

# QTL Scanning

Matthew Gibson

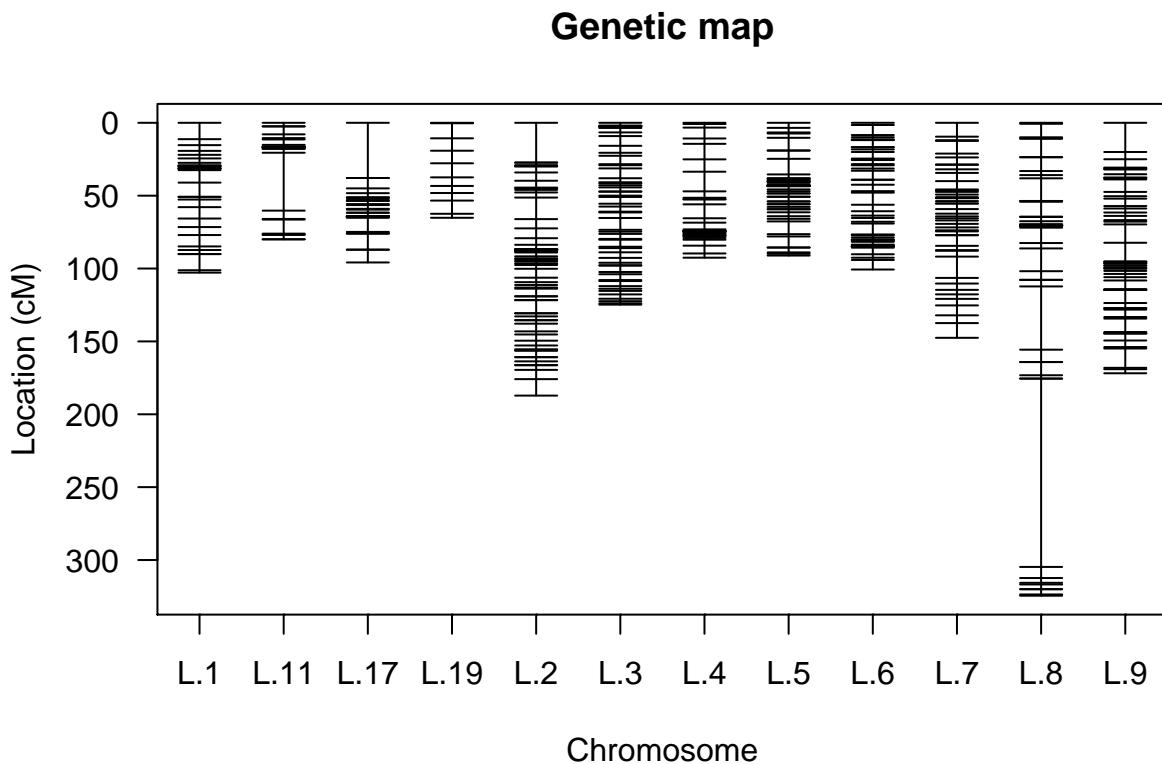
June 8, 2017

## Load the cross

```
mapJal5.1 <- read.cross("csv", pcDir, "final_map_6_15_t.csv", genotypes=c("A", "H"), alleles=c("A", "B"))

## --Read the following data:
## 269 individuals
## 520 markers
## 89 phenotypes
## --Cross type: bc

#write.cross(mapJal5.1, format="csv")
plot.map(mapJal5.1)
```



```
mapJal5.1 <- calc.genoprob(mapJal5.1, step=0.1)
```

## Setup covariates

```
bench <- pull.pheno(mapJal5.1, pheno.col = 3)
hmorph <- pull.pheno(mapJal5.1, pheno.col=c(3, 4))
fmorph <- pull.pheno(mapJal5.1, pheno.col=c(3, 5))
hcolor <- pull.pheno(mapJal5.1, pheno.col=c(3, 6))
fcolor <- pull.pheno(mapJal5.1, pheno.col=c(3, 7))
crossed <- pull.pheno(mapJal5.1, pheno.col=c(3, 8))
trichome <- pull.pheno(mapJal5.1, pheno.col=c(3,8))
veg <- pull.pheno(mapJal5.1, pheno.col=c(3, 10))
```

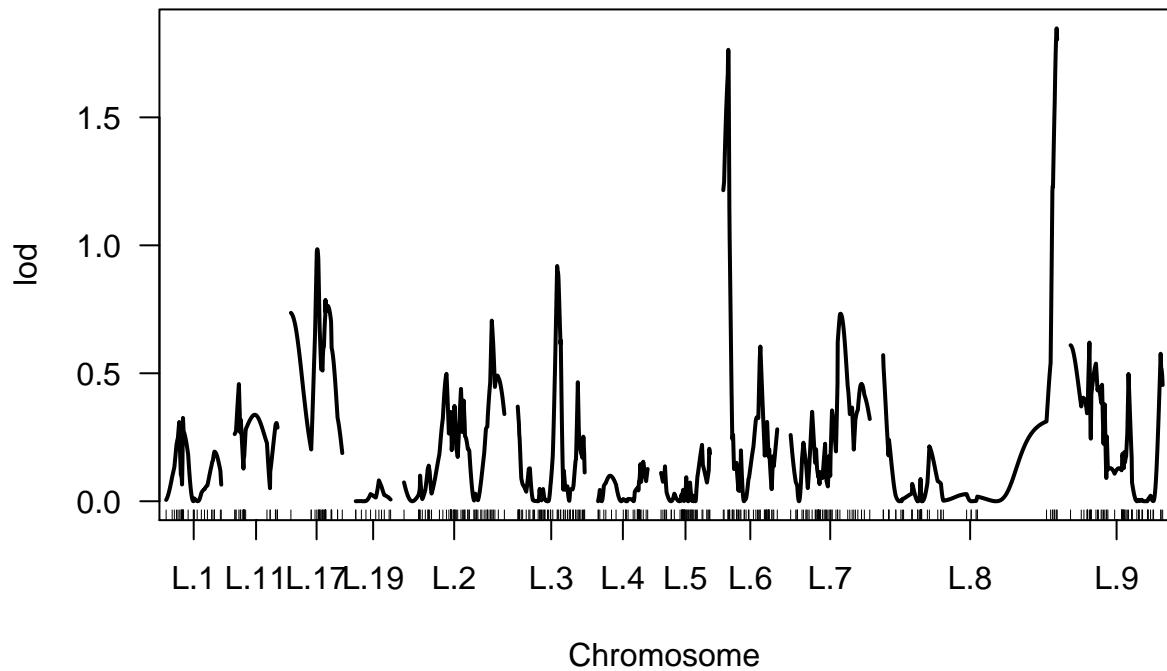
## Scan for QTL

```
#all <- scanone(mapJal5.1, pheno.col=c(3:87))
#summary(all, threshold=3, format="tabByCol")
```

### Trichomes

```
hairs <- scanone(mapJal5.1, pheno.col=11, method="em", model="binary", addcovar=trichome)

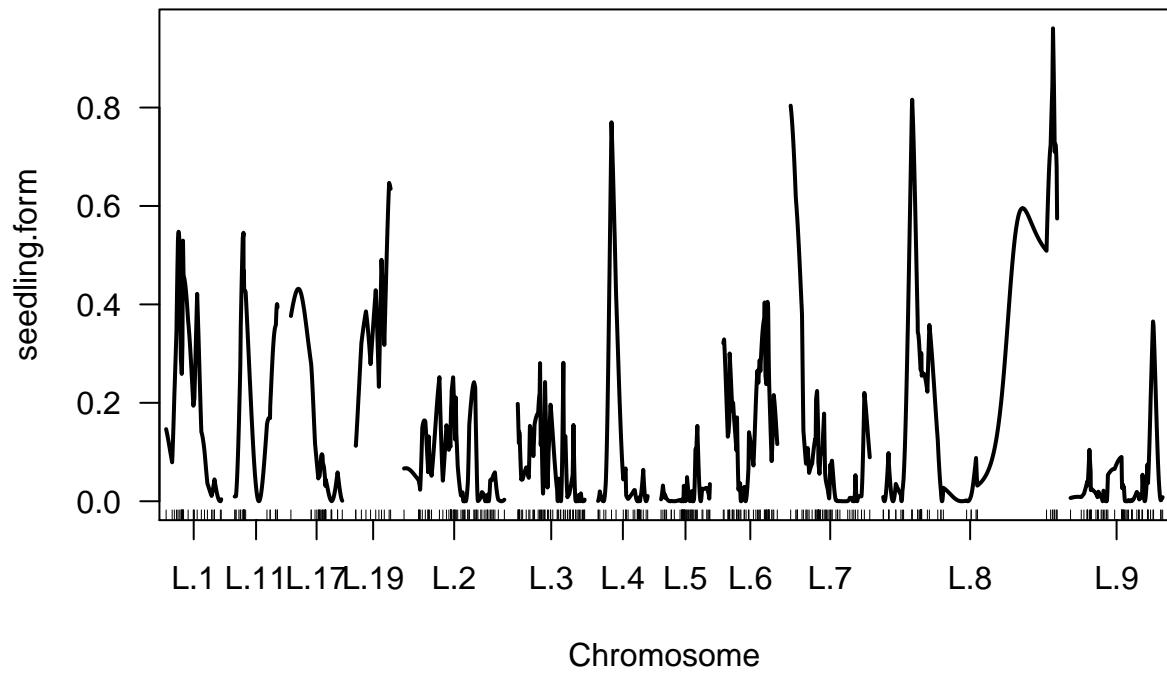
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 47 individuals w
plot(hairs)
abline(3,0,lty=2)
```



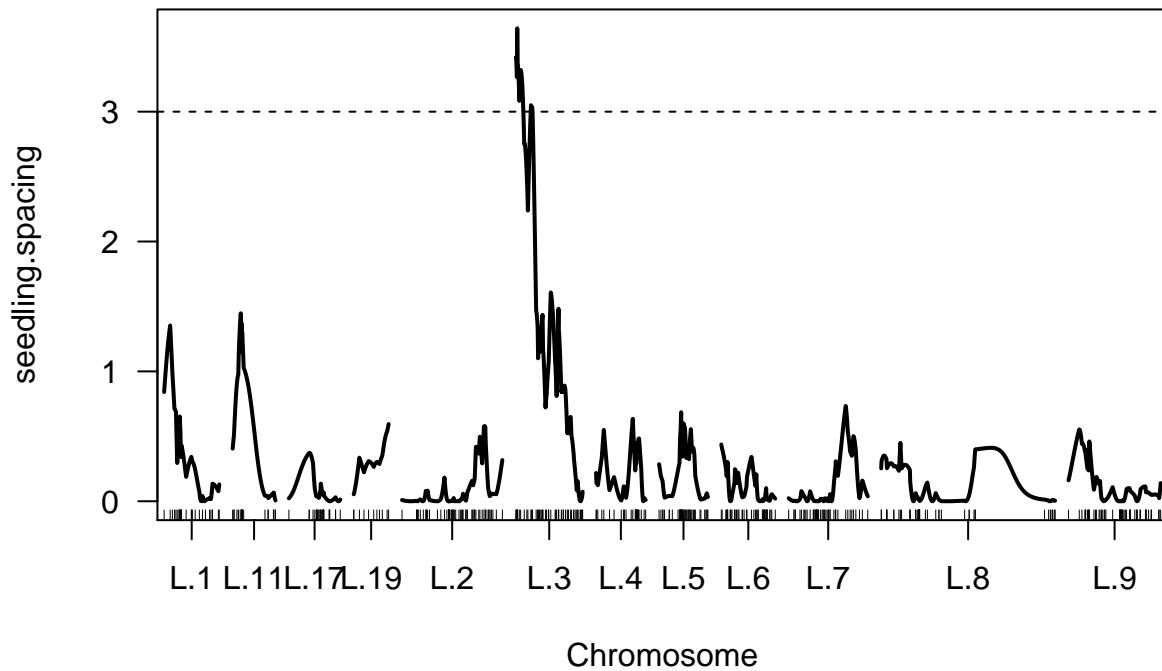
### Seedling form and spacing

```
formSpacing <- scanone(mapJal5.1, pheno.col=c(88,89), method="em", model="binary", addcovar=trichome)

## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 47 individuals w
plot(formSpacing, lodcolumn = 1)
abline(3,0,lty=2)
```



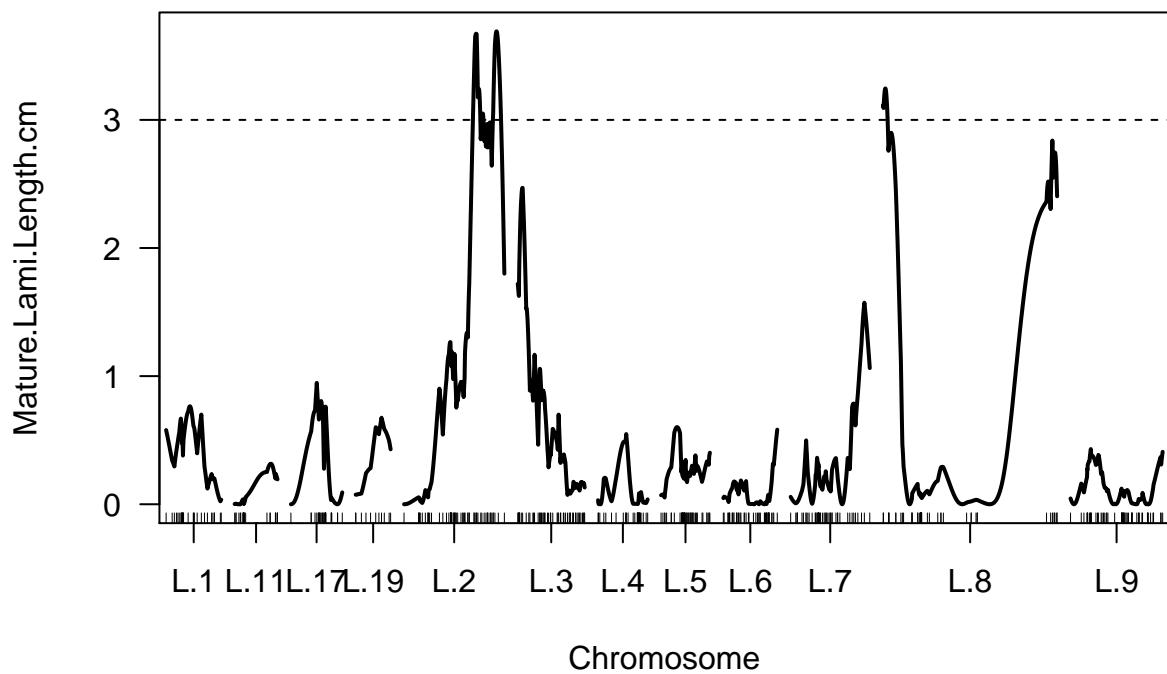
```
plot(formSpacing, lodcolumn = 2)
abline(3,0,lty=2)
```

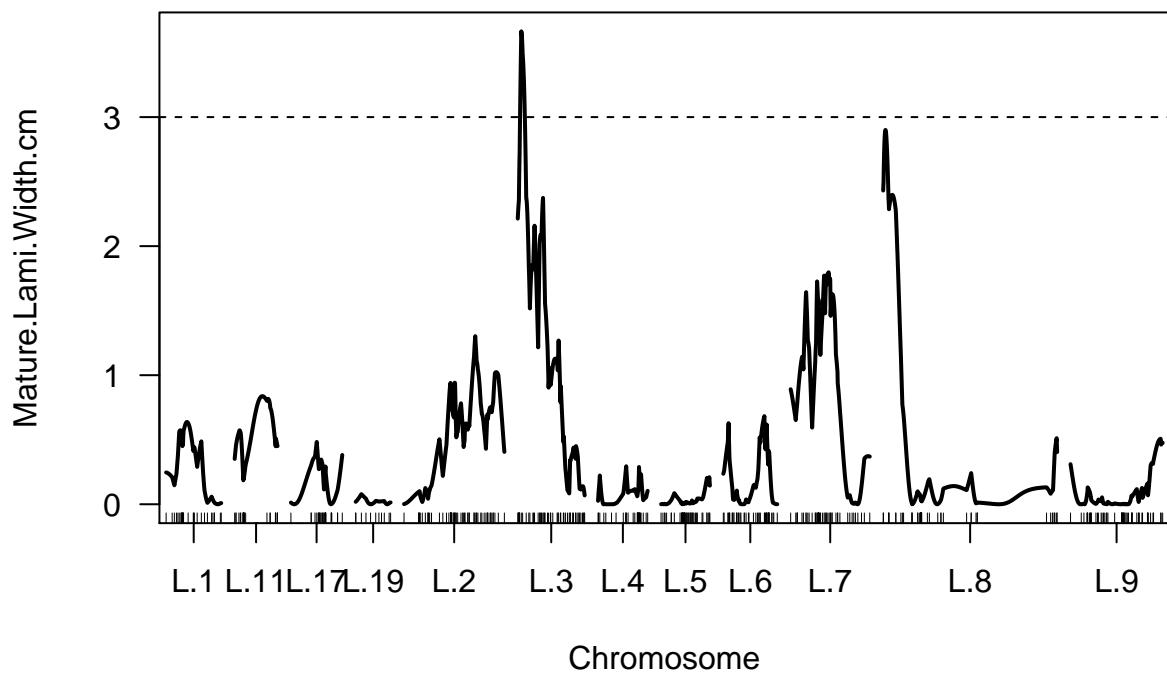


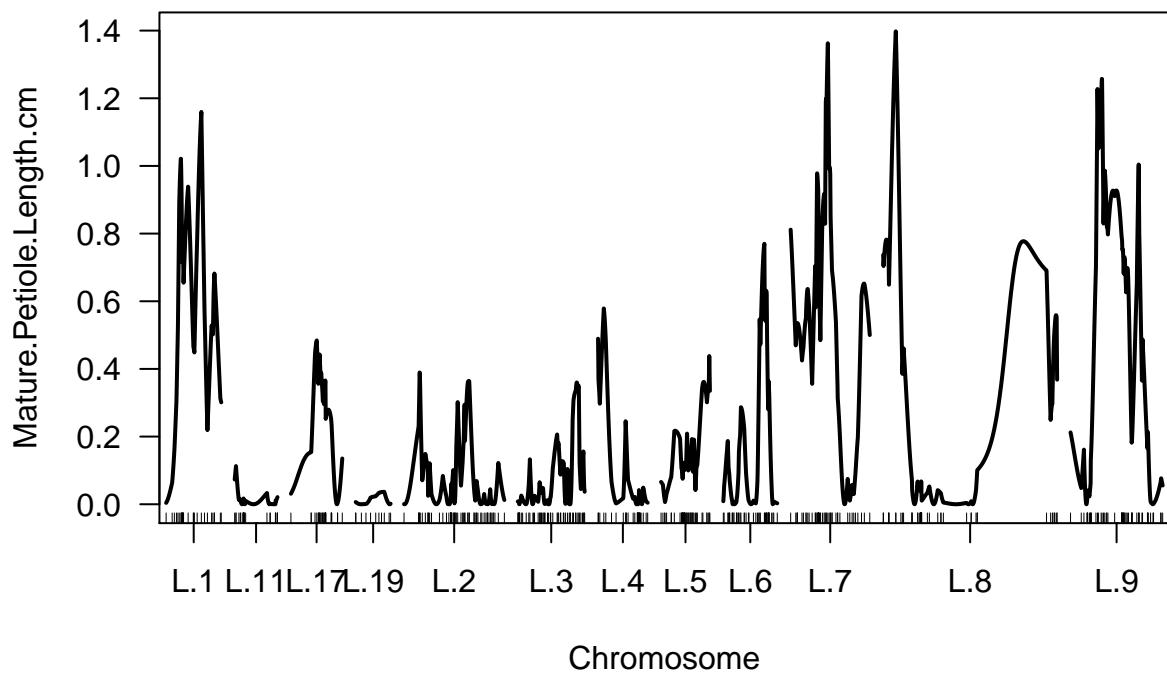
### Vegetative traits

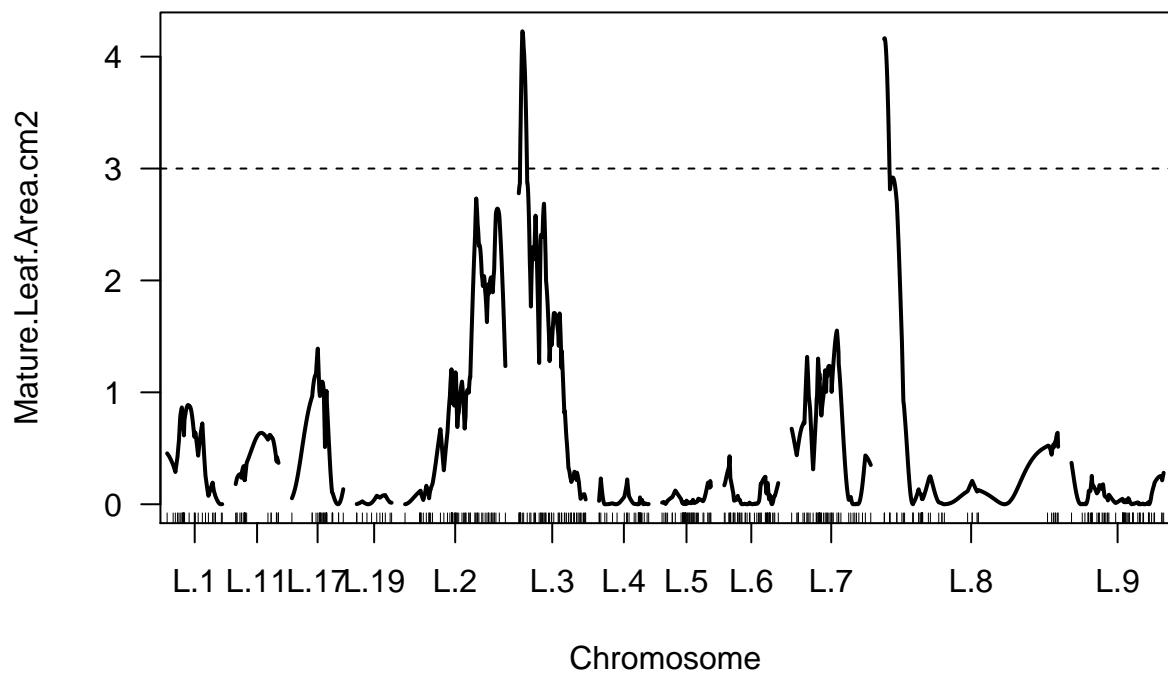
```
vegScan <- scanone(mapJal5.1, pheno.col=c(12:17), method = "em", addcovar=veg)

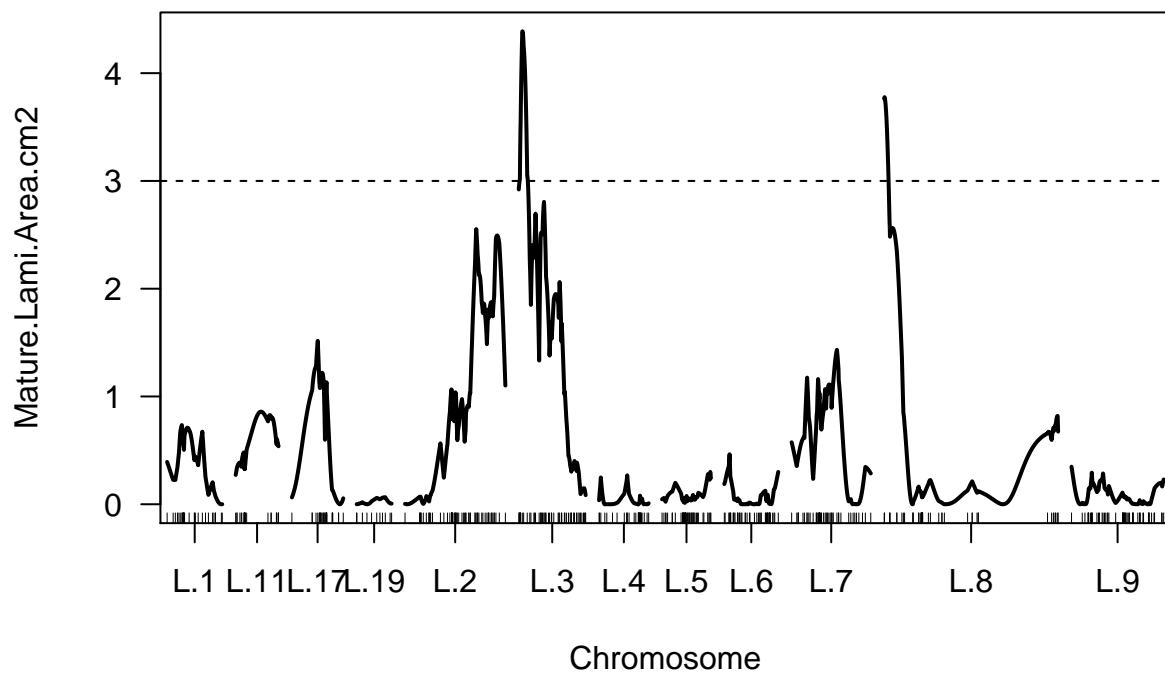
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 10 individuals wi
for (x in 1:6){
  plot(vegScan, lodcolumn = x)
  abline(3,0,lty=2)
}
```

