Proposal QTL scanning

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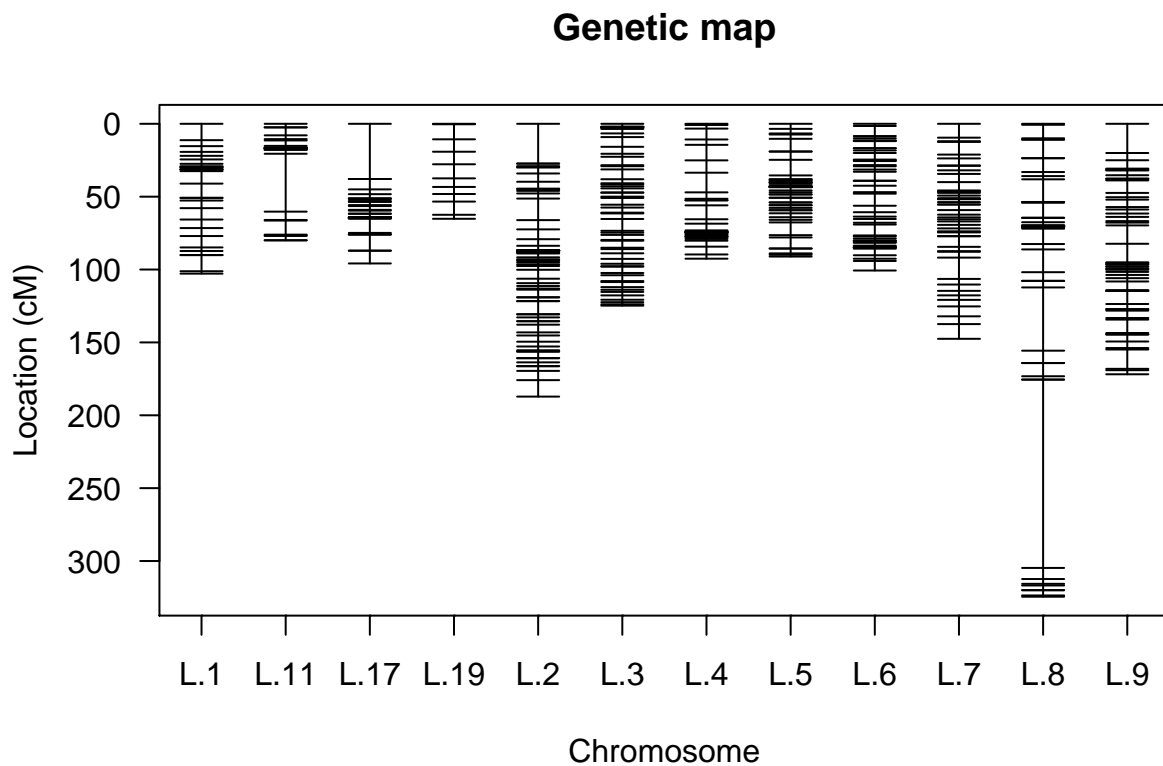
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Load the cross

```
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="csvr")
plot.map(mapJal5.1)
```

Genetic map


```
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))
```
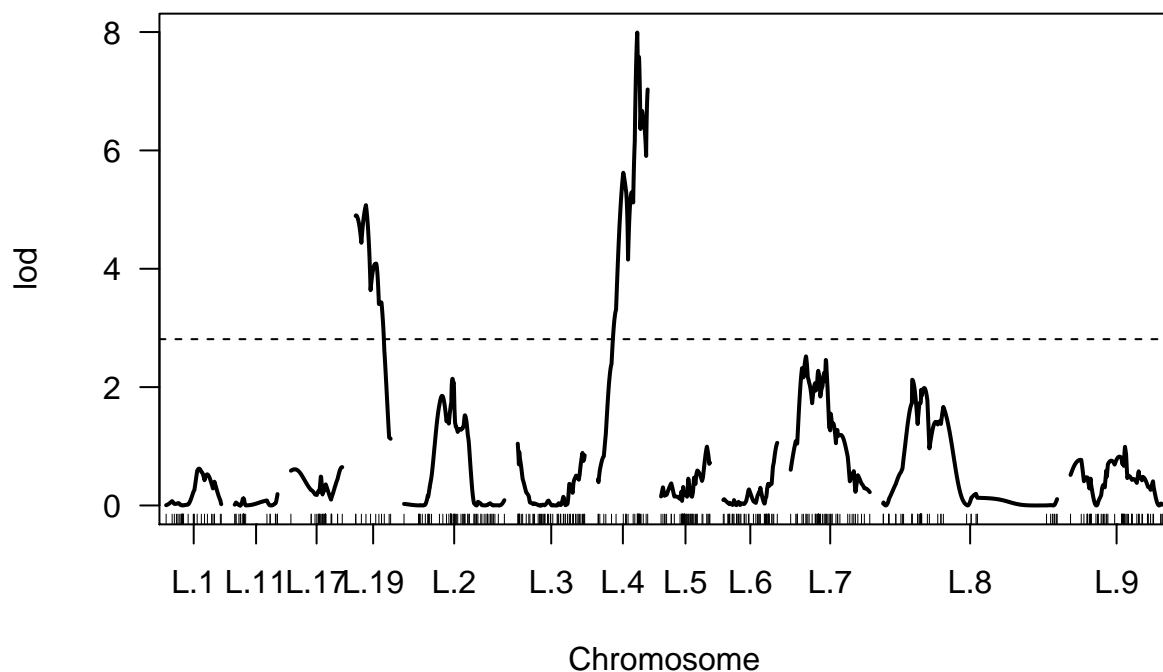
Redo scans of the focal traits

