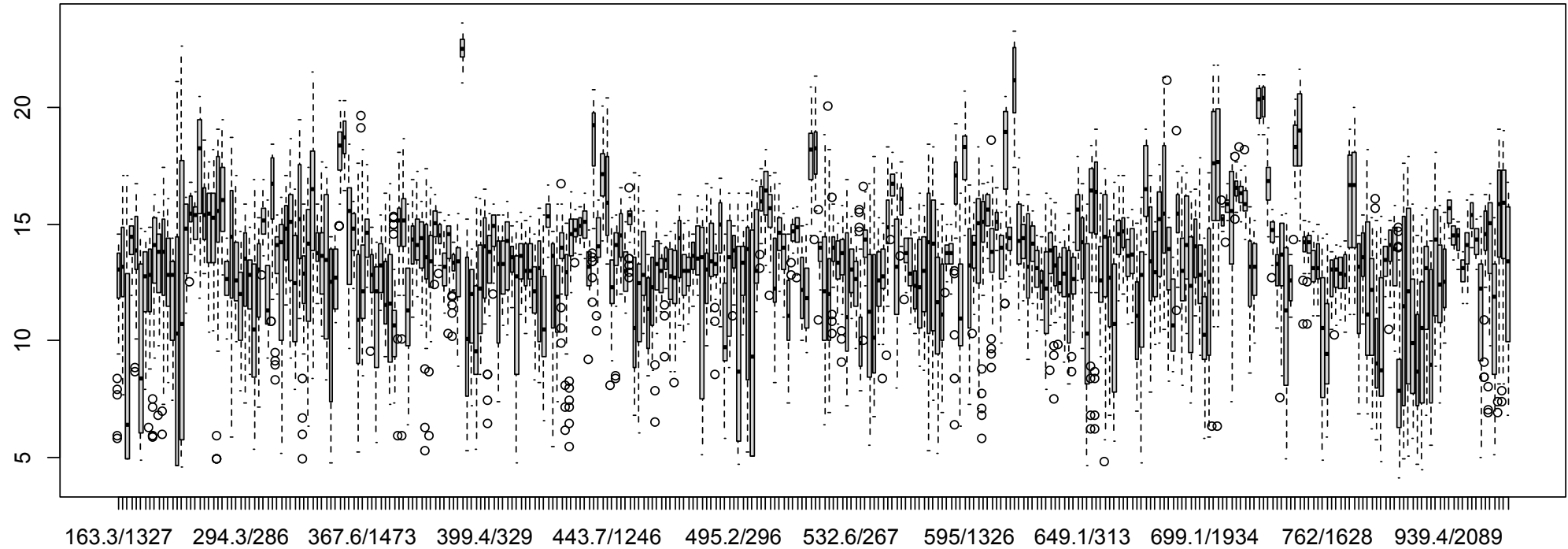
Nach log (spaltenweise = einzelne Pflanzen)

```
dat2 <- as.data.frame(t(apply(dat1, 1, replacezero)))
logdata <- log(dat2, 2)
boxplot(logdata)
```
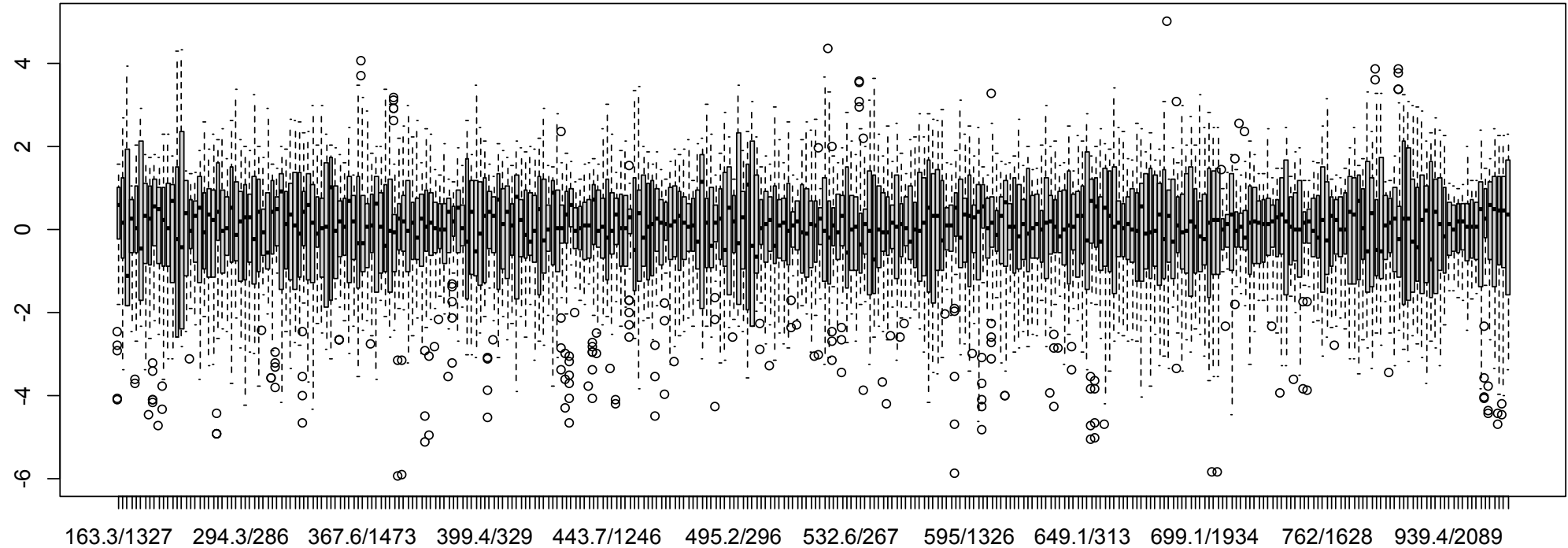
Nach log (zeilenweise = einzelne Metabolite)

boxplot(t(logdata))

Nach Pareto-Scaling (zeilenweise)

```
logdata.pareto <- paretoscale(logdata)
boxplot(t(logdata.pareto))
```

Nach Z-Score-Scaling (zeilenweise)

boxplot(scale(t(logdata)))