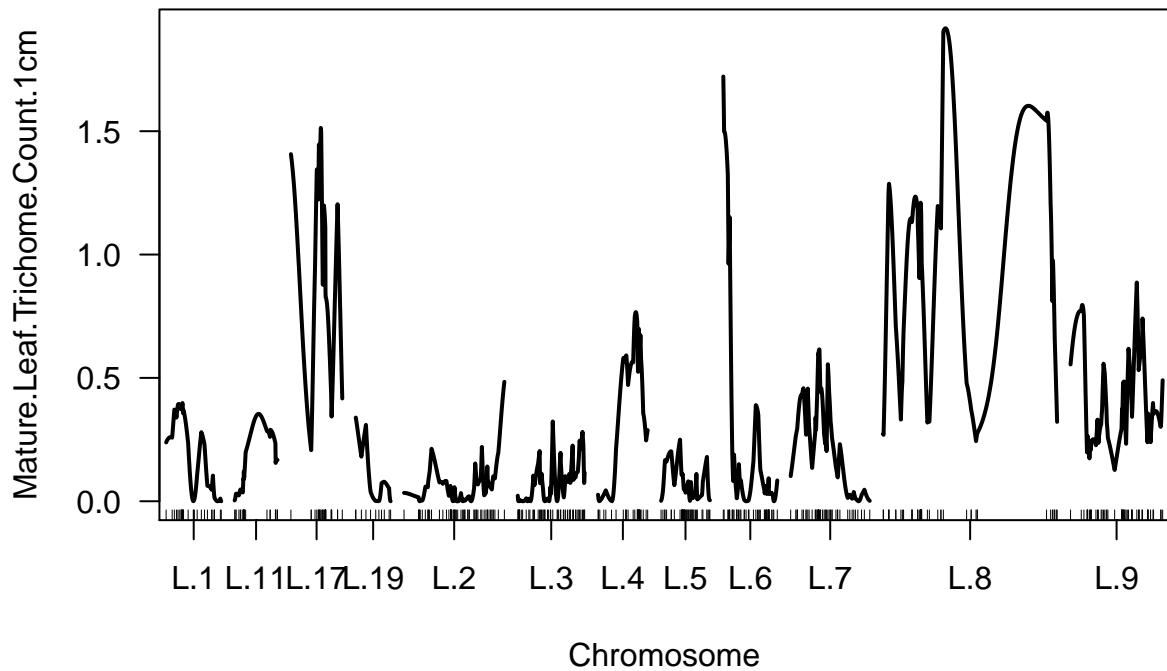








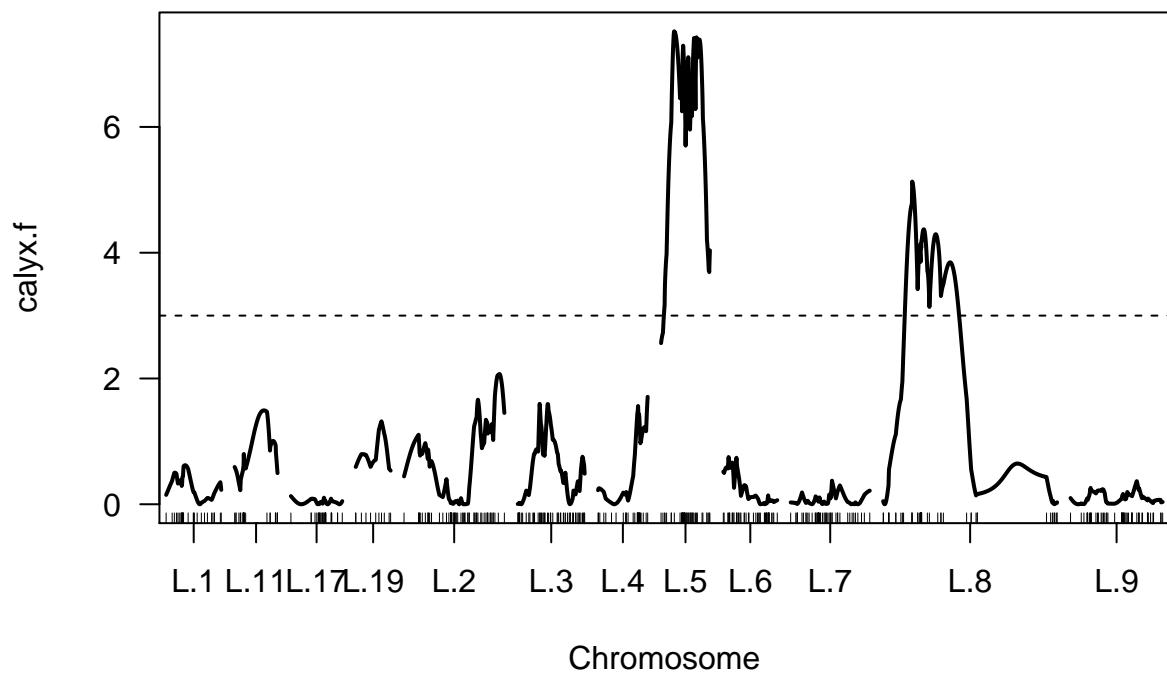


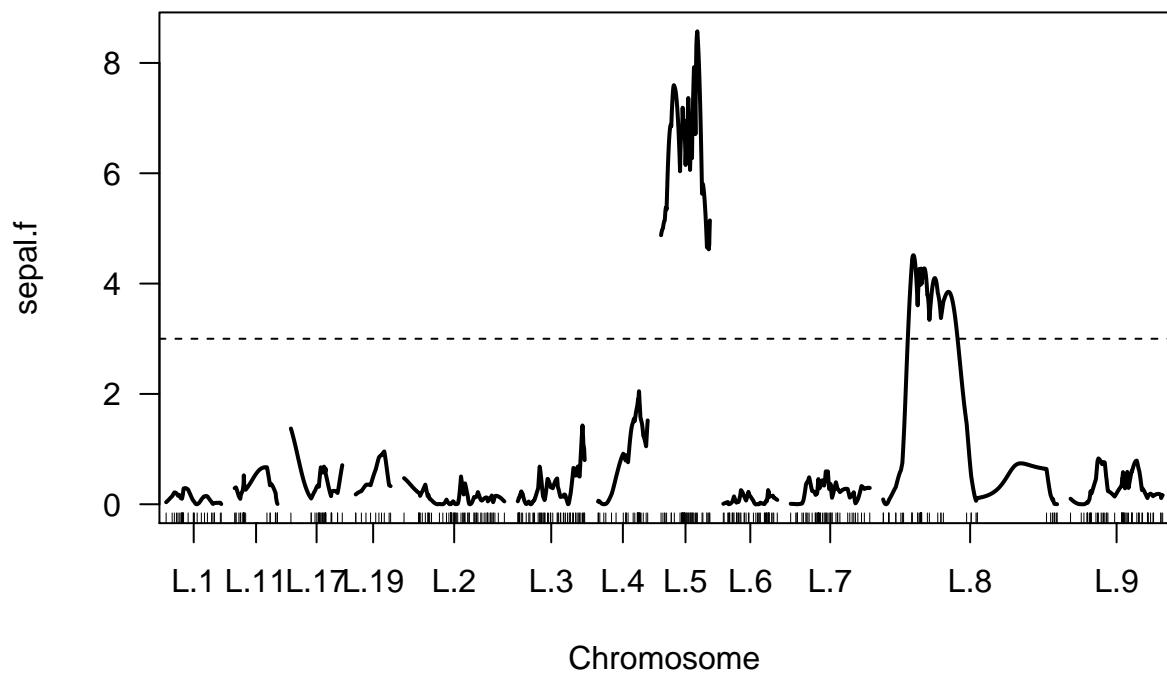


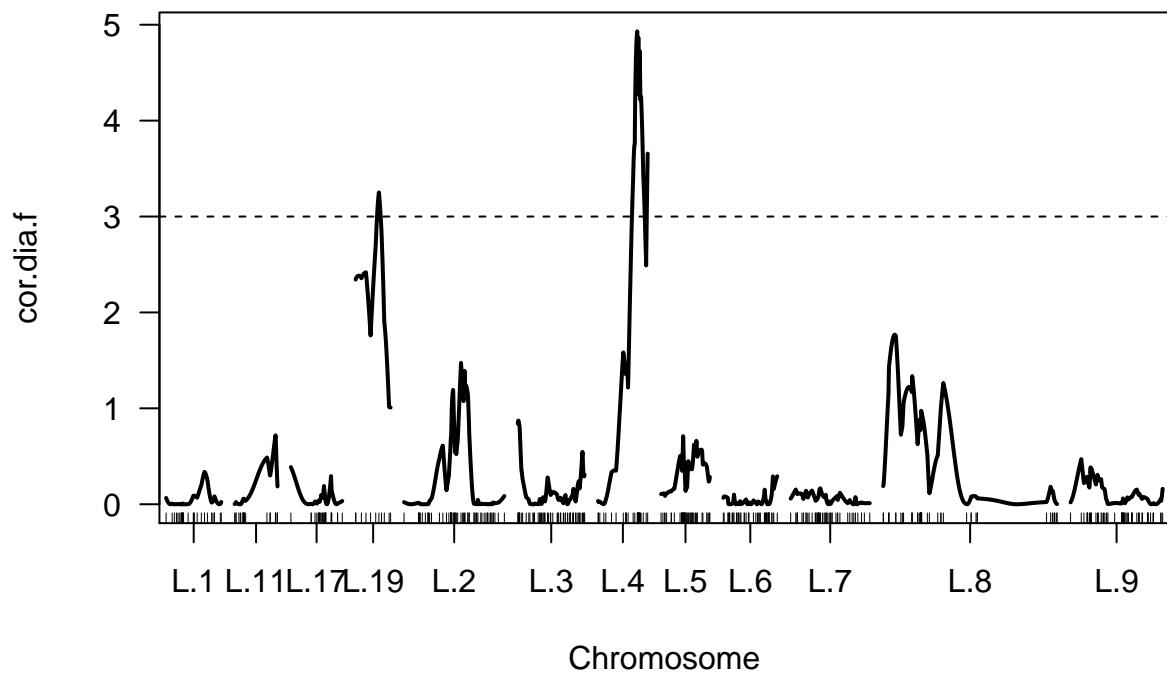
### Female morph

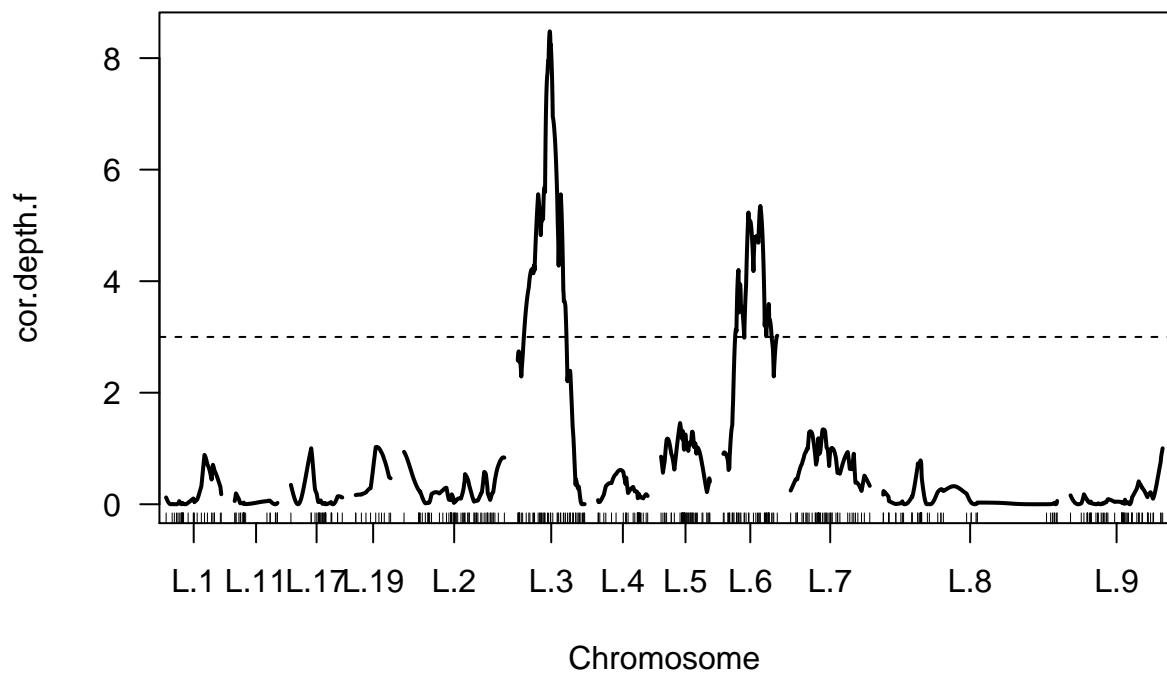
```
femMorph <- scanone(mapJal5.1, pheno.col=c(18:28), method="em", addcovar=fmorph)

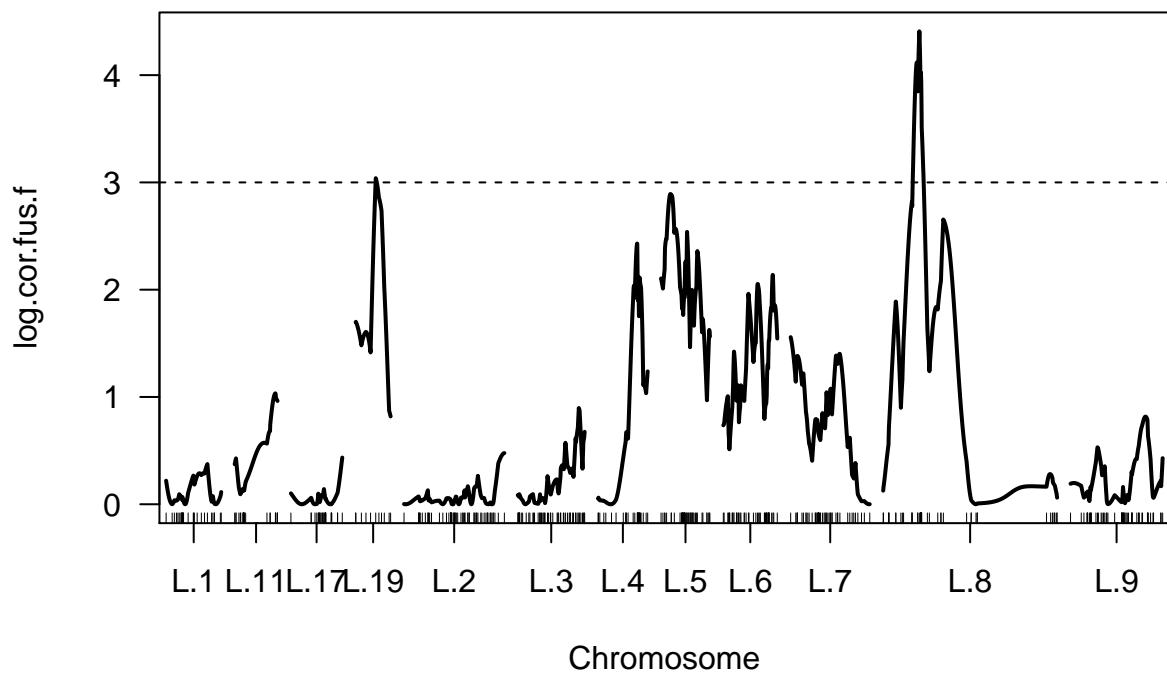
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 46 individuals w
for (x in 1:11){
  plot(femMorph, lodcolumn = x)
  abline(3,0,lty=2)
}
```