Herm corolla diameter

```
herm_cor_diameter <- scanone(mapJal5.1, pheno.col=32, method="em", addcovar=hmorph)
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w:
```

```
plot(herm_cor_diameter)
abline(2.81,0,lty=2)
```



```
lodint(herm_cor_diameter, chr='L.19')
```

```
##              chr      pos      lod
```

2

```
## 14447          L.19  0.00000 4.892238
## 14525          L.19 19.14514 5.074939
## cL.19.loc42.6 L.19 42.60000 3.569321
```

```
lodint(herm_cor_diameter, chr='L.4')
```

```
##            chr      pos      lod
## cL.4.loc69 L.4 69.00000 6.480037
## 16302      L.4 73.12845 7.991513
## 14913      L.4 92.54590 7.029765
```

```
#Explained variance for QTL on L.19
print(R2 <- (1 - 10^(-2*5.074939/(269-45))))
```

```
## [1] 0.09907623
```

```
#Explained variance for QTL on L.4
print(R2 <- (1 - 10^(-2*7.991513/(269-45))))
```
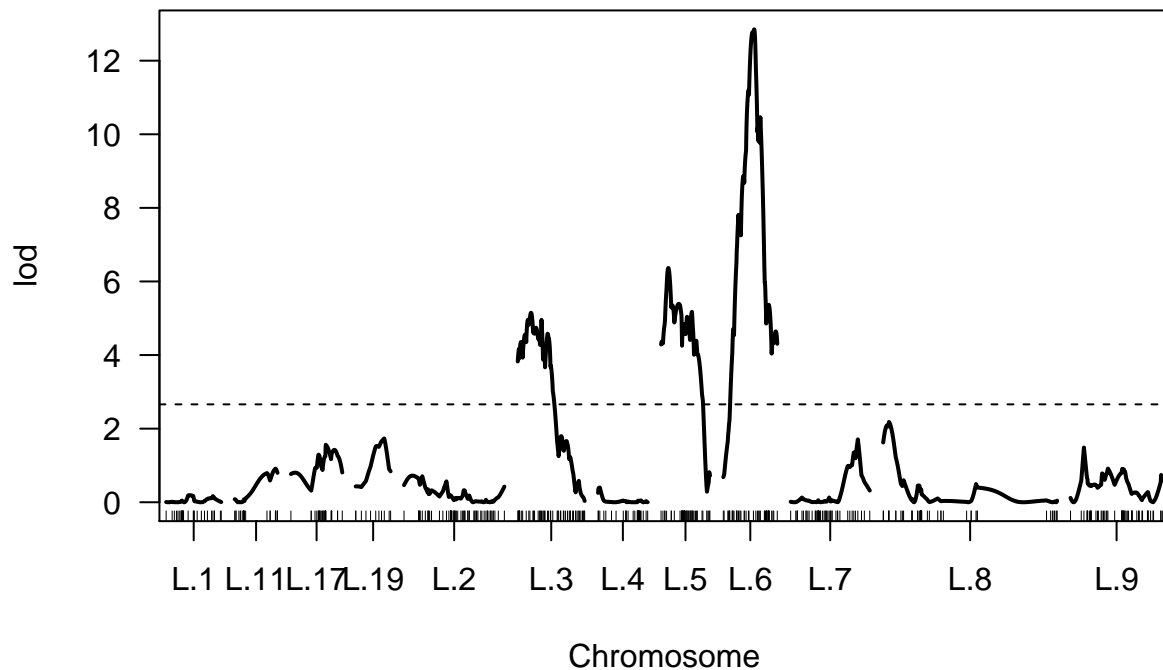
```
## [1] 0.1515091
```

