

jaltomataMapping

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```
library(qtl)
```

```
## Warning: package 'qtl' was built under R version 3.2.5
```

```
macDir <- "~/jaltomataQTL"
```

```
pcDir <- "c:/Users/matth/Documents/bin/jaltomataQTL/maps"
```

```
setwd(pcDir)
```

```
jal_cross <- read.cross("csv",pcDir, "batch_1.genotypes_20_herm.csv", genotypes=c("b", "h"), alleles=c(
```

```
## --Read the following data:
```

```
## 269 individuals
```

```
## 395 markers
```

```
## 79 phenotypes
```

```
## --Cross type: bc
```

Scanning for QTL

Define covariates, calculate genotype probs.

```
h_color <- pull.pheno(jal_cross, pheno.col=c(2, 5))
```

```
h_morph <- pull.pheno(jal_cross, pheno.col=c(2, 3))
```

```
crossed <- pull.pheno(jal_cross, pheno.col=c(2, 57))
```

```
justBench <- pull.pheno(jal_cross, pheno.col=2)
```

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

```
jal_cross <- sim.geno(jal_cross, step=1, n.draws=64)
```

Scan for QTL- all morphological traits

```
scan_all_morph <- scanone(jal_cross, pheno.col=c(6:23), method="em", addcovar=h_morph)
```

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

```
summary(scan_all_morph, threshold=3, format="tabByChr")
```

```
## Chr 2:
```

```
##               chr pos ci.low ci.high lod
## cor.depth.h.mean : c2.loc11  2 11.0    0    26 4.77
## ovary.h.mean : 3890          2 21.4    0    30 4.33
##
```

```
## Chr 4:
```

```
##               chr pos ci.low ci.high lod
## inflor.mean : c4.loc90    4 90.0   25.0   94.0 3.16
## log.inflor.mean : c4.loc90  4 90.0   39.0   91.3 3.94
## calyx.h.mean : c4.loc46    4 46.0   44.5   53.0 8.63
```

```

## sepal.h.mean : c4.loc46      4 46.0   41.0   54.4 7.53
## cor.fus.h.mean : 10749      4 45.7   44.5   48.0 6.06
## log.cor.fus.h.mean : 10749   4 45.7   44.0   48.0 5.93
## cor.fus.prop.h.mean : 11967  4 44.9   21.1   52.6 3.61
## ovary.h.mean : 10749      4 45.7   41.0   48.0 5.86
##
## Chr 5:
##
##          chr  pos ci.low ci.high  lod
## calyx.h.mean : c5.loc13      5 13.0     8    36 5.68
## sepal.h.mean : c5.loc14      5 14.0     9    34 5.81
## cor.depth.h.mean : c5.loc7    5  7.0     0    31 5.74
## cor.fus.h.mean : c5.loc4      5  4.0     0    27 4.18
## log.cor.fus.h.mean : 15186    5 18.9     0    27 4.32
## cor.fus.prop.h.mean : c5.loc7  5  7.0     0    29 5.52
## stamen.h.mean : 14608        5 20.0     0    34 3.16
## style.h.mean : 15864         5  0.0     0    12 10.27
## log.style.h.mean : 15864      5  0.0     0    13  9.96
## herkogamy.h.mean : 15864      5  0.0     0    27  5.27
## log.herkogamy.h.mean.x.3. : 15864  5  0.0     0    29  4.37
##
## Chr 6:
##          chr  pos ci.low ci.high  lod
## cor.dia.h.mean : c6.loc61     6 61.0   54.0   67.0 7.86
## cor.fus.h.mean : 14584        6 95.3   56.4  104.0 4.15
## log.cor.fus.h.mean : 14584    6 95.3   55.0  104.0 4.06
## petal.h.mean : 16302         6 57.0   48.0   99.7 5.34
## log.petal.h.mean : 16302      6 57.0   49.0   99.0 5.51
## ovary.h.mean : 14629         6 98.0   82.0  107.4 3.45
##
## Chr 8:
##          chr  pos ci.low ci.high  lod
## cor.depth.h.mean : c8.loc63    8 63.0    60   69.0 13.47
## cor.fus.h.mean : 18692         8 63.4    27   67.0  6.09
## log.cor.fus.h.mean : 18692     8 63.4    55   66.1  6.24
## petal.h.mean : c8.loc26        8 26.0     0   88.9  3.09
## log.petal.h.mean : c8.loc27    8 27.0     0   88.9  3.14
##
## Chr 11:
##          chr  pos ci.low ci.high  lod
## stamen.h.mean : 8060          11 68.5     0   84.0  3.15
## log.style.h.mean : 7758        11 44.2    36   55.0  3.14
## herkogamy.h.mean : c11.loc43   11 43.0    36   74.0  6.67
## log.herkogamy.h.mean.x.3. : 7758 11 44.2    36   74.6  5.70
summary(scan_all_morph, threshold=3, format="tabByCol")

## inflor.mean:
##          chr pos ci.low ci.high  lod
## c4.loc90   4  90     25     94 3.16
##
## log.inflor.mean:
##          chr pos ci.low ci.high  lod
## c4.loc90   4  90     39    91.3 3.94
##
## calyx.h.mean:

```

```

##          chr pos ci.low ci.high lod
## c4.loc46   4  46   44.5    53 8.63
## c5.loc13   5  13    8.0    36 5.68
##
## sepal.h.mean:
##          chr pos ci.low ci.high lod
## c4.loc46   4  46    41    54.4 7.53
## c5.loc14   5  14     9    34.0 5.81
##
## cor.dia.h.mean:
##          chr pos ci.low ci.high lod
## c6.loc61   6  61    54    67 7.86
##
## cor.depth.h.mean:
##          chr pos ci.low ci.high lod
## c2.loc11   2  11     0    26 4.77
## c5.loc7    5   7     0    31 5.74
## c8.loc63   8  63    60    69 13.47
##
## cor.fus.h.mean:
##          chr pos ci.low ci.high lod
## 10749      4 45.7   44.5    48 6.06
## c5.loc4    5  4.0    0.0    27 4.18
## 14584      6 95.3   56.4   104 4.15
## 18692      8 63.4   27.0    67 6.09
##
## log.cor.fus.h.mean:
##          chr pos ci.low ci.high lod
## 10749      4 45.7    44    48.0 5.93
## 15186      5 18.9     0    27.0 4.32
## 14584      6 95.3    55   104.0 4.06
## 18692      8 63.4    55    66.1 6.24
##
## cor.fus.prop.h.mean:
##          chr pos ci.low ci.high lod
## 11967      4 44.9   21.1    52.6 3.61
## c5.loc7    5  7.0    0.0    29.0 5.52
##
## petal.h.mean:
##          chr pos ci.low ci.high lod
## 16302      6  57    48    99.7 5.34
## c8.loc26   8  26     0    88.9 3.09
##
## log.petal.h.mean:
##          chr pos ci.low ci.high lod
## 16302      6  57    49    99.0 5.51
## c8.loc27   8  27     0    88.9 3.14
##
## stamen.h.mean:
##          chr pos ci.low ci.high lod
## 14608      5 20.0     0    34 3.16
## 8060      11 68.5     0    84 3.15
##
## ovary.h.mean:

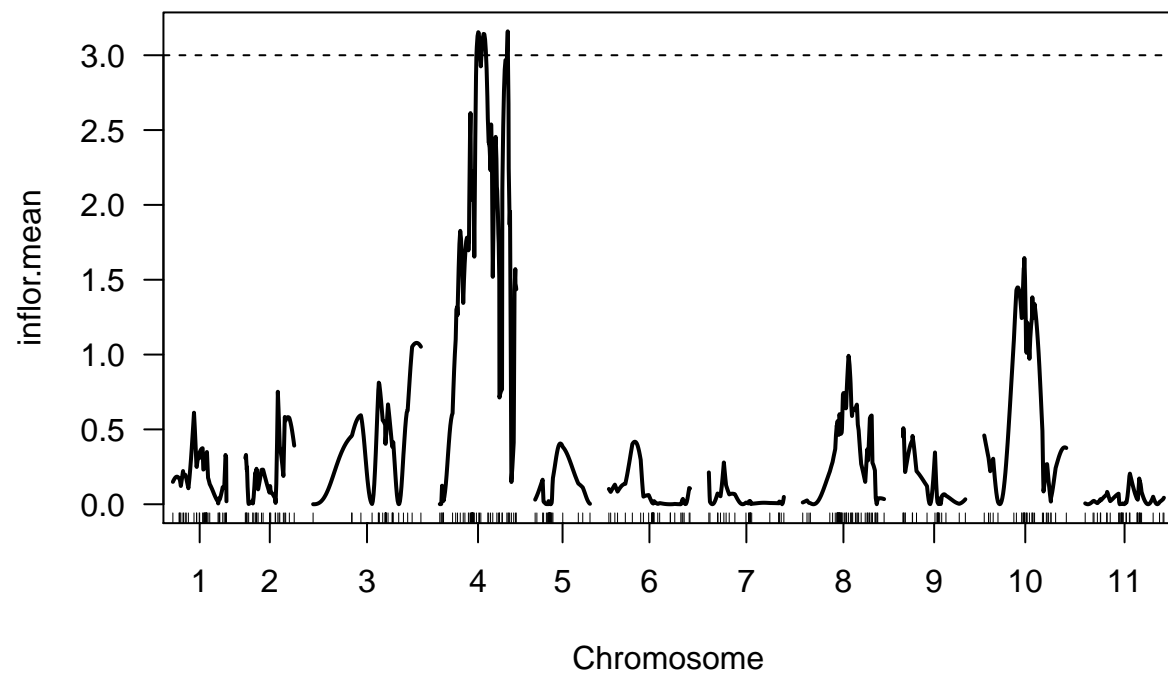
```

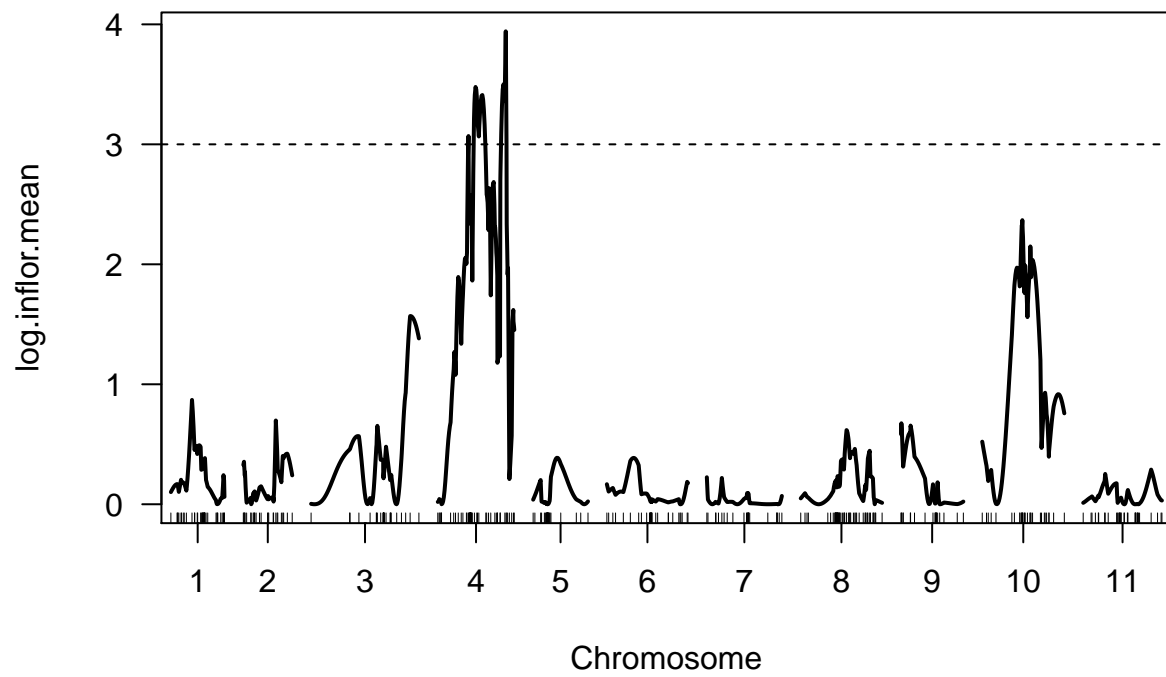
```

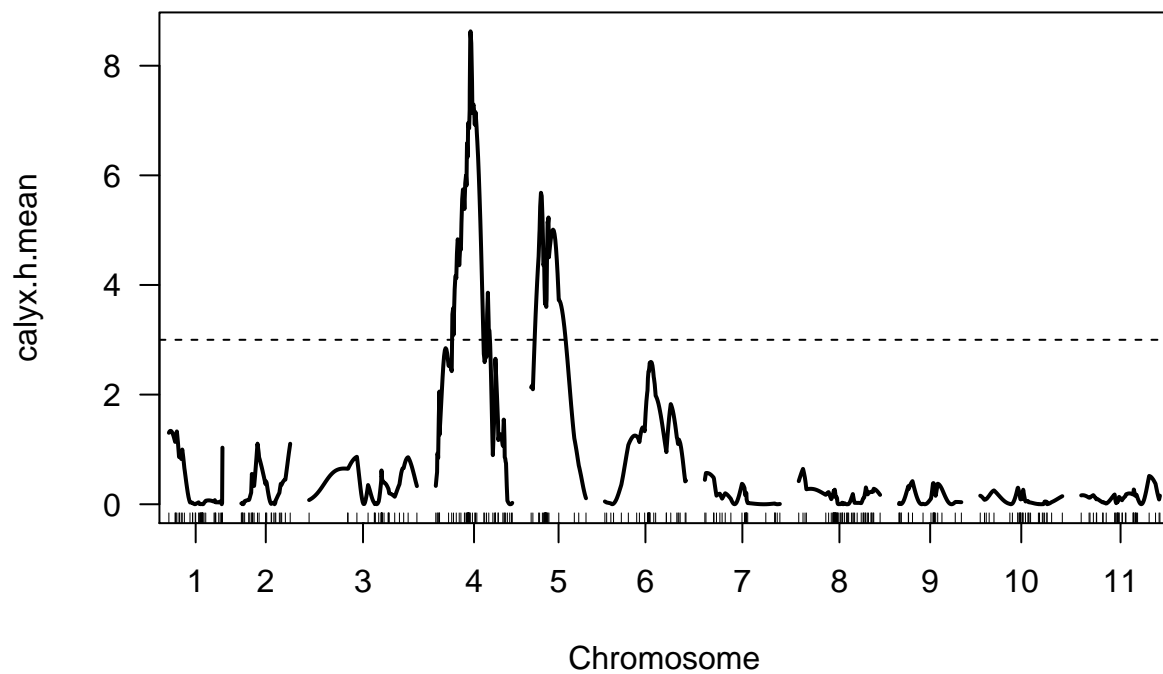
##      chr  pos ci.low ci.high  lod
## 3890   2 21.4    0      30 4.33
## 10749  4 45.7   41      48 5.86
## 14629  6 98.0   82     107 3.45
##
## style.h.mean:
##      chr pos ci.low ci.high  lod
## 15864  5  0      0      12 10.3
##
## log.style.h.mean:
##      chr  pos ci.low ci.high  lod
## 15864  5 0.0      0      13 9.96
## 7758   11 44.2   36      55 3.14
##
## herkogamy.h.mean:
##      chr pos ci.low ci.high  lod
## 15864    5  0      0      27 5.27
## c11.loc43 11 43   36      74 6.67
##
## log.herkogamy.h.mean.x.3.:
##      chr  pos ci.low ci.high  lod
## 15864  5 0.0      0     29.0 4.37
## 7758   11 44.2   36     74.6 5.70

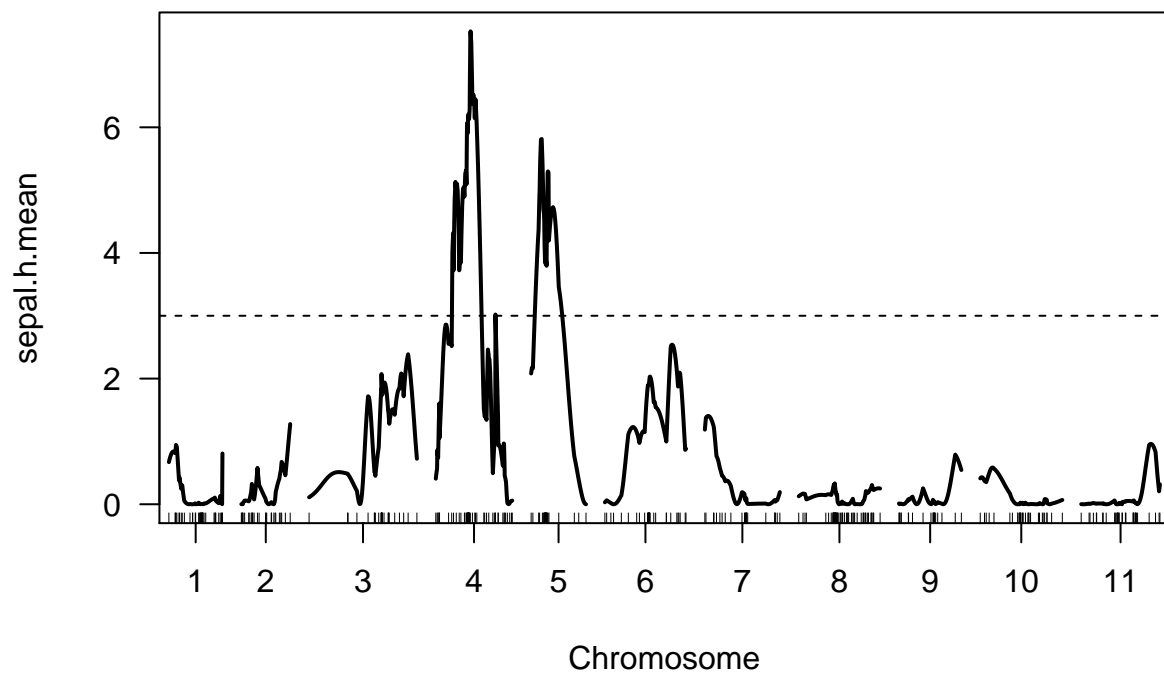
#par(mfrow=c(3,1))
for (x in 1:18){
  plot(scan_all_morph, lodcolumn = x)
  abline(3,0,lty=2)
}