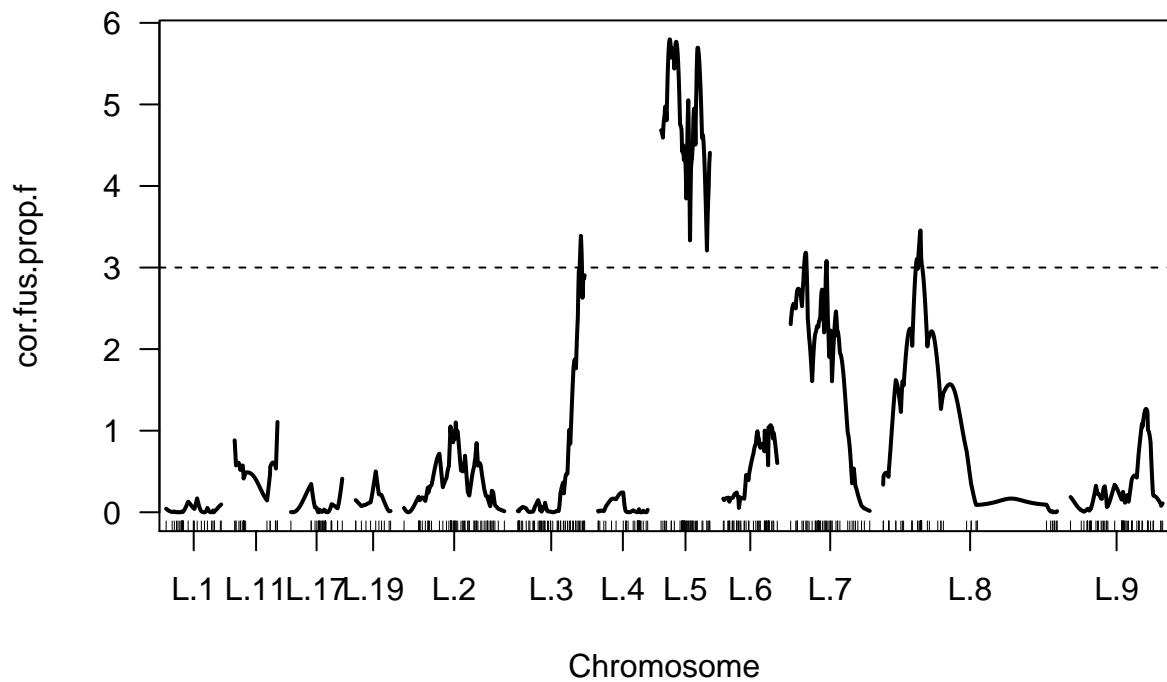


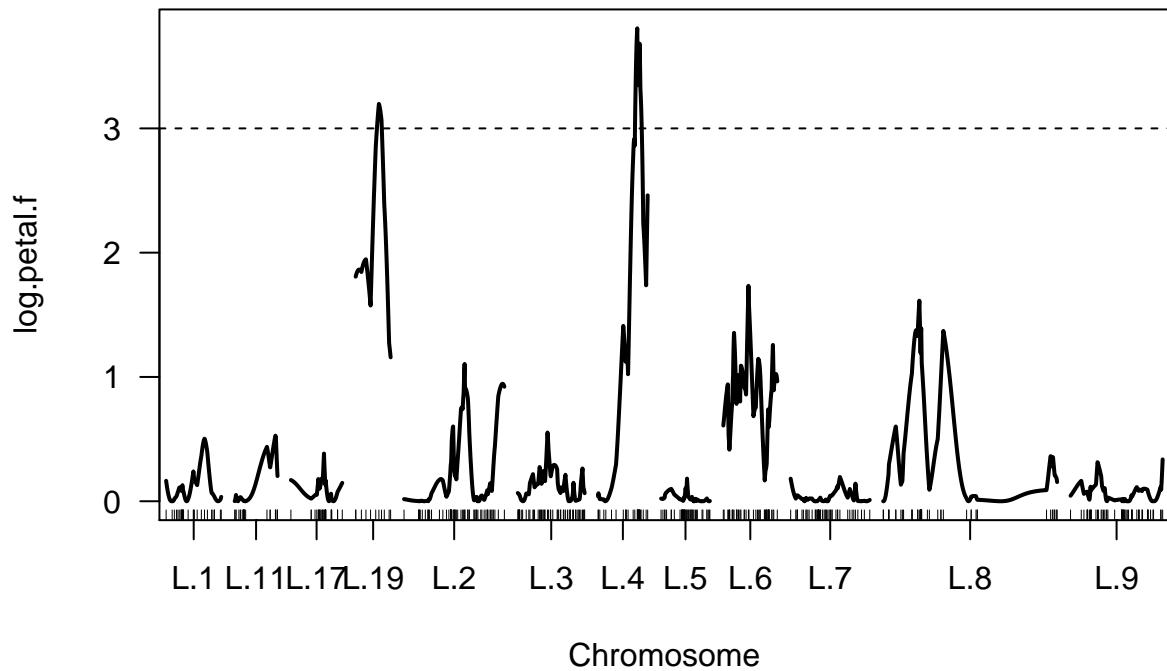


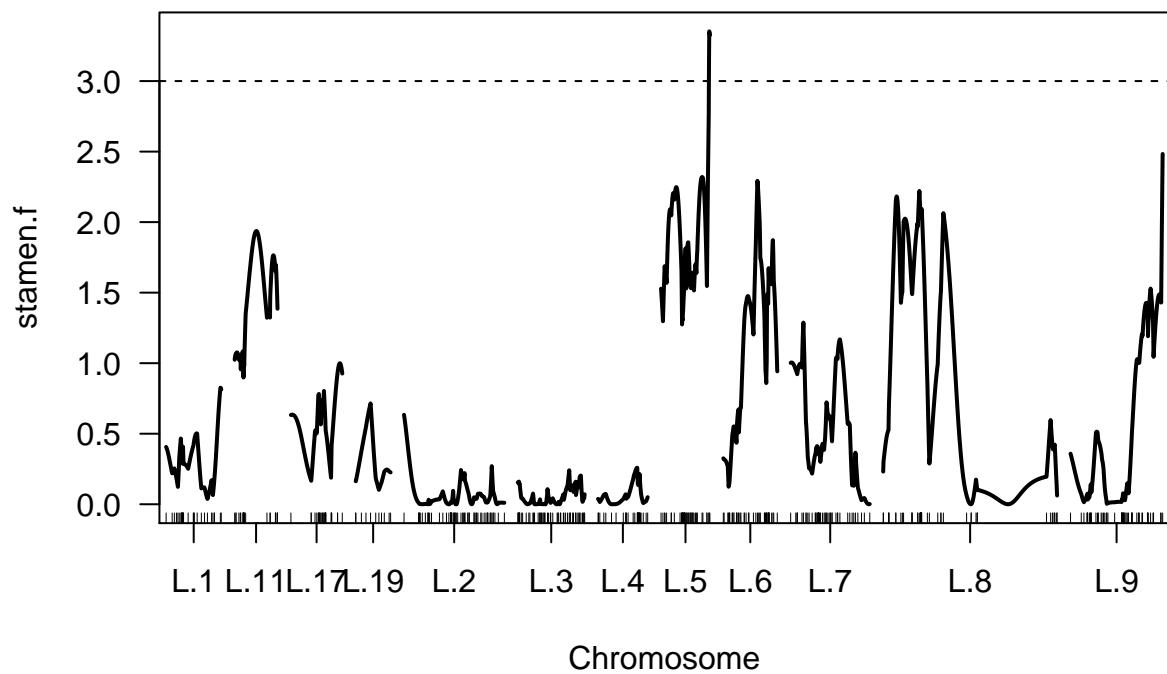


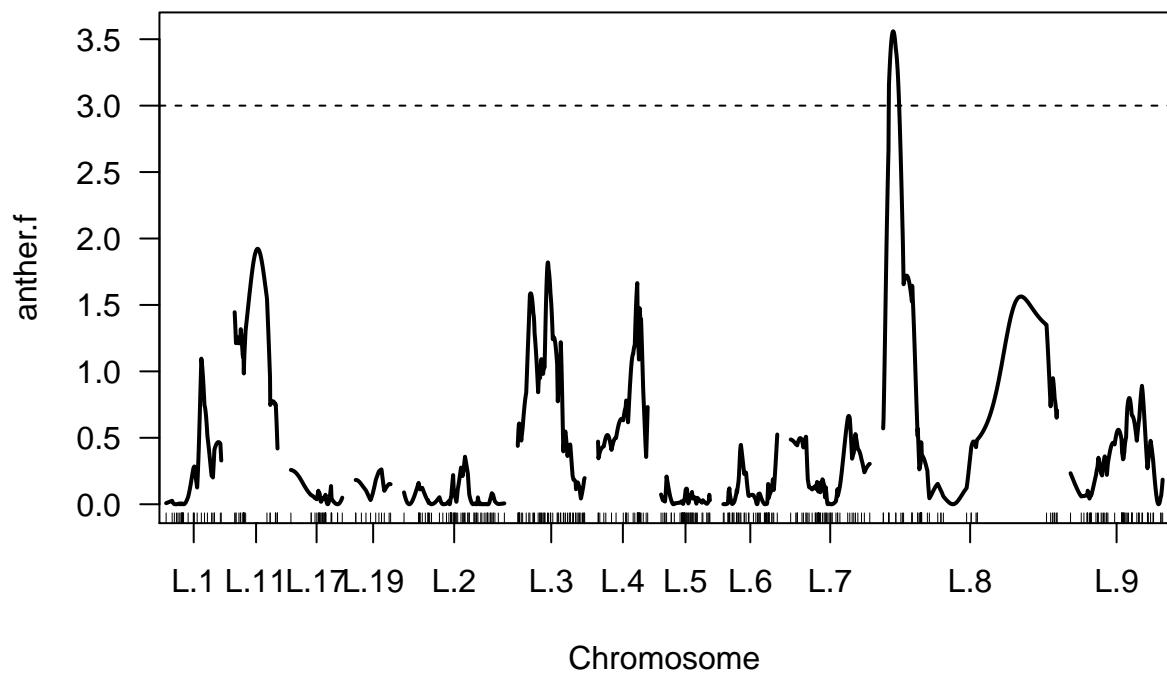


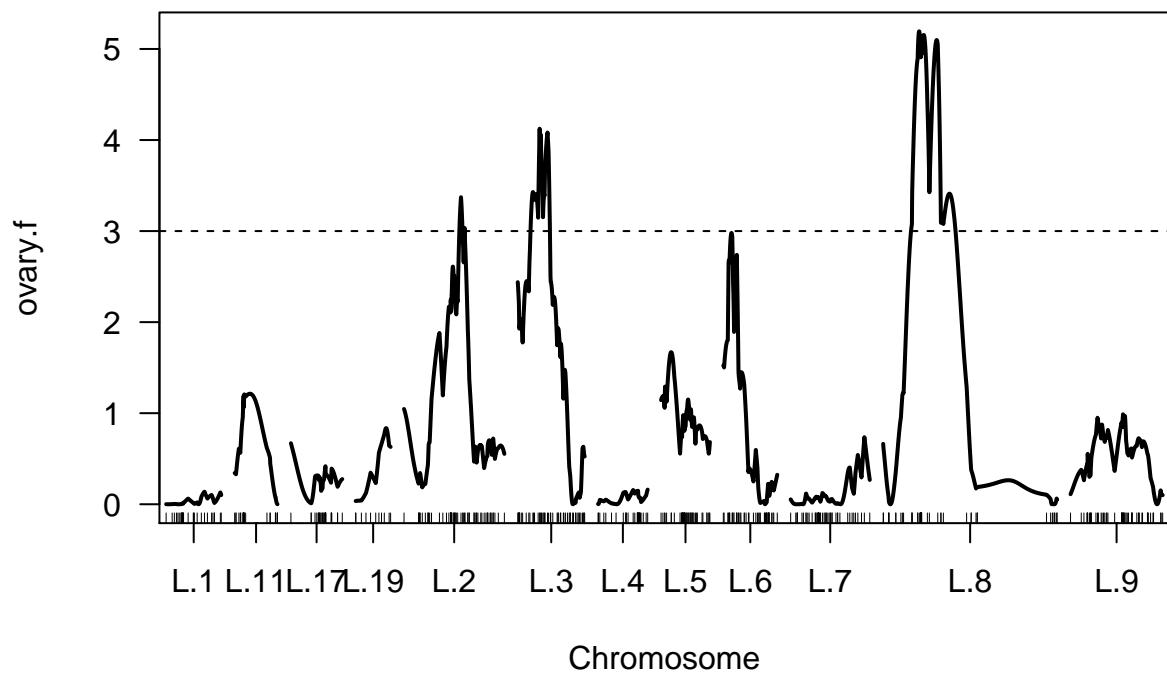


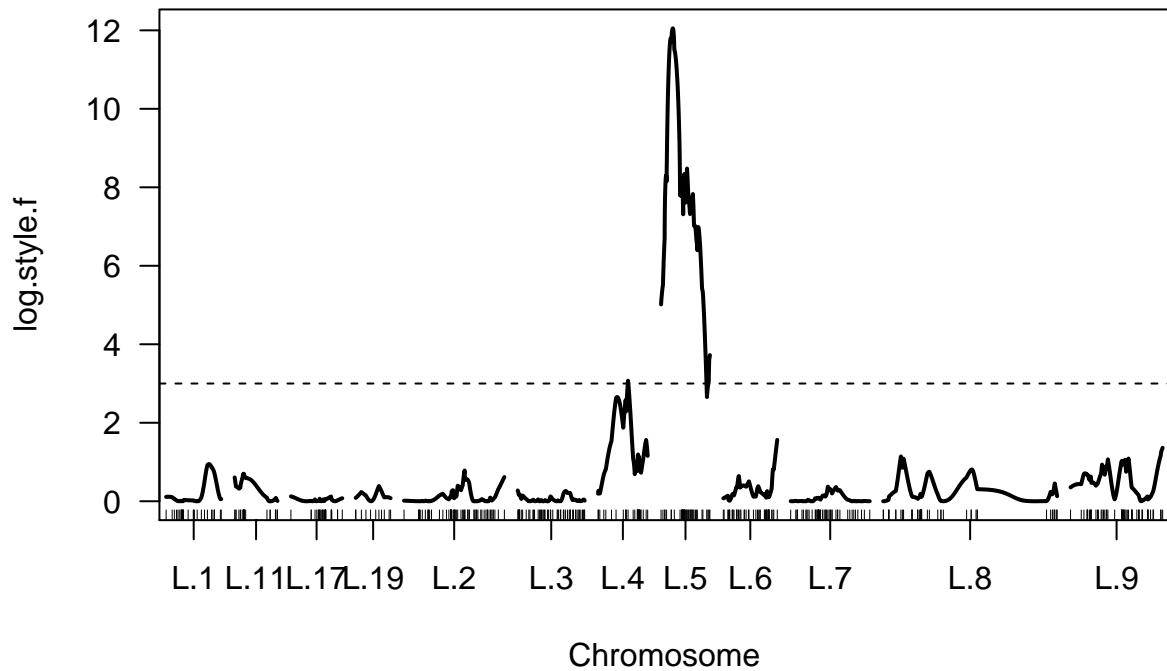












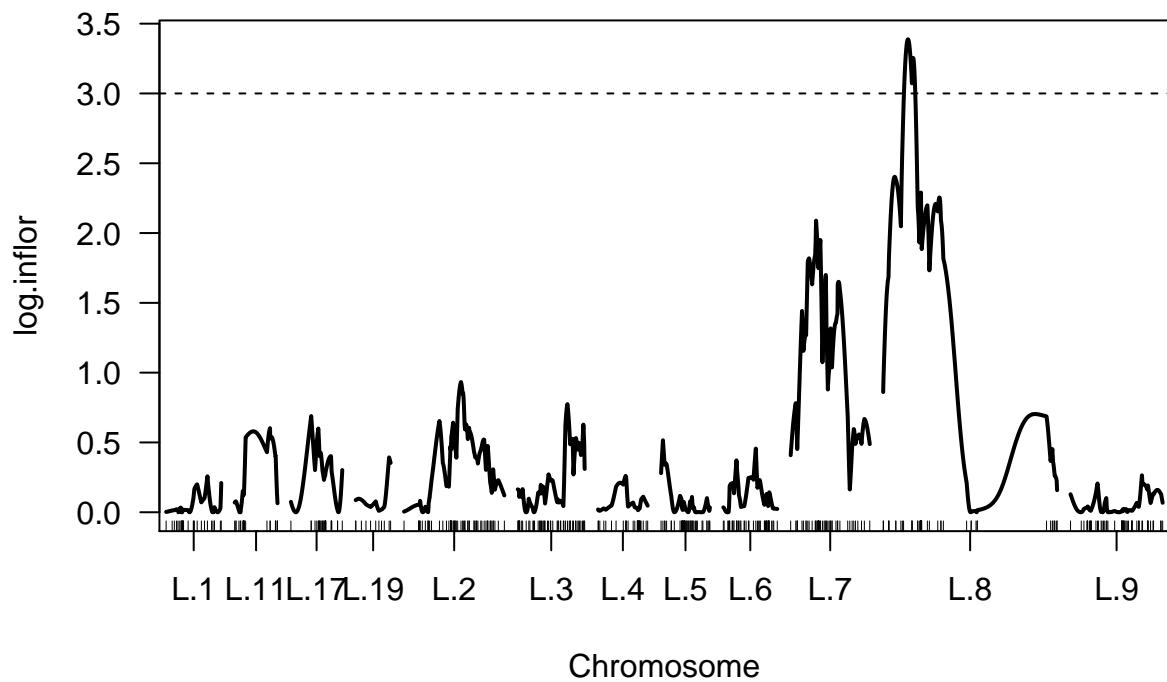
### Herm morph

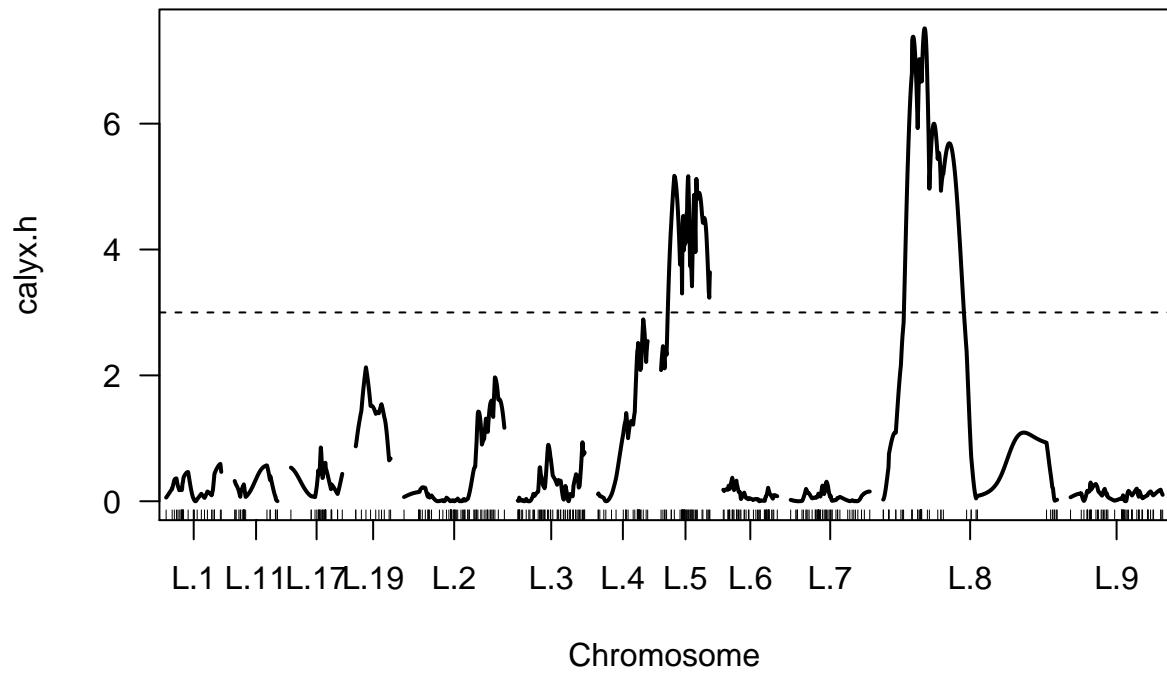
```

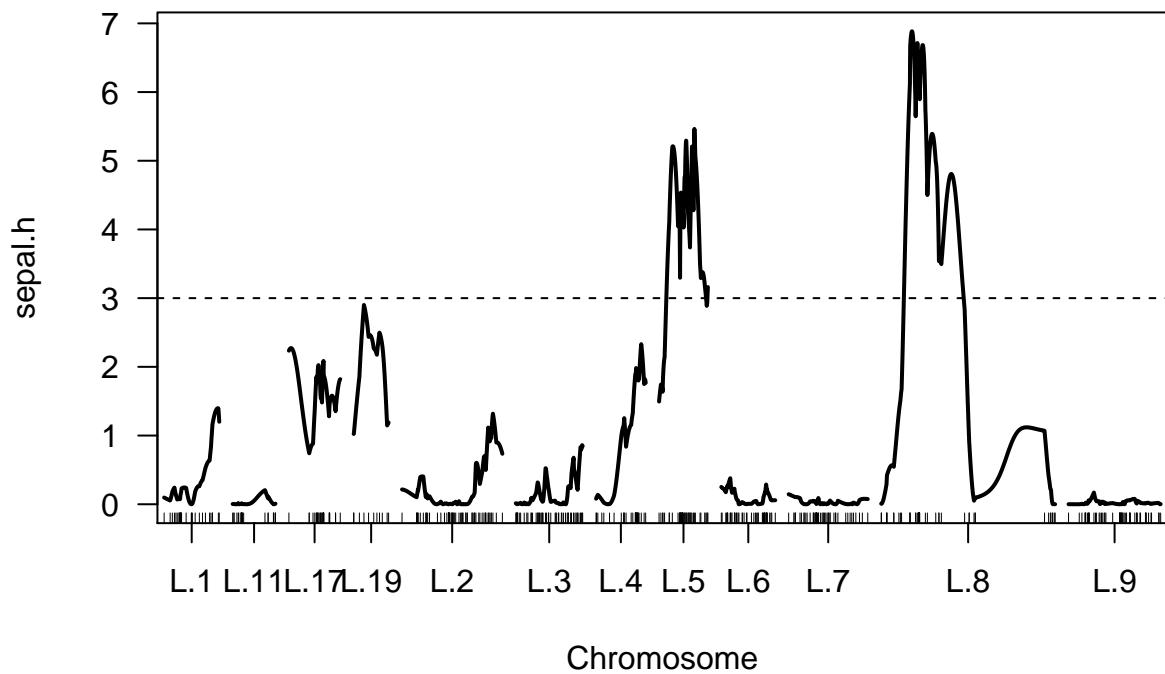
hermMorph <- scanone(mapJal5.1, pheno.col=c(29:41), method="em", addcovar=hmorph)

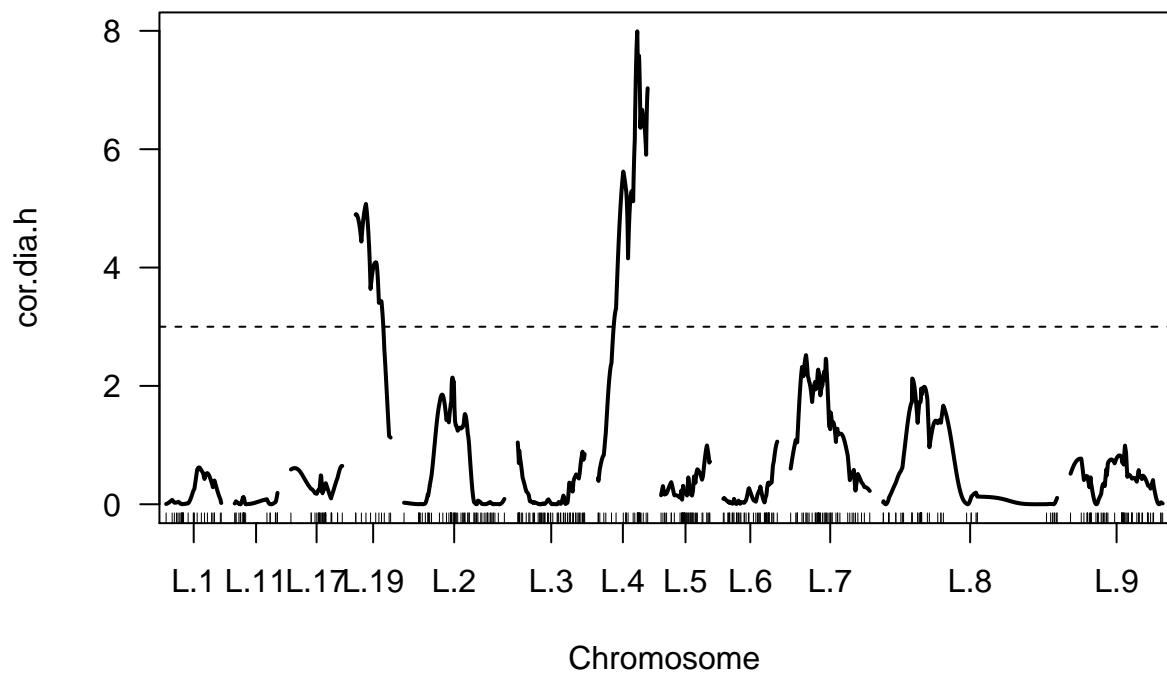
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w
for (x in 1:13){
  plot(hermMorph, lodcolumn = x)
  abline(3,0,lty=2)
}

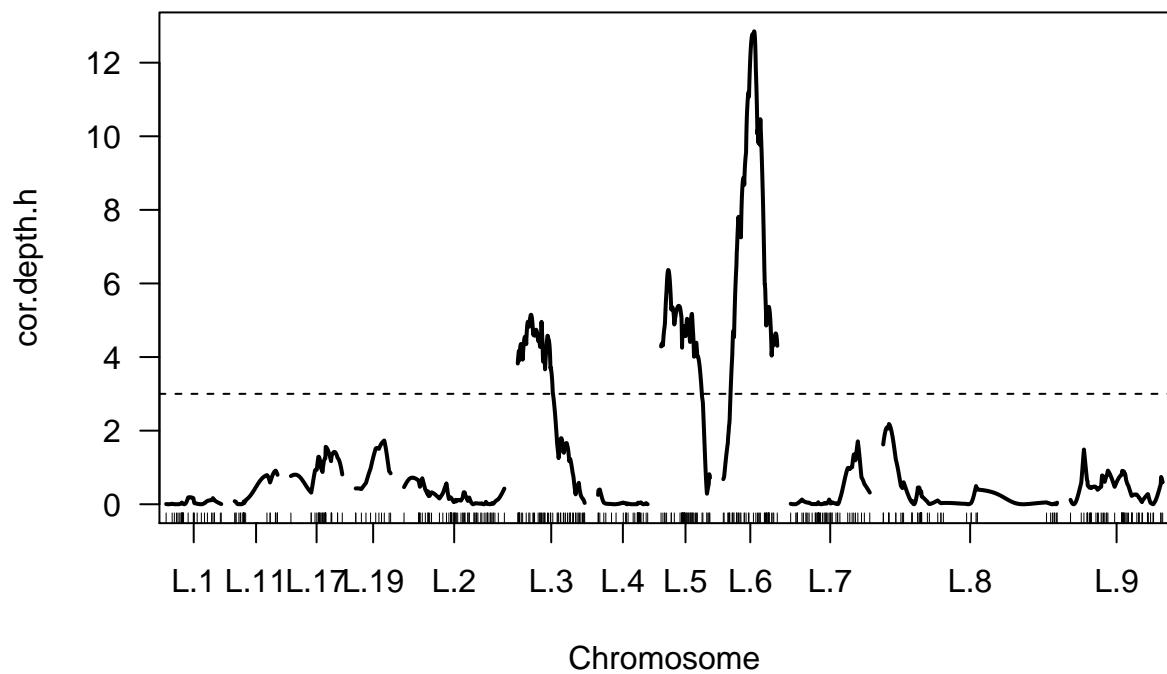
```