Herm corolla depth

```
herm_cor_dep <- scanone(mapJal5.1, pheno.col=33, method="em", addcovar=hmorph)
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w
```

```
plot(herm_cor_dep)
abline(2.66,0,lty=2)
```

```r
lodint(herm_cor_dep, chr='L.3')
```

```
##               chr  pos      lod
## 3447          L.3  0.0 3.824543
## cL.3.loc24.8  L.3 24.8 5.148749
## cL.3.loc62.3  L.3 62.3 3.647239
```

```r
lodint(herm_cor_dep, chr='L.5')
```

```
##              chr  pos     lod
## cL.5.loc6.8  L.5  6.8 4.86266
## cL.5.loc13.5 L.5 13.5 6.36536
## cL.5.loc58.9 L.5 58.9 4.85858
```

```r
lodint(herm_cor_dep, chr='L.6')
```

```
##              chr  pos      lod
## cL.6.loc48.4 L.6 48.4 11.33746
## cL.6.loc57.6 L.6 57.6 12.85144
## cL.6.loc61.8 L.6 61.8 11.31222
```

```r
#Explained variance for QTL on L.3
print(R2 <- (1 - 10^(-2*5.148749/(269-45))))
```

```
## [1] 0.1004423
```

```r
#Explained variance for QTL on L.5
print(R2 <- (1 - 10^(-2*6.36536/(269-45))))
```

```
## [1] 0.122663
```

```r
#Explained variance for QTL on L.6
print(R2 <- (1 - 10^(-2*12.85144/(269-45))))
```
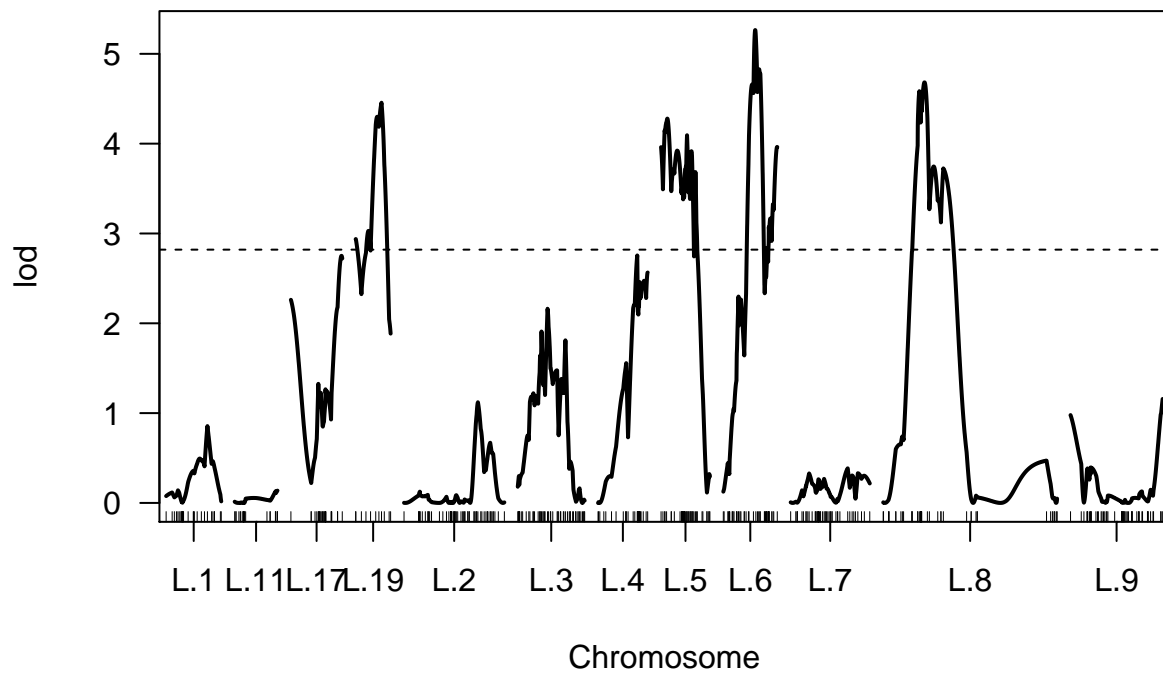
```
## [1] 0.2321878
```