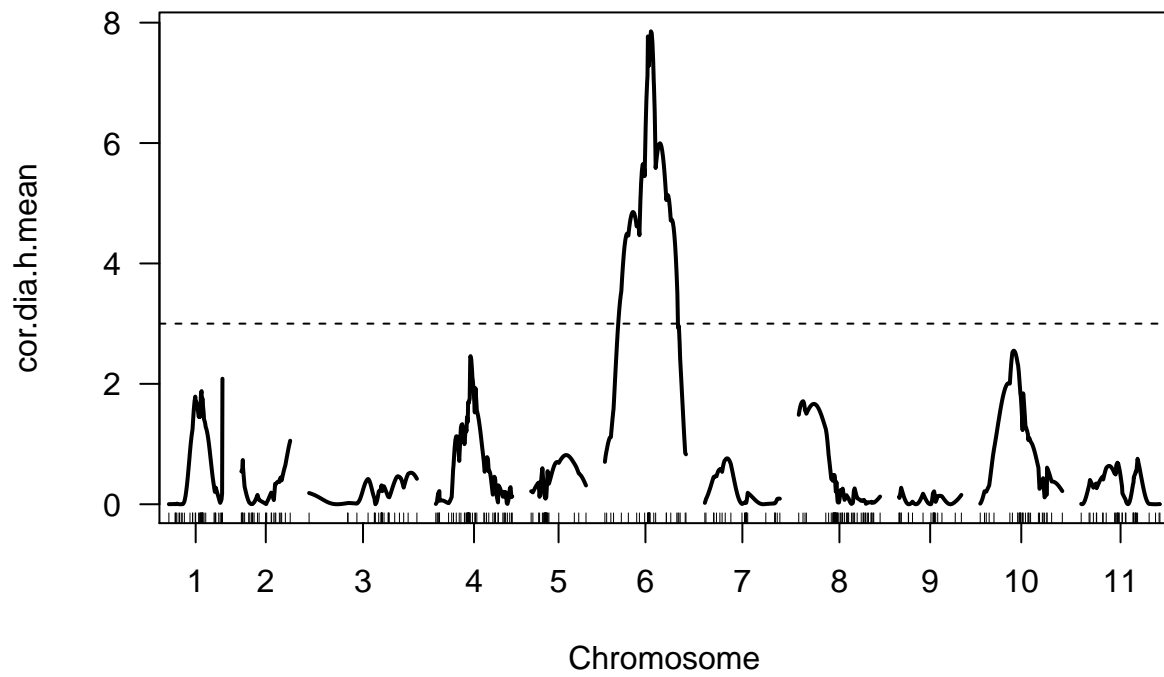
```

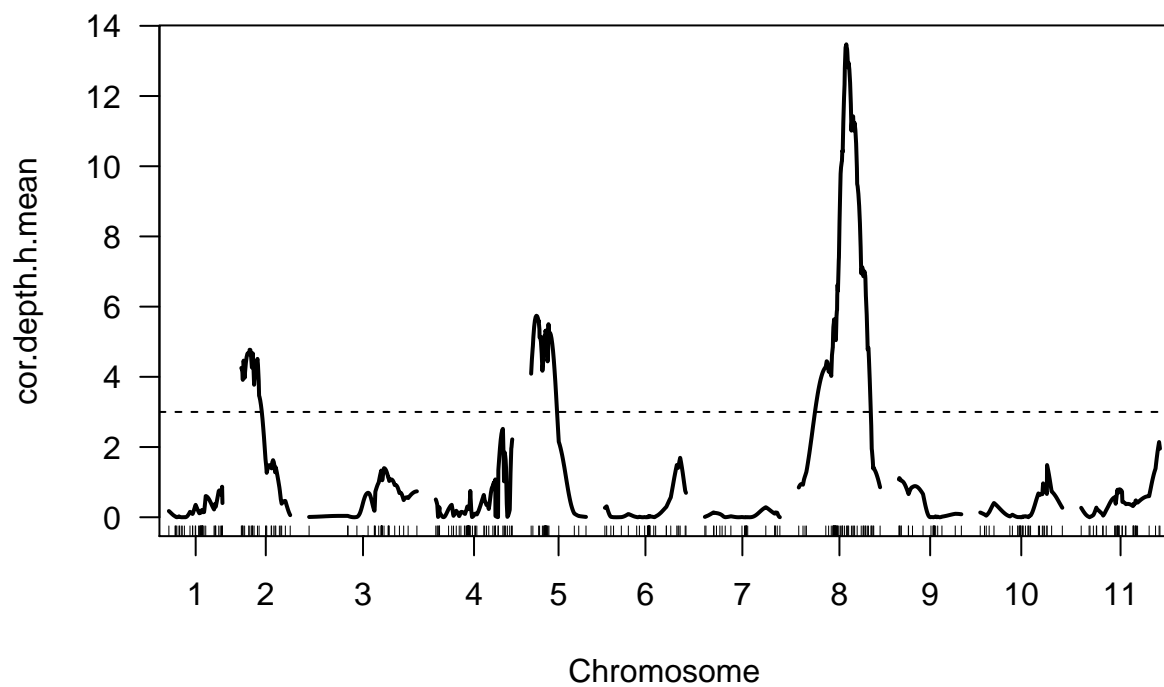


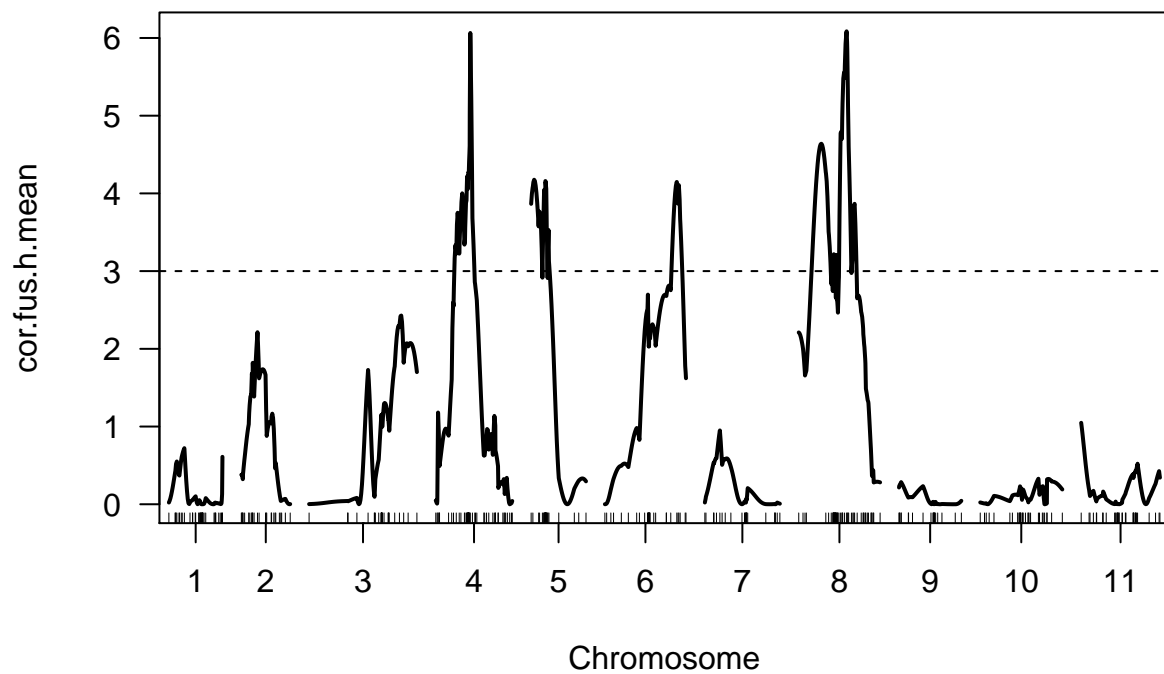


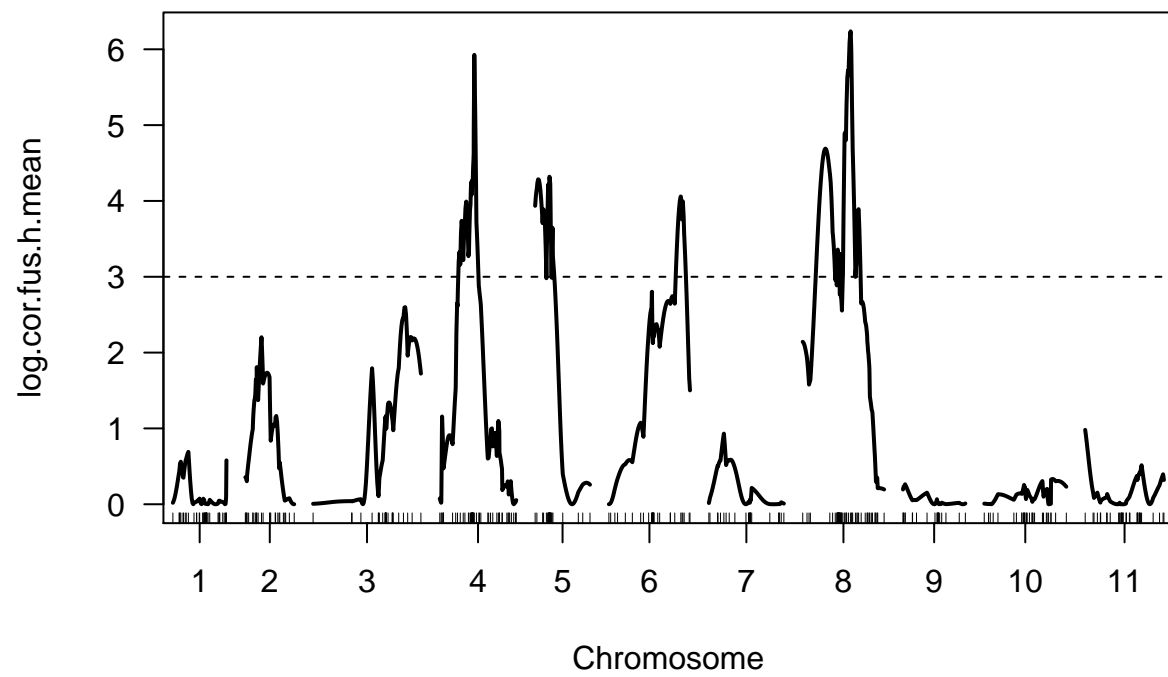


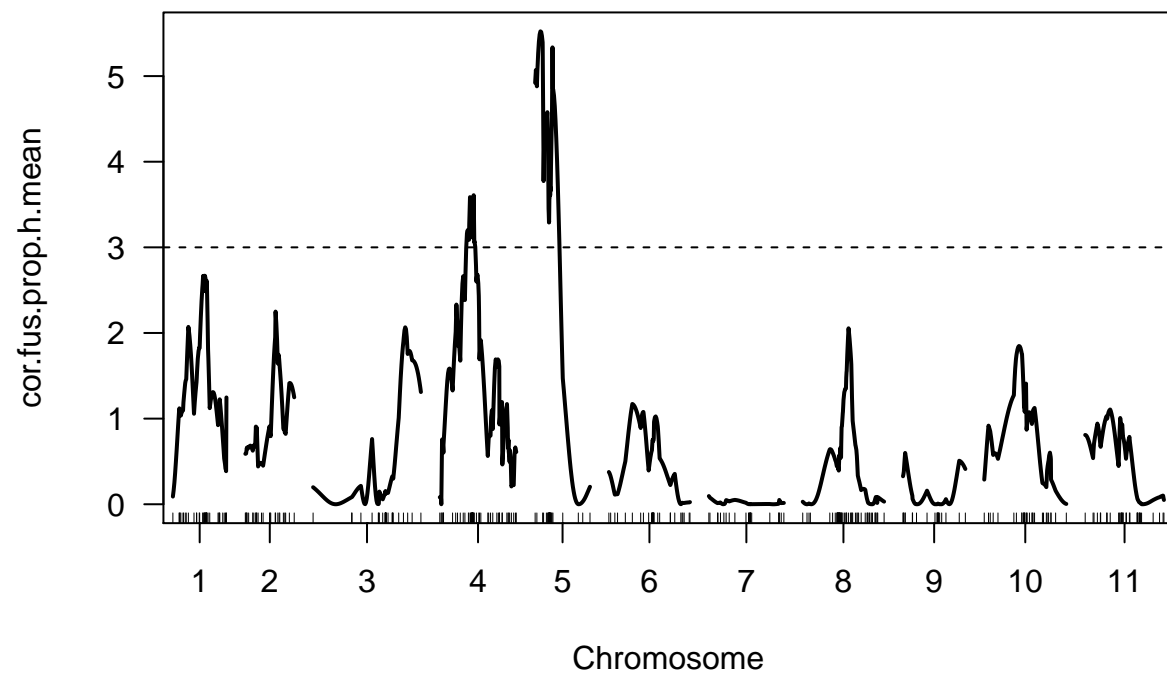


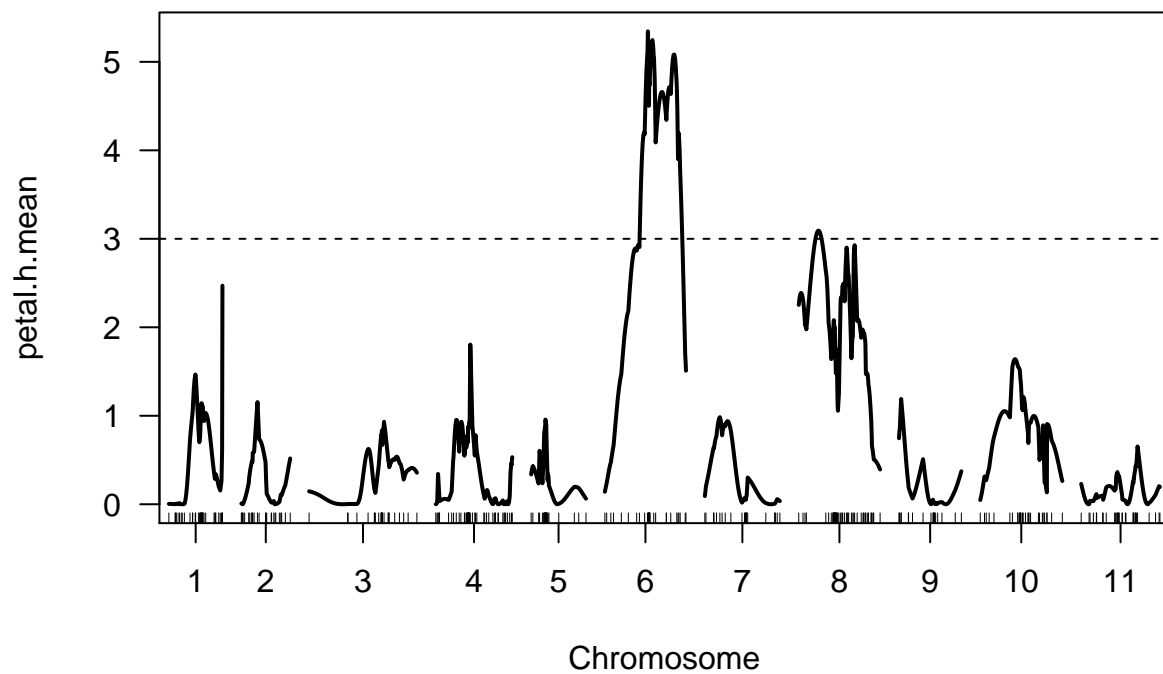


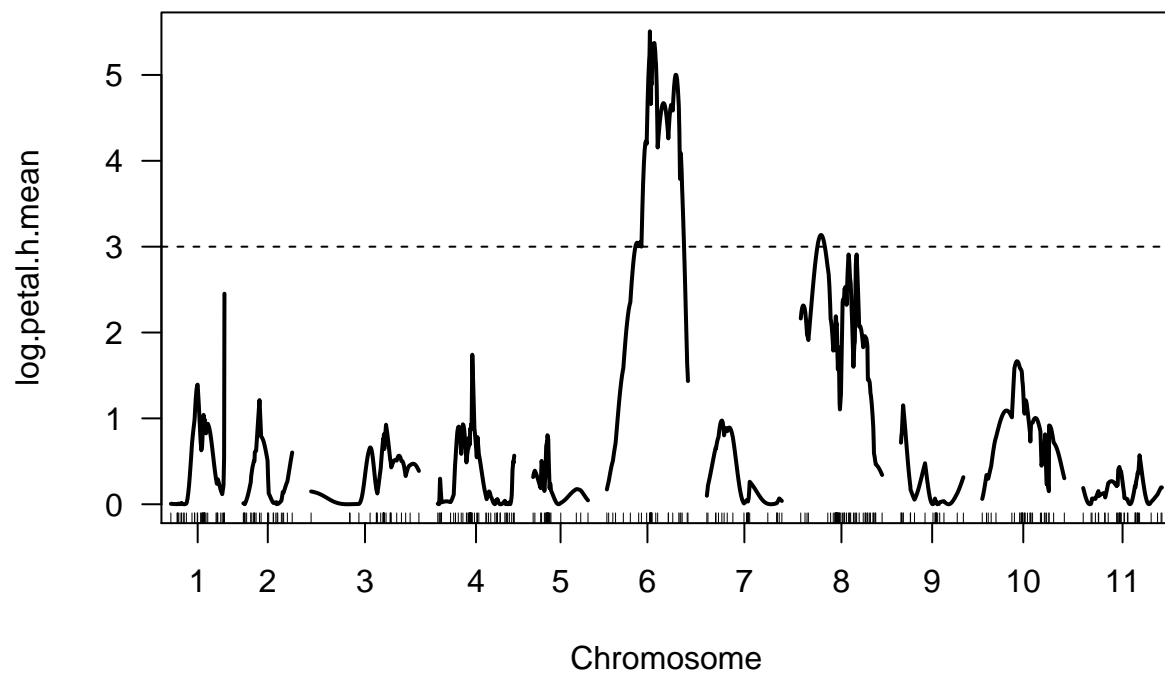


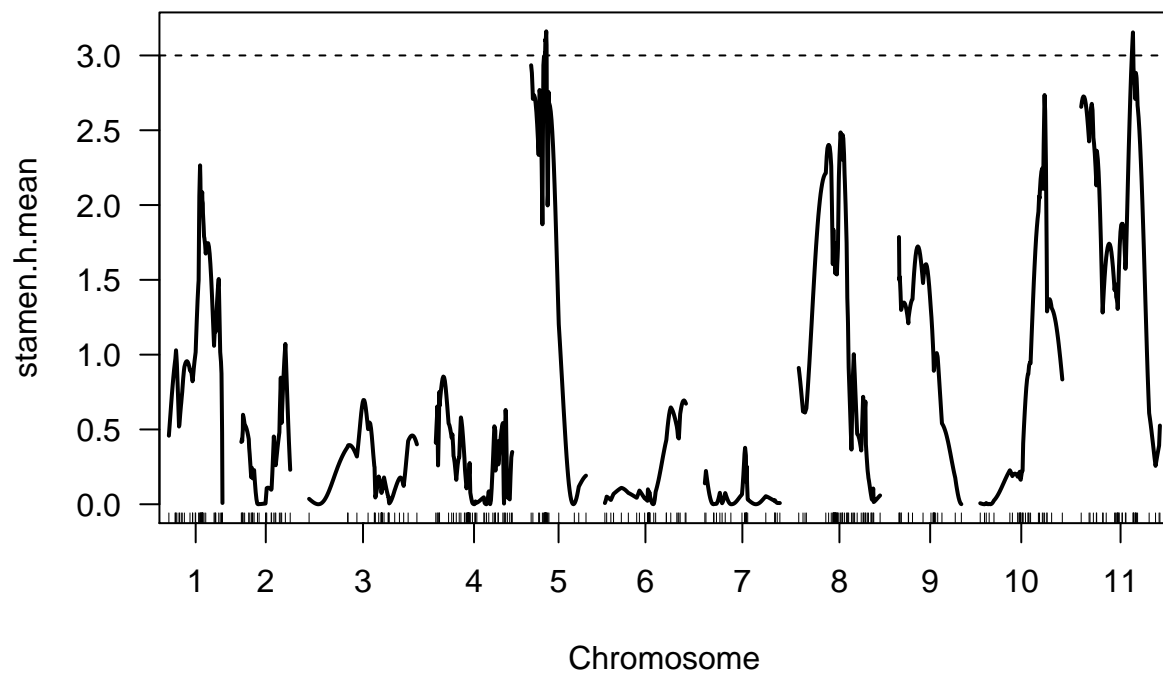


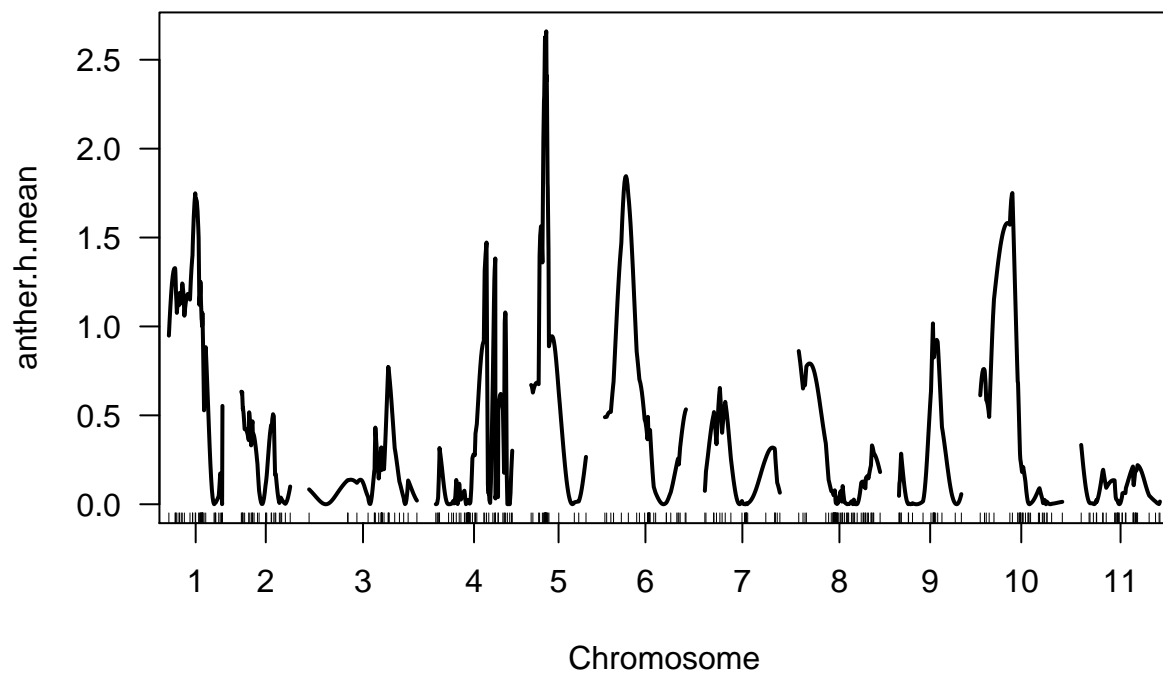


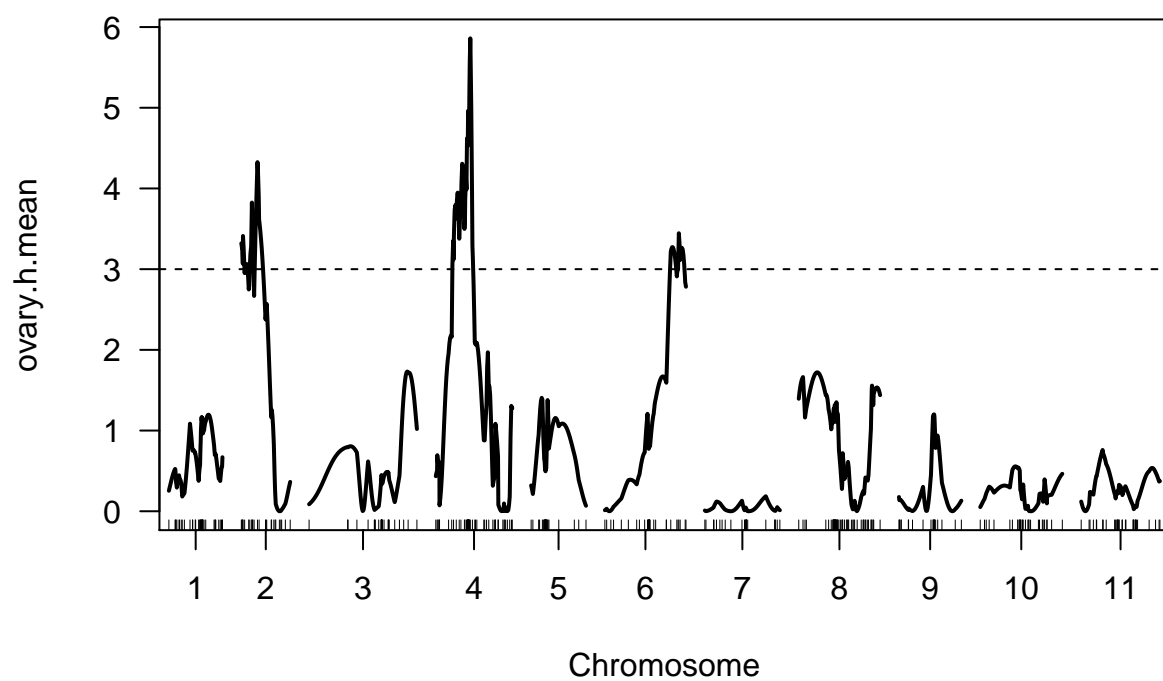


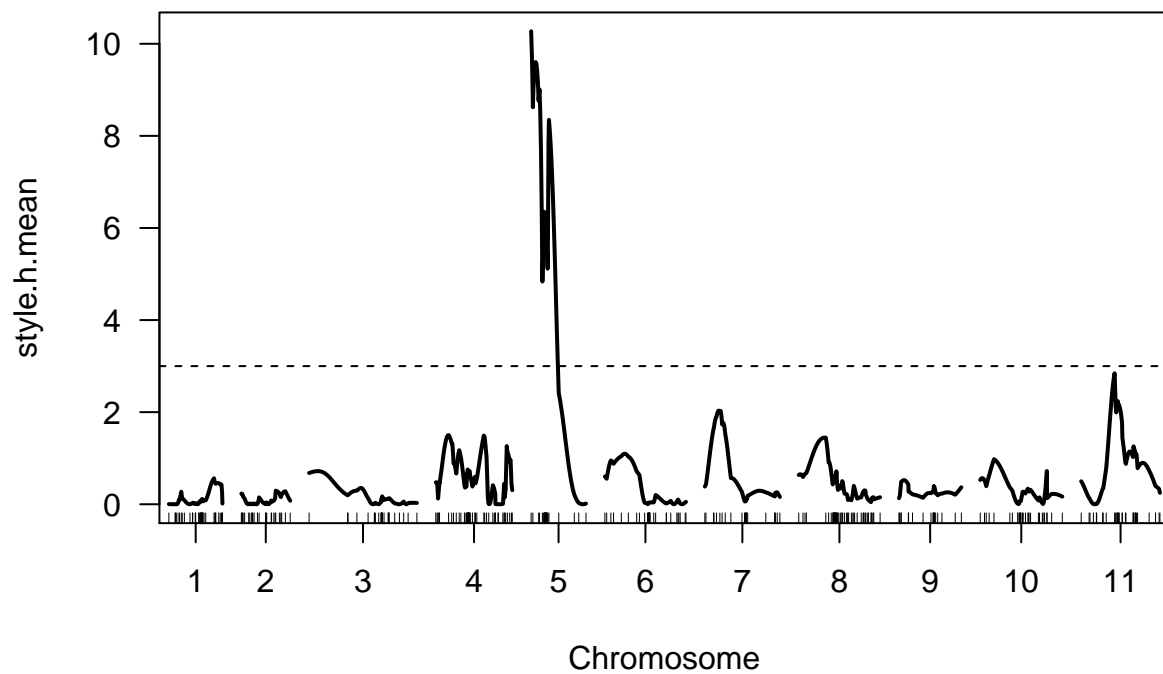


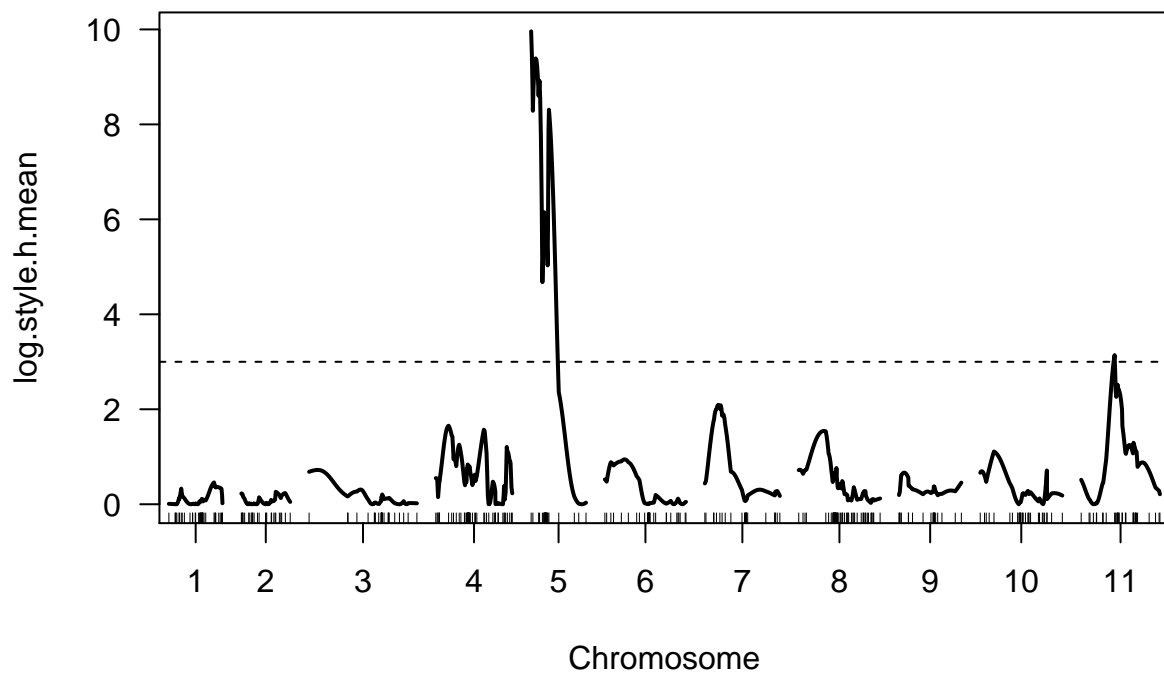


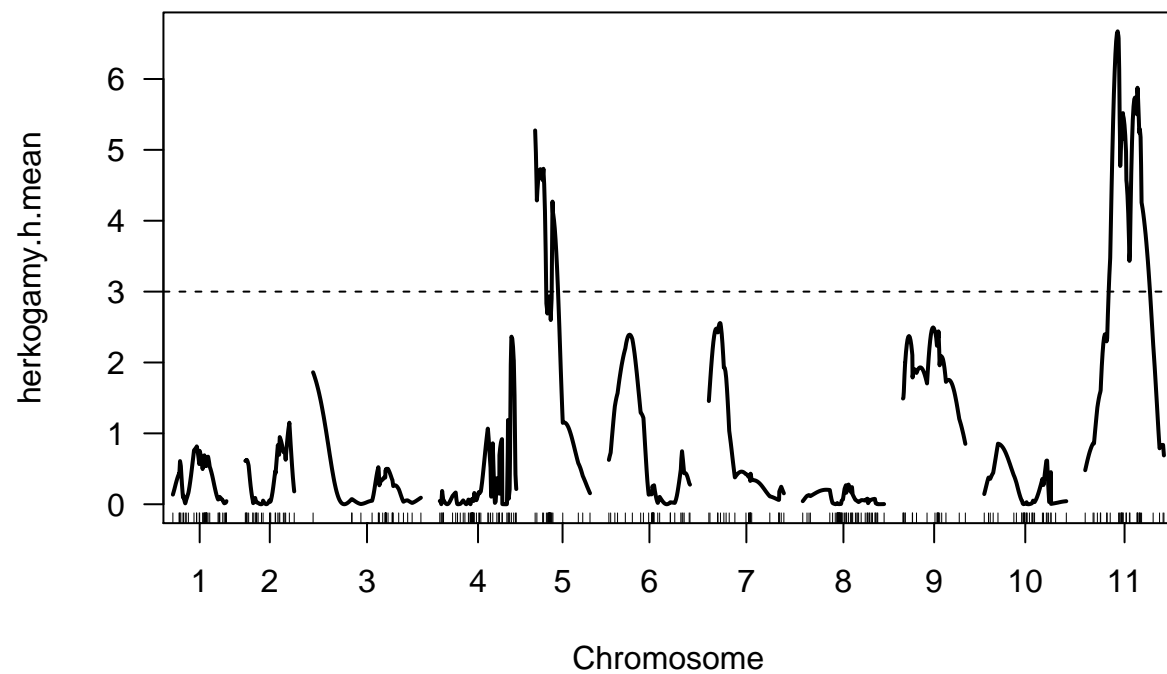


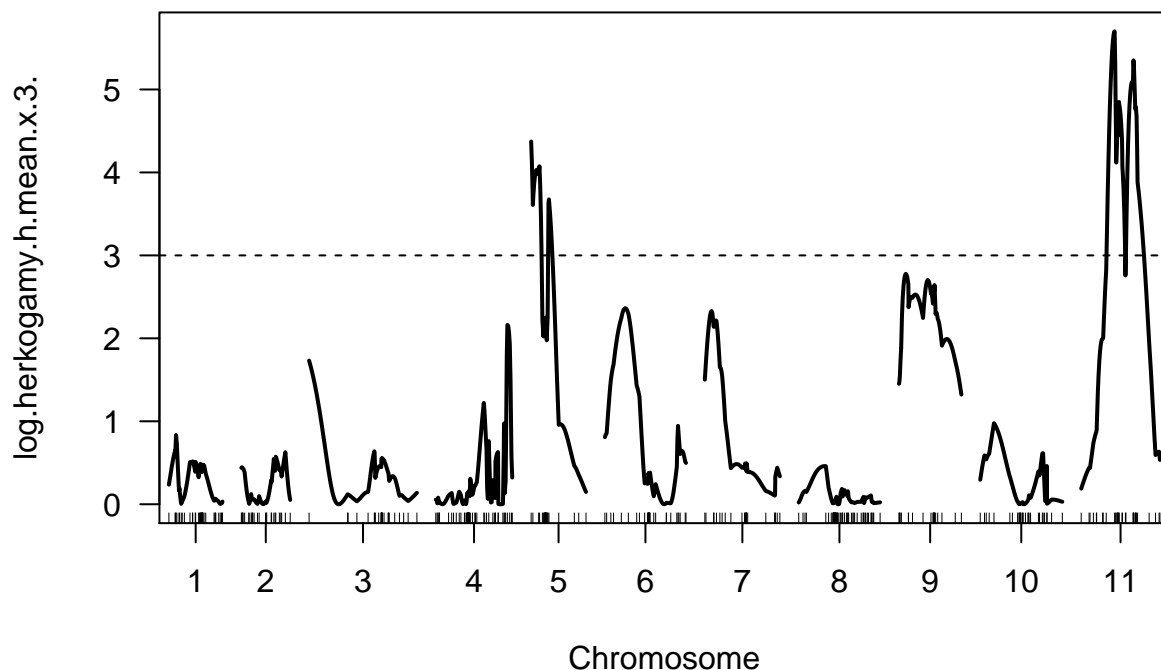












Scan for QTL- all color traits