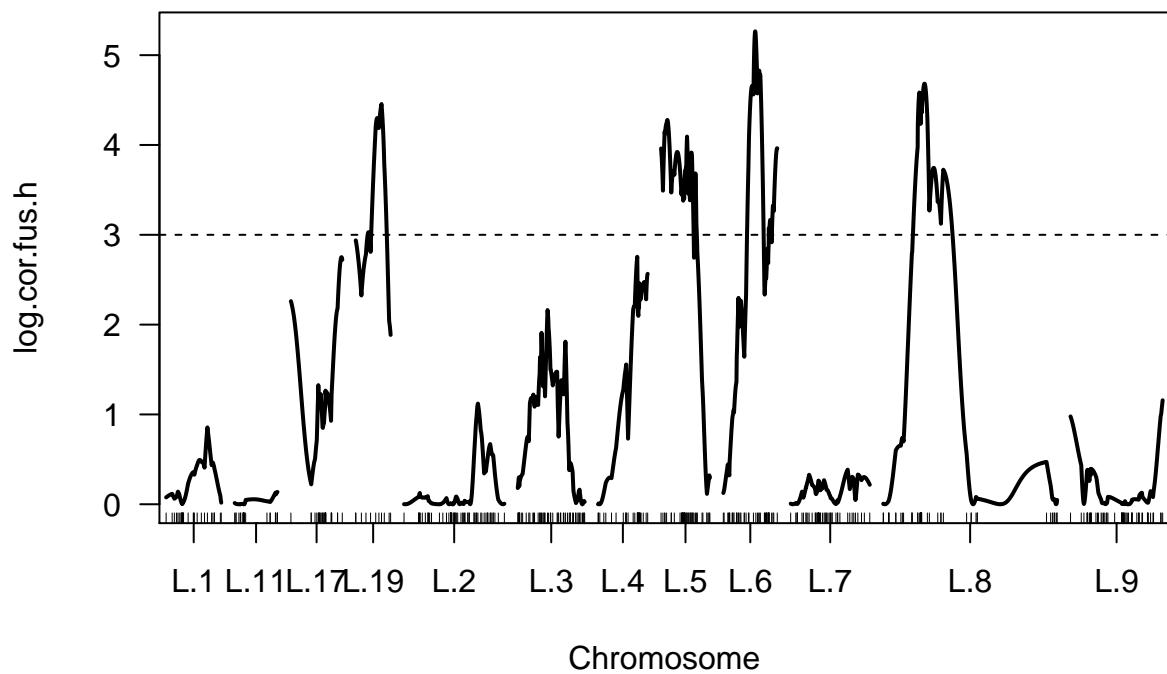


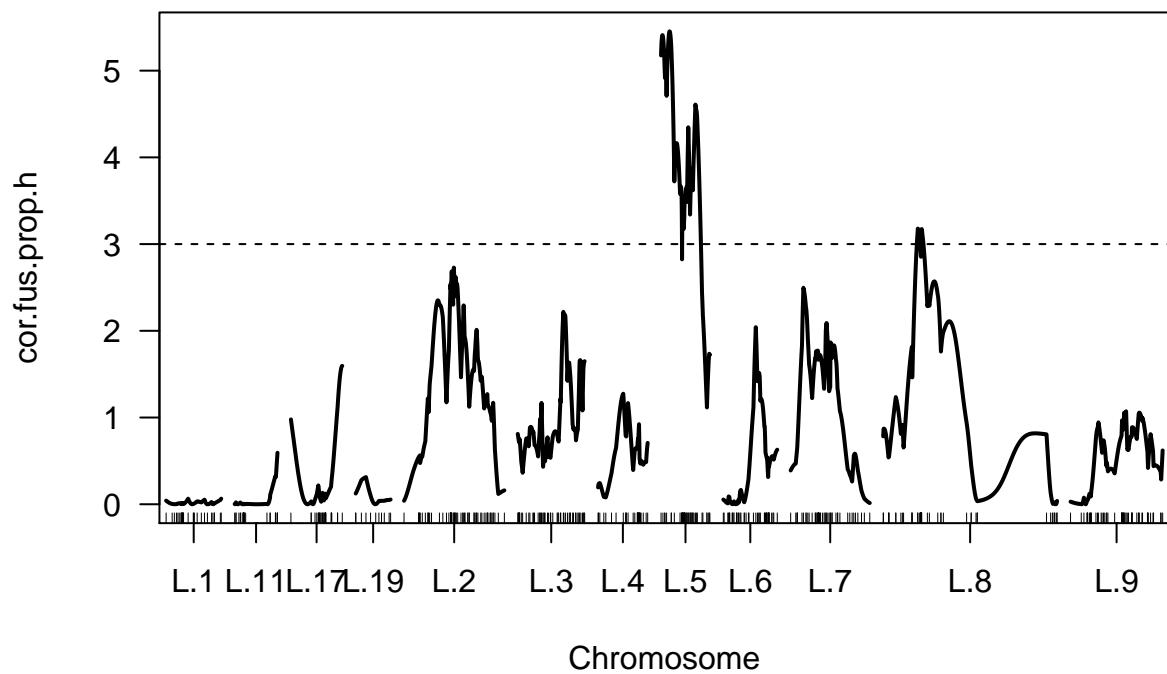


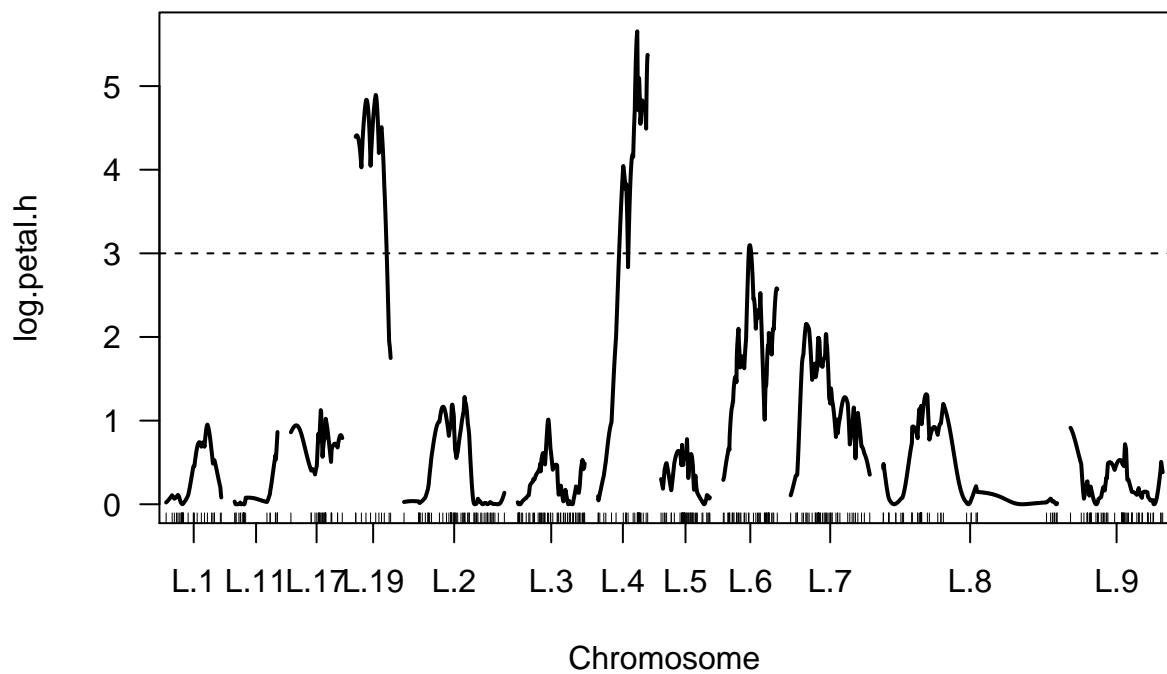


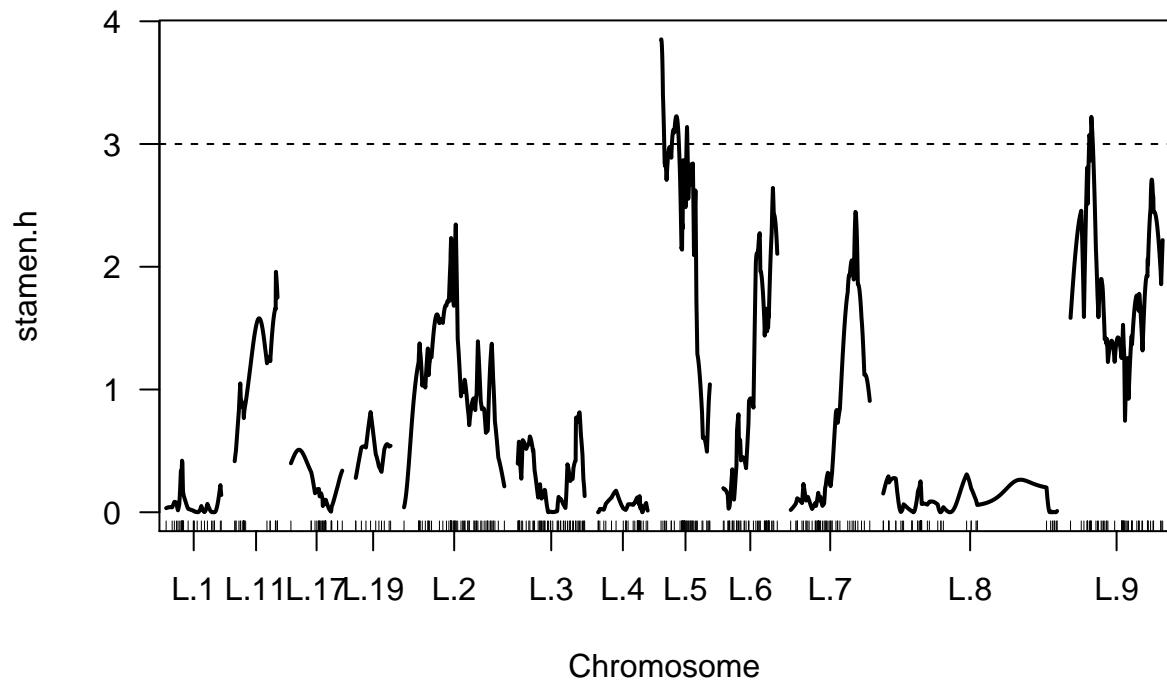


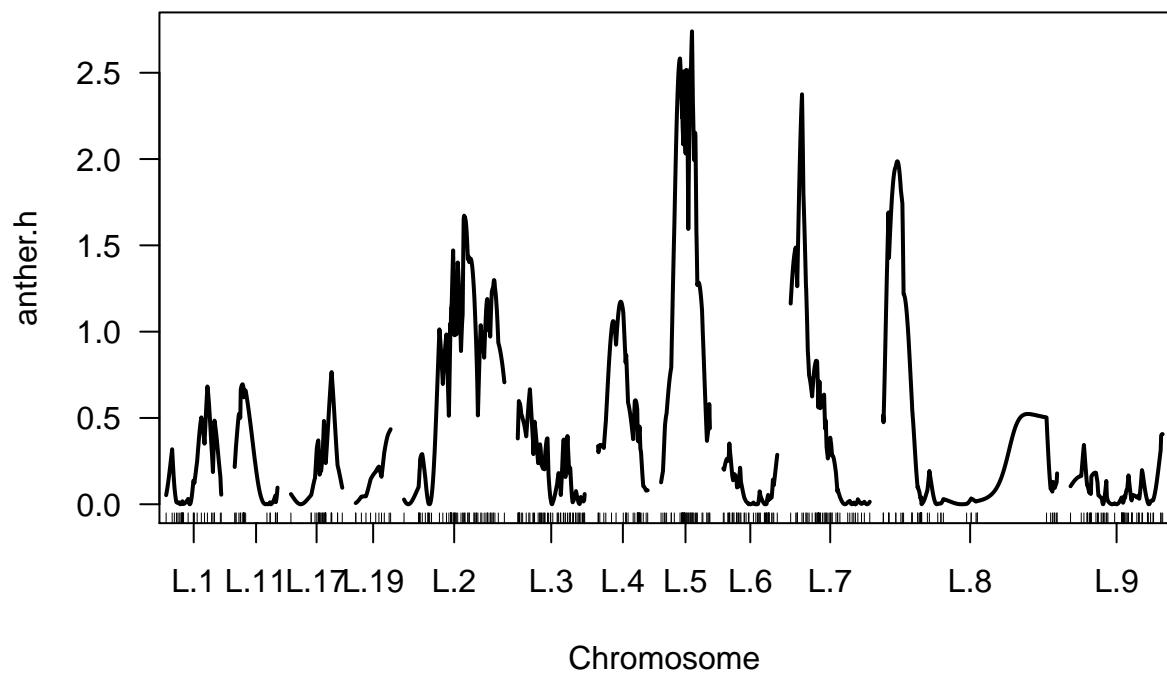


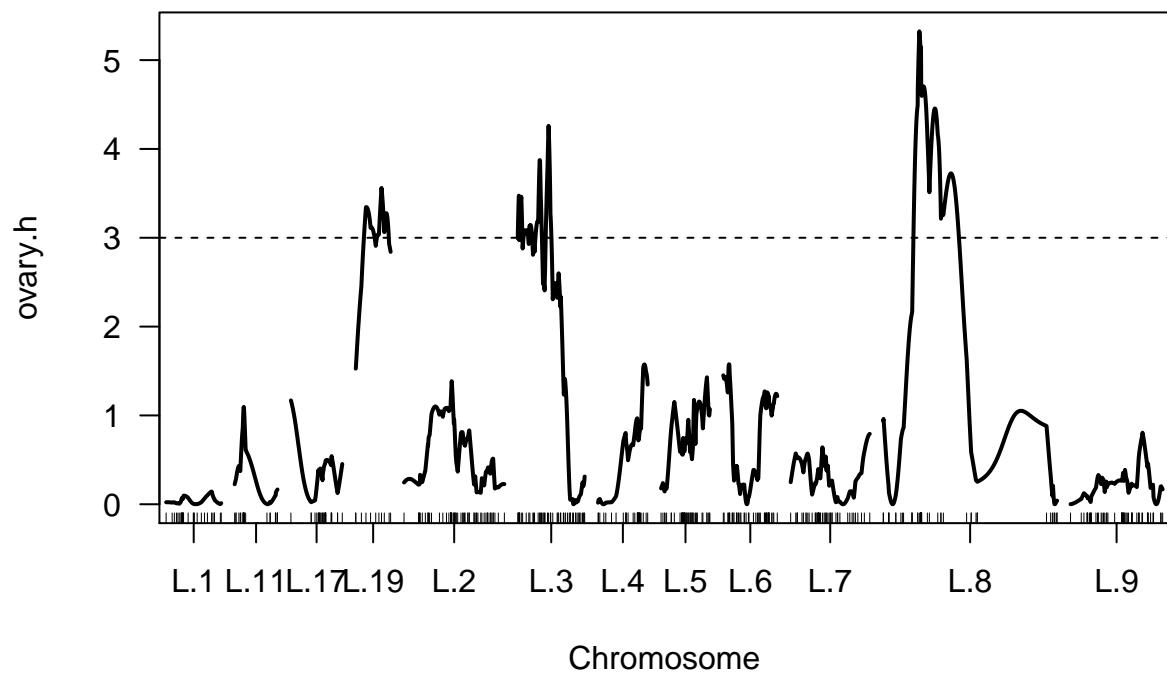


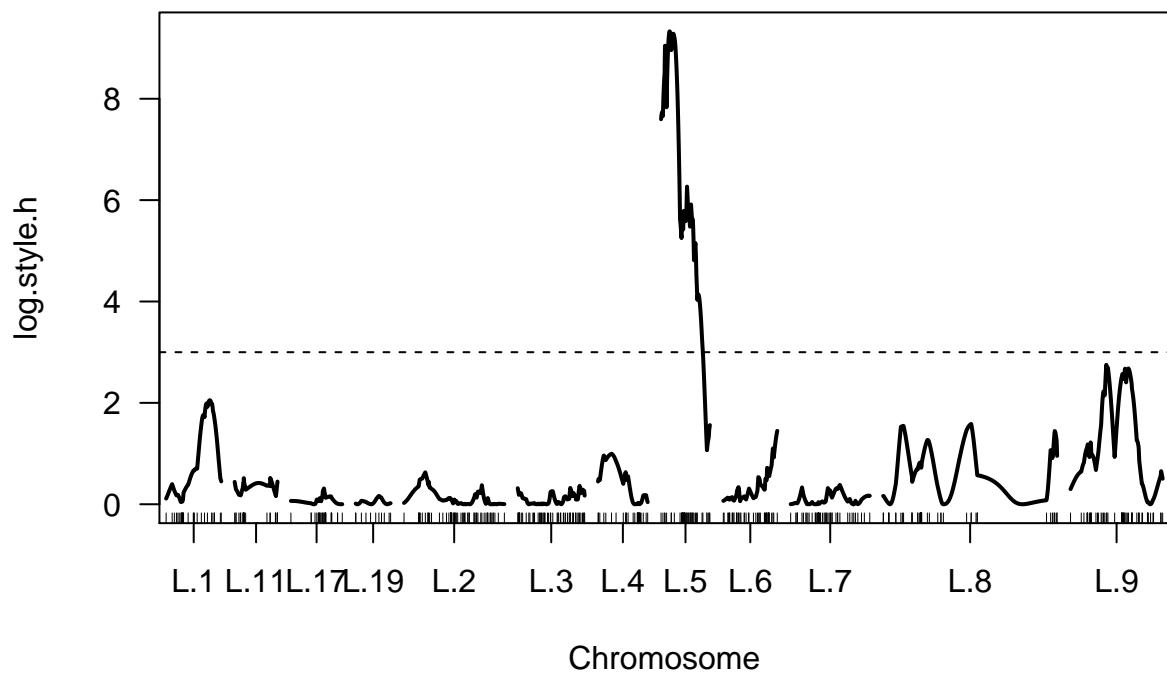


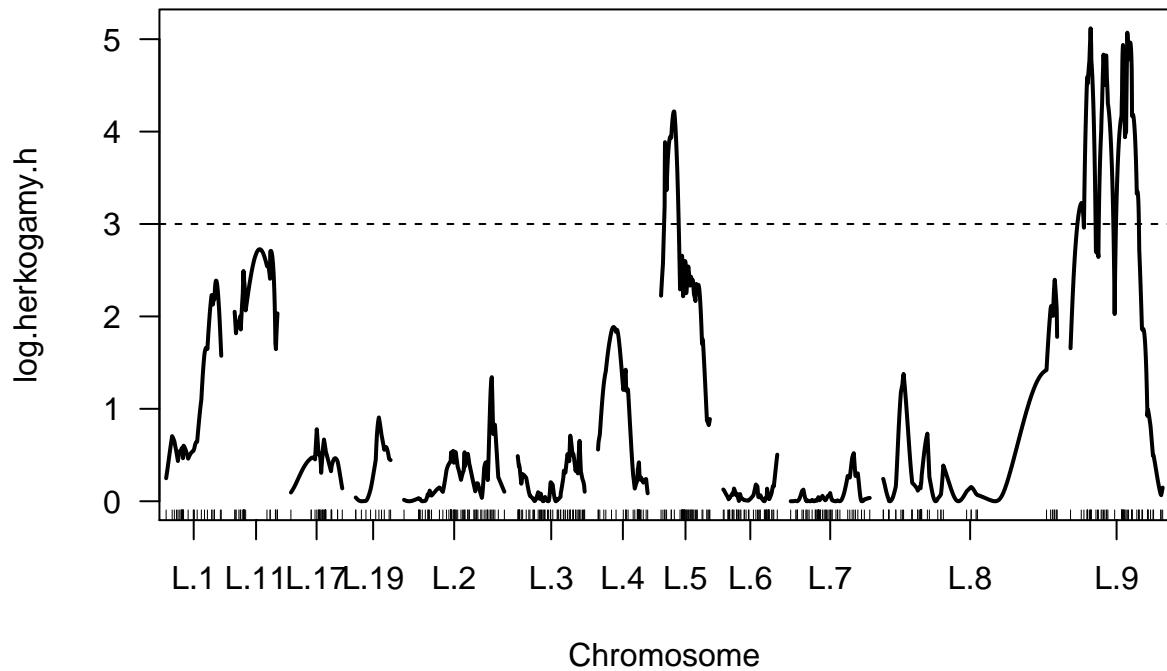








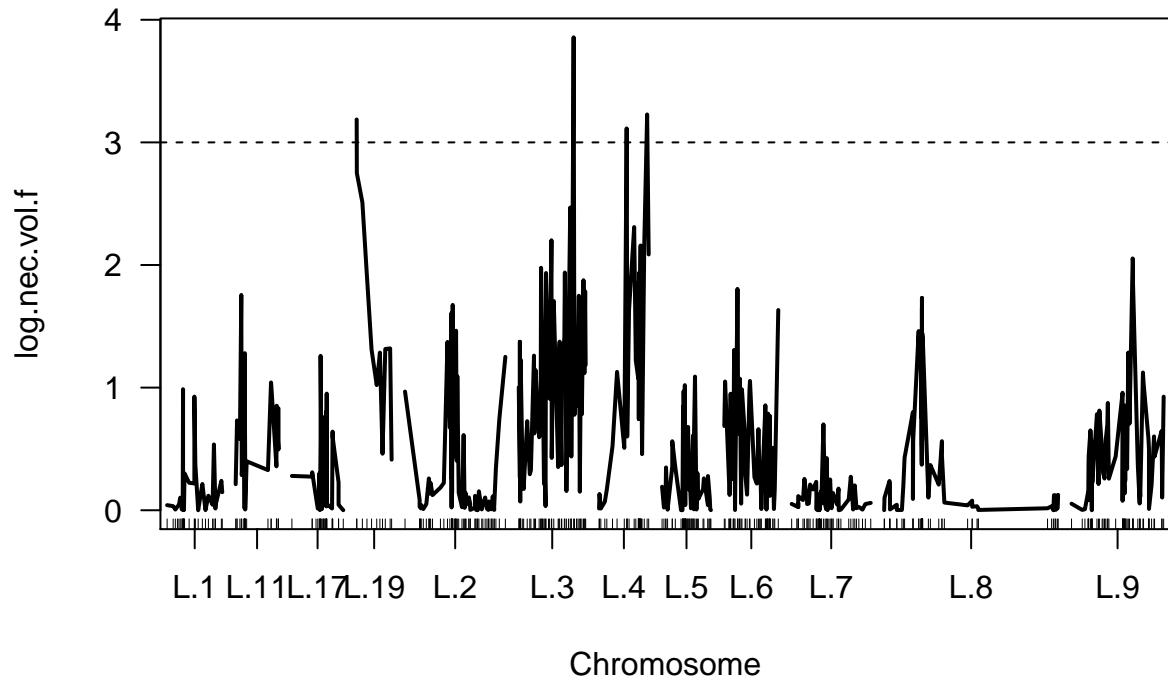


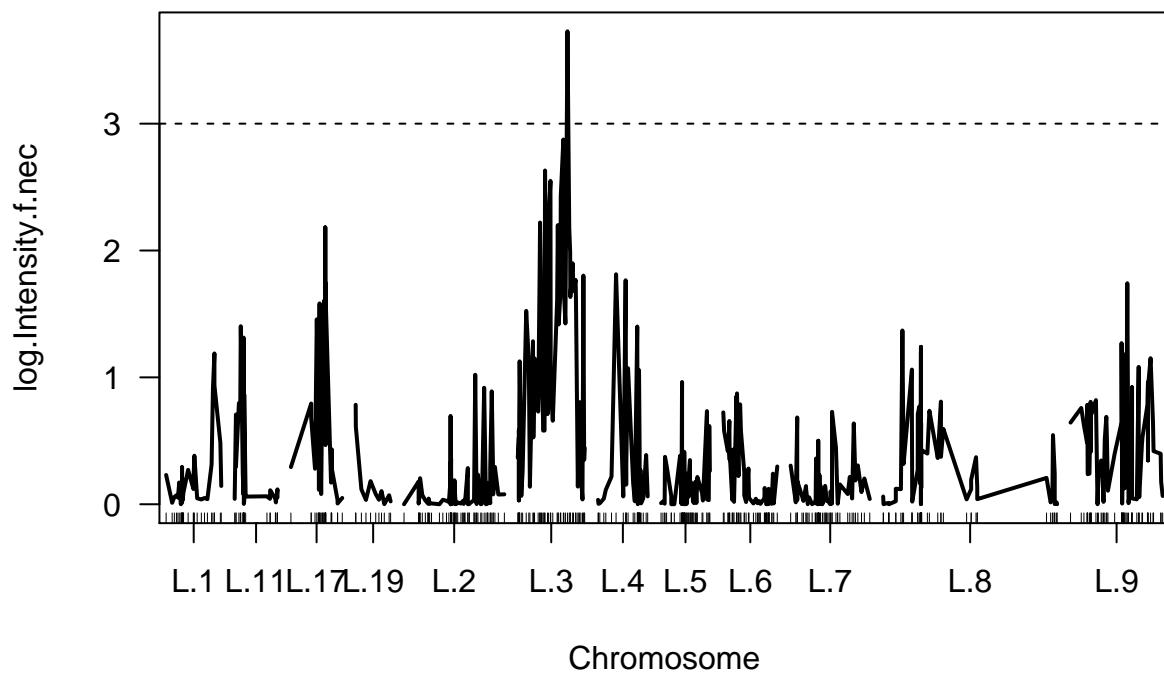