Herm log corolla fusion

```r
herm_log_cor_fus <- scanone(mapJal5.1, pheno.col=34, method="em", addcovar=hmorph)
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w
```

```r
plot(herm_log_cor_fus)
abline(2.82,0,lty=2)
```



```r
lodint(herm_log_cor_fus, chr='L.19')
```

```
##                 chr      pos      lod
## cL.19.loc21.4 L.19 21.40000 2.954828
## 14629         L.19 48.17938 4.455928
## cL.19.loc58.3 L.19 58.30000 2.948192
```

```r
lodint(herm_log_cor_fus, chr='L.5')
```

```
##                chr  pos      lod
## 16404          L.5  0.0 3.961218
## cL.5.loc11.7   L.5 11.7 4.278688
```

```
## cL.5.loc67.9 L.5 67.9 2.774268
```

```r
lodint(herm_log_cor_fus, chr='L.6')
```

```
##              chr      pos      lod
## cL.6.loc46.8 L.6  46.8000 3.743512
## cL.6.loc59.5 L.6  59.5000 5.265163
## 13785        L.6 100.6749 3.961144
```

```r
lodint(herm_log_cor_fus, chr='L.8')
```

```
##               chr   pos      lod
## cL.8.loc56.7  L.8  56.7 3.178811
## cL.8.loc77.1  L.8  77.1 4.682373
## cL.8.loc127.1 L.8 127.1 3.181991
```

```r
#Explained variance for QTL on L.19
print(R2 <- (1 - 10^(-2*4.455928/(269-45))))
```

```
## [1] 0.0875377
```

```r
#Explained variance for QTL on L.5
print(R2 <- (1 - 10^(-2*4.278688/(269-45))))
```

```
## [1] 0.08420677
```

```r
#Explained variance for QTL on L.6
print(R2 <- (1 - 10^(-2*5.265163/(269-45))))
```

```
## [1] 0.1025927
```

```r
#Explained variance for QTL on L.8
print(R2 <- (1 - 10^(-2*4.682373/(269-45))))
```
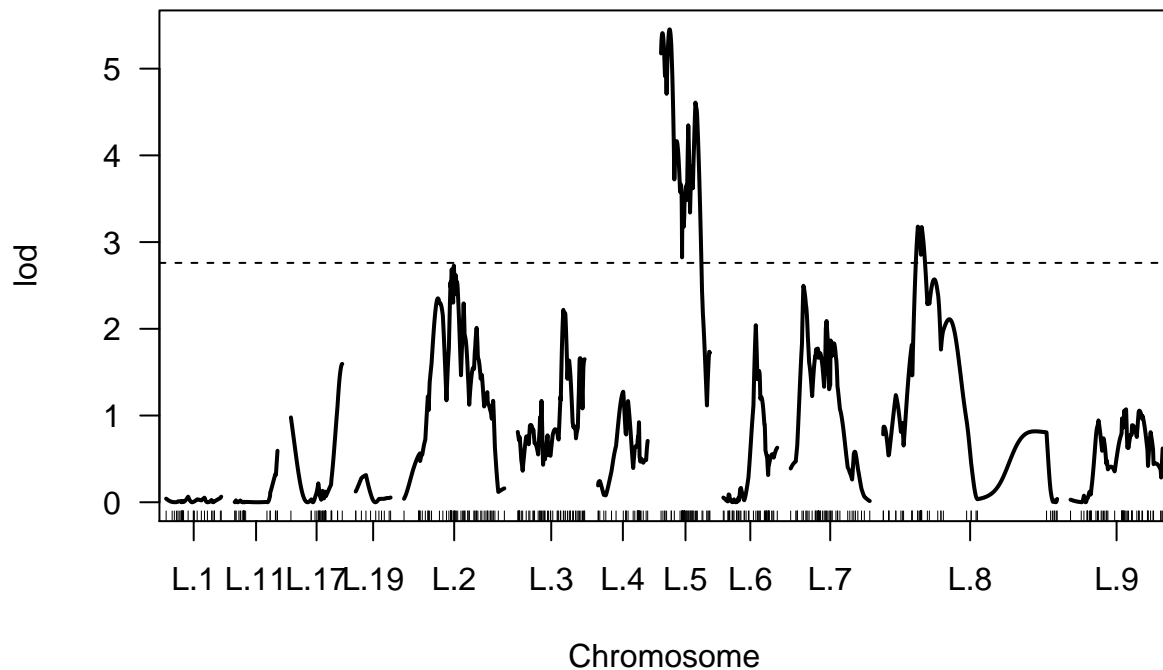
```
## [1] 0.09177574
```