```
scan_all_color <- scanone(jal_cross, pheno.col=c(24:56), method="em", addcovar=h_color)
```

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

```
summary(scan_all_color, threshold=3, format="tabByChr")
```

```
## Chr 1:
```

```
##
##          chr pos ci.low ci.high lod
## mean.a.h.nec.mean : 10117      1 44.9  31.6    57 4.59
## log.mean.a.h.nec.mean.x.25. : 10435  1 43.6  32.0    56 4.90
##
```

```
## Chr 2:
```

```
##
##          chr pos ci.low ci.high lod
## mean.Intensity.h.nec : c2.loc48      2 48.0  39.5    52.0 8.06
## log.mean.Intensity.h.nec : c2.loc48      2 48.0  39.5    52.0 7.56
## mean.RGB.h.nec : c2.loc47      2 47.0  40.0    52.0 7.89
## log.mean.RGB.h.nec.x.300. : c2.loc47      2 47.0  43.1    50.4 10.03
## mean.G.h.nec : c2.loc48      2 48.0  35.0    63.0 3.97
## log.mean.G.h.nec : c2.loc48      2 48.0  28.0    64.0 3.82
## mean.B.h.nec : c2.loc47      2 47.0  40.0    52.0 8.25
## log.mean.B.h.nec : c2.loc47      2 47.0  28.0    56.0 5.39
## mean.L.h.nec.mean : c2.loc49      2 49.0  32.1    57.0 5.69
## log.mean.L.h.nec.mean : c2.loc49      2 49.0  32.1    57.0 5.65
```

```
## mean.b.h.nec.mean : c2.loc47      2 47.0   29.0   57.0  5.96
## mean.Intensity.h.pet : c2.loc26    2 26.0   20.0   37.0  3.65
## log.mean.Intensity.h.pet : c2.loc26 2 26.0   20.0   36.0  3.86
## mean.R.h.pet : c2.loc26            2 26.0   21.4   36.0  4.82
## log.mean.R.h.pet : c2.loc26        2 26.0   21.4   36.0  5.10
## mean.G.h.pet : c2.loc26            2 26.0   21.4   34.0  5.41
## log.mean.G.h.pet : c2.loc26        2 26.0   21.4   32.0  5.51
## mean.L.h.pet : c2.loc24            2 24.0   19.0   31.0  3.49
## log.L.h.pet : c2.loc24             2 24.0   20.0   31.0  3.64
## mean.a.h.pet : 3974                2 23.5   21.4   29.0 11.09
## log.mean.a.h.pet.x.2. : 3974       2 23.5   14.8   29.0  8.46
## mean.b.h.pet : c2.loc26            2 26.0   22.0   30.0 14.38
## log.mean.b.h.pet.x.3. : c2.loc26    2 26.0   22.0   31.0 15.89
```

```
##
## Chr 5:
##                chr pos ci.low ci.high lod
## mean.a.h.pet : 15397      5 16.2    12   23.6 6.01
## log.mean.a.h.pet.x.2. : 15397  5 16.2    12   23.6 7.46
```

```
##
## Chr 8:
##                chr pos ci.low ci.high lod
## mean.Intensity.h.nec : 2474      8 88.3   80.0   91.0  9.29
## log.mean.Intensity.h.nec : 2474  8 88.3   80.0   91.3  9.07
## mean.RGB.h.nec : 2474           8 88.3   81.0   92.0 12.45
## log.mean.RGB.h.nec.x.300. : 2474  8 88.3   83.0   92.0 13.36
## log.mean.G.h.nec : c8.loc72      8 72.0   50.5   92.3  3.02
## mean.B.h.nec : 2474            8 88.3   82.7   92.0 12.80
## log.mean.B.h.nec : 2474         8 88.3   80.0   92.0  9.89
## mean.b.h.nec.mean : 2474        8 88.3   82.7   92.3 10.66
```

```
##
## Chr 11:
##                chr pos ci.low ci.high lod
## mean.Intensity.h.nec : c11.loc11  11 11.0     0    21  3.03
## log.mean.Intensity.h.nec : 18363  11 10.4     0    21  3.02
## mean.RGB.h.nec : c11.loc13        11 13.0     1    22  3.61
## log.mean.RGB.h.nec.x.300. : c11.loc14 11 14.0     1    23  3.58
## mean.B.h.nec : c11.loc12          11 12.0     0    22  3.58
## log.mean.B.h.nec : 18367          11 11.6     0    22  3.29
## mean.b.h.nec.mean : c11.loc13     11 13.0     1    23  3.49
```

```
summary(scan_all_color, threshold=3, format="tabByCol")
```

```
## mean.Intensity.h.nec:
##      chr pos ci.low ci.high lod
## c2.loc48  2 48.0   39.5    52  8.06
## 2474      8 88.3   80.0    91  9.29
## c11.loc11 11 11.0    0.0    21  3.03
##
## log.mean.Intensity.h.nec:
##      chr pos ci.low ci.high lod
## c2.loc48  2 48.0   39.5    52.0 7.56
## 2474      8 88.3   80.0    91.3 9.07
## 18363     11 10.4    0.0    21.0 3.02
##
## mean.RGB.h.nec:
```

```

##          chr pos ci.low ci.high lod
## c2.loc47   2 47.0   40    52 7.89
## 2474       8 88.3   81    92 12.45
## c11.loc13 11 13.0    1    22 3.61
##
## log.mean.RGB.h.nec.x.300.:
##          chr pos ci.low ci.high lod
## c2.loc47   2 47.0  43.1   50.4 10.03
## 2474       8 88.3  83.0   92.0 13.36
## c11.loc14 11 14.0   1.0   23.0 3.58
##
## mean.G.h.nec:
##          chr pos ci.low ci.high lod
## c2.loc48   2 48    35    63 3.97
##
## log.mean.G.h.nec:
##          chr pos ci.low ci.high lod
## c2.loc48   2 48   28.0   64.0 3.82
## c8.loc72   8 72   50.5   92.3 3.02
##
## mean.B.h.nec:
##          chr pos ci.low ci.high lod
## c2.loc47   2 47.0  40.0    52 8.25
## 2474       8 88.3  82.7    92 12.80
## c11.loc12 11 12.0   0.0    22 3.58
##
## log.mean.B.h.nec:
##          chr pos ci.low ci.high lod
## c2.loc47   2 47.0   28    56 5.39
## 2474       8 88.3   80    92 9.89
## 18367      11 11.6    0    22 3.29
##
## mean.L.h.nec.mean:
##          chr pos ci.low ci.high lod
## c2.loc49   2 49   32.1    57 5.69
##
## log.mean.L.h.nec.mean:
##          chr pos ci.low ci.high lod
## c2.loc49   2 49   32.1    57 5.65
##
## mean.a.h.nec.mean:
##          chr pos ci.low ci.high lod
## 10117      1 44.9   31.6    57 4.59
##
## log.mean.a.h.nec.mean.x.25.:
##          chr pos ci.low ci.high lod
## 10435      1 43.6    32    56 4.9
##
## mean.b.h.nec.mean:
##          chr pos ci.low ci.high lod
## c2.loc47   2 47.0  29.0   57.0 5.96
## 2474       8 88.3  82.7   92.3 10.66
## c11.loc13 11 13.0   1.0   23.0 3.49
##

```

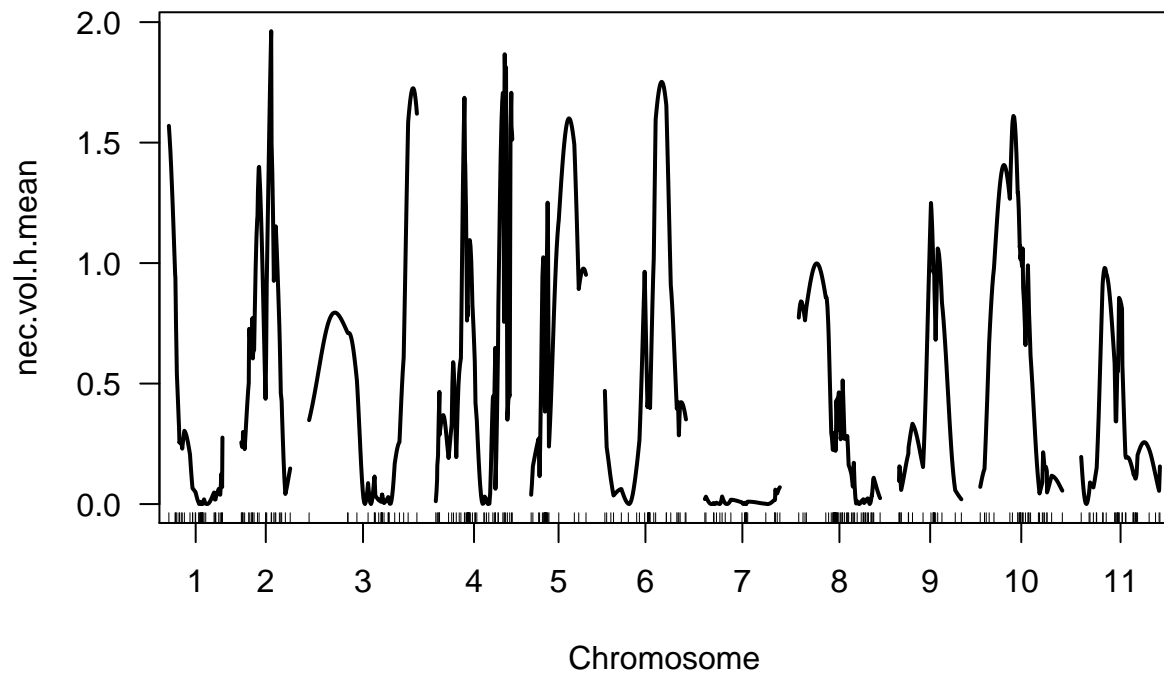


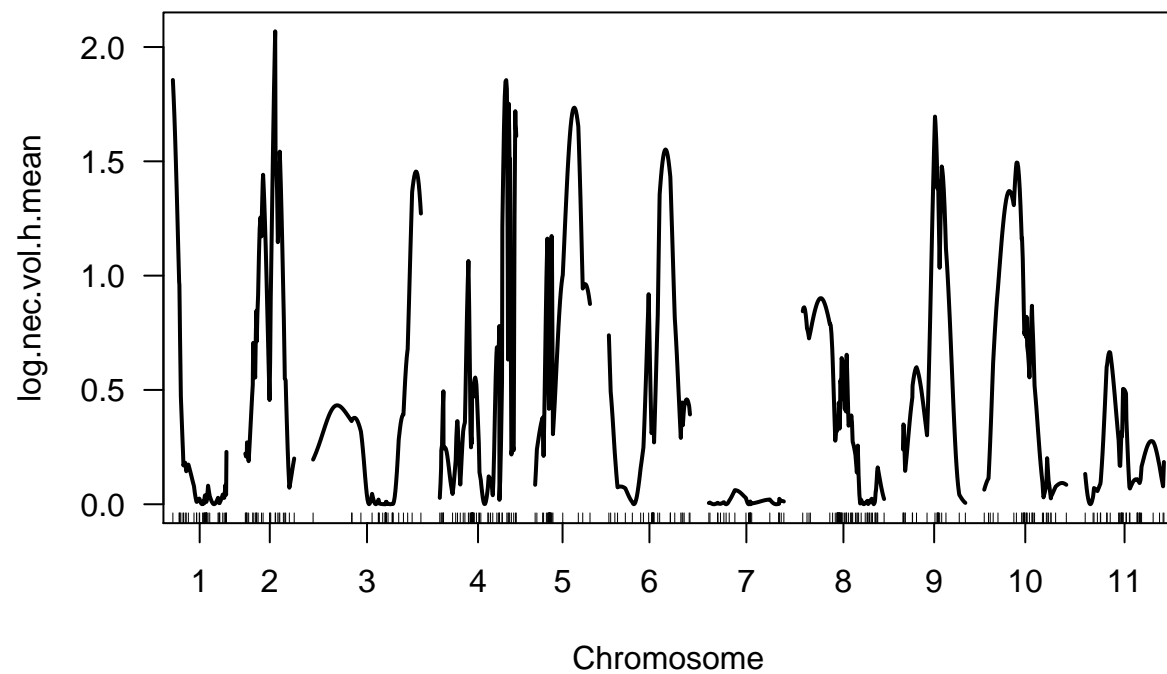
```

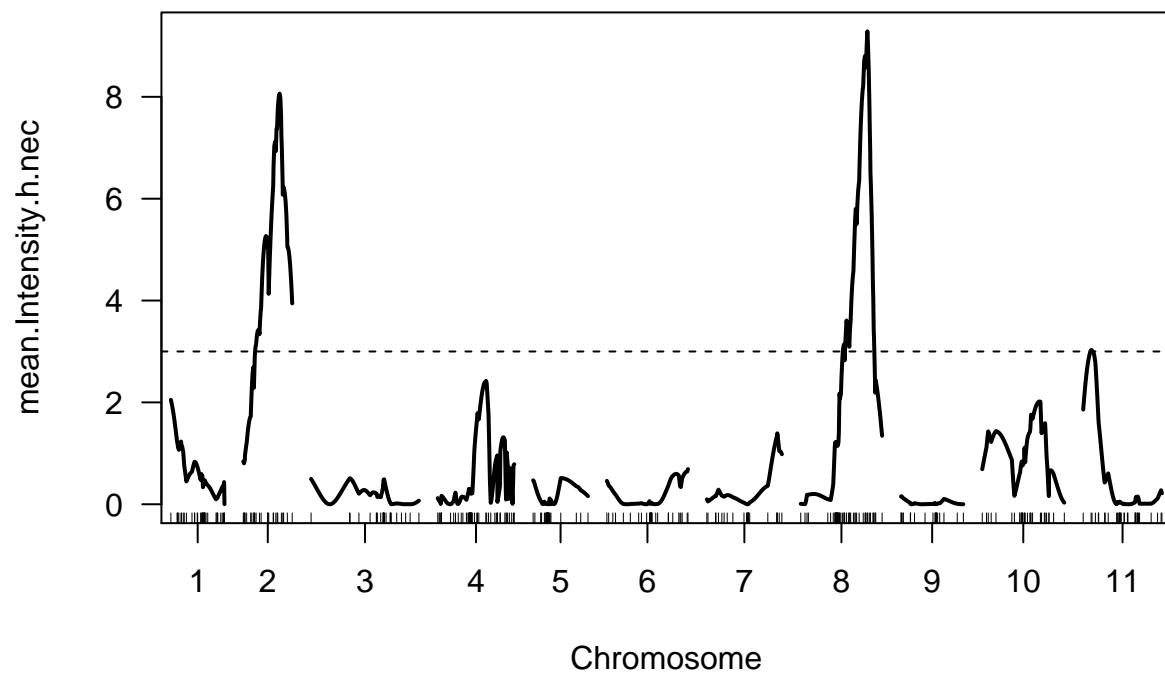
## mean.Intensity.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26      20      37 3.65
##
## log.mean.Intensity.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26      20      36 3.86
##
## mean.R.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26     21.4      36 4.82
##
## log.mean.R.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26     21.4      36 5.1
##
## mean.G.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26     21.4      34 5.41
##
## log.mean.G.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26     21.4      32 5.51
##
## mean.L.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc24  2 24      19      31 3.49
##
## log.L.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc24  2 24      20      31 3.64
##
## mean.a.h.pet:
##      chr pos ci.low ci.high lod
## 3974    2 23.5    21.4    29.0 11.09
## 15397   5 16.2    12.0    23.6  6.01
##
## log.mean.a.h.pet.x.2.:
##      chr pos ci.low ci.high lod
## 3974    2 23.5    14.8    29.0  8.46
## 15397   5 16.2    12.0    23.6  7.46
##
## mean.b.h.pet:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26      22      30 14.4
##
## log.mean.b.h.pet.x.3.:
##      chr pos ci.low ci.high lod
## c2.loc26  2 26      22      31 15.9
##
##par(mfrow=c(3,1))
for (x in 1:33){
  plot(scan_all_color, lodcolumn = x)
  abline(3,0,lty=2)
}