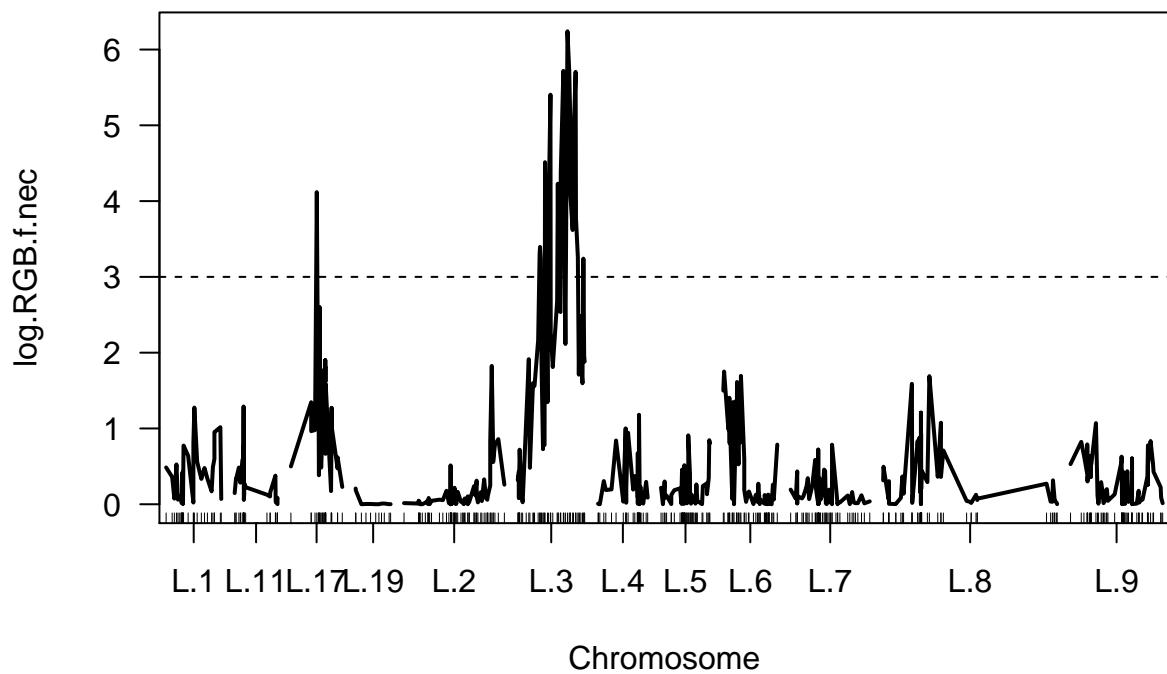
#### Female color

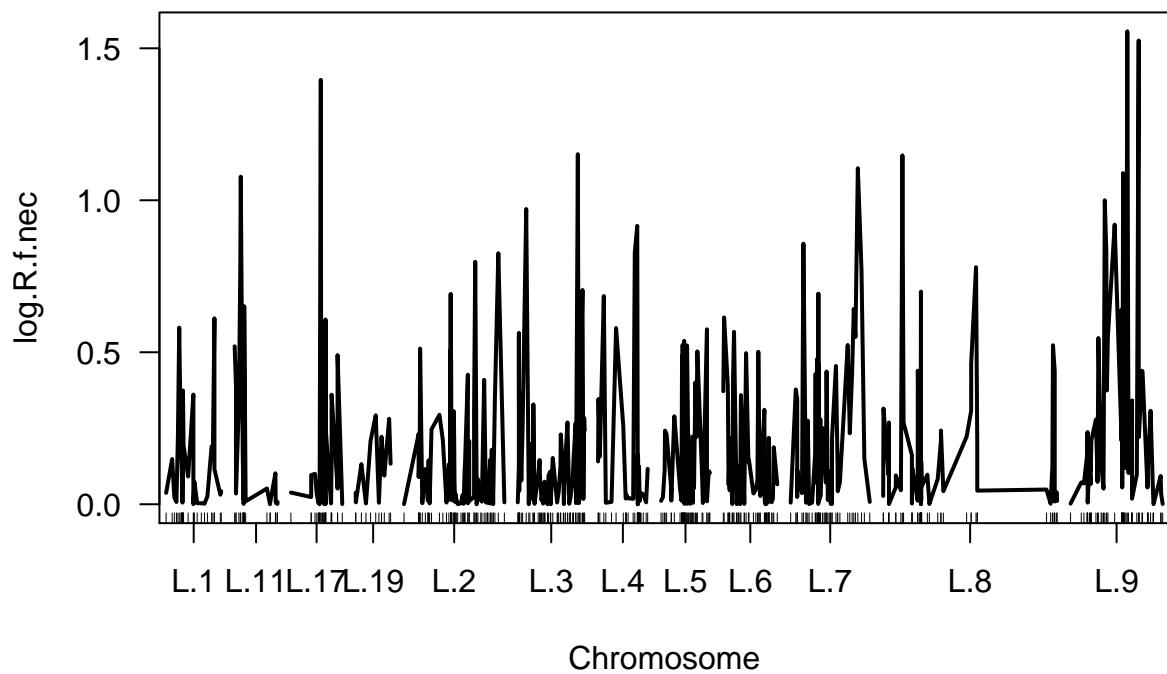
```
femColor <- scanone(mapJal5.1, pheno.col=c(42:58), method="mr", addcovar=fcolor)

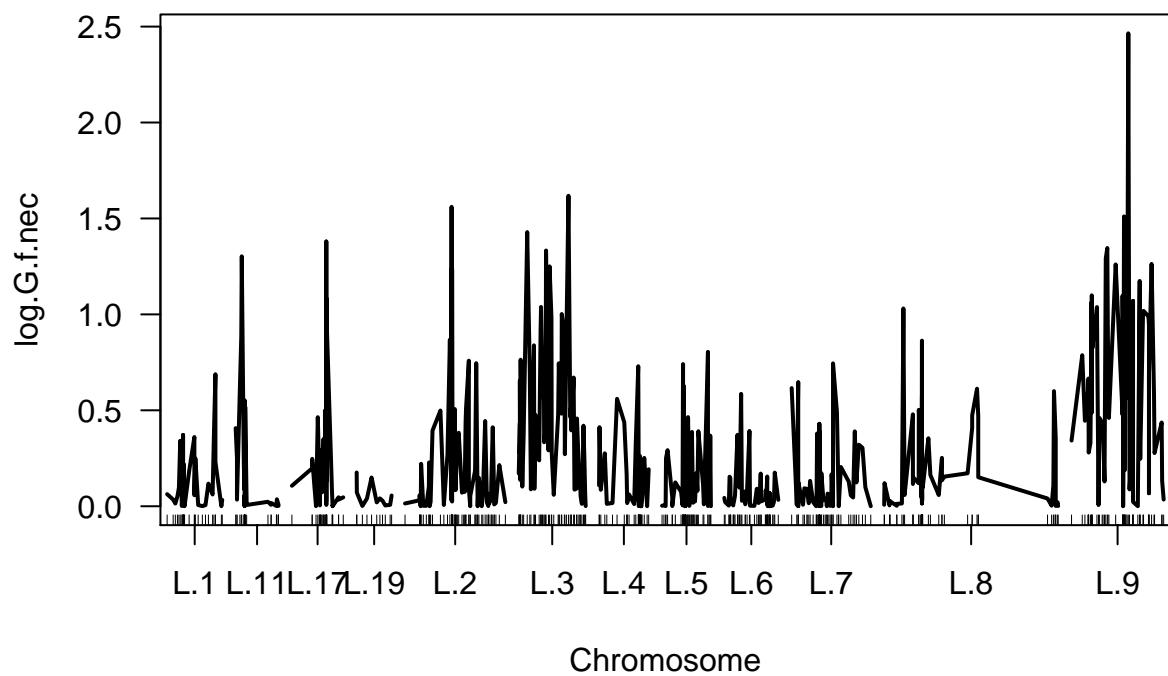
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 46 individuals w
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 4 individuals wi
for (x in 1:17){
  plot(femColor, lodcolumn = x)
  abline(3,0,lty=2)
}
```