Log corolla fusion proportion

```r
herm_log_cor_fus_prop <- scanone(mapJal5.1, pheno.col=35, method="em", addcovar=hmorph)
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w:
```

```r
plot(herm_log_cor_fus_prop)
abline(2.76,0,lty=2)
```

```
lodint(herm_log_cor_fus_prop, chr='L.5')
```

```
##               chr  pos      lod
## 16404        L.5  0.0 5.175655
## cL.5.loc15.9 L.5 15.9 5.453092
## cL.5.loc70.2 L.5 70.2 3.953035
```

```
lodint(herm_log_cor_fus_prop, chr='L.8')
```

```
##               chr      pos      lod
## cL.8.loc50.7  L.8   50.70000 1.675979
## 16231         L.8   64.62369 3.178532
## cL.8.loc140.3 L.8 140.30000 1.675106
```

```r
#Explained variance for QTL on L.5
print(R2 <- (1 - 10^(-2*5.453092/(269-45))))
```

```
## [1] 0.1060532
```
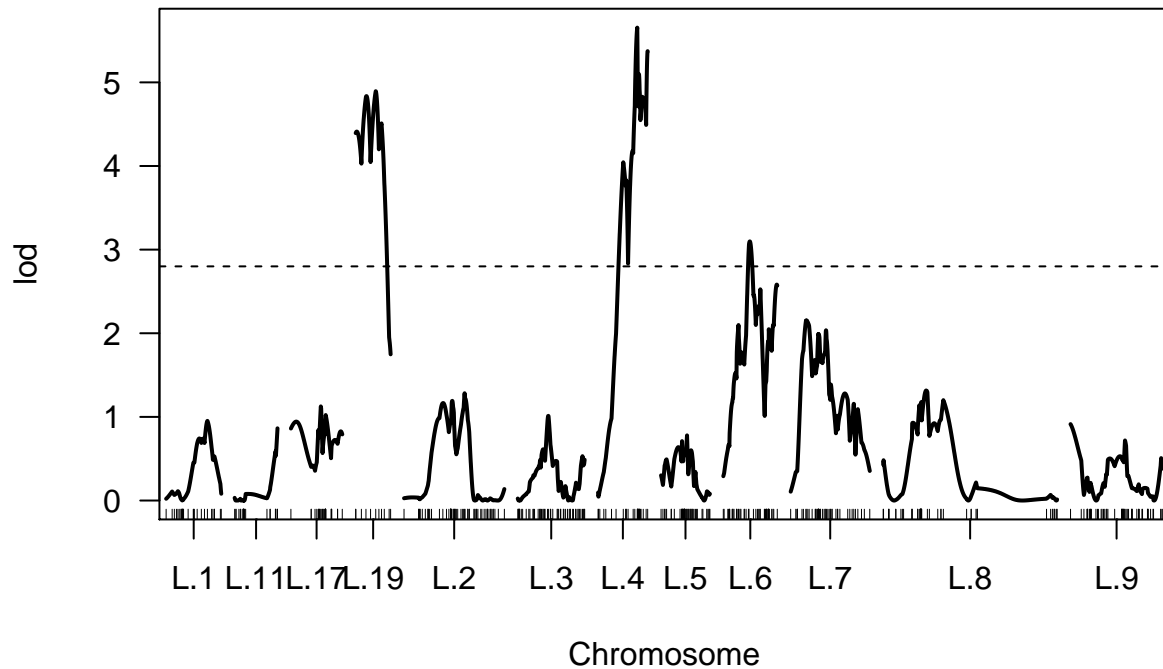
```r
#Explained variance for QTL on L.8
print(R2 <- (1 - 10^(-2*3.178532/(269-45))))
```

```
## [1] 0.06325745
```