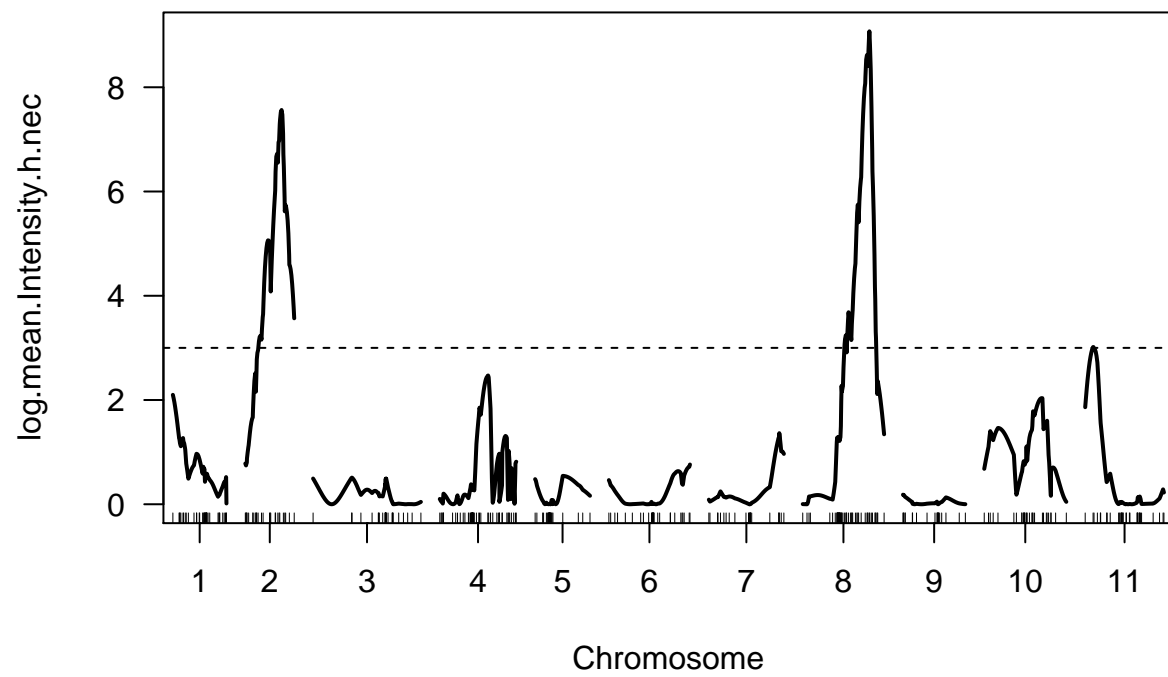
```

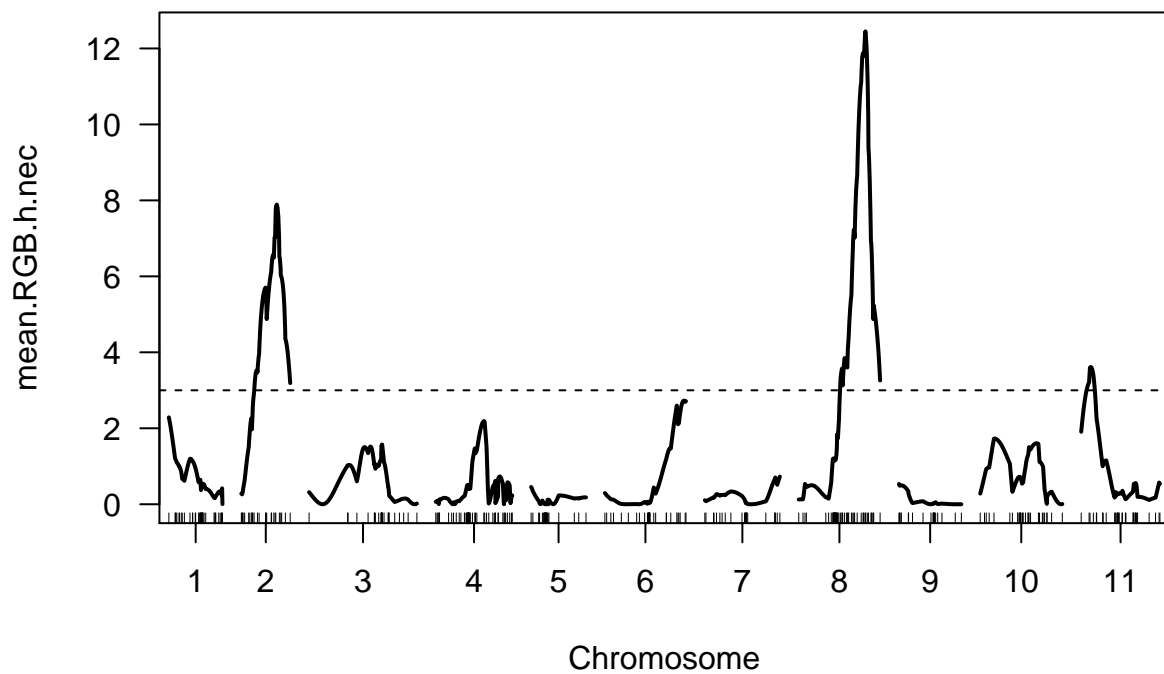
}

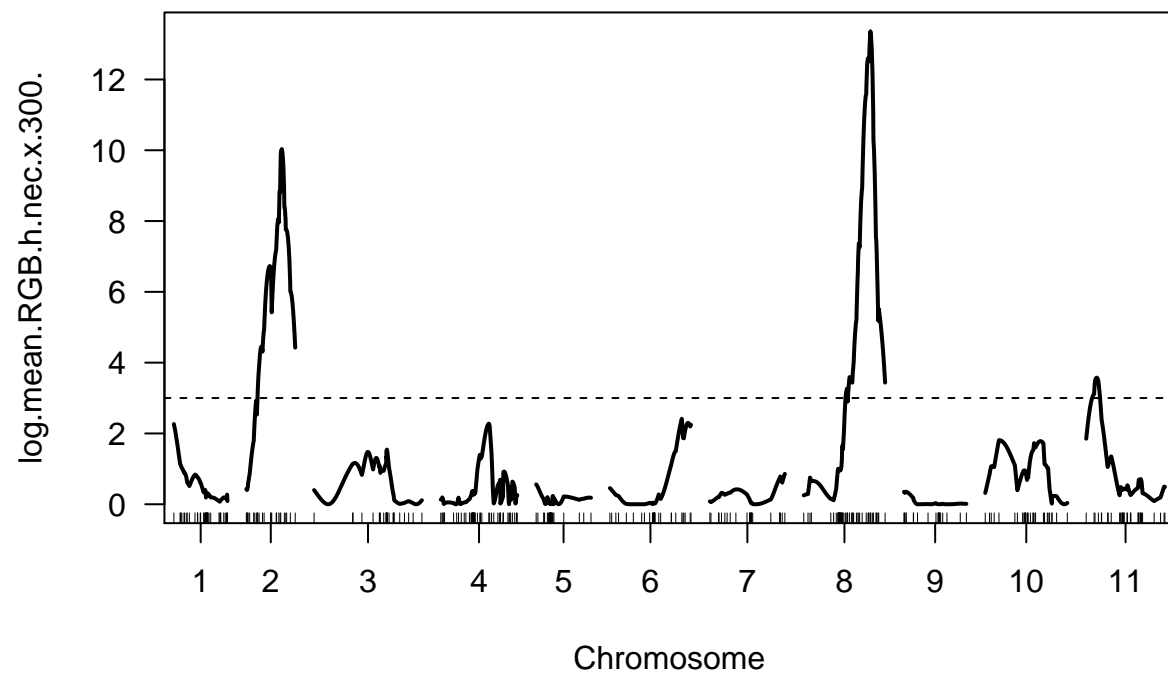


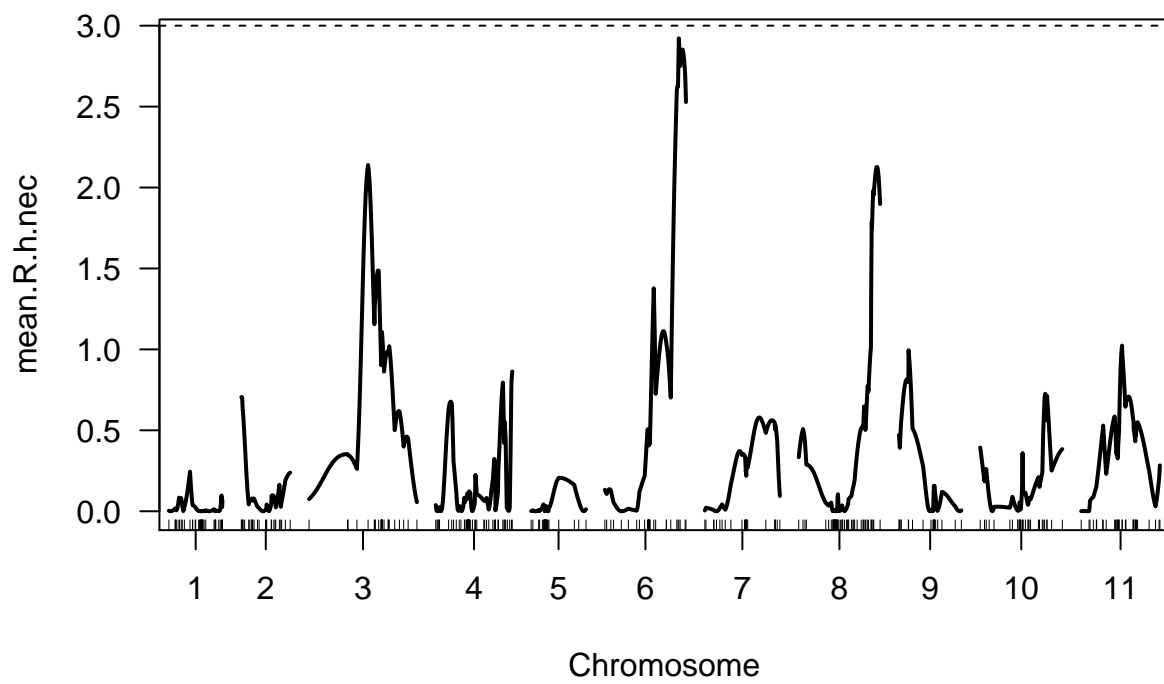


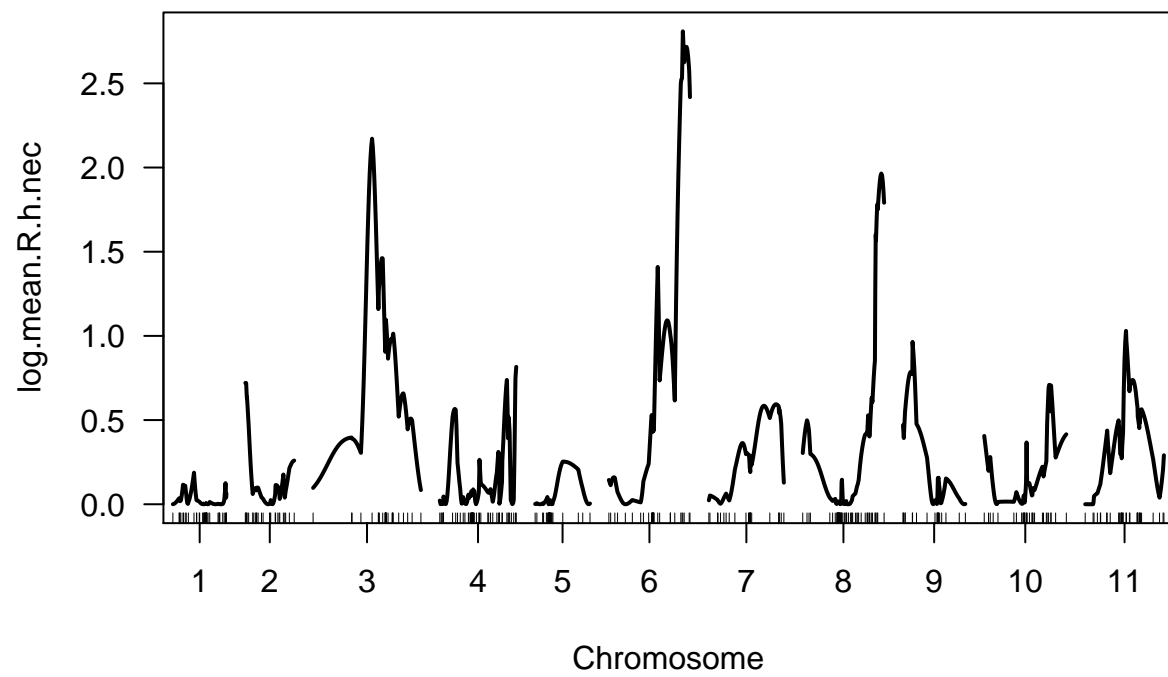


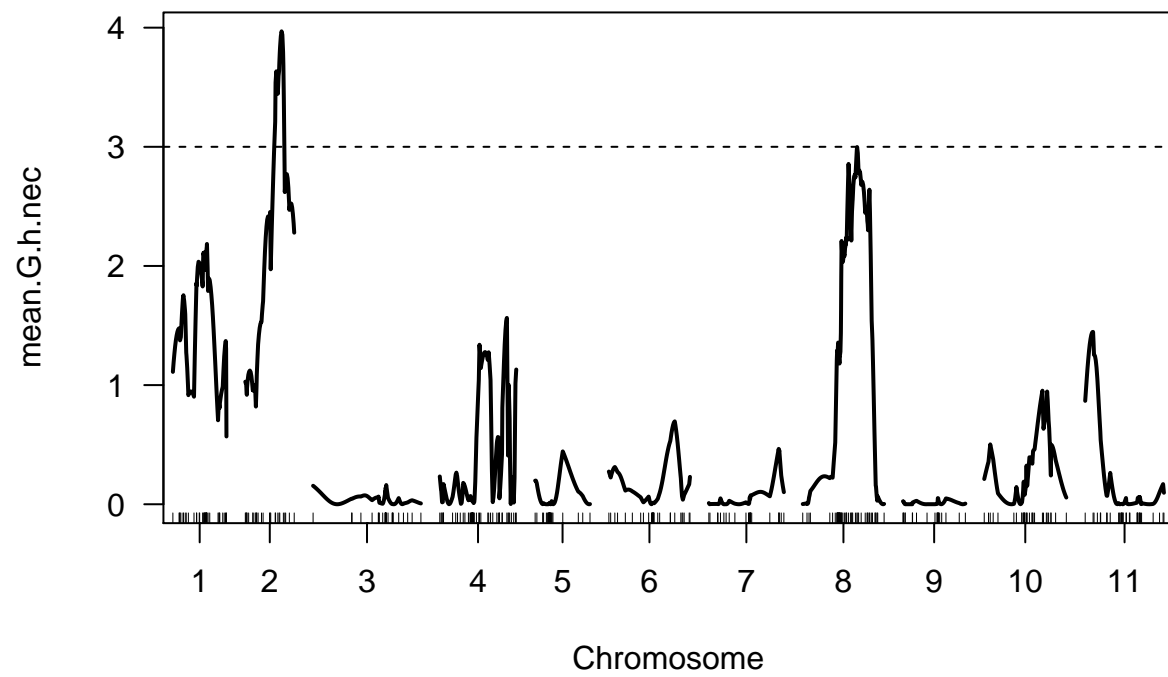


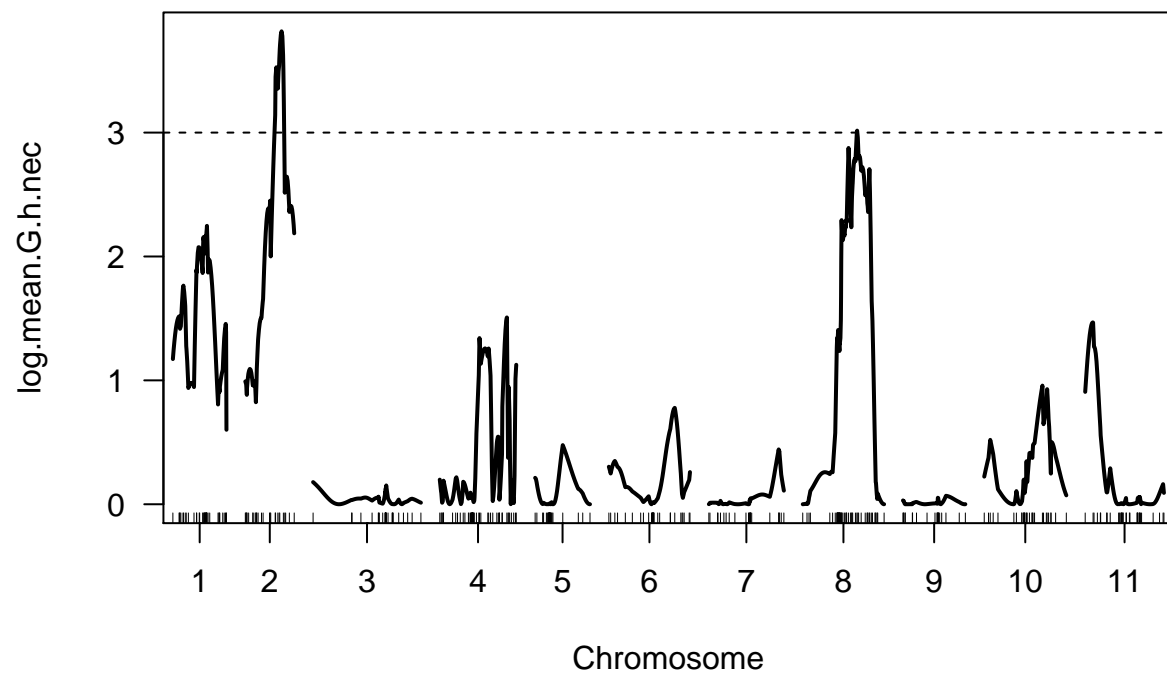


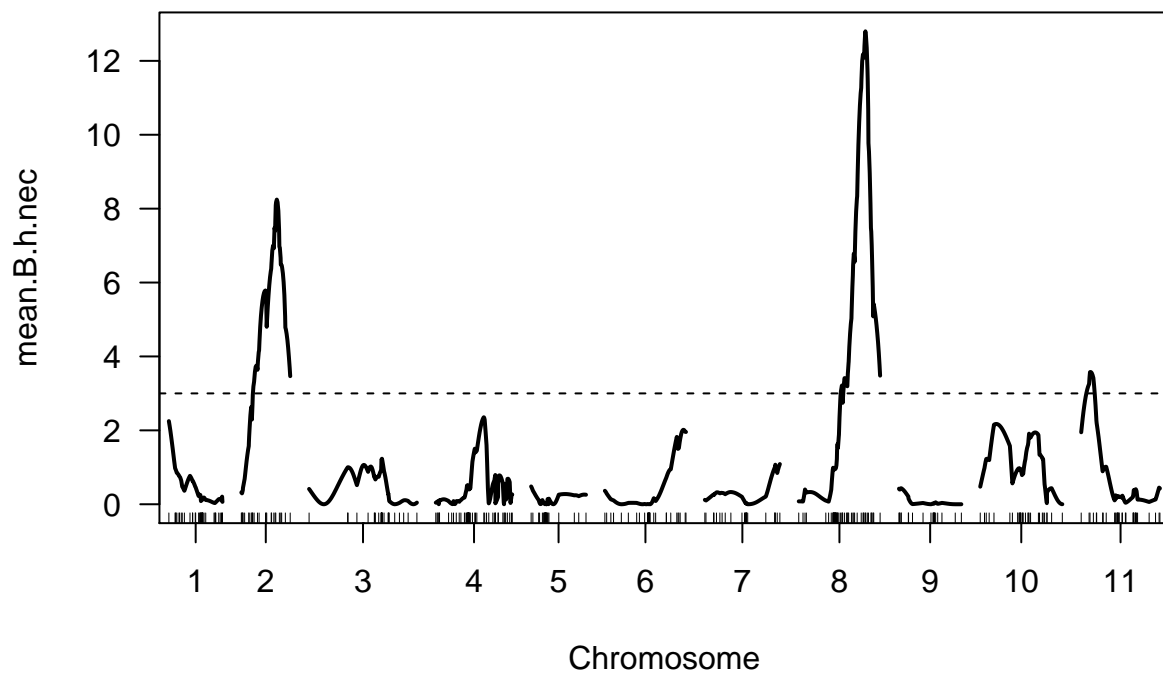


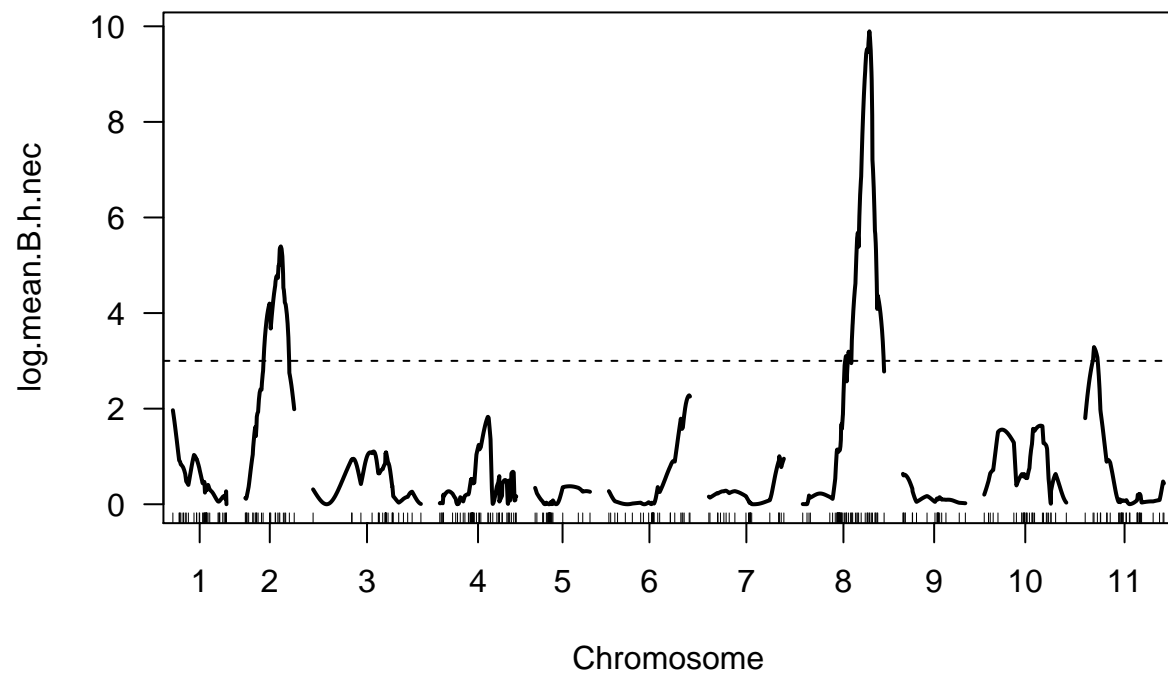


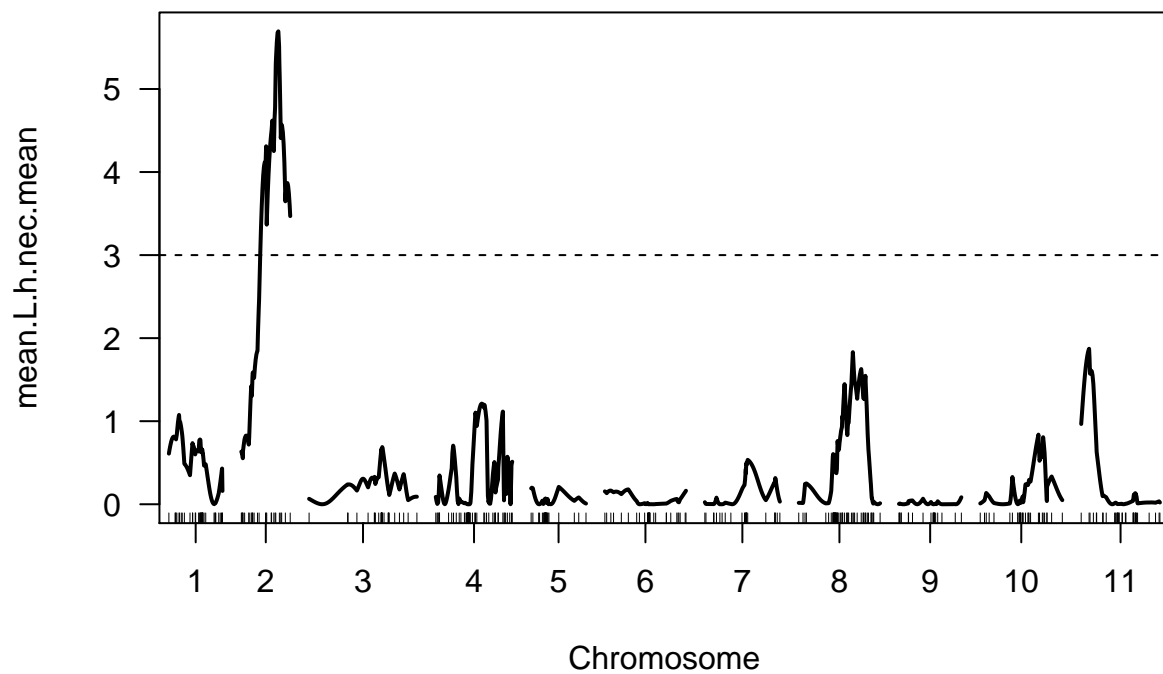


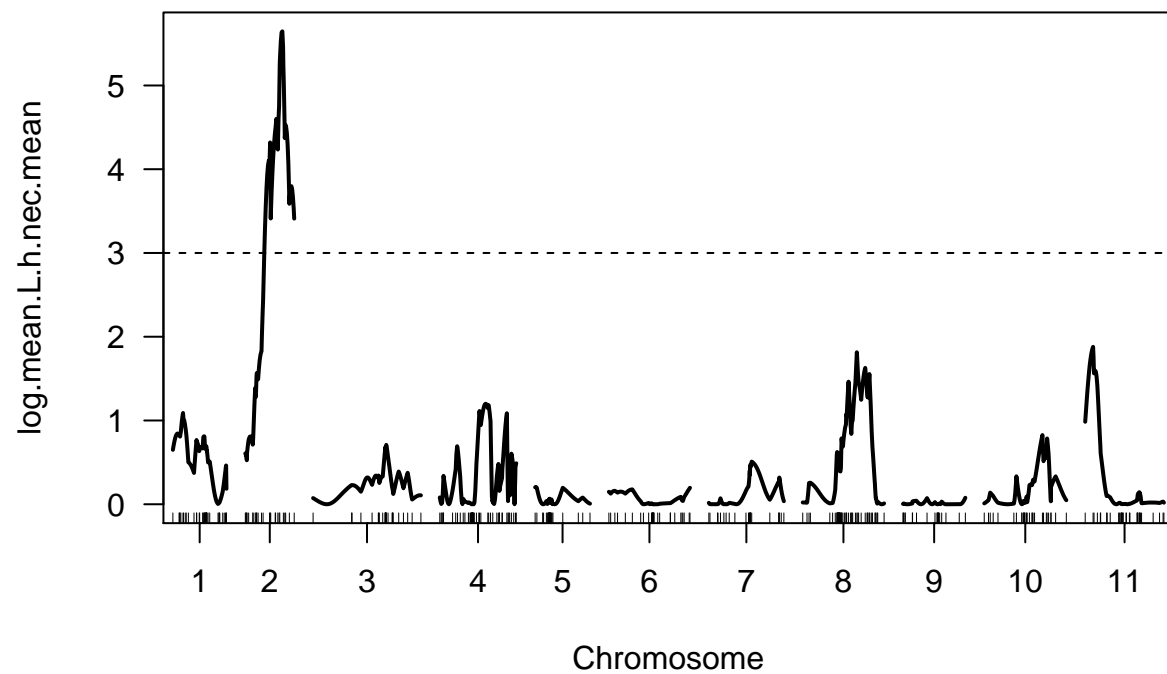


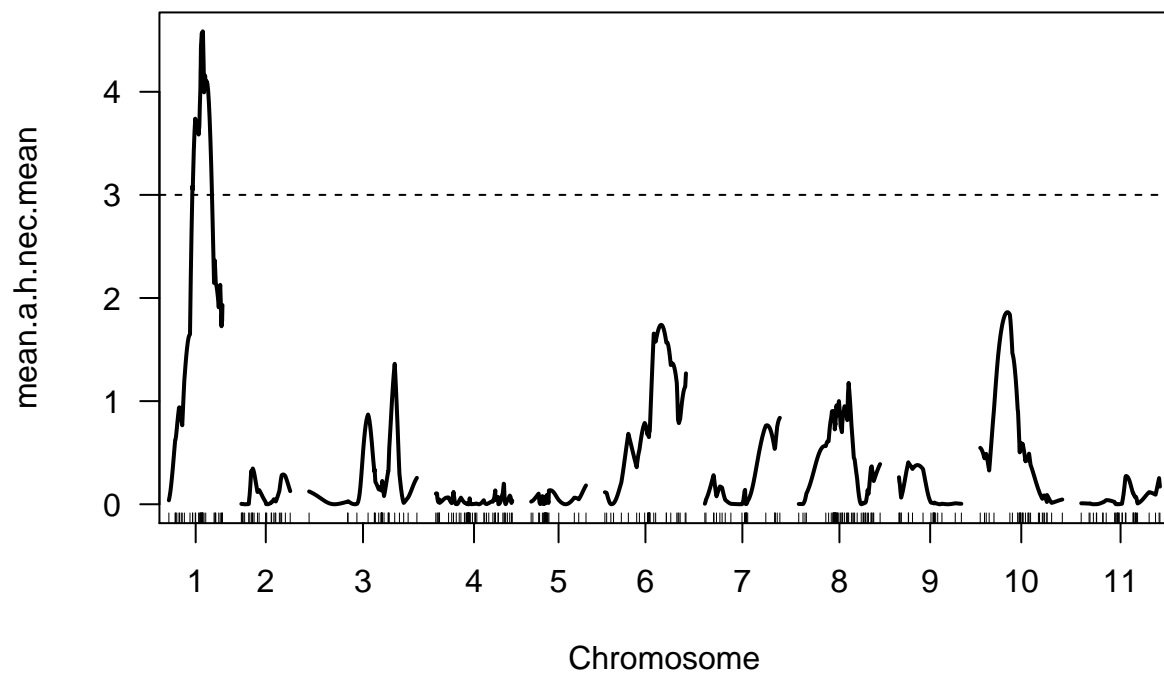


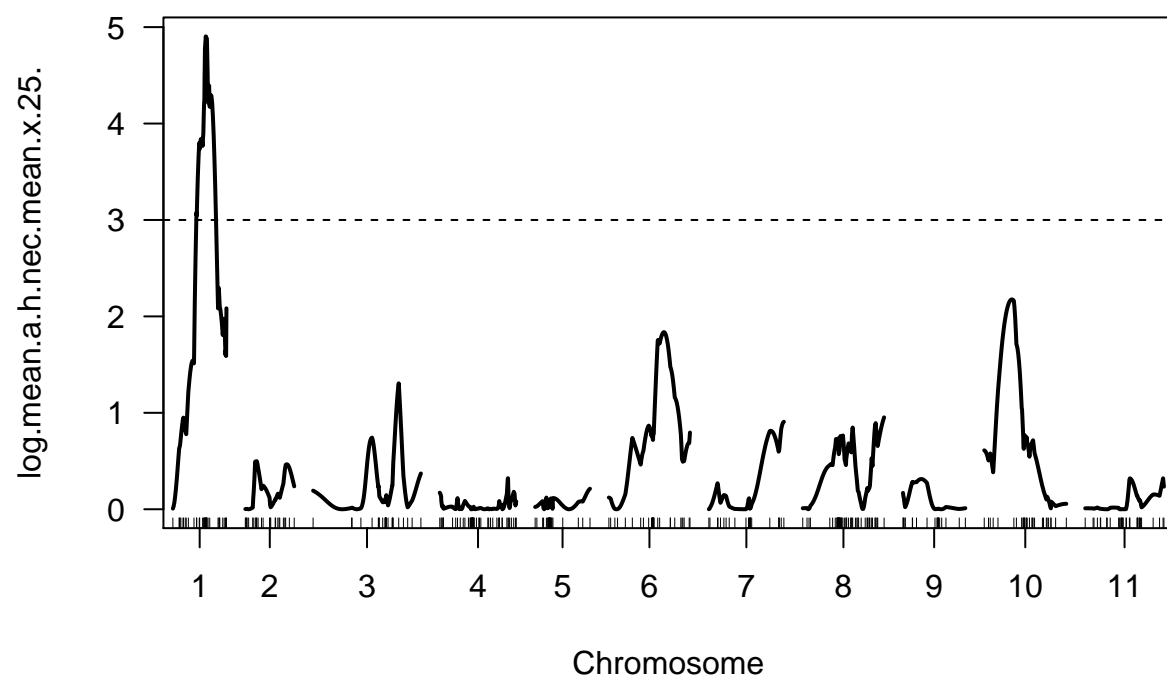


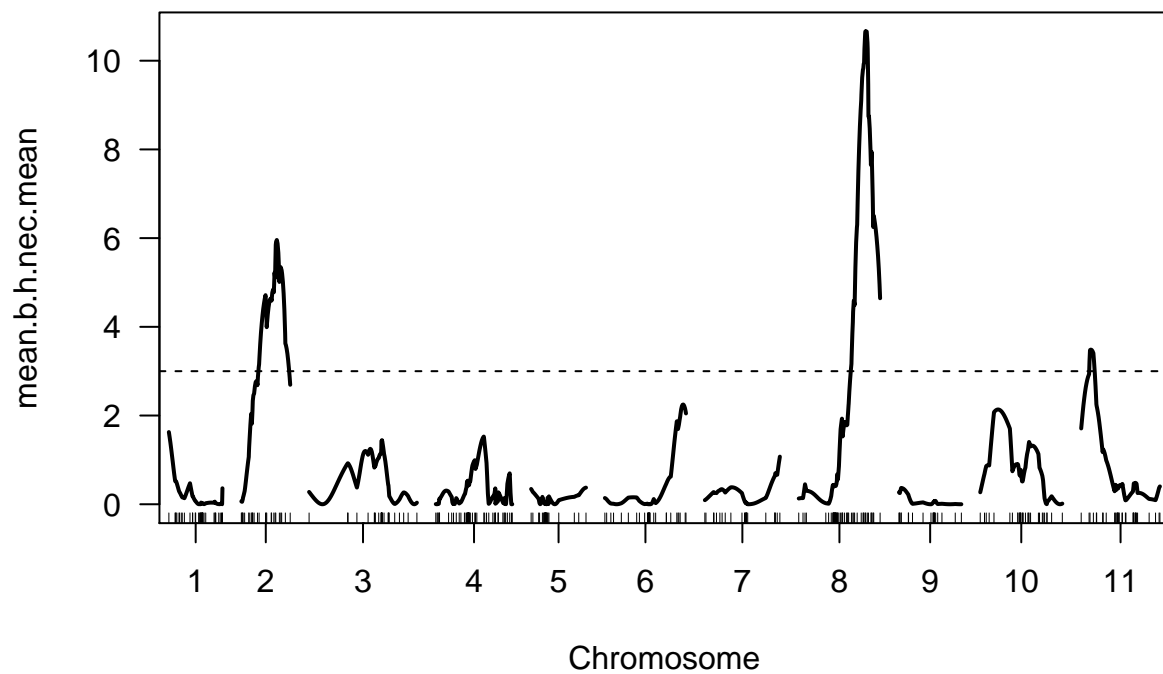


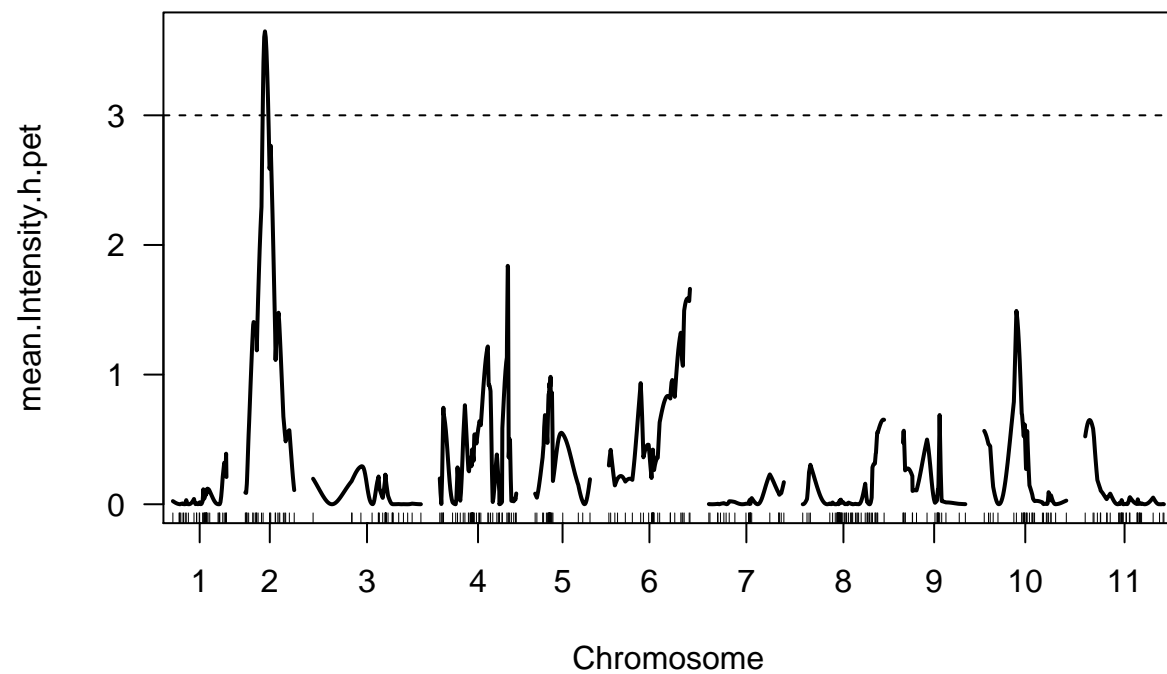


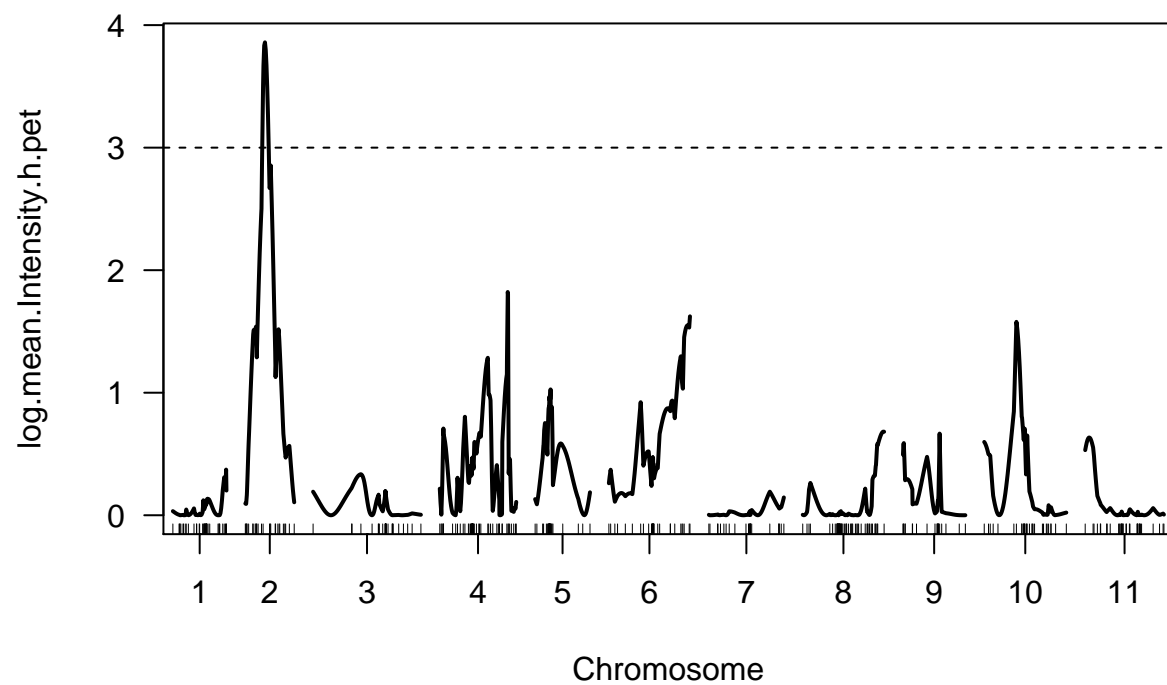


