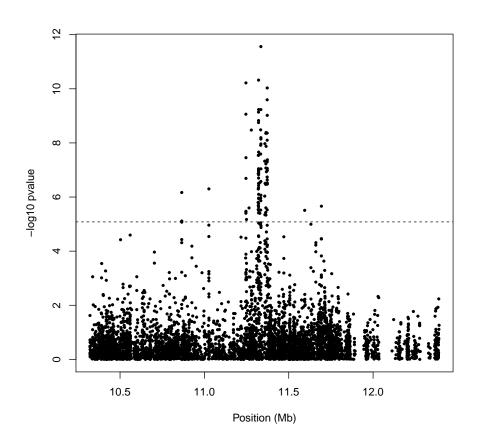
```
library(pcev)
## PCEV: Principal components of explained variance
data(methylation)
data(pheno)
data(position)
```

```
# Compute nominal pvalues
fit <- lm(methylation ~ pheno)
pval <- vapply(summary(fit), function(sum) {
   pvalue <- sum$coef[2,4]
   return(pvalue)
}, numeric(1))

# Manhattan plot univariate
plot(position$Pos/1e6, -log10(pval), xlab="Position (Mb)",
        ylab="-log10 pvalue", pch=19, cex=0.5)
abline(h=-log10(8.3*10^-6), lty=2)</pre>
```



```
for (j in unique(index)) {
   p <- length(index[index == j])</pre>
    if (p > 30) {
      q \leftarrow floor(p/2); r \leftarrow p - q
      index[index == j] <- c(rep_len(maxInd, q),</pre>
                             rep_len(maxInd + 1, r))
     maxInd \leftarrow maxInd + 2
 blockLengths <- table(index)</pre>
cl <- index
index <- cl
counter <- 0
for(j in sort(unique(cl))) {
 counter <- counter + 1
 index[index == j] <- counter</pre>
table(table(index))
##
                         6
                           7
                                 8
                                   9 10 11 12 13 14 15 16 17 18
## 303 160 72 68 56 31 28
                                                        6 17 24 14 15
                               30 17 18 13
                                                 9
                                                   15
   19 20 21 22 23 24
                            25
                               26 27 28 29 30
## 13 13 8 9 4 9 4 4 3 4 5
pcev_out <- computePCEV(methylation, covariate = pheno,</pre>
```