Herm petal length

```r
herm_petal_length <- scanone(mapJal5.1, pheno.col=36, method="em", addcovar=hmorph)
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 45 individuals w
plot(herm_petal_length)
abline(2.8,0,lty=2)
```



```
lodint(herm_petal_length, chr='L.19')
```

```
##                 chr      pos      lod
## 14447          L.19  0.00000 4.393192
## 14584          L.19 37.42937 4.894433
## cL.19.loc55.9 L.19 55.90000 3.393809
```

```
lodint(herm_petal_length, chr='L.4')
```

```
##                chr      pos      lod
## cL.4.loc63.3 L.4 63.30000 4.154427
## 16302        L.4 73.12845 5.654602
## 14913        L.4 92.54590 5.371882
```

```
lodint(herm_petal_length, chr='L.6')
```

```
##               chr      pos      lod
## cL.6.loc24.8 L.6  24.8000 1.593065
## cL.6.loc49.4 L.6  49.4000 3.098091
## 13785        L.6 100.6749 2.569013
```

```
#Explained variance for QTL on L.19
print(R2 <- (1 - 10^(-2*4.894433/(269-45))))
```

```
## [1] 0.09572671
```
```
#Explained variance for QTL on L.4
print(R2 <- (1 - 10^(-2*5.654602/(269-45))))
```
```
## [1] 0.109749
```
```
#Explained variance for QTL on L.6
print(R2 <- (1 - 10^(-2*3.098091/(269-45))))
```
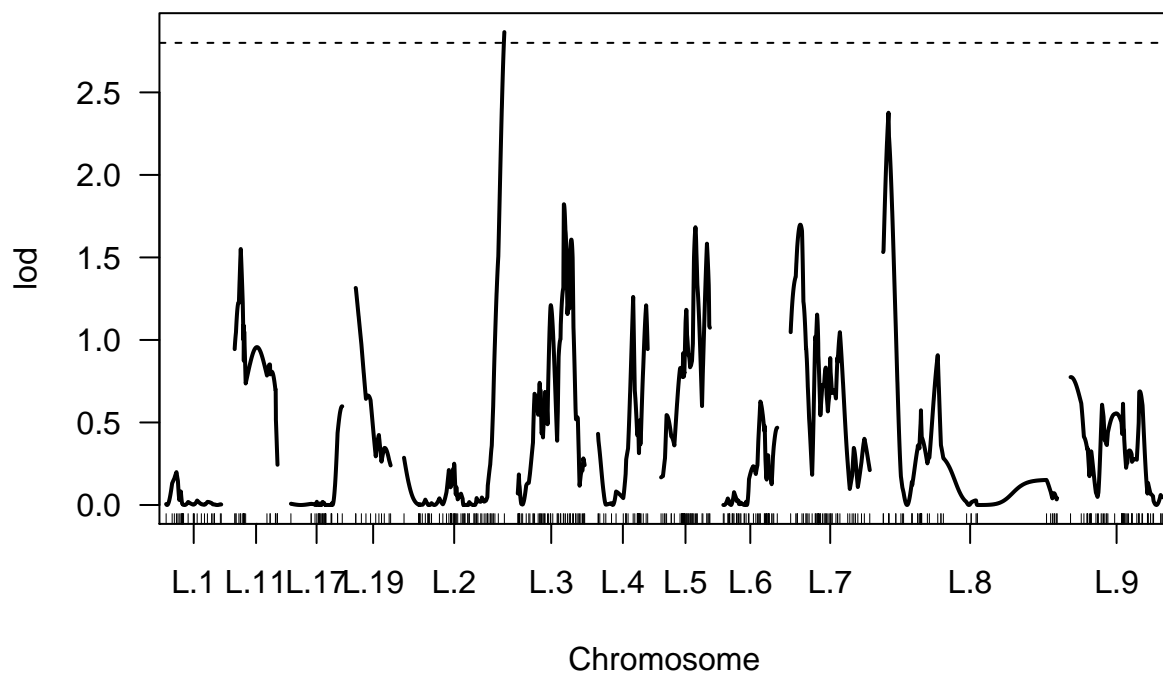```
[1] 0.06170701
```

**Herm nectar volume**

```
herm_nec_volume <- scanone(mapJal5.1, pheno.col=59, 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
```
```
plot(herm_nec_volume)
abline(2.8,0,lty=2)
```



```
lodint(herm_nec_volume, chr='L.2')
```
```
chr   pos   lod
cL.2.loc173.7 L.2 173.7000 1.363344
11364   L.2 187.1877 2.865291
```

```
## 11364          L.2 187.1877 2.865291
```

```r
#Explained variance for QTL on L.2
print(R2 <- (1 - 10^(-2*2.865291/(269-48))))
```

```
## [1] 0.05795909
```

```r
herm_nec_color_rgb <- scanone(mapJal5.1, pheno.col=61, 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
```

```r
plot(herm_nec_color_rgb)
abline(2.73,0,lty=2)
```
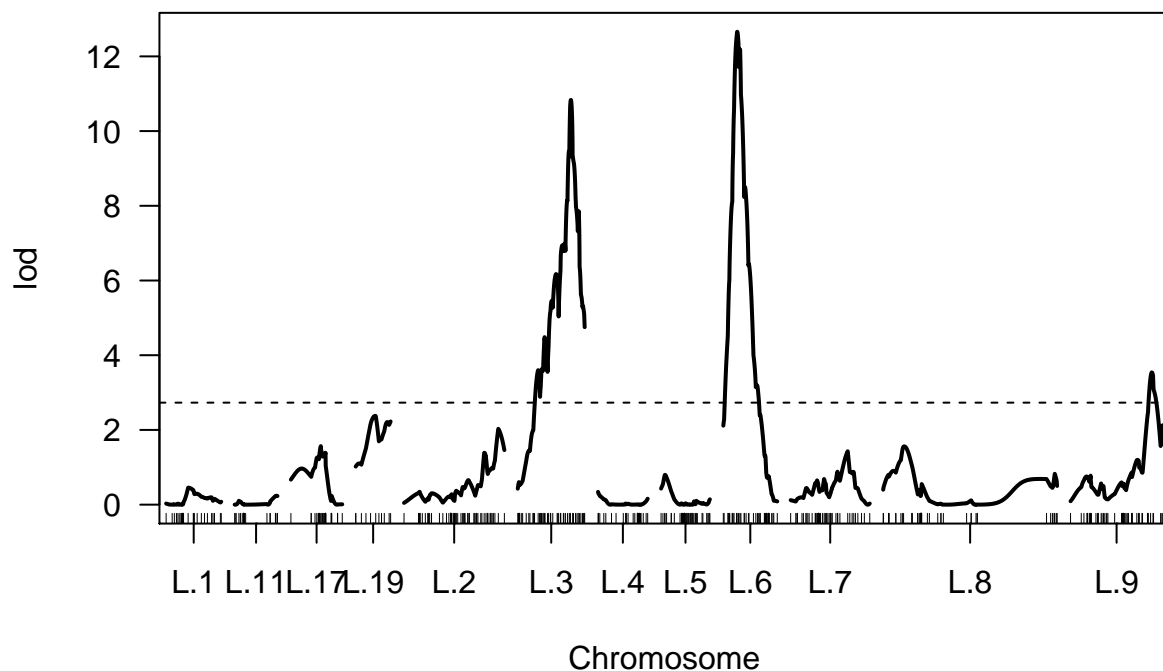