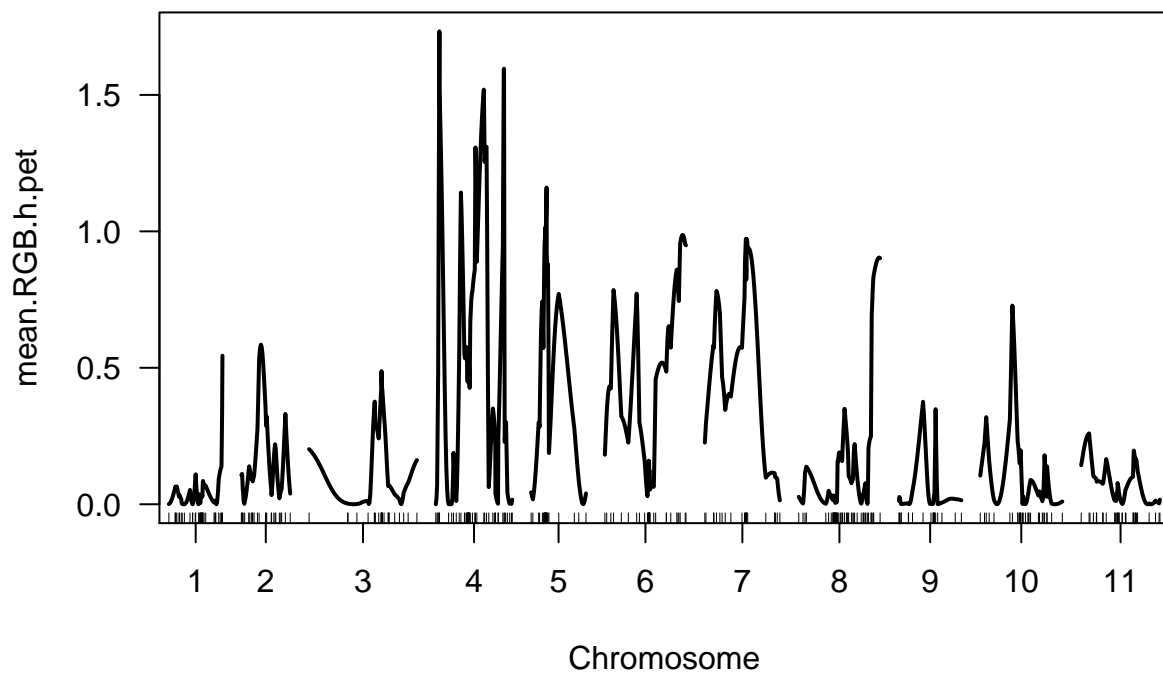


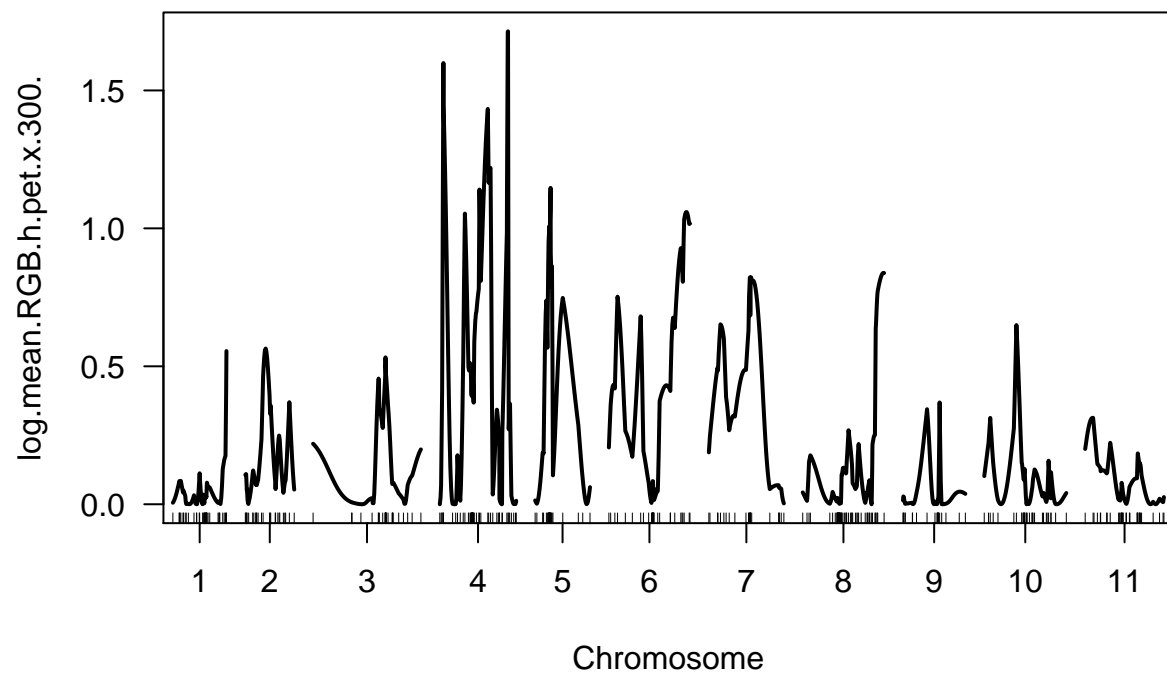


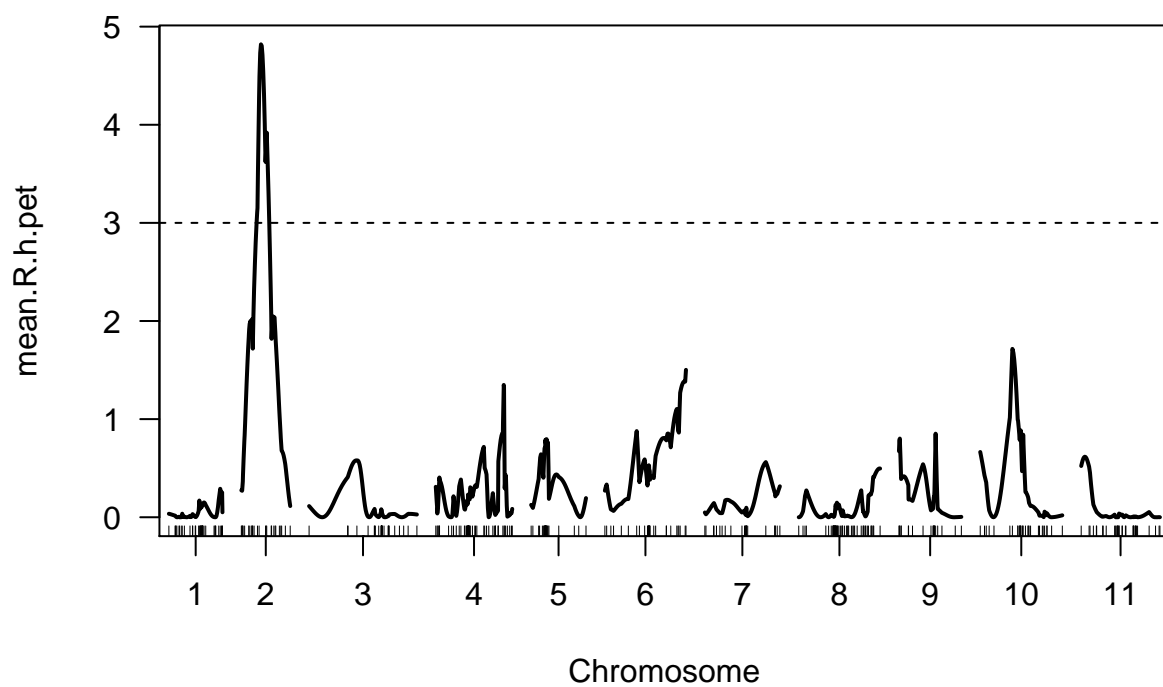


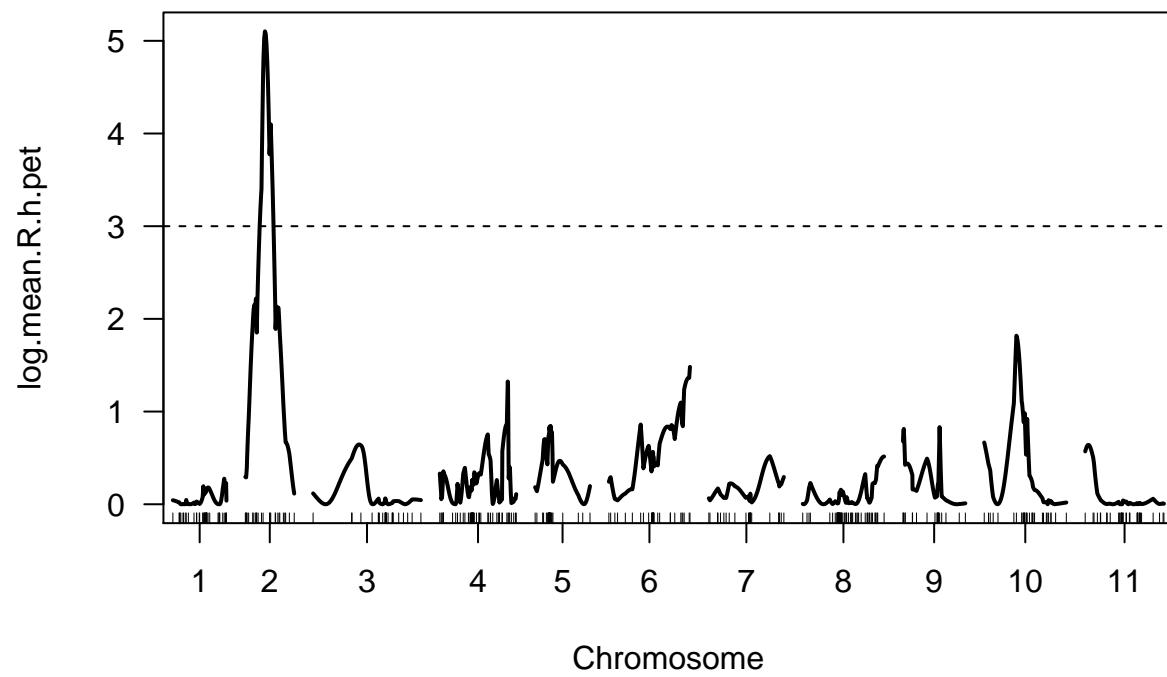


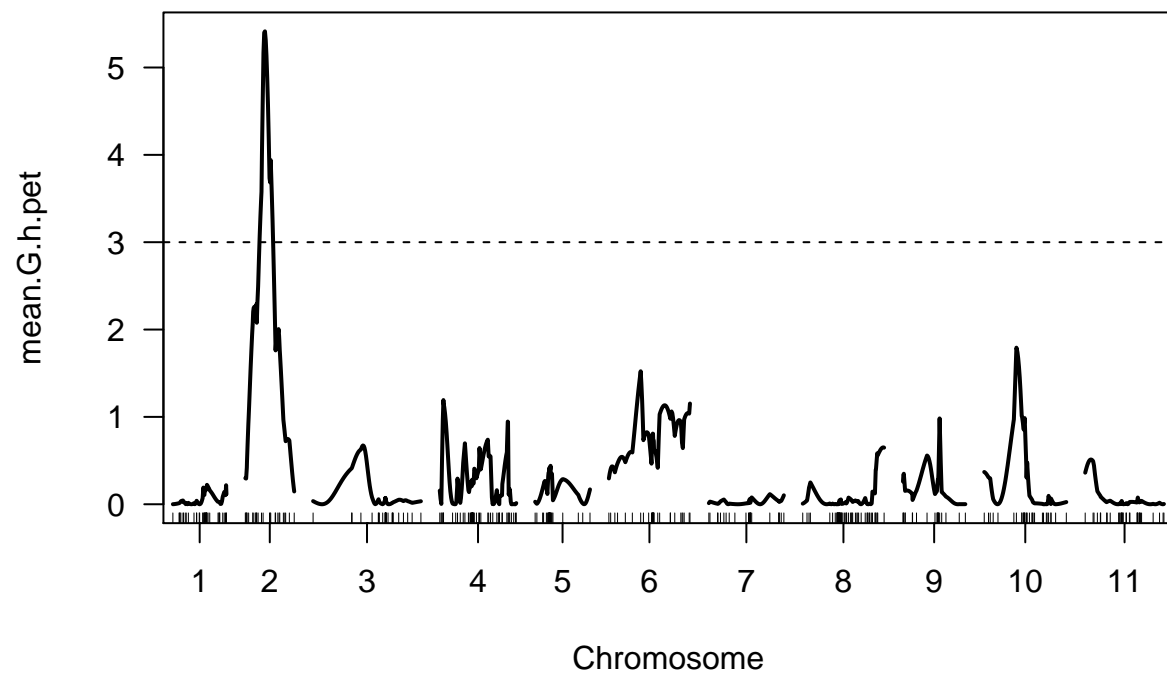


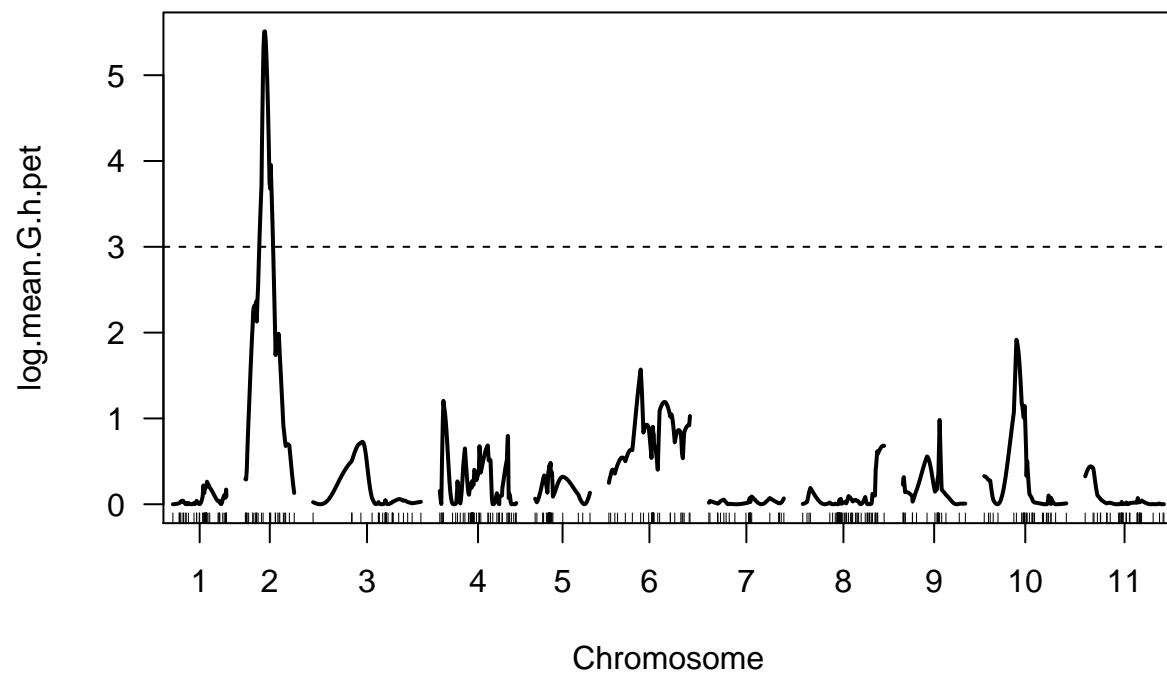


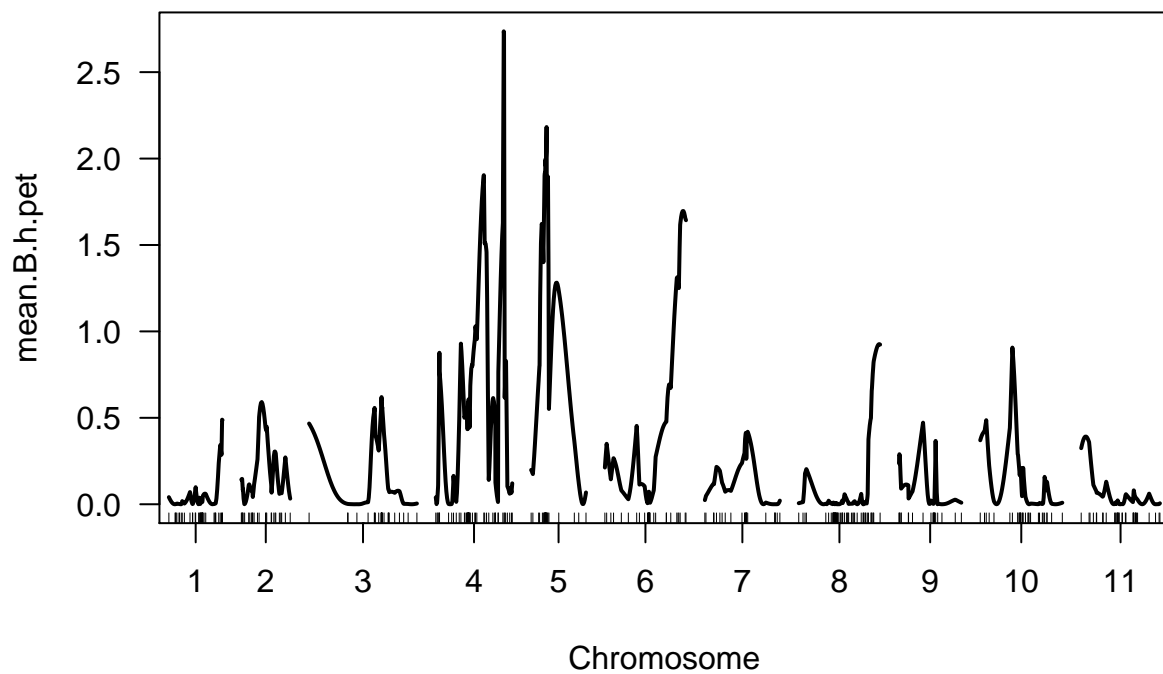


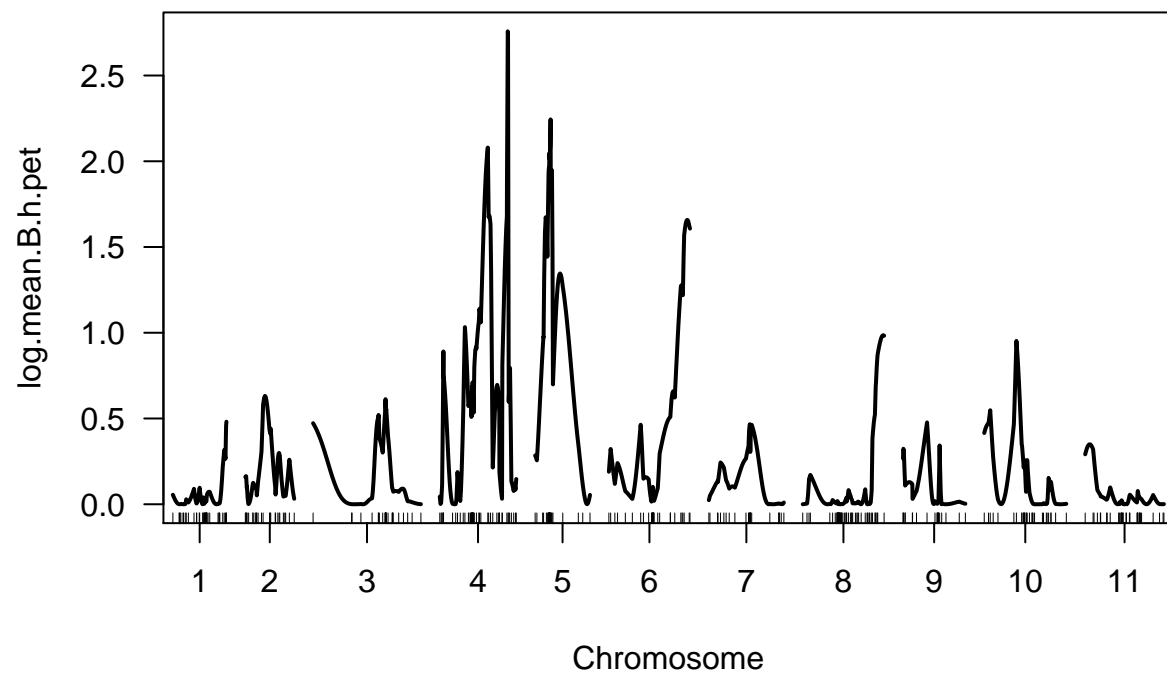


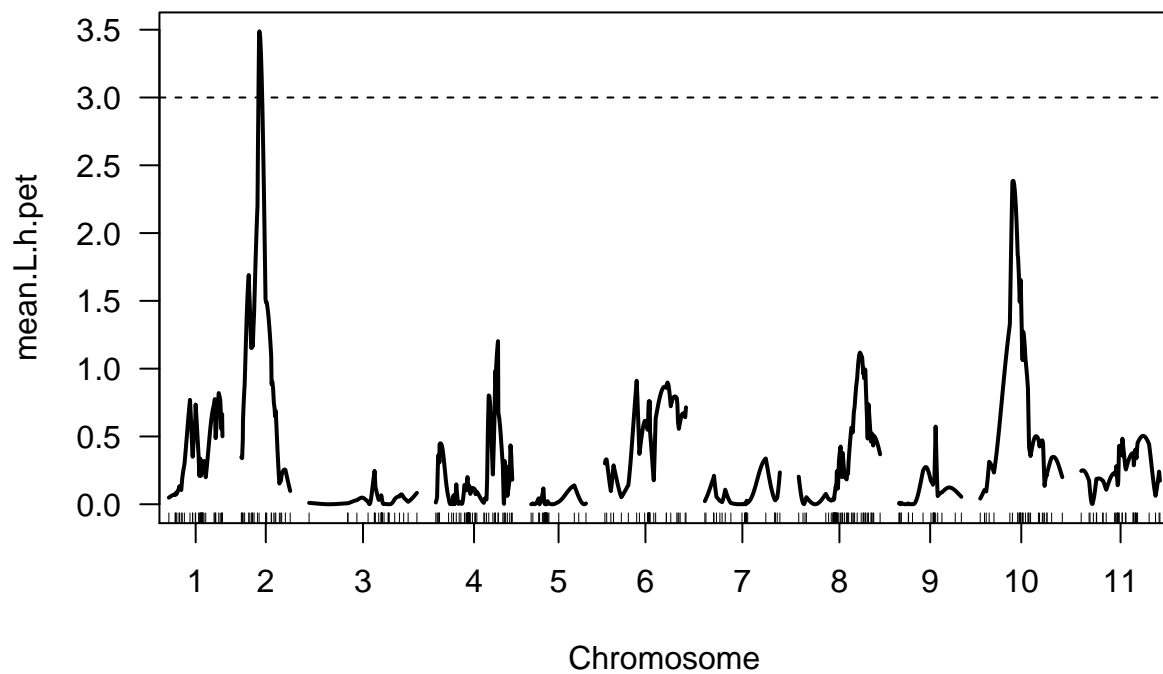


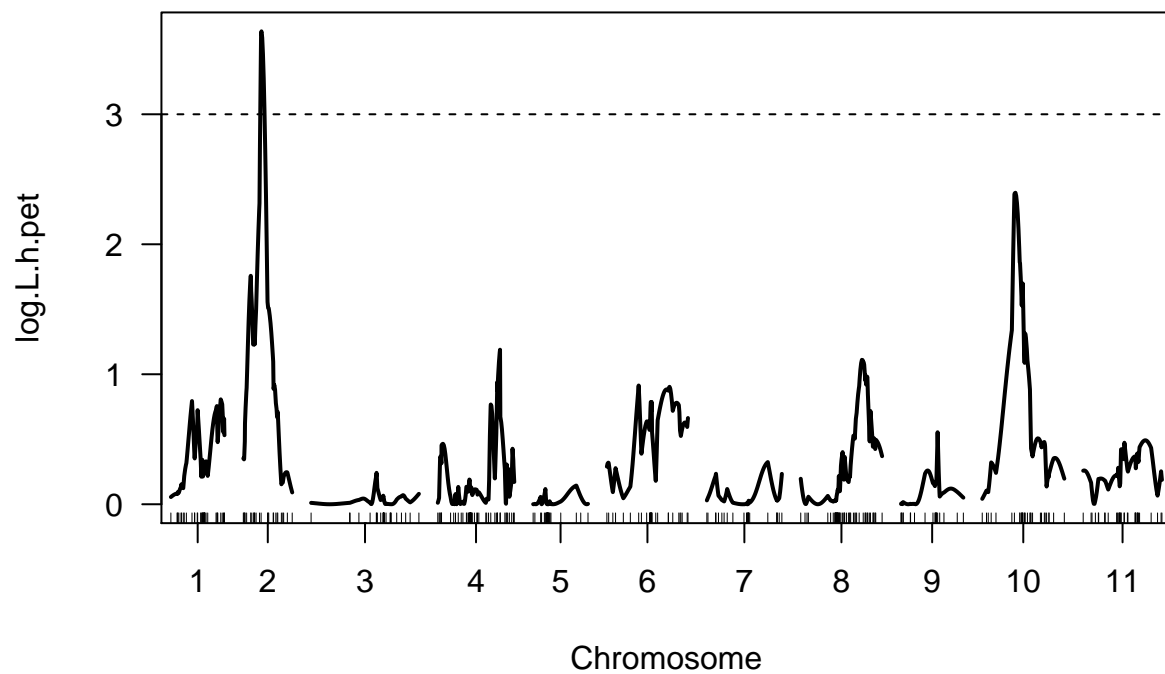


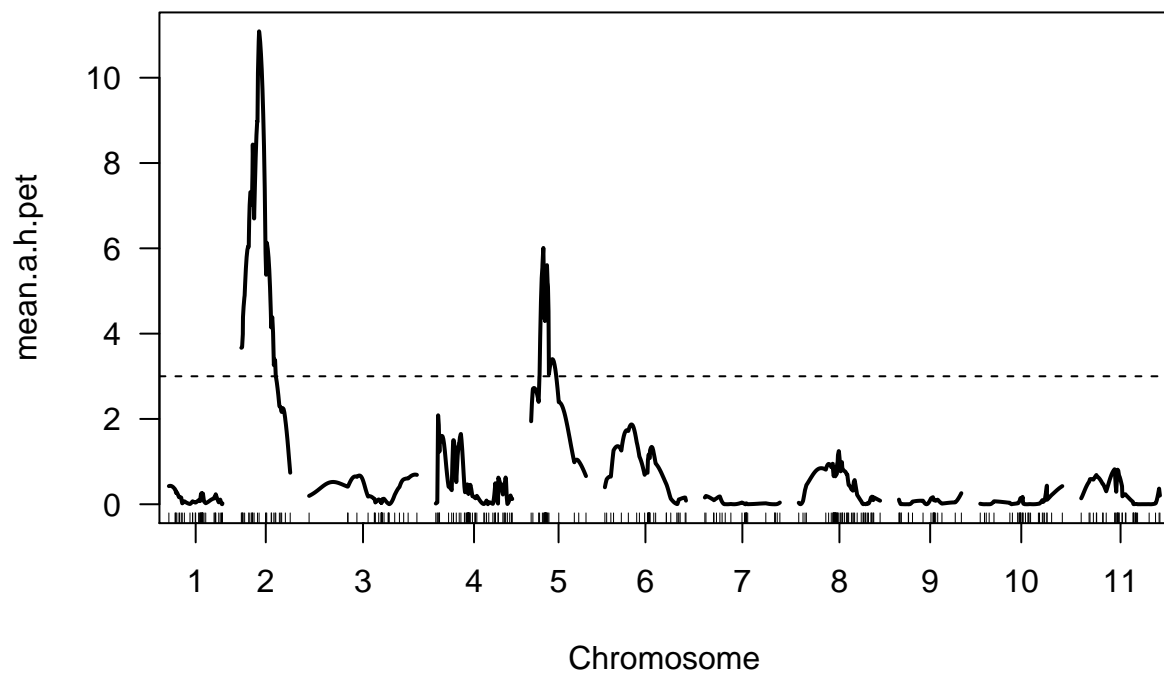


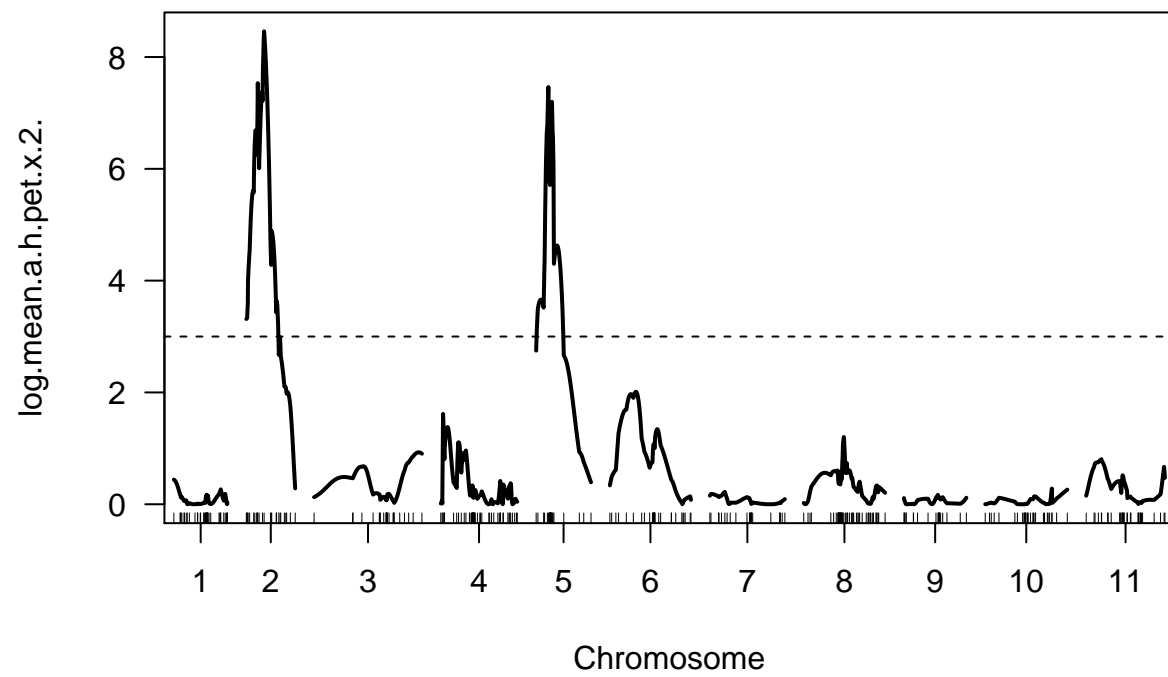


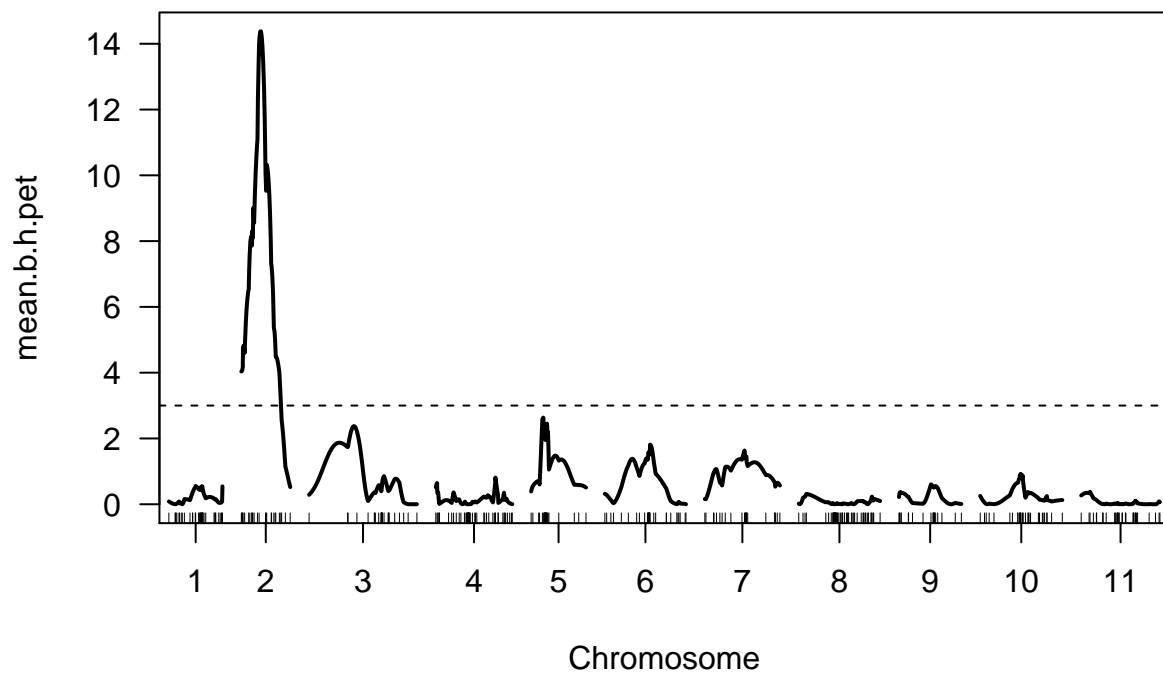


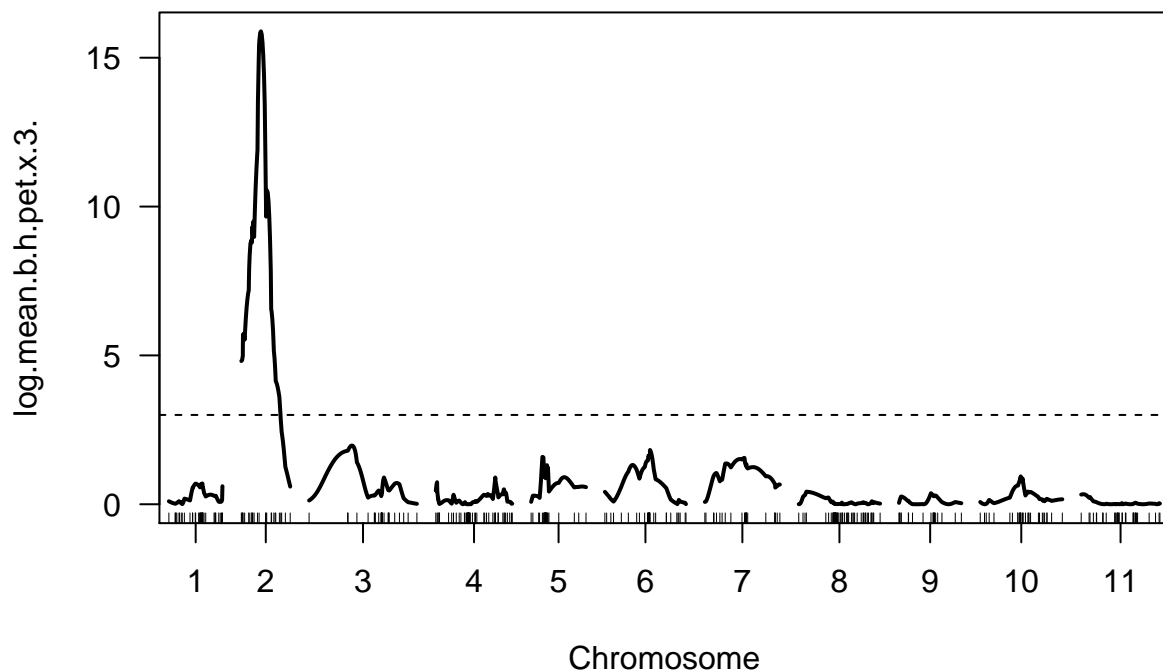












Scan for QTL- all seed and fruit traits (non-selfed; pollen from Sinosa)