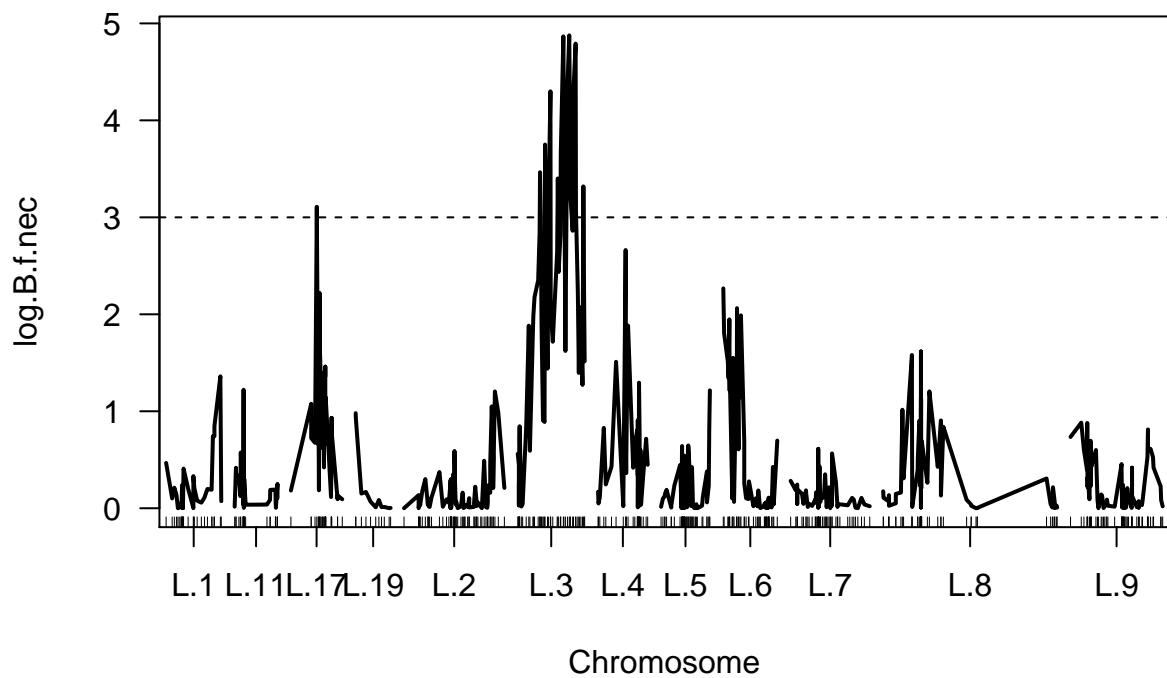


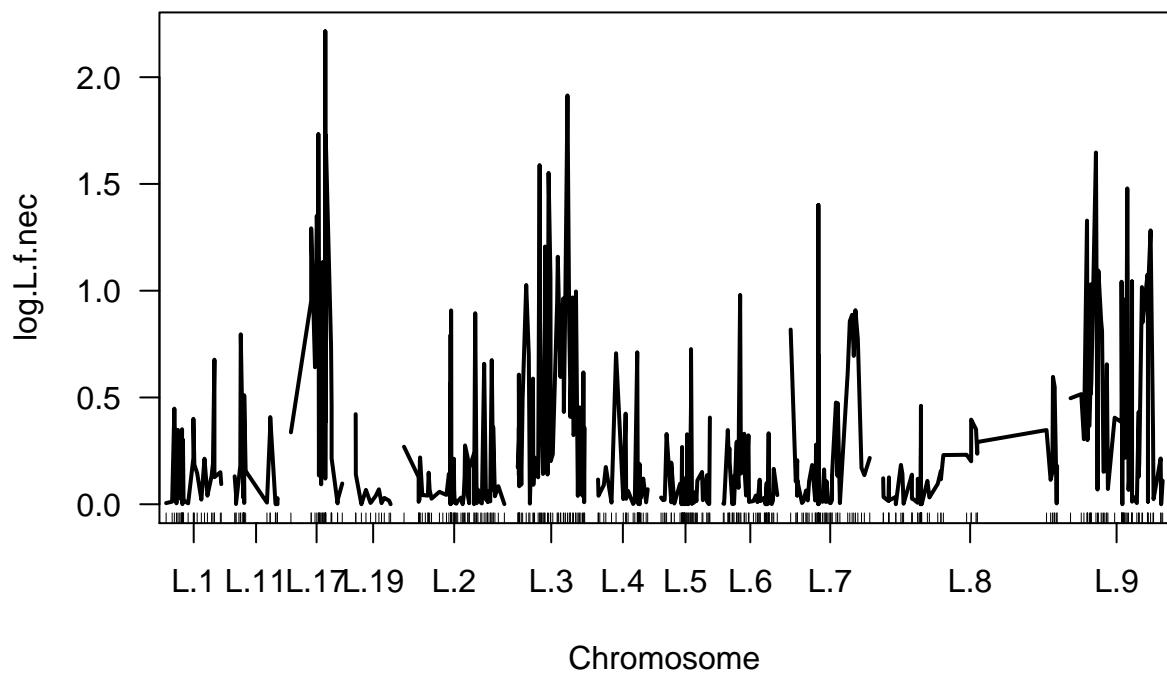


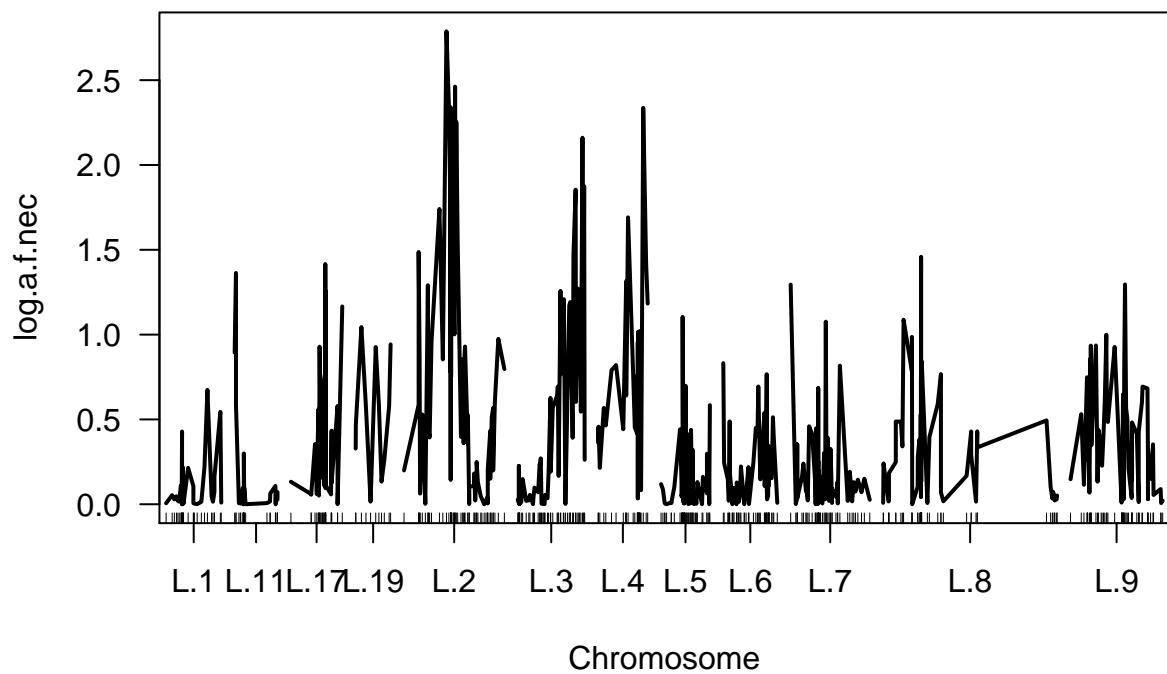


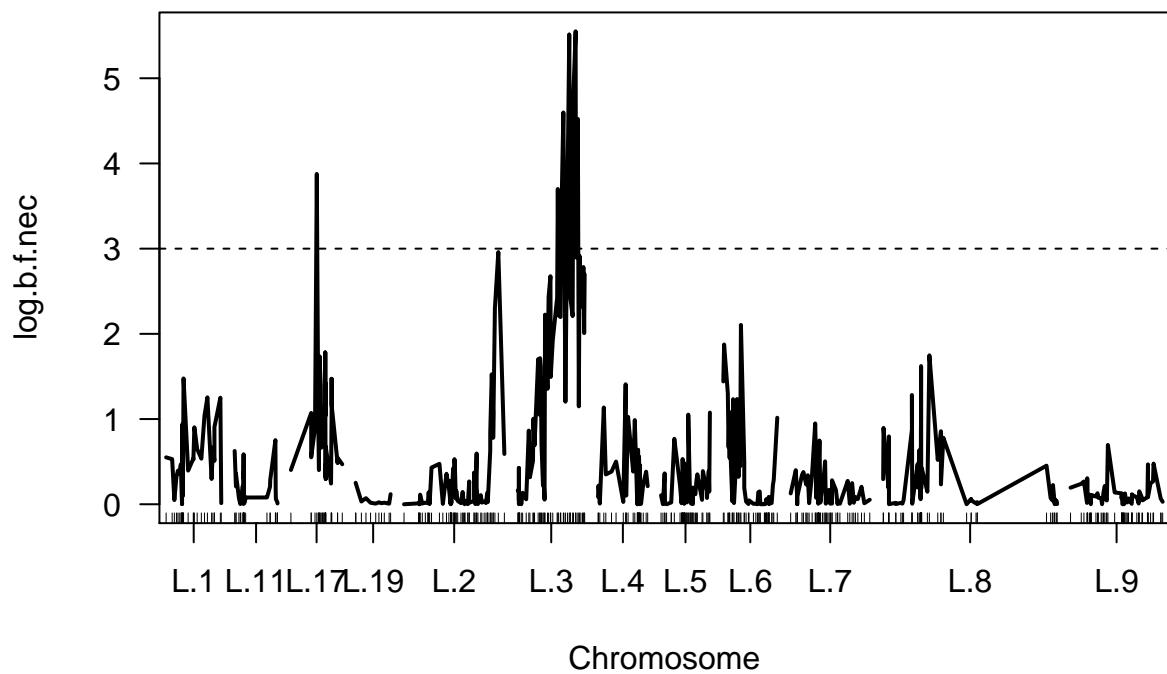


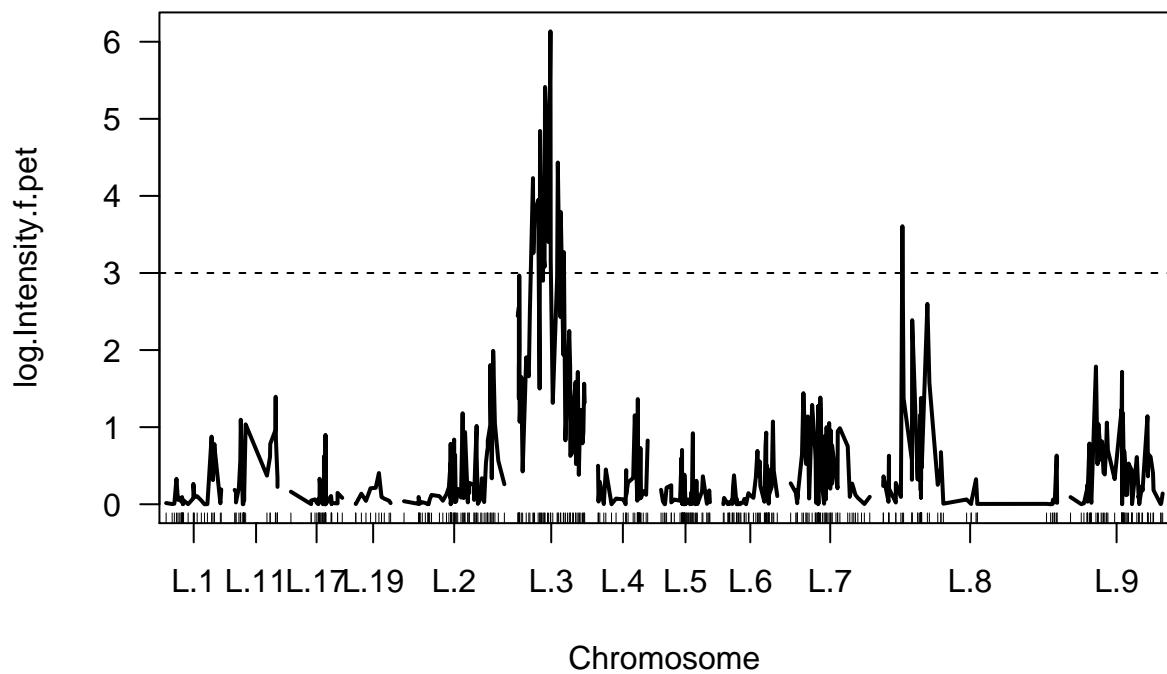


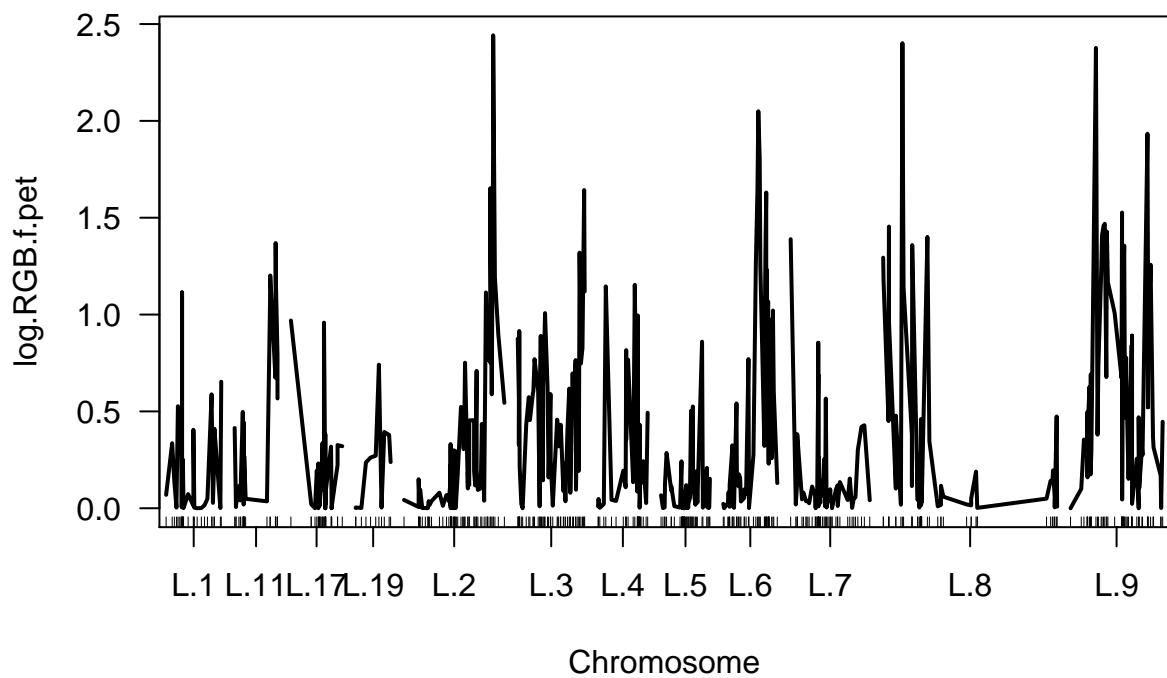


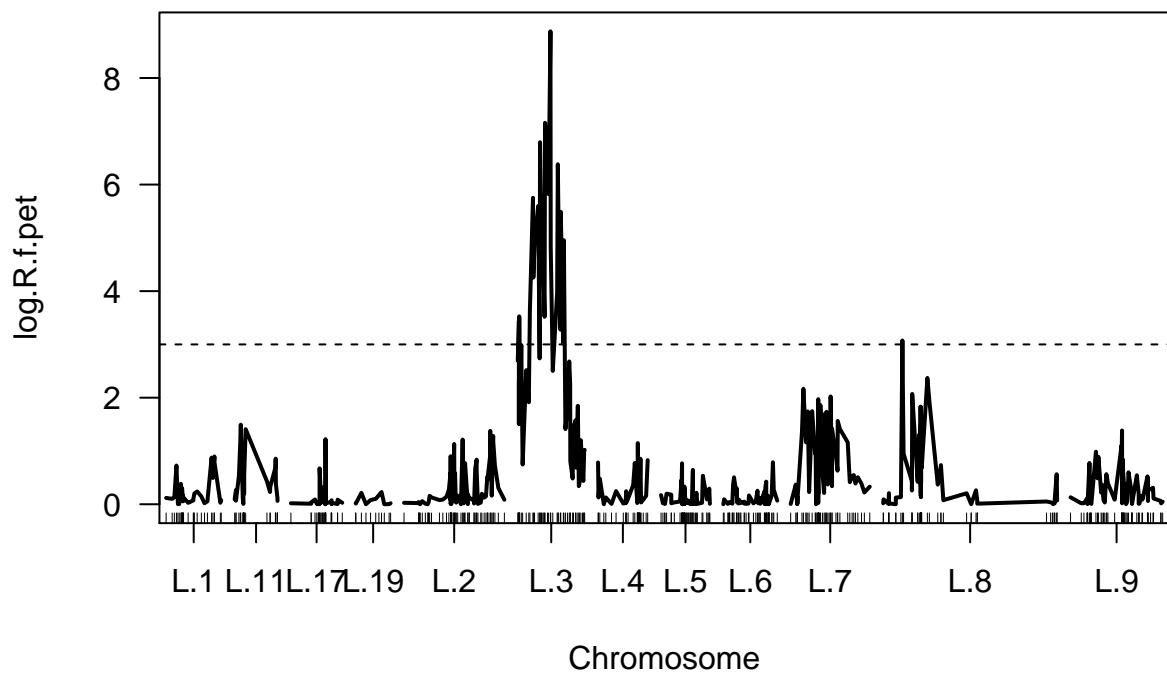


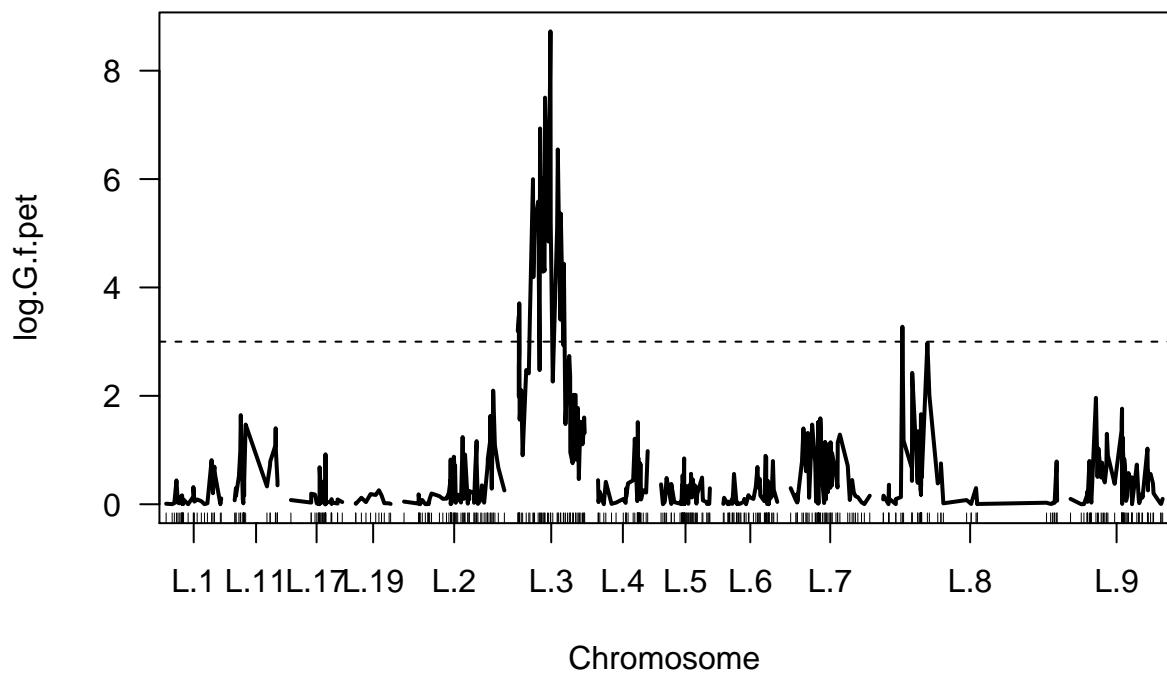


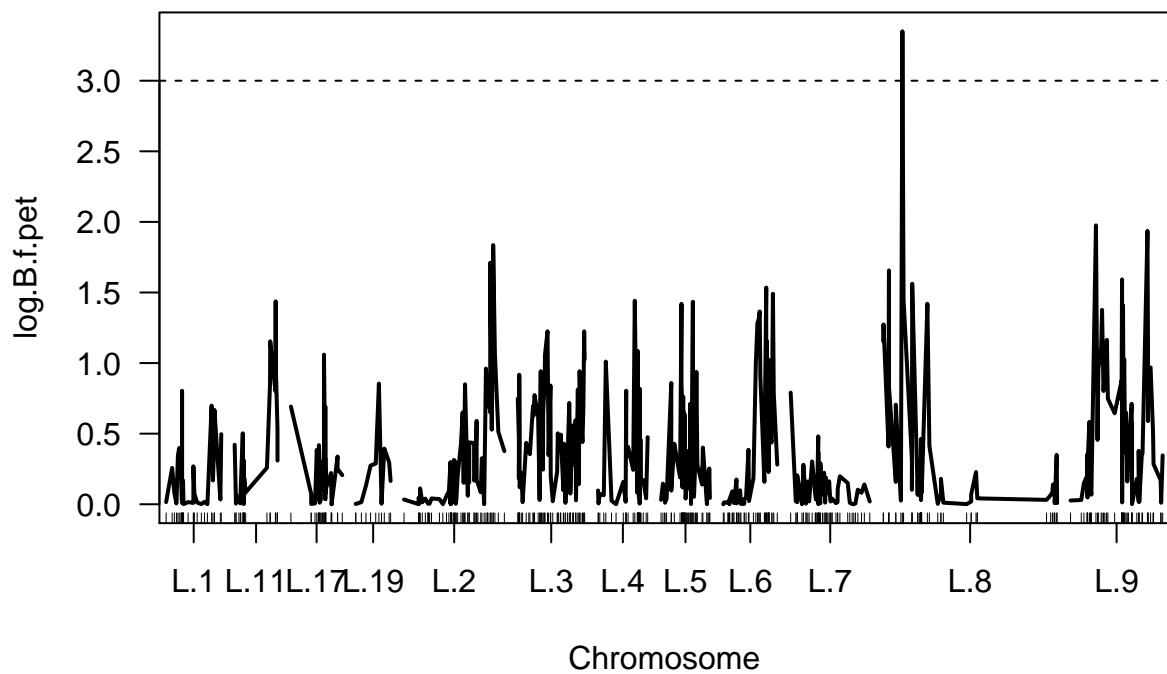


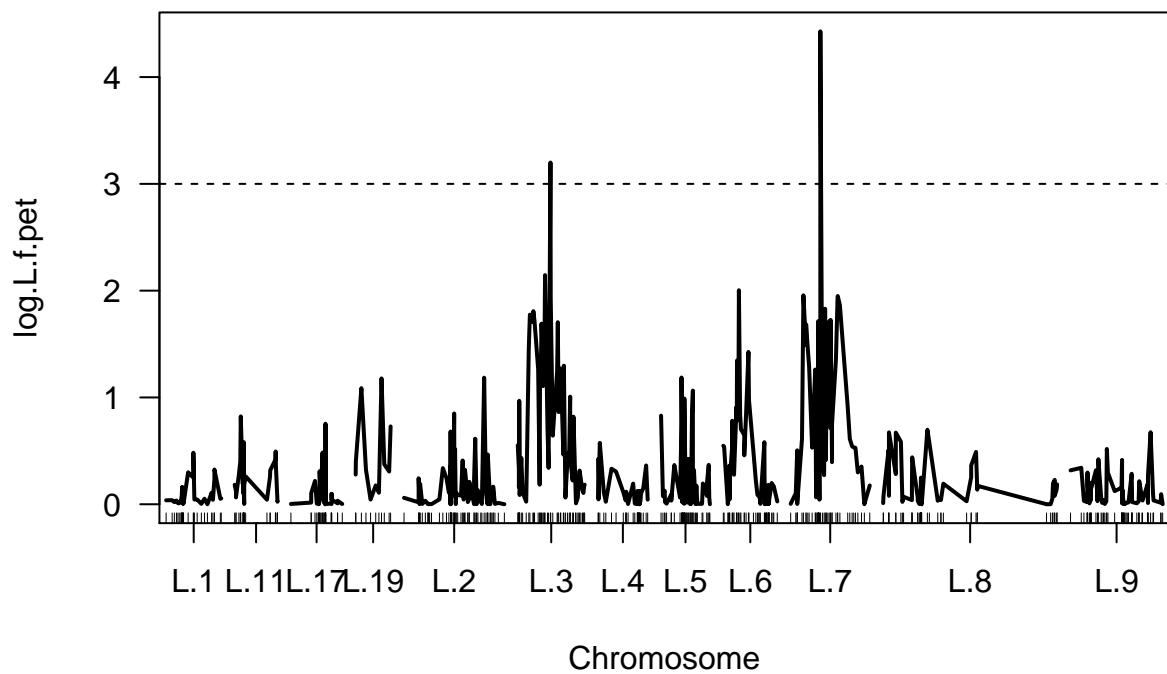


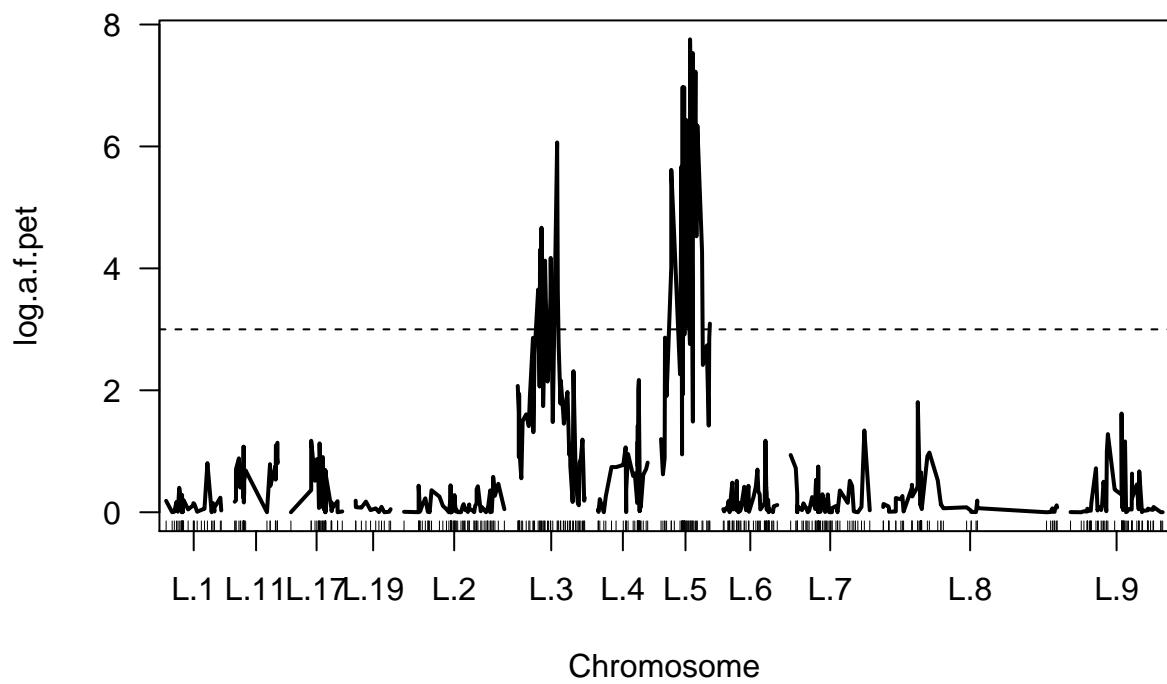