```r
lodint(herm_nec_color_rgb, chr='L.3')
```

```
##               chr     pos      lod
## cL.3.loc94.6 L.3  94.6000  9.319011
## cL.3.loc99   L.3  99.0000 10.834672
## 4489         L.3 102.3608  9.307060
```

```r
lodint(herm_nec_color_rgb, chr='L.6')
```

```
##               chr  pos      lod
## cL.6.loc20.8 L.6 20.8 11.15518
## cL.6.loc26   L.6 26.0 12.65906
## cL.6.loc32.8 L.6 32.8 11.09665
```

```r
lodint(herm_nec_color_rgb, chr='L.9')
```

```
##                  chr      pos       lod
## cL.9.loc141.3 L.9 141.3000 2.036742
## cL.9.loc151.8 L.9 151.8000 3.540315
## 18537         L.9 171.8665 2.125763
```

```r
#Explained variance for QTL on L.3
print(R2 <- (1 - 10^(-2*10.834672/(269-48))))
```

```
## [1] 0.2020996
```

```r
#Explained variance for QTL on L.6
print(R2 <- (1 - 10^(-2*12.65906/(269-48))))
```

```
## [1] 0.2318636
```

```r
#Explained variance for QTL on L.9
print(R2 <- (1 - 10^(-2*3.540315/(269-48))))
```
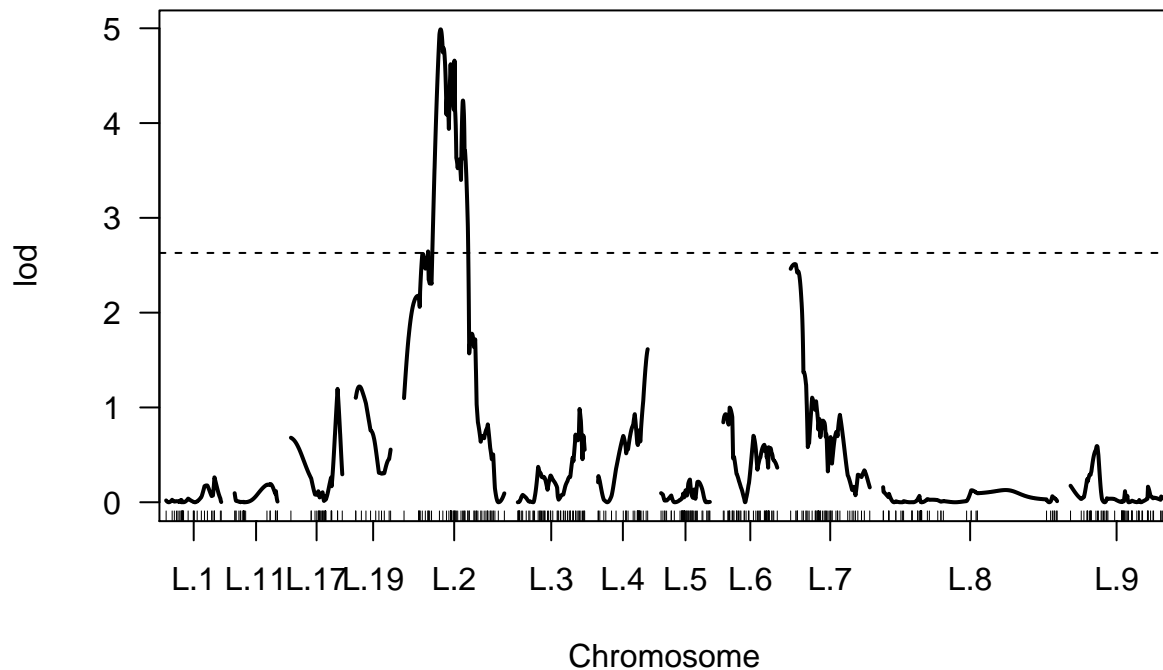
```
## [1] 0.07111714
```

Herm nectar color a