```
scan_all_seedFruit <- scanone(jal_cross, pheno.col=c(58:71), 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 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 50 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 50 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 50 individuals w
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 50 individuals w
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 50 individuals w
```

```
## Warning in checkcovar(cross, pheno.col, addcovar, intcovar, perm.strata, : Dropping 50 individuals w
```

```
summary(scan_all_seedFruit, threshold=3, format="tabByChr")
```

```
## Chr 4:
```

```
##               chr pos ci.low ci.high lod
## mean.fruit.mass : c4.loc29      4 29  21.1  44.0 6.96
## log.mean.fruit.mass.x.1. : c4.loc29  4 29  21.1  41.8 7.05
## mean.fruit.dia : c4.loc29      4 29  21.1  49.0 5.83
## log.mean.fruit.dia.x.1. : c4.loc29  4 29  21.1  50.0 5.52
## mean.seed : c4.loc33      4 33   2.0  53.0 3.46
```

```
##
```

```
## Chr 6:
```

```
##               chr pos ci.low ci.high lod
## mean.fruit.mass : 14447      6 81.4   63   93 3.27
## log.mean.fruit.mass.x.1. : 14447  6 81.4   63   94 3.15
```

```
##
```

```
## Chr 9:
```

```
##               chr pos ci.low ci.high lod
## mean.fruit.mass : 17983      9 0.518    0   21 4.49
## log.mean.fruit.mass.x.1. : 17983  9 0.518    0   20 4.62
## mean.fruit.dia : 17983      9 0.518    0   20 4.26
## log.mean.fruit.dia.x.1. : 17983  9 0.518    0   21 3.96
## mean.seed : 17983      9 0.518    0   19 5.23
## log.mean.seed : 17983      9 0.518    0   12 5.57
## mean.via.seed : 17983      9 0.518    0   10 3.82
## log.mean.via.seed : 17982      9 0.000    0    9 4.46
```

```
summary(scan_all_seedFruit, threshold=3, format="tabByCol")
```

```
## mean.fruit.mass:
```

```
##      chr pos ci.low ci.high lod
## c4.loc29  4 29.000  21.1   44 6.96
## 14447      6 81.400  63.0   93 3.27
## 17983      9  0.518   0.0   21 4.49
```

```
##
```

```
## log.mean.fruit.mass.x.1.:
```

```
##      chr pos ci.low ci.high lod
## c4.loc29  4 29.000  21.1   41.8 7.05
## 14447      6 81.400  63.0   94.0 3.15
## 17983      9  0.518   0.0   20.0 4.62
```

```
##
```

```
## mean.fruit.dia:
```

```
##      chr pos ci.low ci.high lod
## c4.loc29  4 29.000  21.1   49 5.83
## 17983      9  0.518   0.0   20 4.26
```