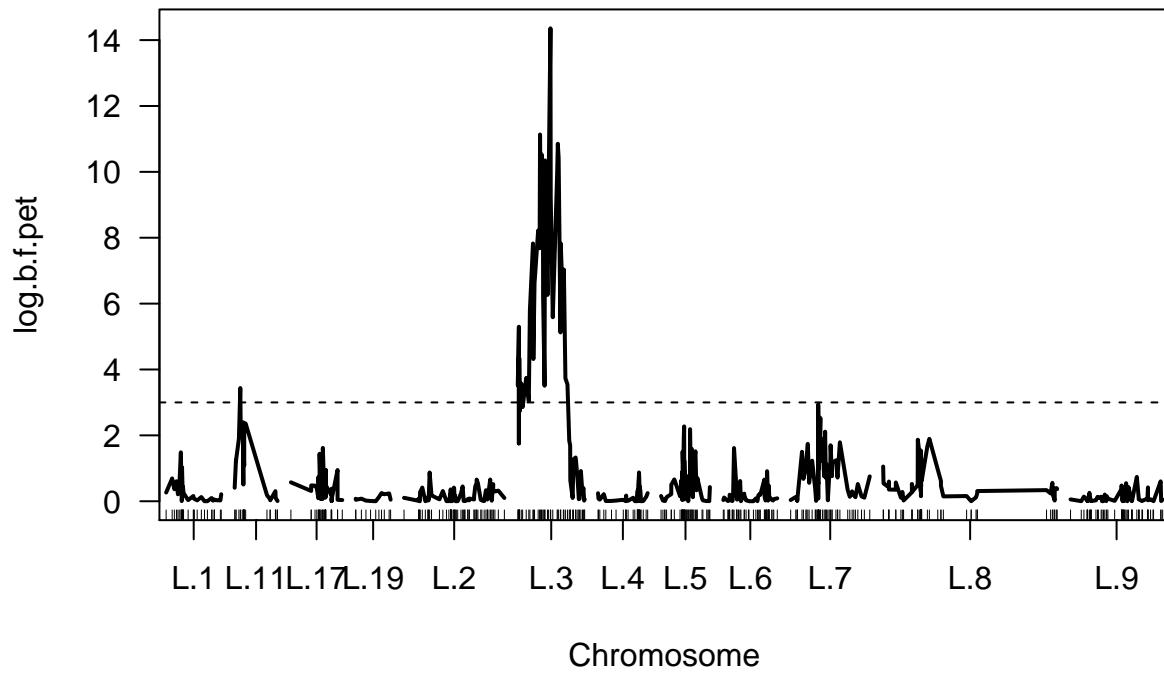








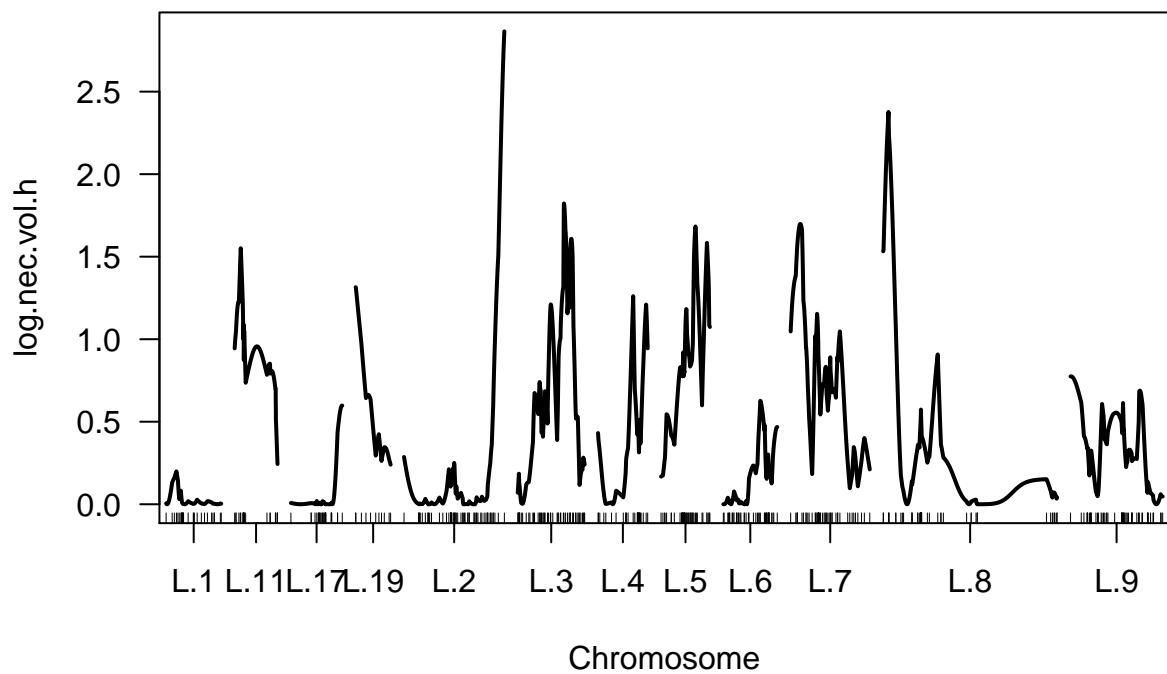


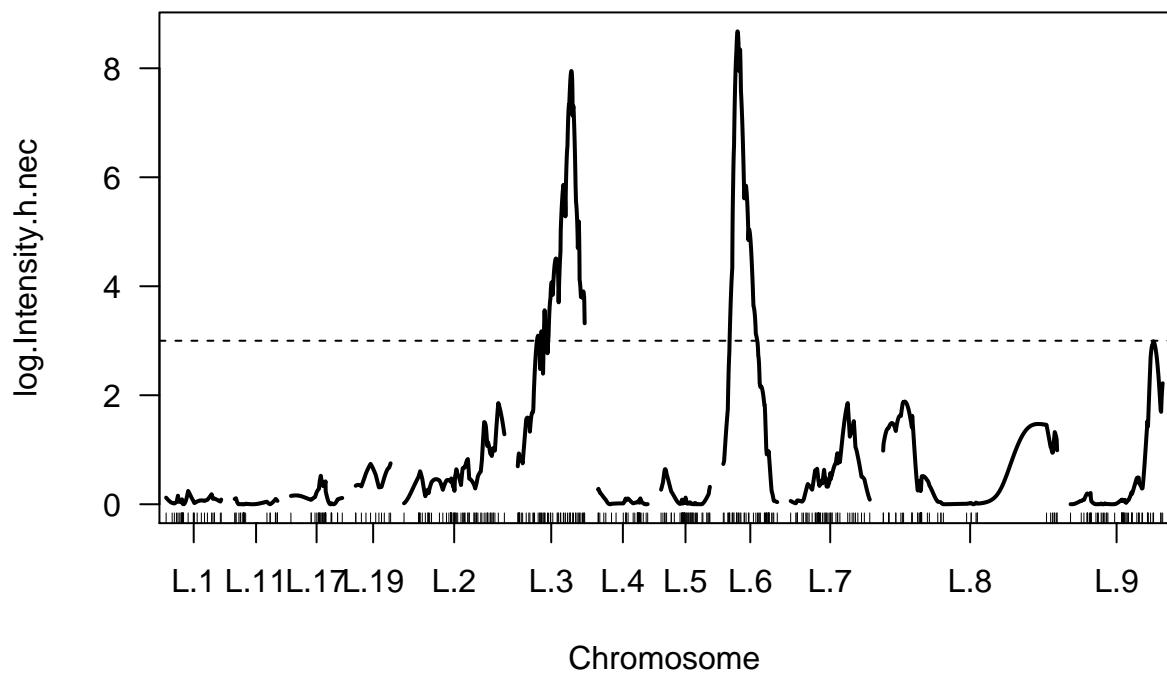


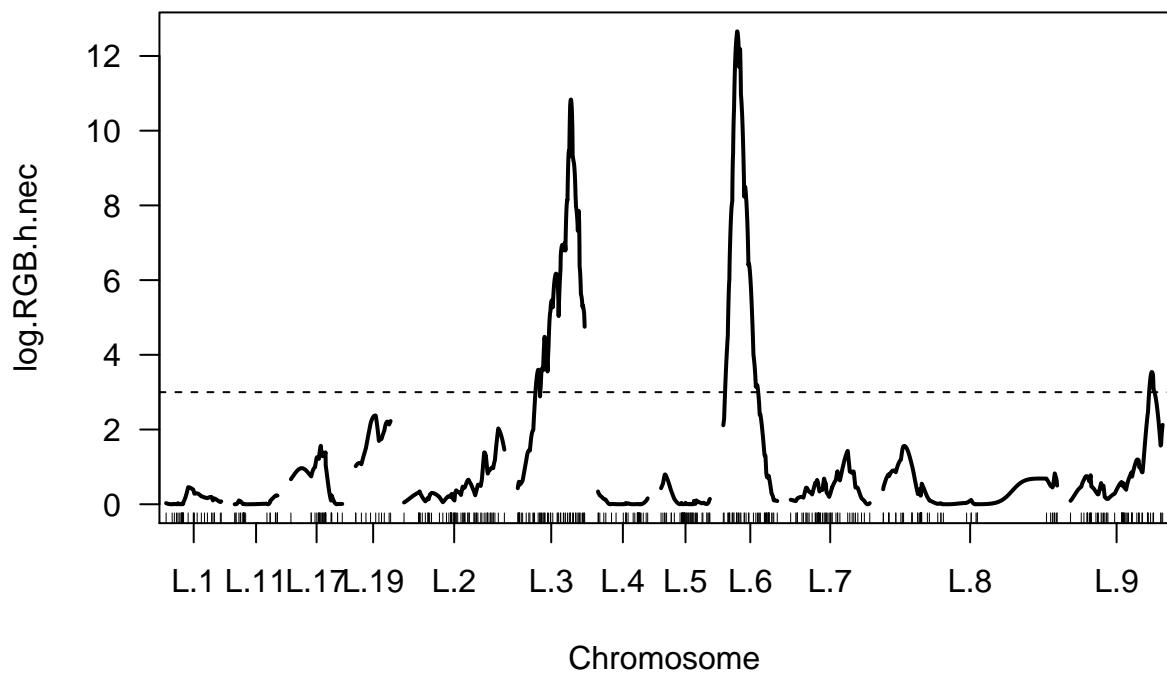
### Herm color

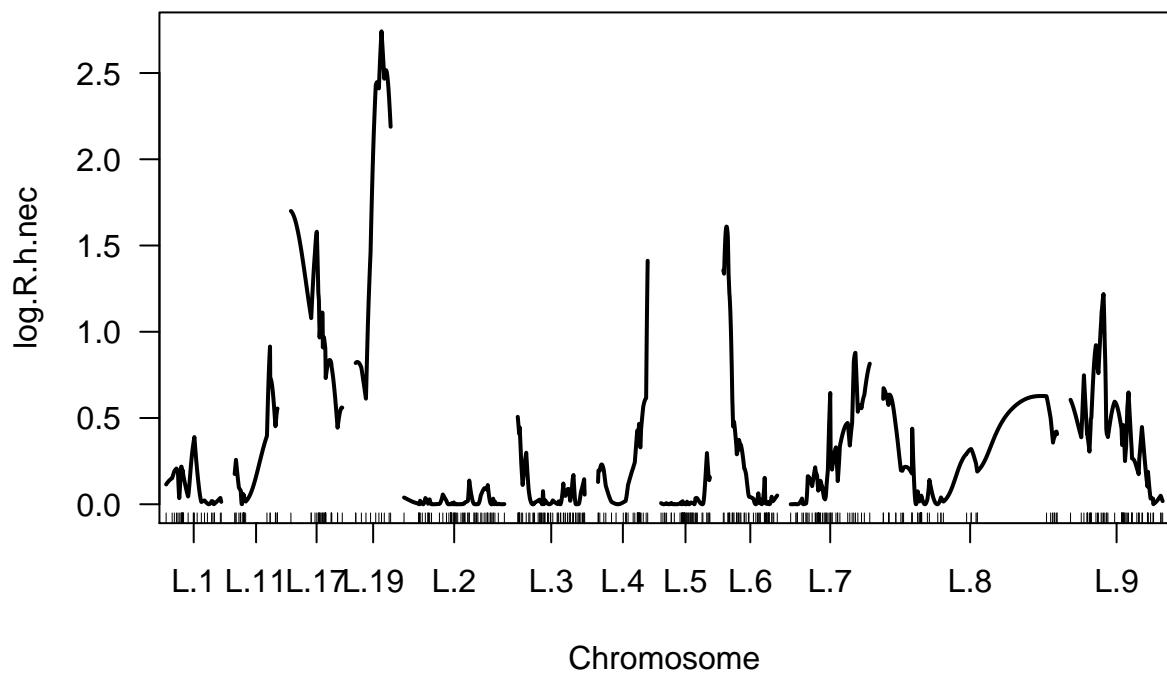
```
hermColor <- scanone(mapJal5.1, pheno.col=c(59:75), method="em", addcovar=hcolor)

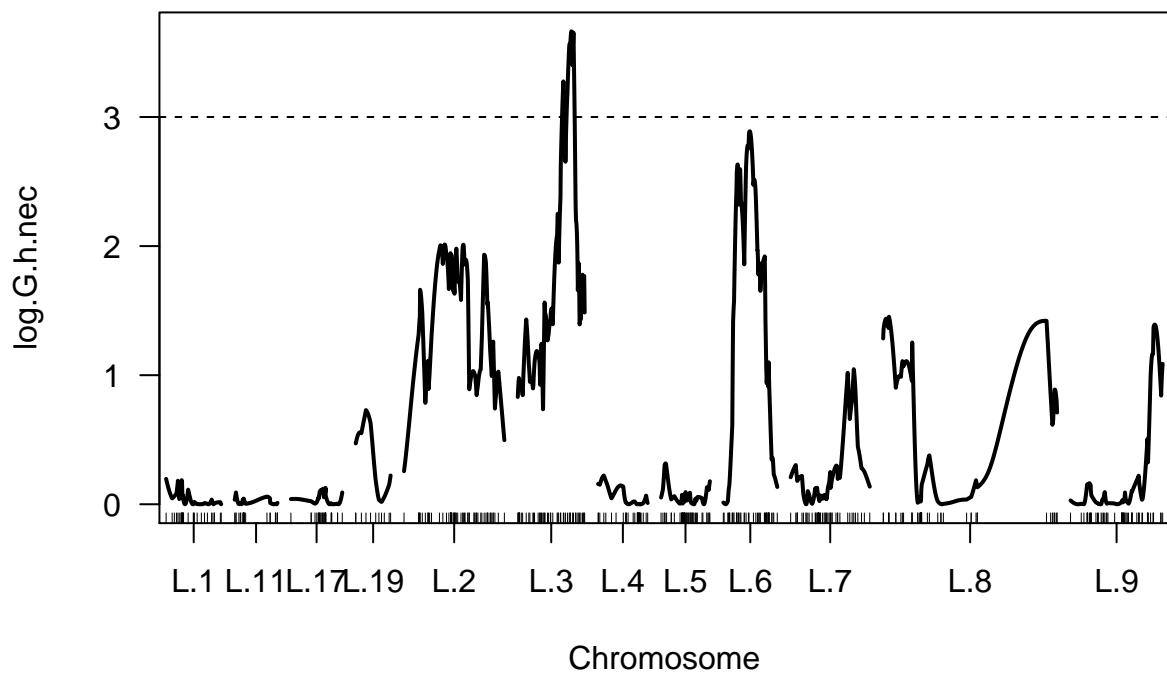
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 3 individuals wi
for (x in 1:17){
  plot(hermColor, lodcolumn = x)
  abline(3,0,lty=2)
}
```