```r
herm_nec_color_a <- scanone(mapJal5.1, pheno.col=66, 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
```

```r
plot(herm_nec_color_a)
abline(2.63,0,lty=2)
```

```r
lodint(herm_nec_color_a, chr='L.2')
```

```
##               chr   pos      lod
## cL.2.loc56.8  L.2  56.8 3.488374
## cL.2.loc68.3  L.2  68.3 4.988582
## cL.2.loc115.9 L.2 115.9 3.482529
```

```r
#Explained variance for QTL on L.3
print(R2 <- (1 - 10^(-2*4.988582/(269-48))))
```

```
## [1] 0.09873094
```
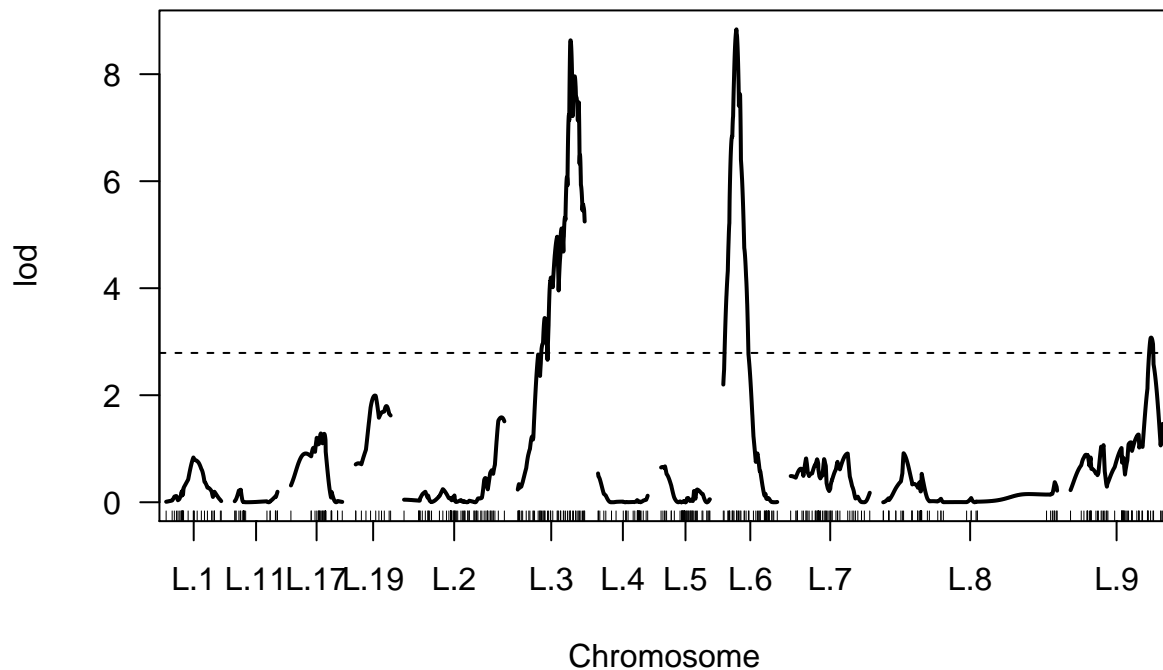
Herm nectar color b

```r
herm_nec_color_b <- scanone(mapJal5.1, pheno.col=67, 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
```

```r
plot(herm_nec_color_b)
abline(2.79,0,lty=2)
```

```
lodint(herm_nec_color_b, chr='L.3')
```

```
##                chr   pos      lod
## cL.3.loc94.6   L.3  94.6 7.113538
## cL.3.loc98.5   L.3  98.5 8.632559
## cL.3.loc114.6  L.3 114.6 7.072445
```

```
lodint(herm_nec_color_b, chr='L.6')
```

```
##                chr     pos      lod
## cL.6.loc18.5   L.6 18.5000 7.328038
## 2487           L.6 24.5554 8.837499
## cL.6.loc31.9   L.6 31.9000 7.320357
```

```
lodint(herm_nec_color_b, chr='L.9')
```

```
##                chr   pos      lod
## cL.9.loc138.4  L.9 138.4 1.569922
## cL.9.loc150.3  L.9 150.3 3.076774
## cL.9.loc164.7  L.9 164.7 1.565235
```

```
#Explained variance for QTL on L.3
print(R2 <- (1 - 10^(-2*8.632559/(269-48))))
```

```
## [1] 0.164633
```

```
#Explained variance for QTL on L.6
print(R2 <- (1 - 10^(-2*8.837499/(269-48))))
```

```
## [1] 0.1681929
```

```r
#Explained variance for QTL on L.9
print(R2 <- (1 - 10^(-2*3.076774/(269-48))))
```

```
## [1] 0.06210139
```