```
##
```

```
## log.mean.fruit.dia.x.1.:
```

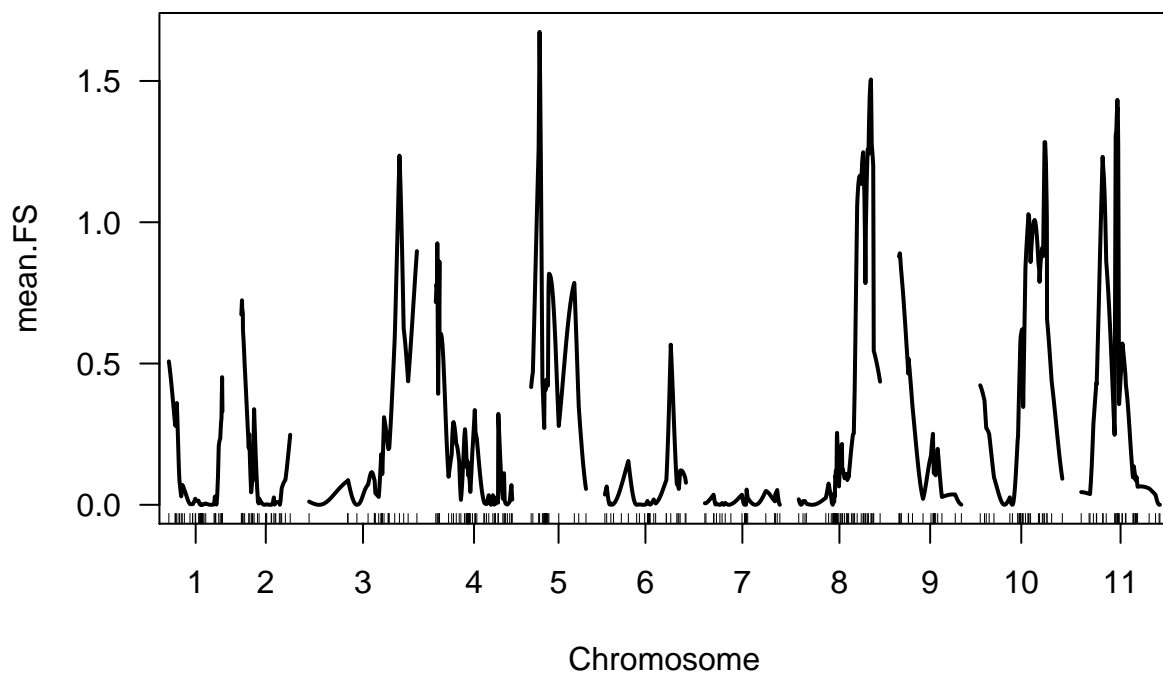
```
##      chr pos ci.low ci.high lod
## c4.loc29  4 29.000  21.1   50 5.52
## 17983      9  0.518   0.0   21 3.96
```

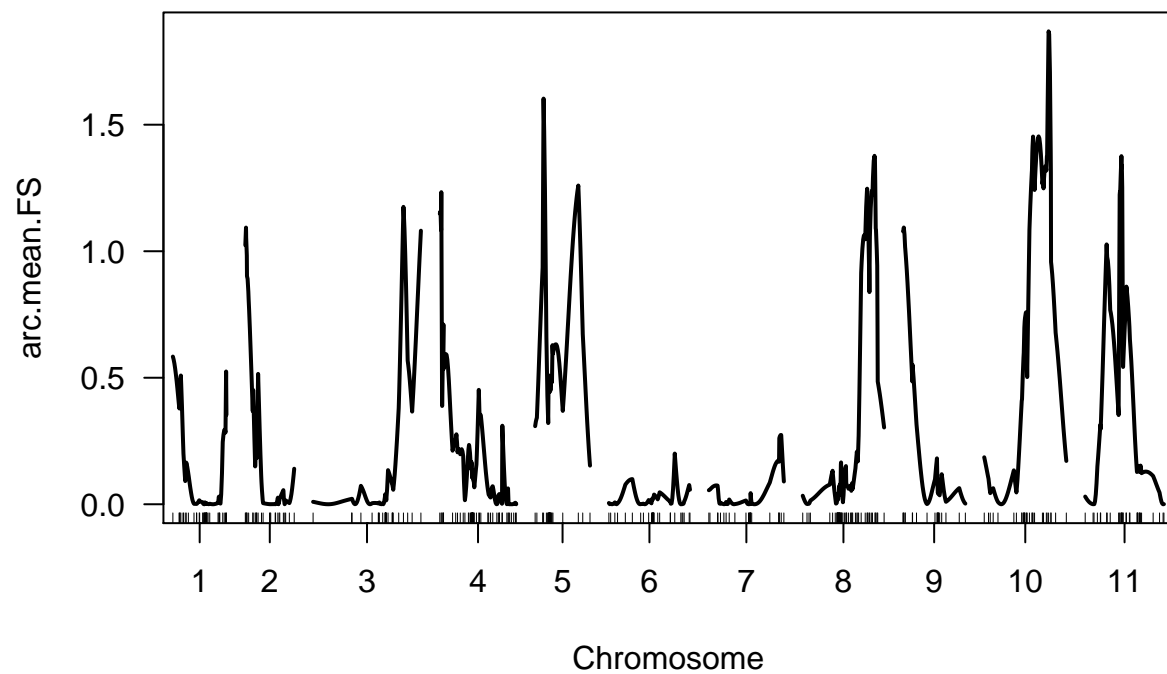
```
##
```

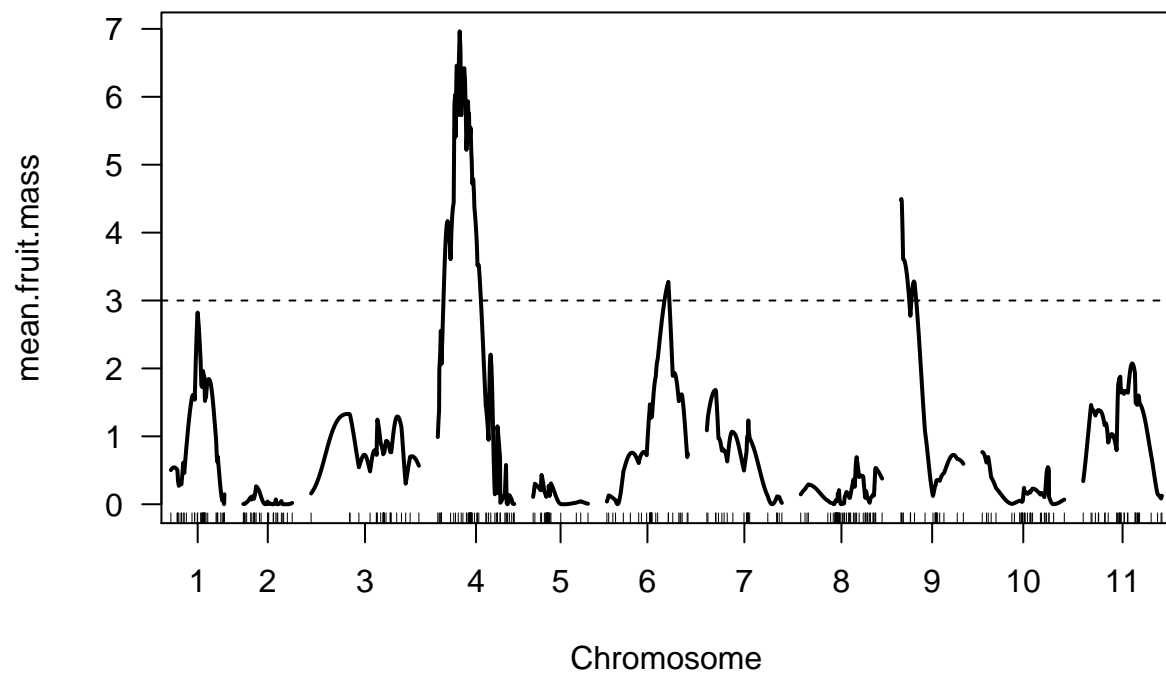
```
## mean.seed:
```

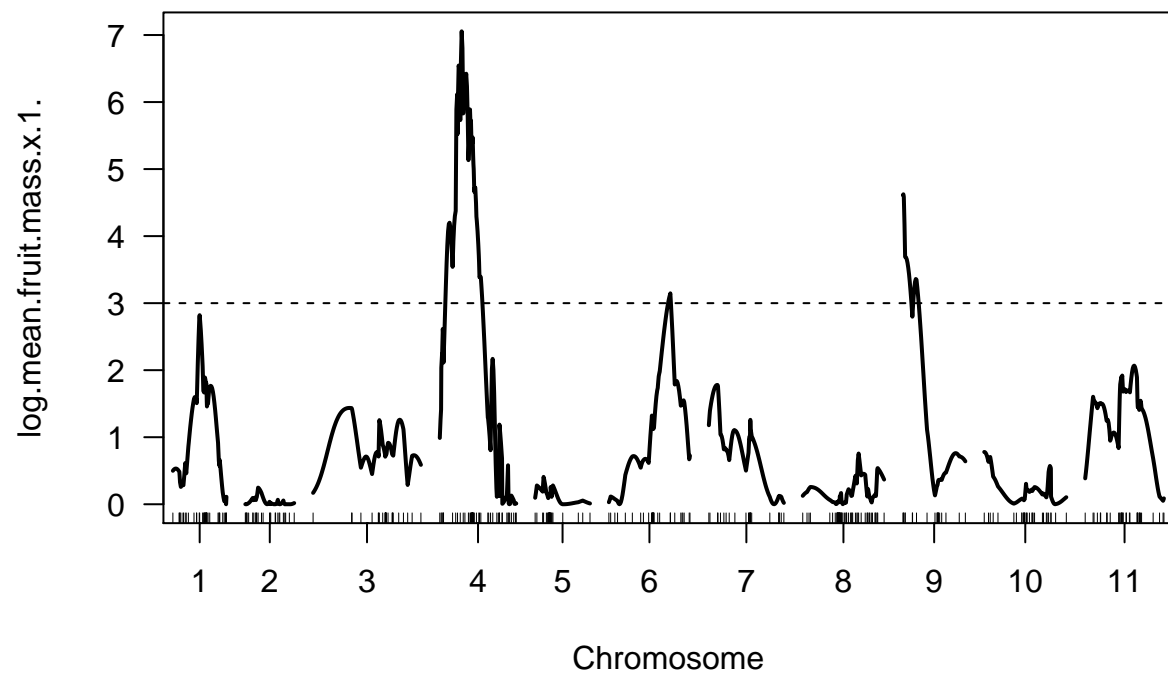
```
##          chr    pos ci.low ci.high  lod
## c4.loc33    4 33.000      2      53 3.46
## 17983       9  0.518      0      19 5.23
##
## log.mean.seed:
##          chr    pos ci.low ci.high  lod
## 17983       9  0.518      0      12 5.57
##
## mean.via.seed:
##          chr    pos ci.low ci.high  lod
## 17983       9  0.518      0      10 3.82
##
## log.mean.via.seed:
##          chr pos ci.low ci.high  lod
## 17982       9  0      0      9 4.46
```

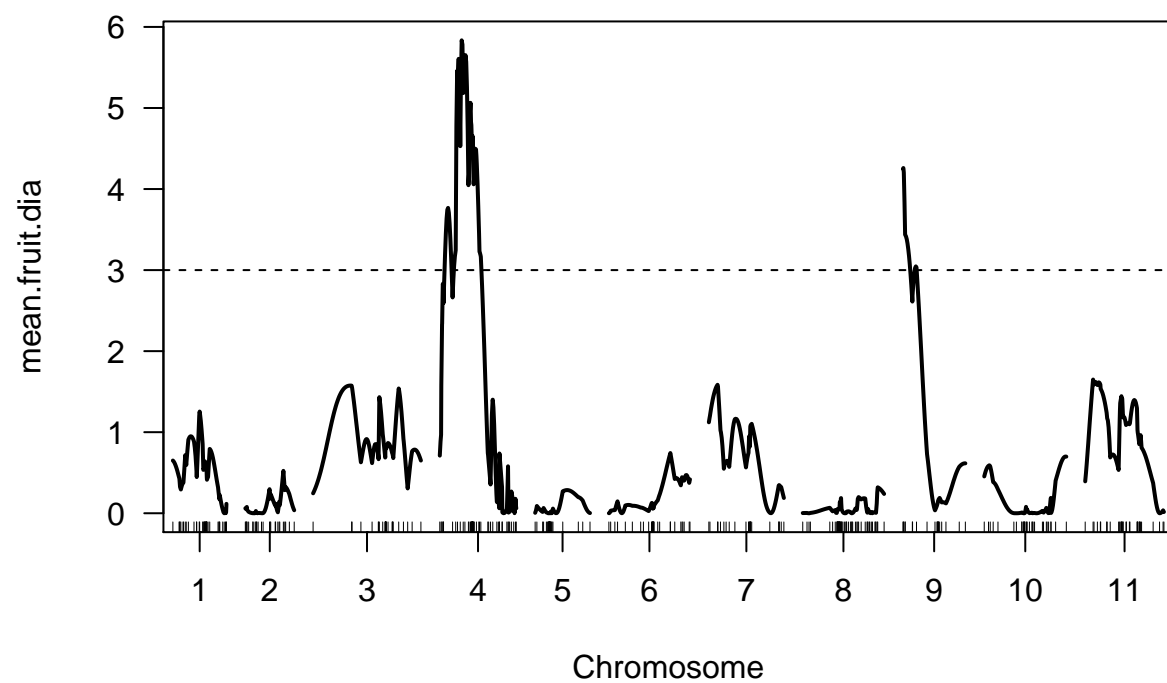
```
#par(mfrow=c(3,1))
for (x in 1:13){
  plot(scan_all_seedFruit, lodcolumn = x)
  abline(3,0,lty=2)
}
```

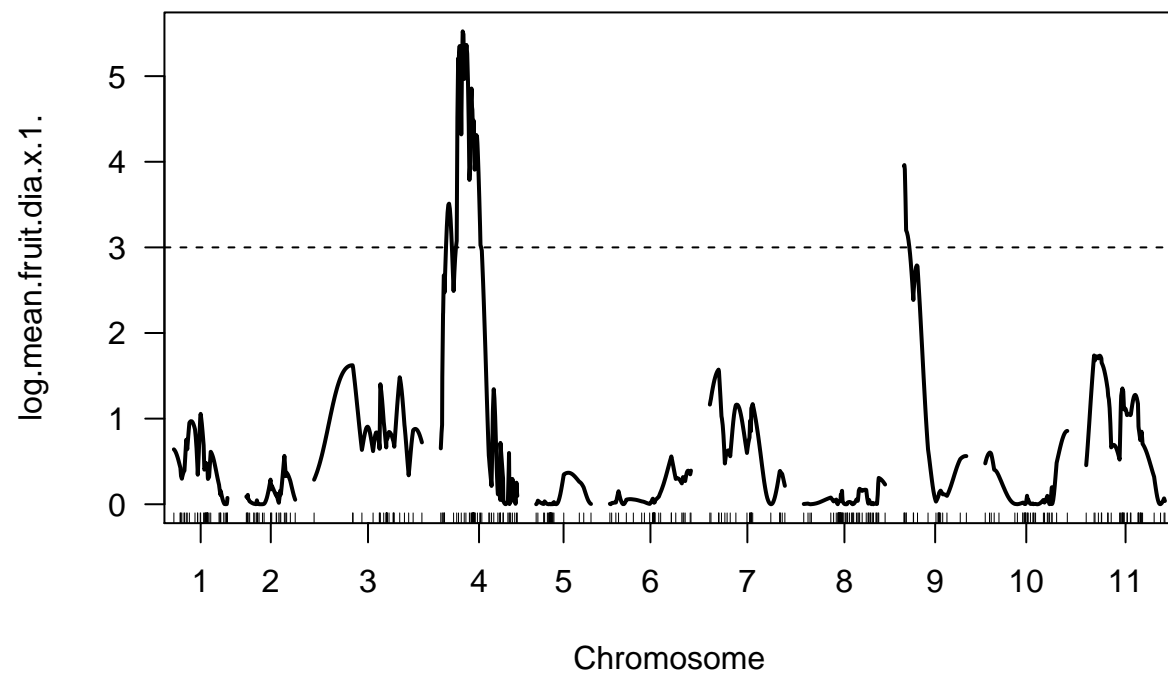


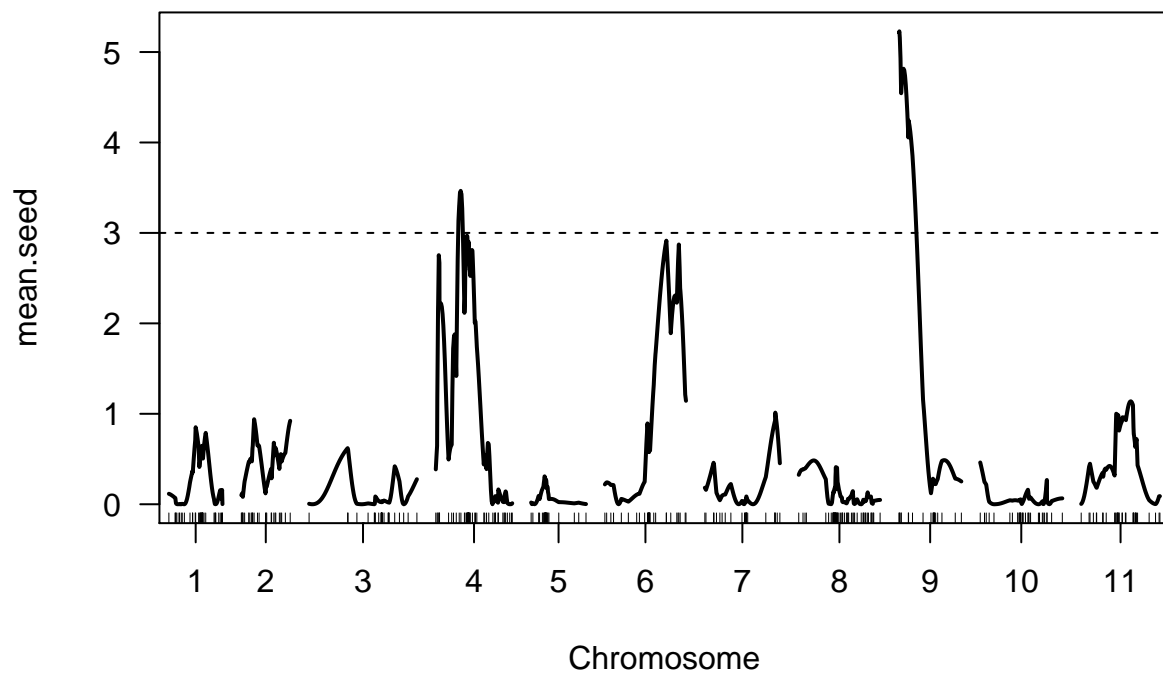


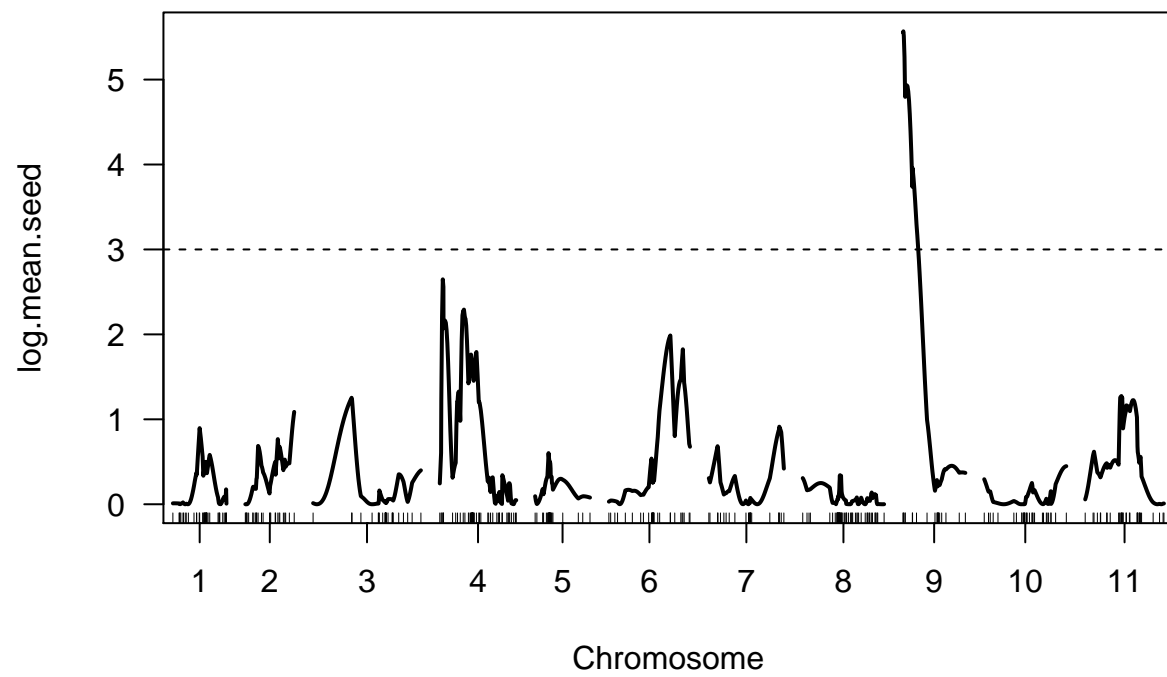


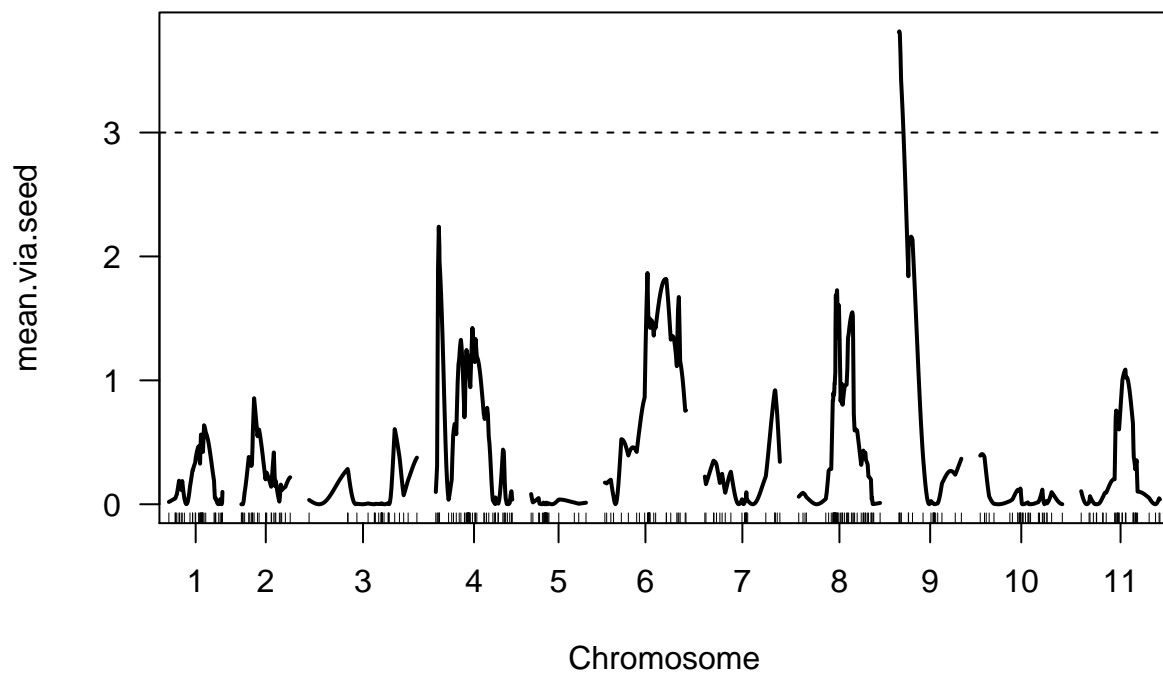


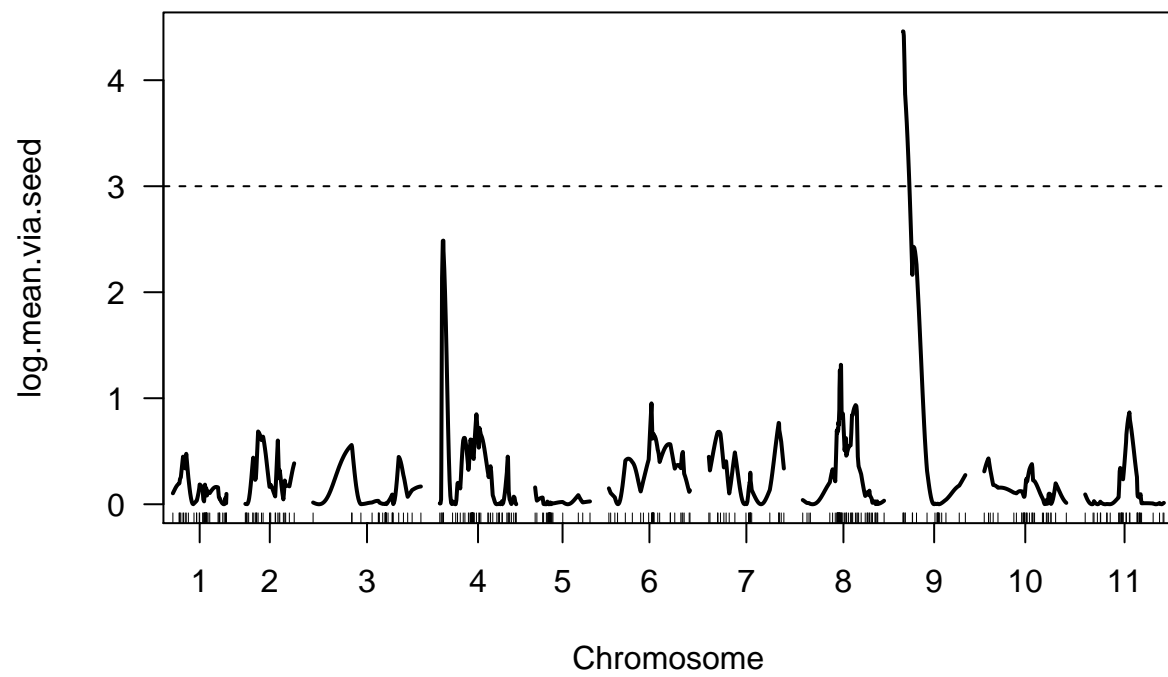


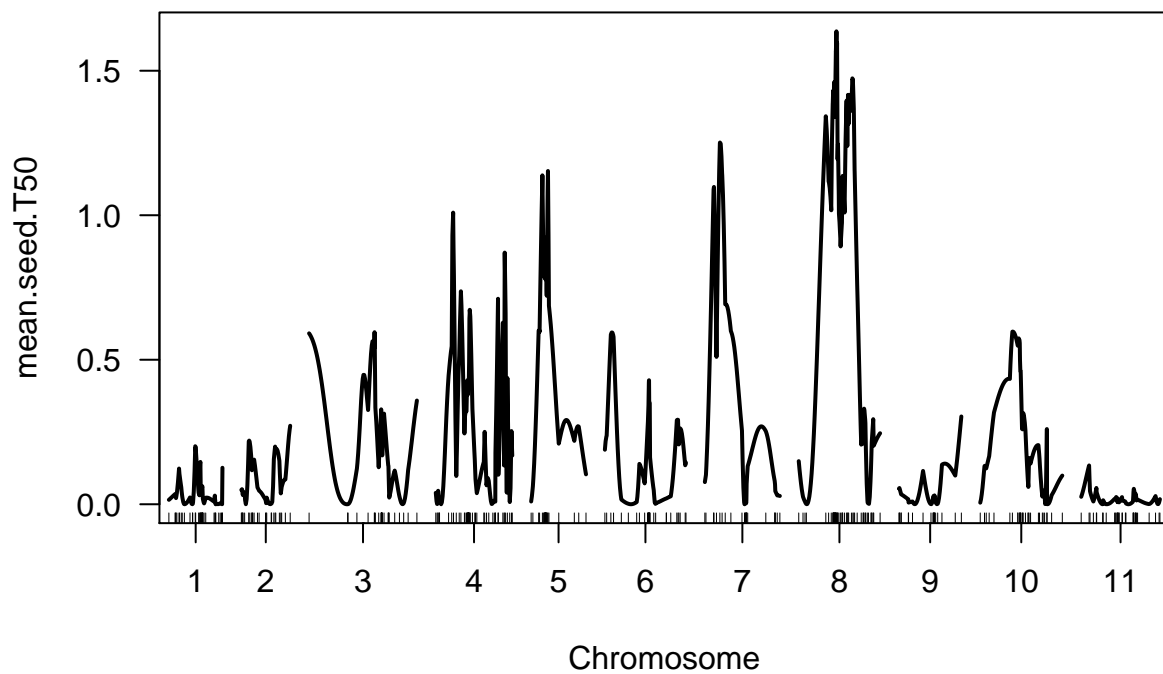


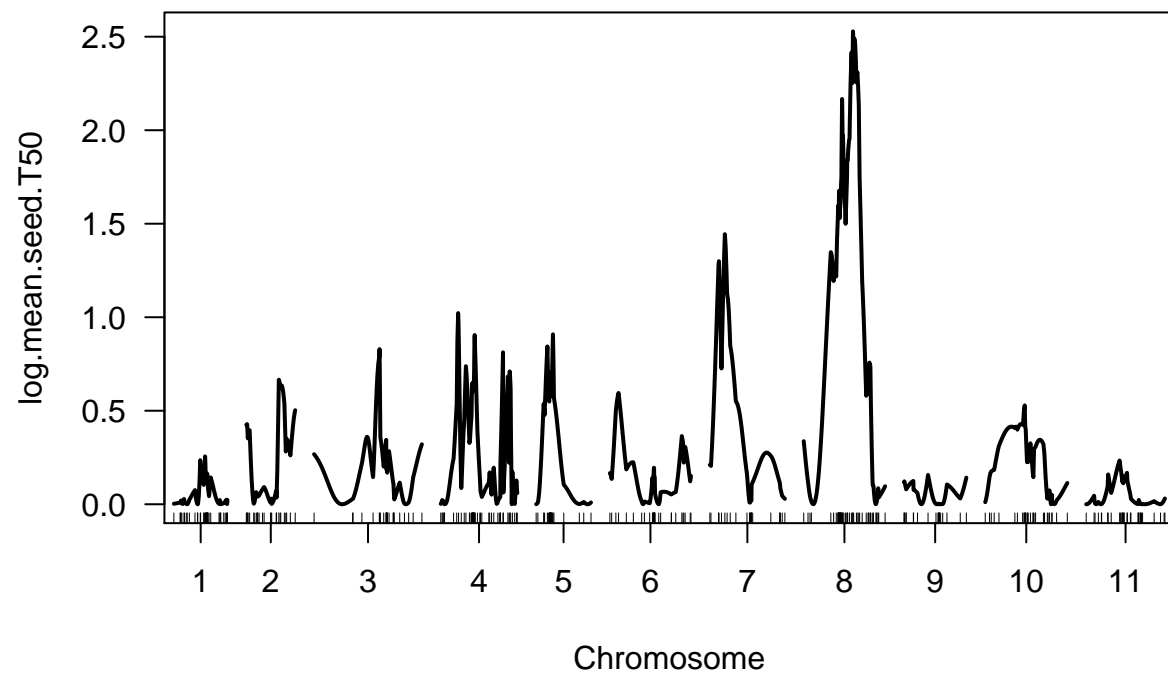


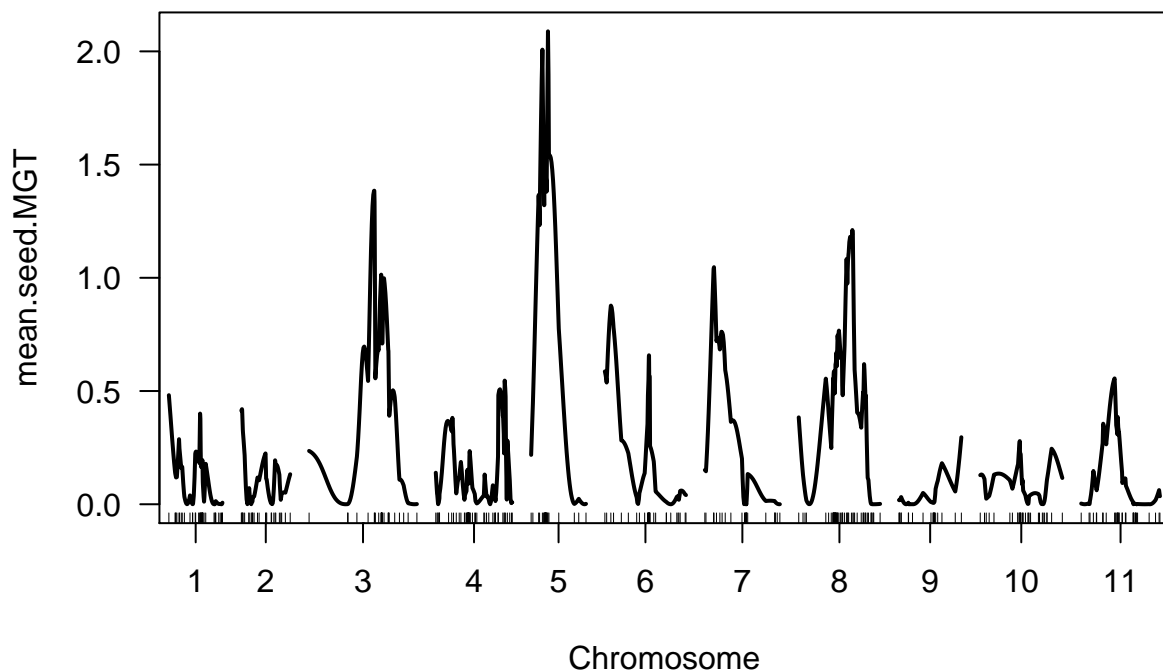












Scan for QTL- seed, pollen, and fruit traits (selfed)