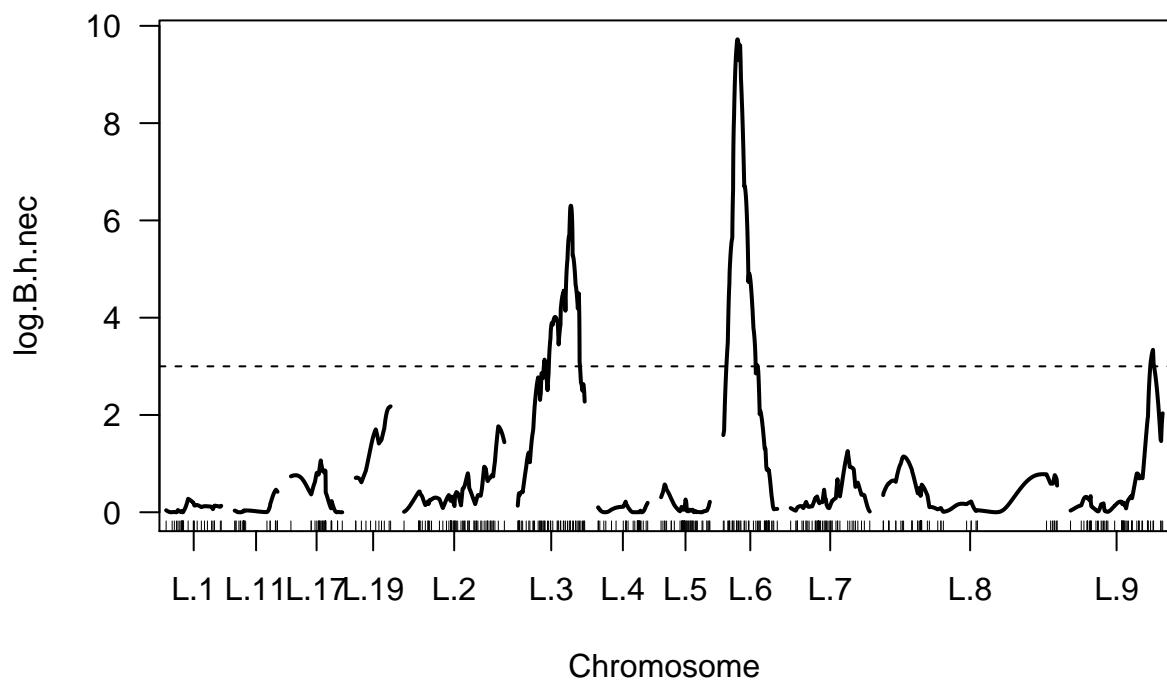


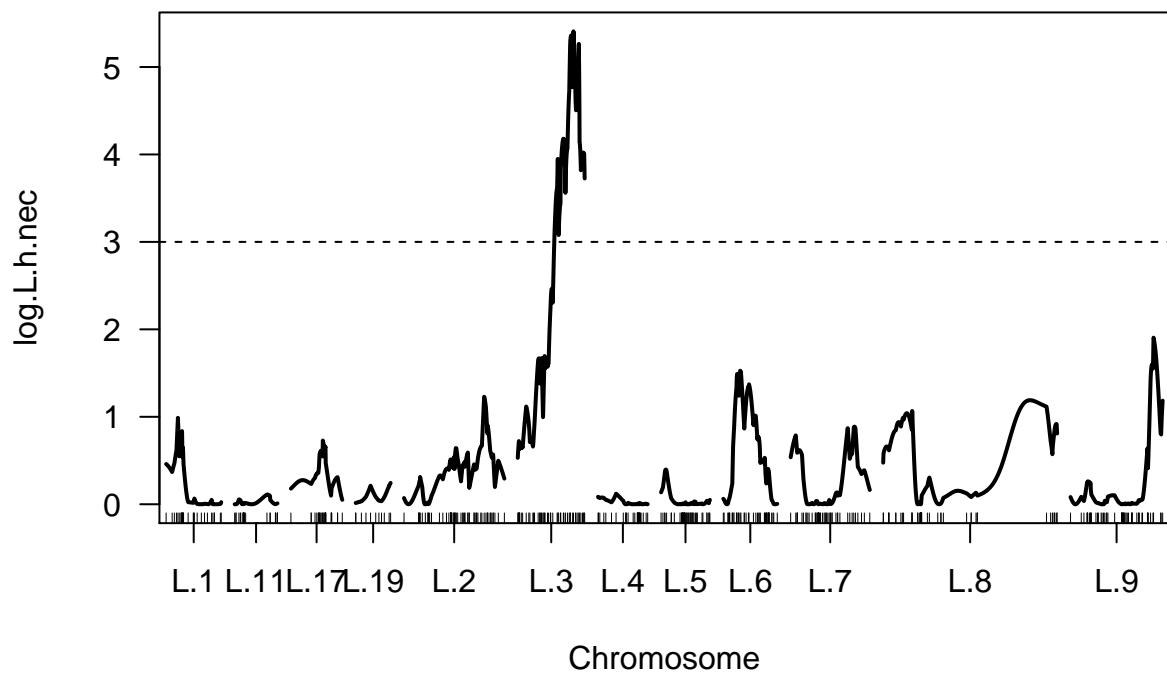


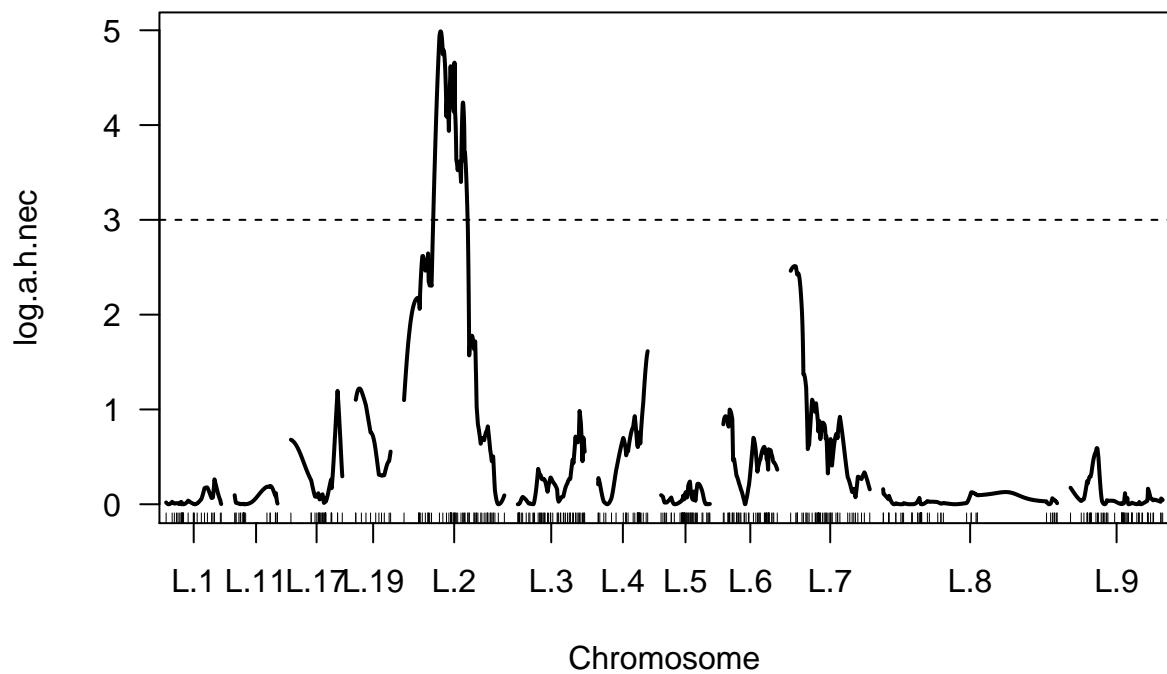


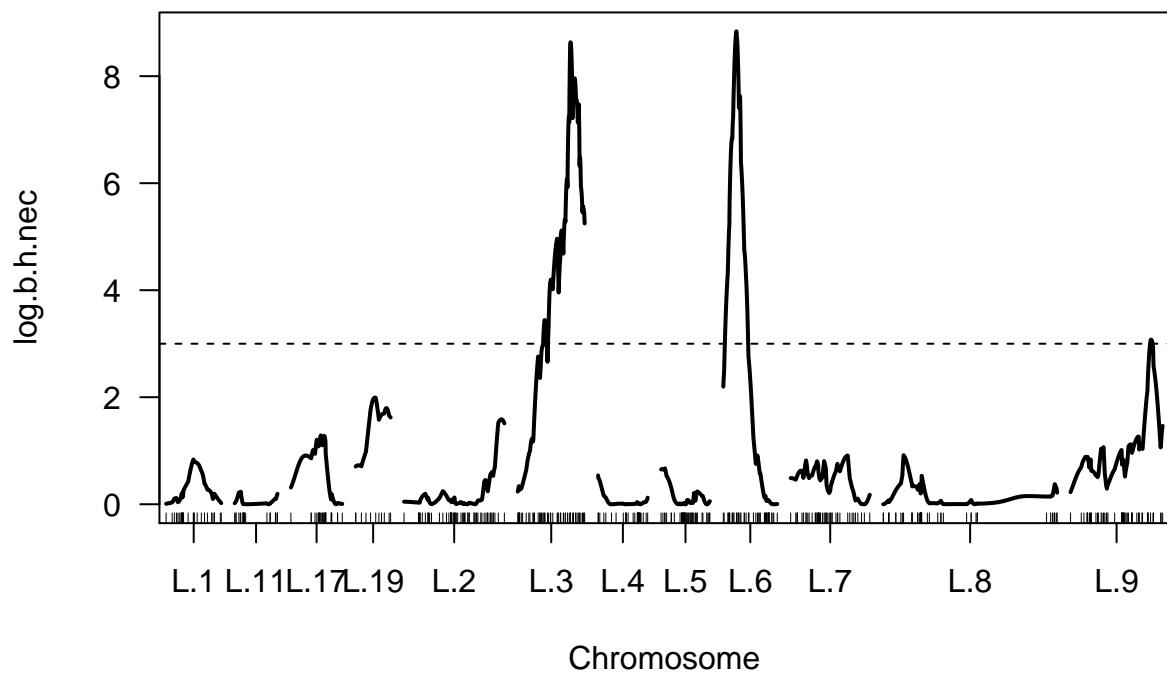


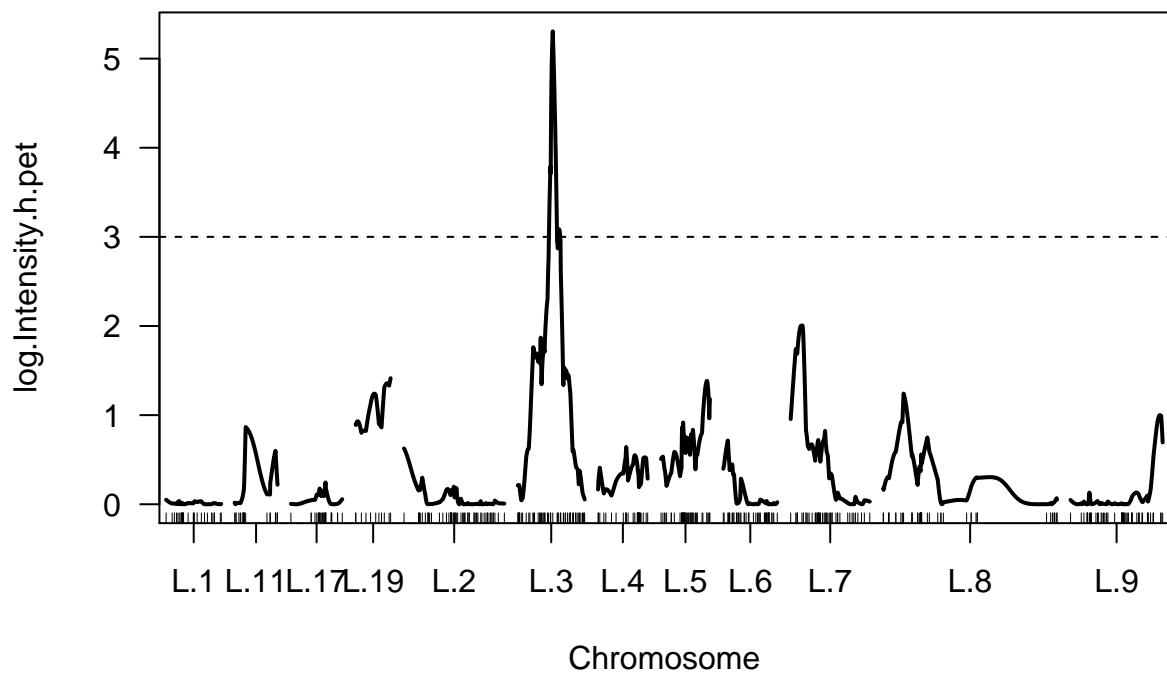


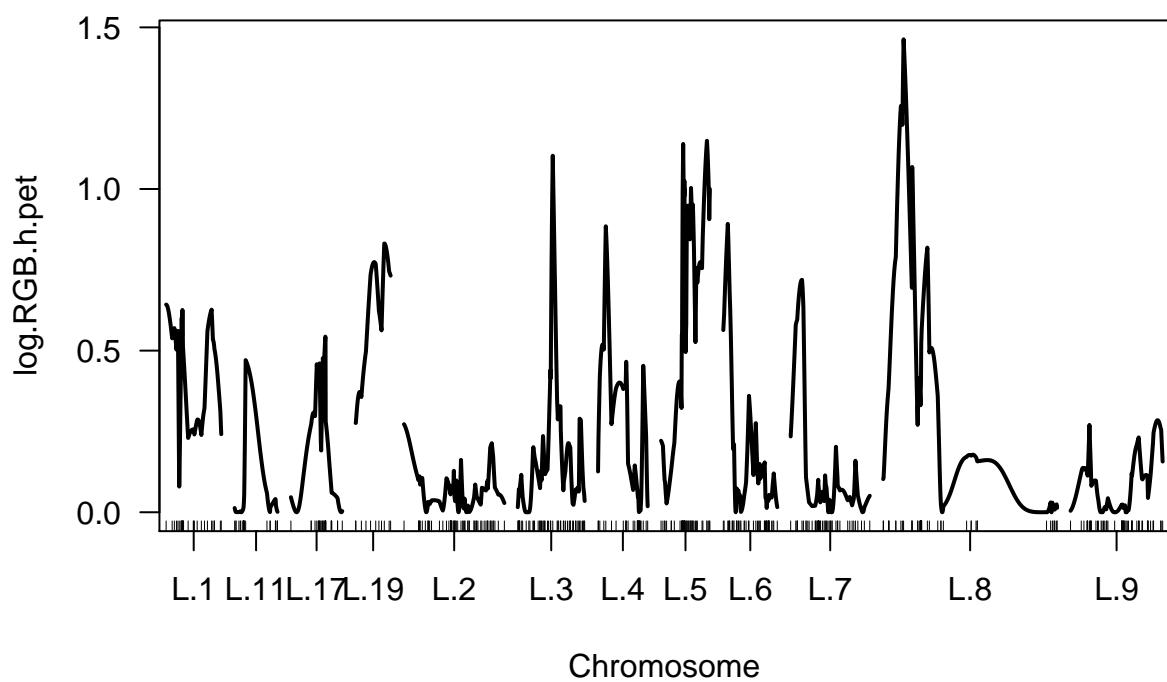


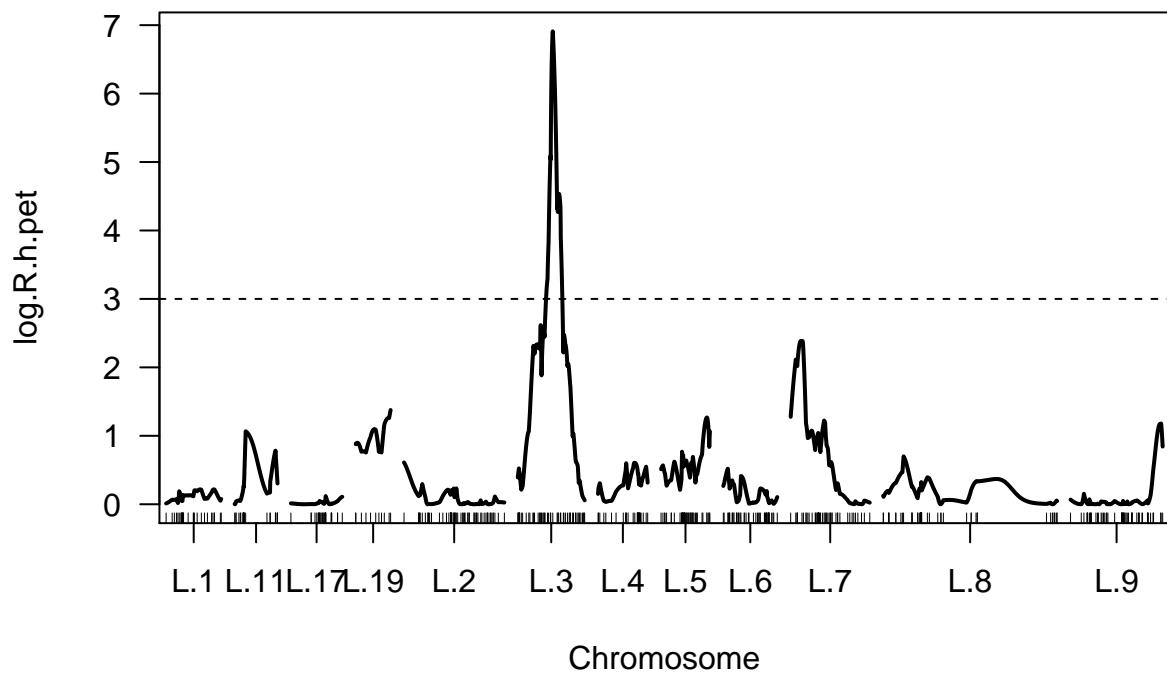


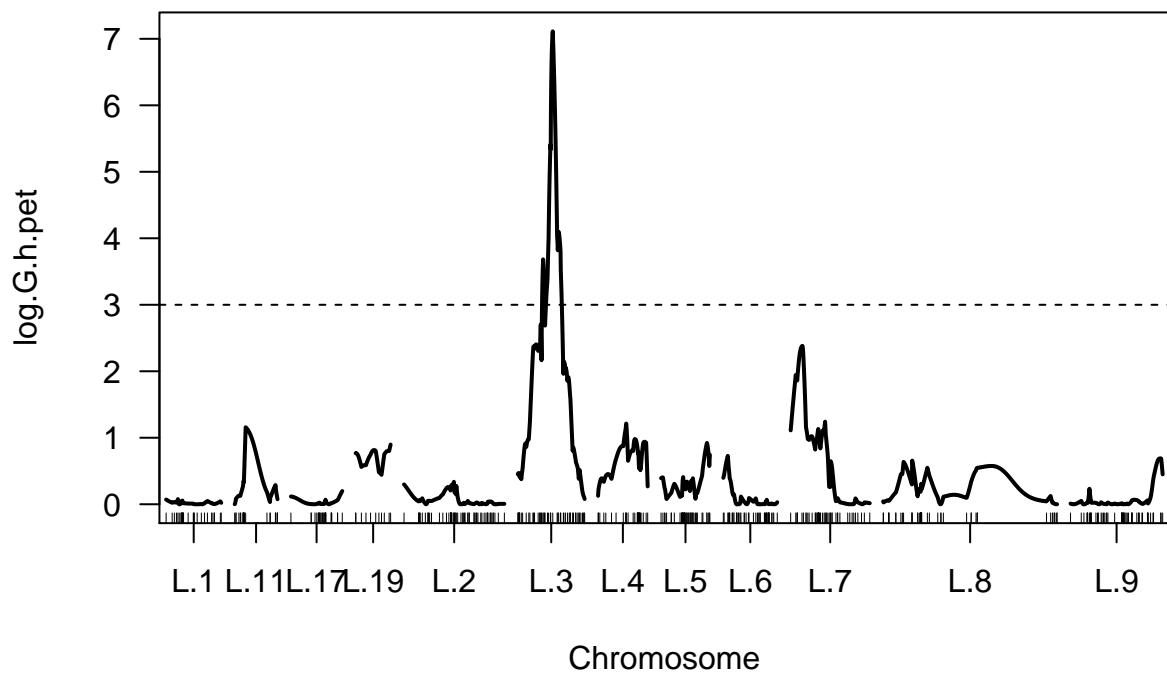


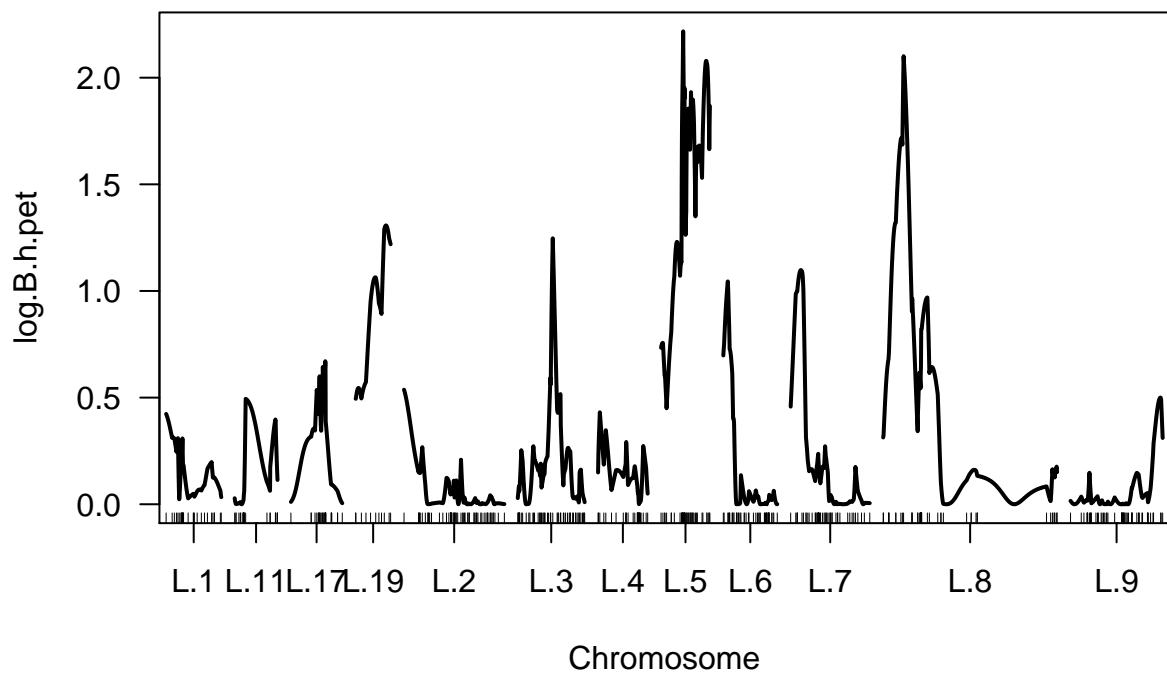


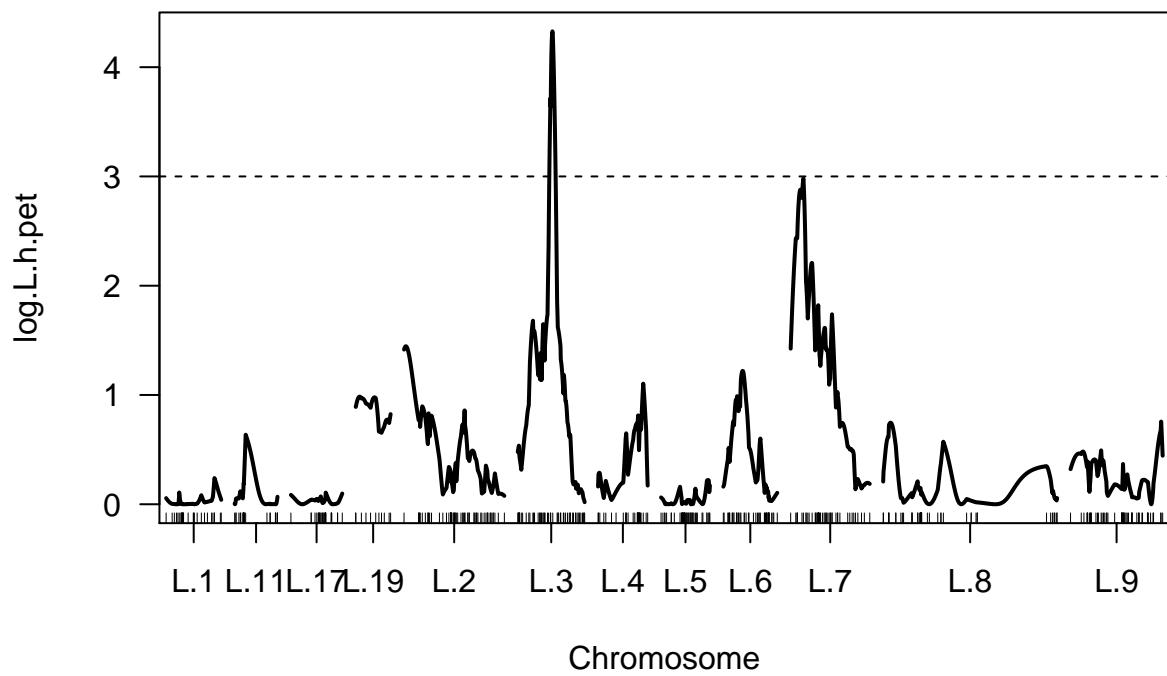


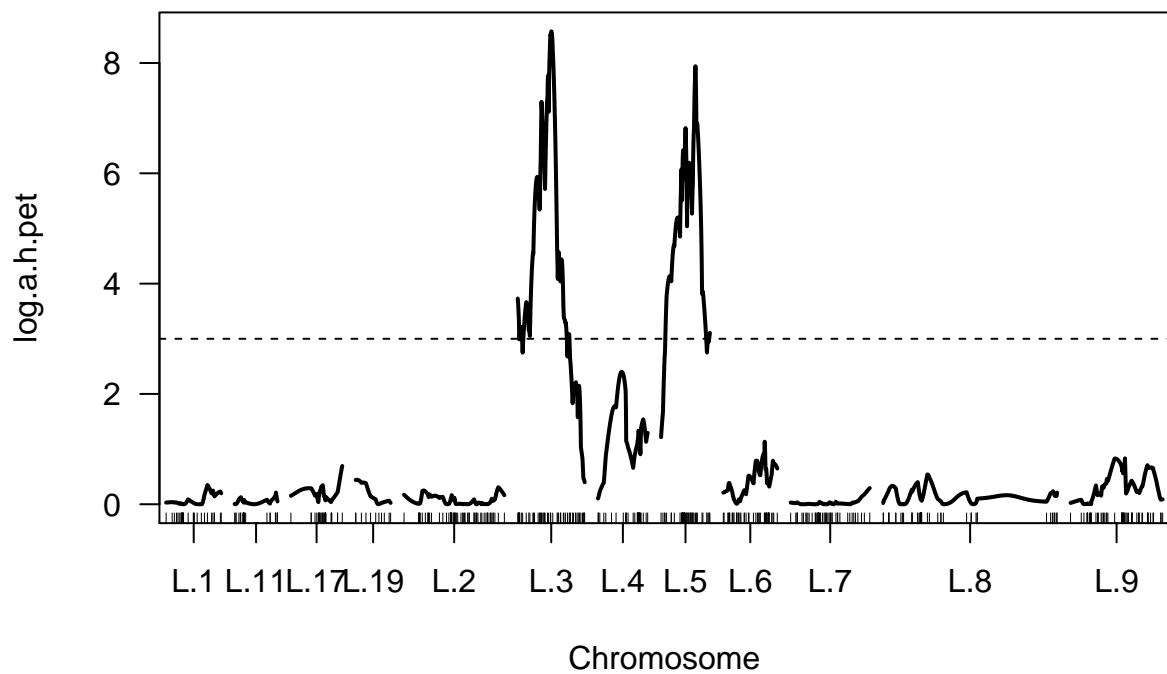


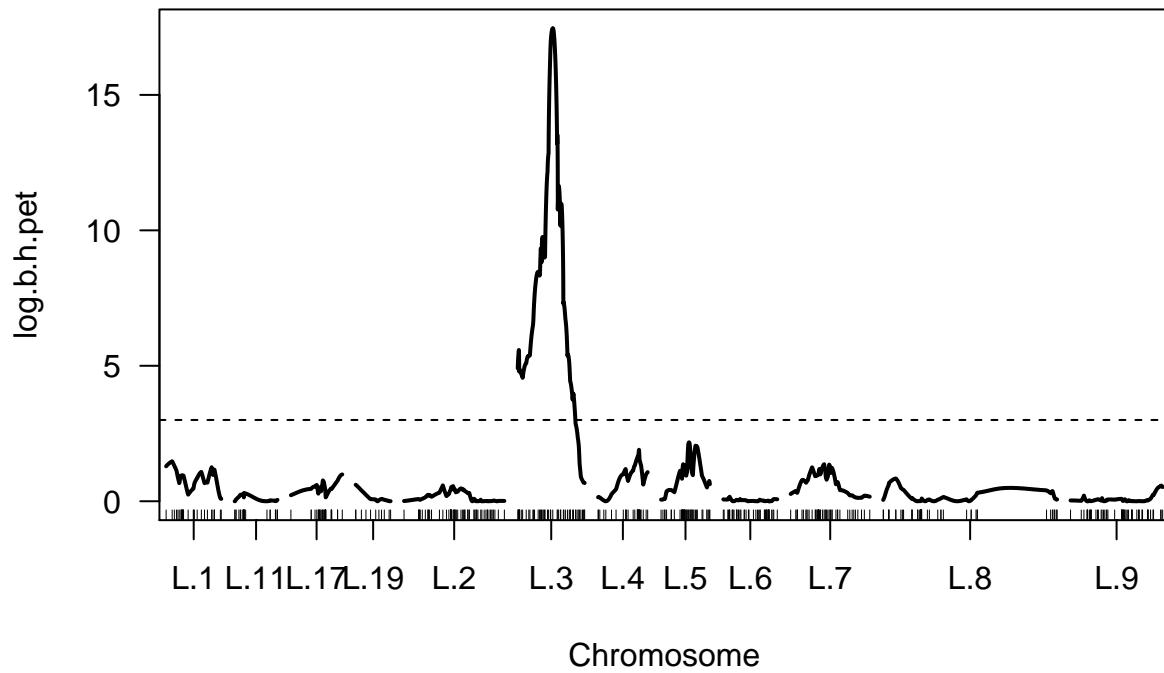












### Fertility and fruit traits

```
fertility <- scanone(mapJal5.1, pheno.col=c(76:87), method="em", addcovar=crossed)

## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 47 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 51 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 191 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 1 individuals wi...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 191 individuals w...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 1 individuals wi...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 1 individuals wi...
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 188 individuals w...
```

```

## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 1 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 46 individuals w
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 2 individuals wi
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 46 individuals w
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 2 individuals wi
for (x in 1:11){
  plot(fertility, lodcolumn = x)
  abline(3,0,lty=2)
}

```