```
scan_all_self <- scanone(jal_cross, pheno.col=c(72:79), method="em", addcovar=justBench)
```

```
## 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 191 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 188 individuals w
```

```
## 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 46 individuals w
```

```
## 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 46 individuals w
```

```
summary(scan_all_self, threshold=3, format="tabByChr")
```

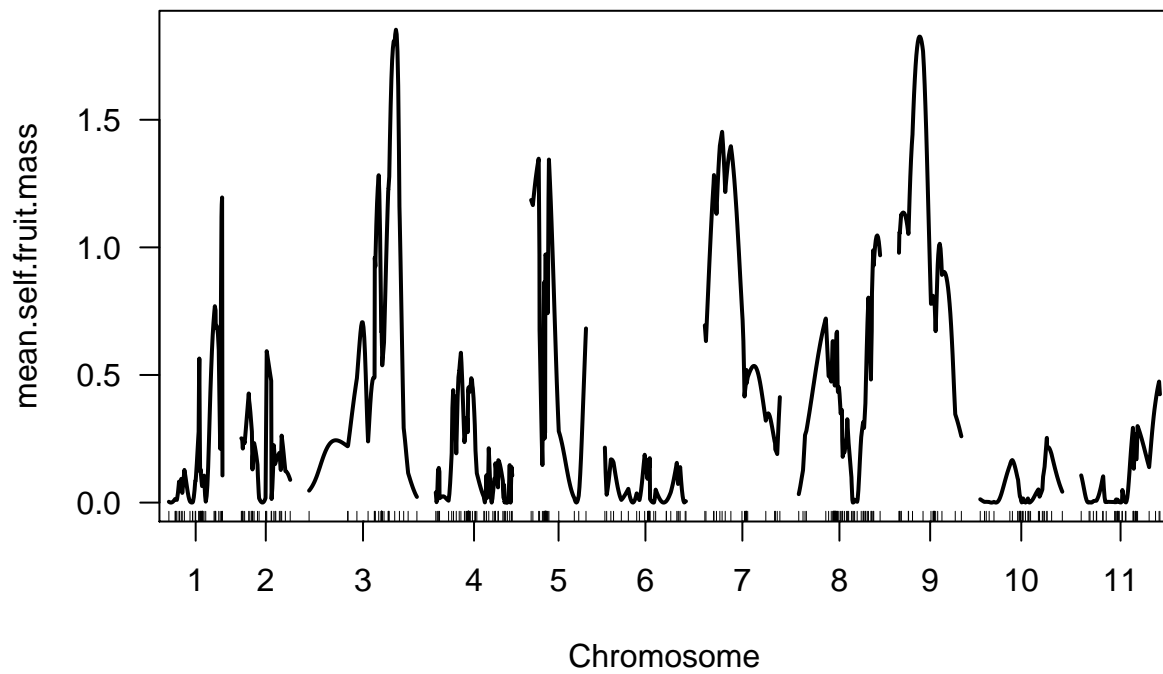
```
##      There were no LOD peaks above the threshold.
```

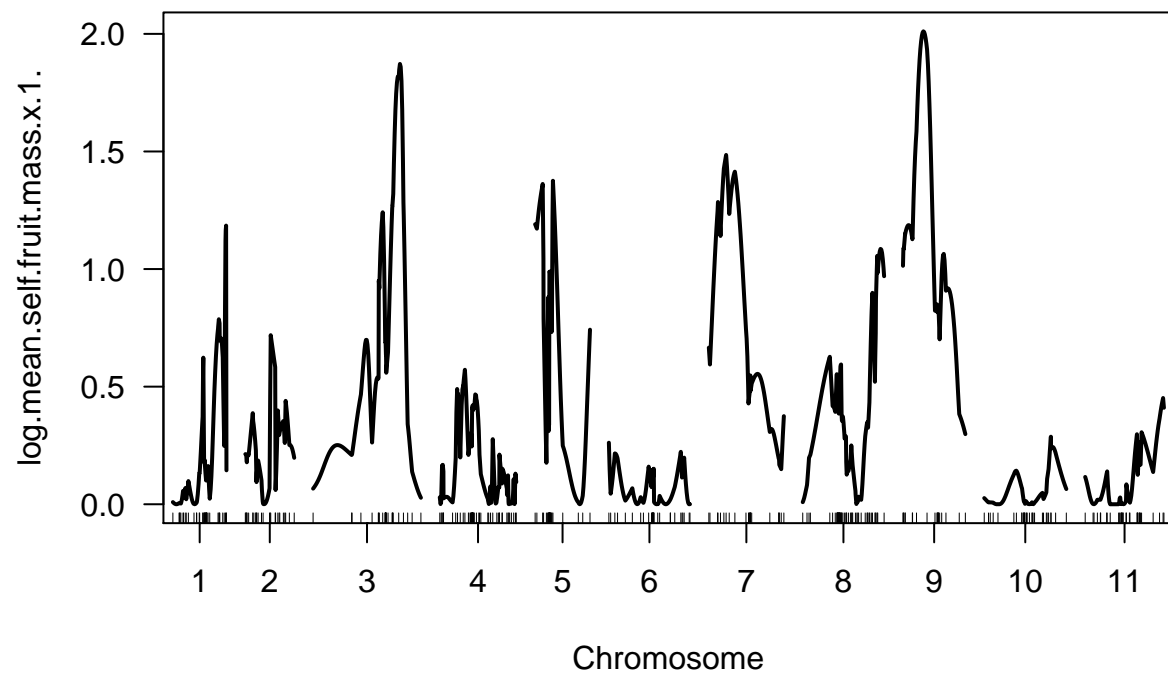
```
summary(scan_all_self, threshold=3, format="tabByCol")
```

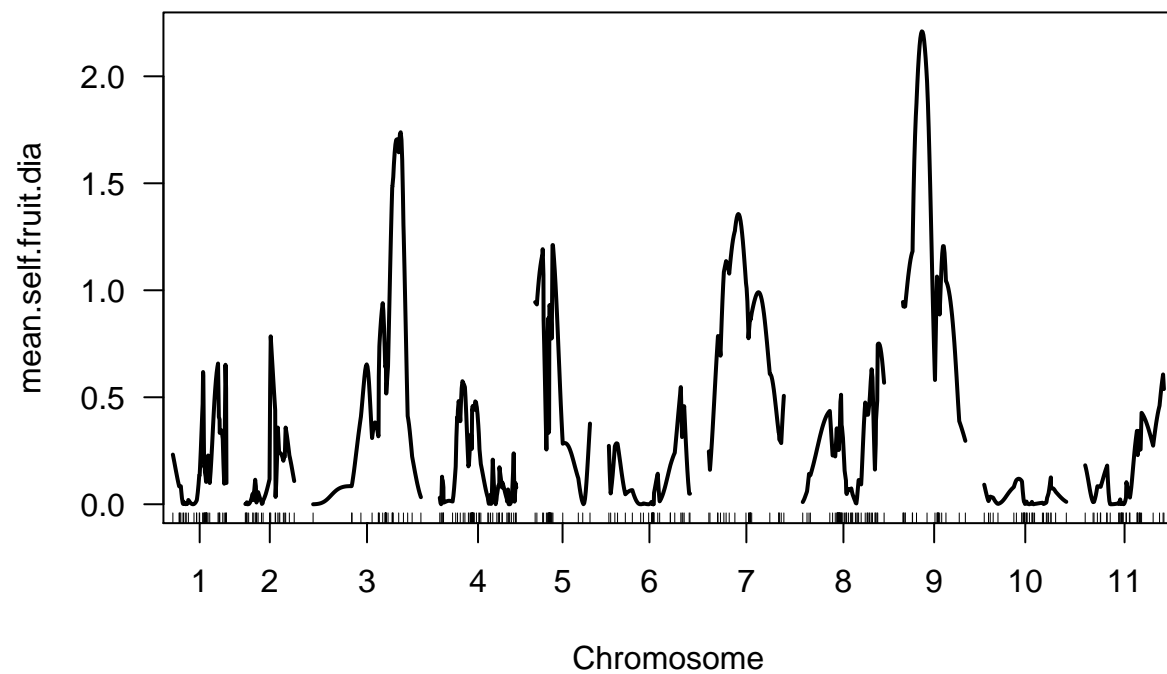
```
##      There were no LOD peaks above the threshold.
```

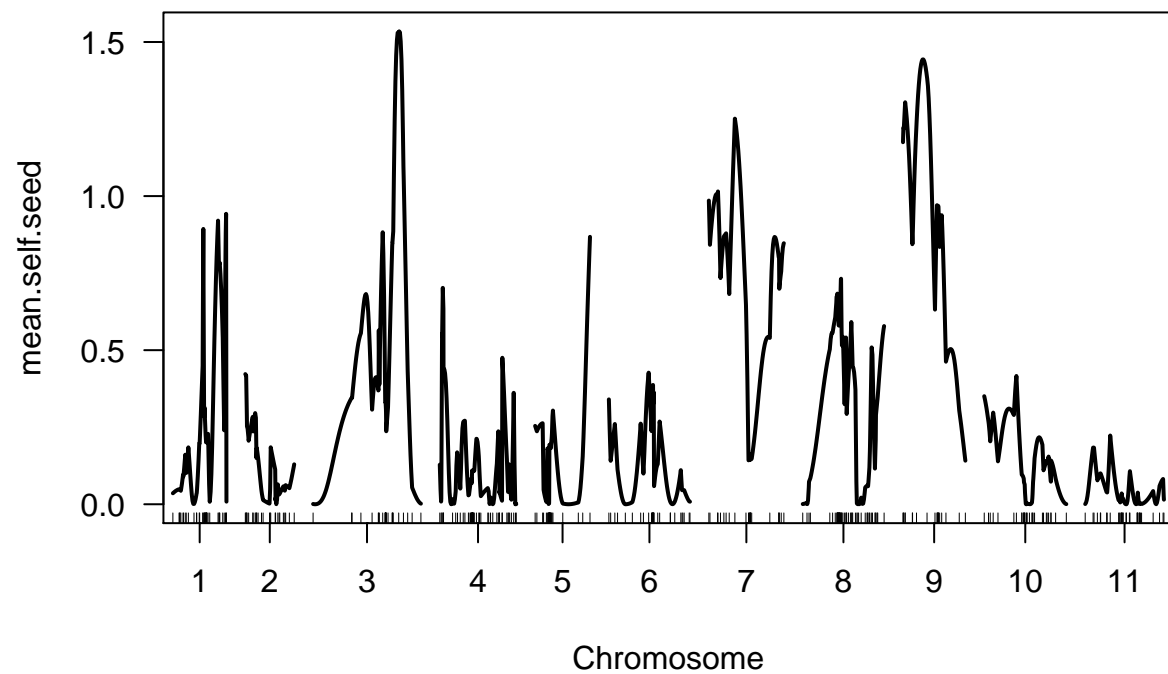


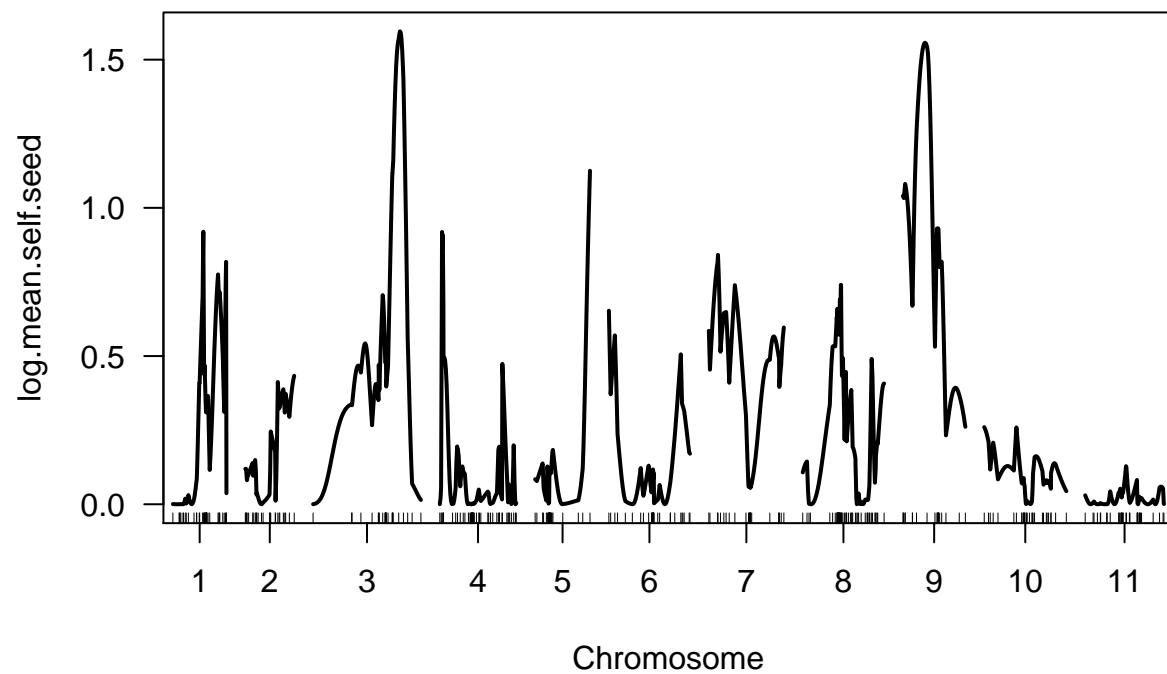
```
#par(mfrow=c(3,1))
for (x in 1:8){
  plot(scan_all_self, lodcolumn = x)
  abline(3,0,lty=2)
}
```

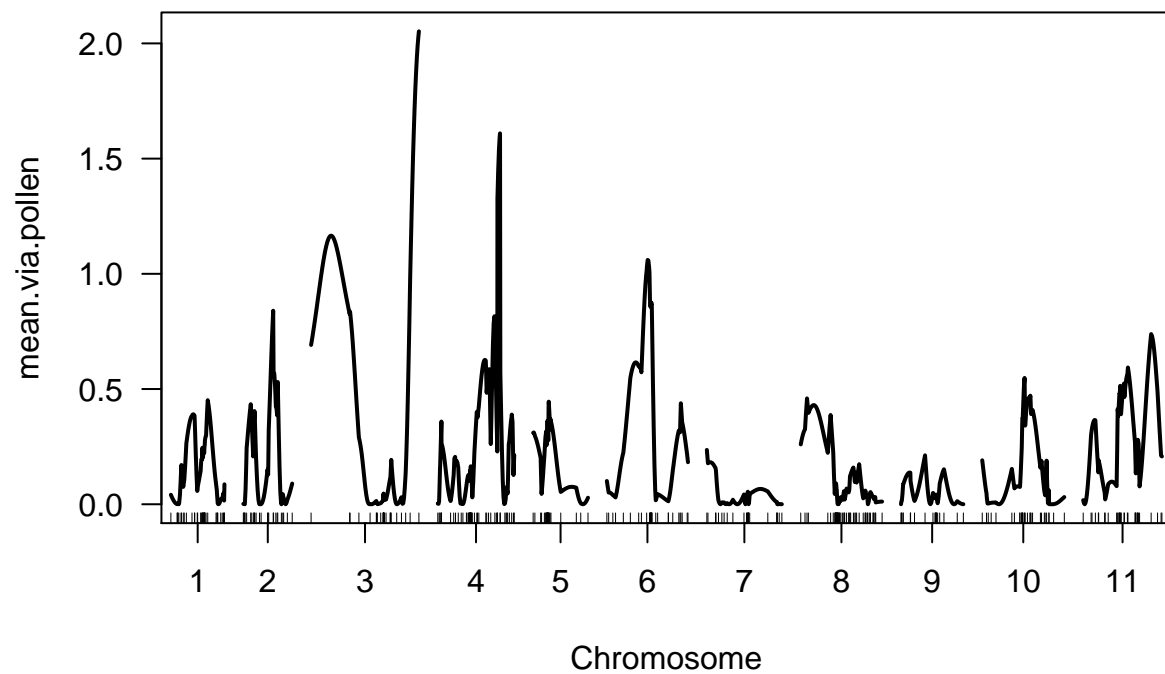


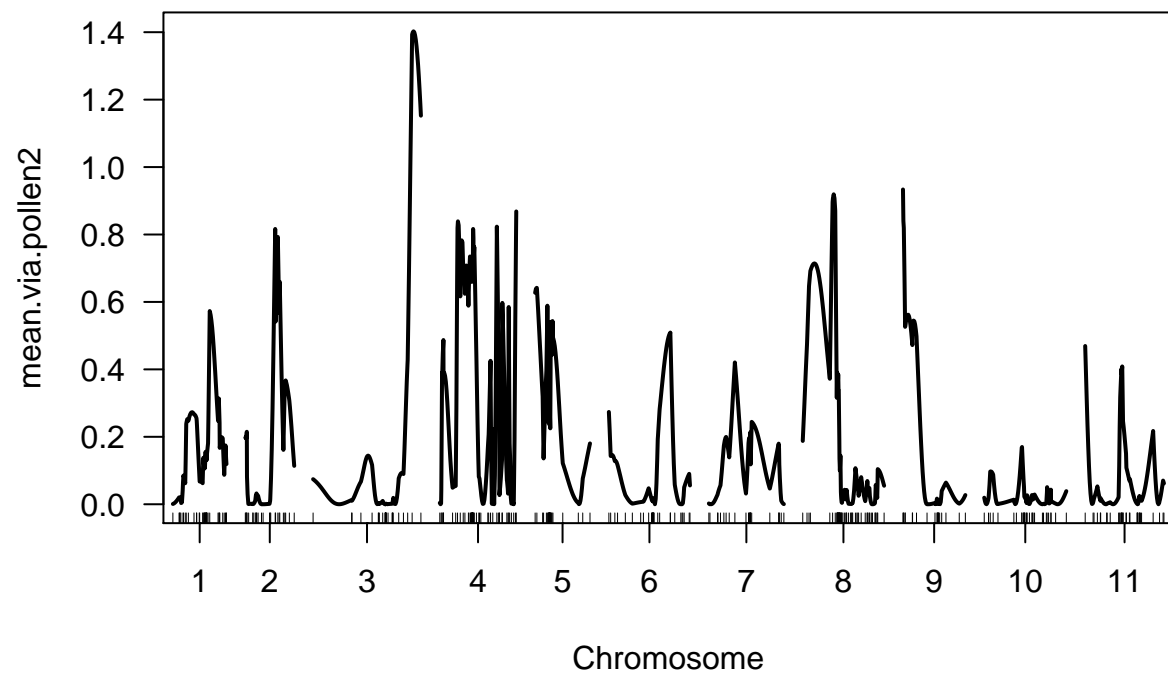


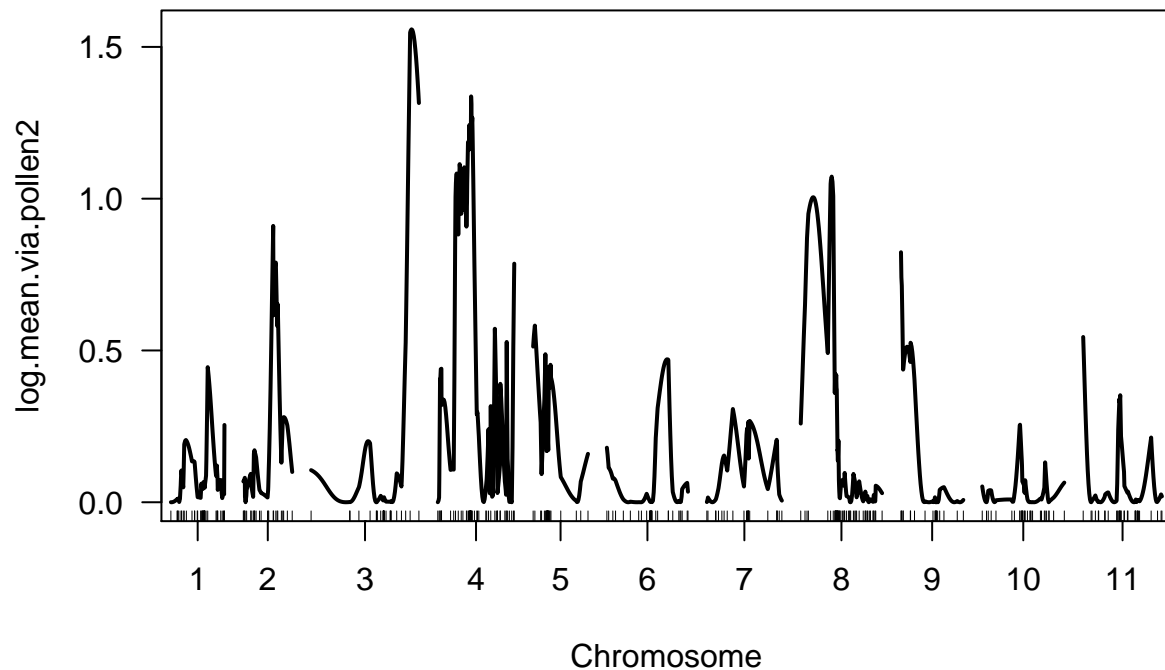












“{r}

Nectar Volume

```
log.nec.vol.mean.h <- scanone(jal_cross, pheno.col=37, method="em", addcovar=h_morph) plot(log.nec.vol.mean.h)
#No QTL for nectar volume
```

Nectar Color

```
log.comp.rgb.h.nec <- scanone(jal_cross, pheno.col=59, method = "em", addcovar = h_color)
plot(log.comp.rgb.h.nec, main="Log Composite RGB (H) Nectar")

log.mean.B.h.nec <- scanone(jal_cross, pheno.col=65, method = "em", addcovar = h_color)
plot(log.mean.B.h.nec, main="Log Mean B-Color (H) Nectar")

plot(log.comp.rgb.h.nec, log.mean.B.h.nec)
```



```
max(out.hk)
```

```
mar <- find.marker(sug, chr=7, pos=47.7)
```

```
plotPVG(sug, marker=mar
```

Global max on 8

```
max(log.comp.rgb.h.nec)
```

Local max on 2

```
max(log.comp.rgb.h.nec[log.comp.rgb.h.nec$chr=='2',])
```

```
mar2 <- find.marker(jal_cross, chr=2, pos=47)
```

```
mar <- find.marker(jal_cross, chr=8, pos=88.3)
```

```
plotPVG(jal_cross,marker=mar, pheno.col = 59, infer=F)
```

```
effectplot(jal_cross, mname1=mar, mname2=mar2, pheno.col=59)
```

Possible weak epistasis

Petal Colors

```
log.comp.rgb.h.pet <- scanone(jal_cross, pheno.col=91, method="em", addcovar=h_color) plot(log.comp.rgb.h.pet,  
main="Log Composite RGB (H) Petals")
```

```
log.mean.B.h.pet <- scanone(jal_cross, pheno.col=97, method="em", addcovar=h_color) plot(log.mean.B.h.pet,  
main="Log Mean B-Color (H) Petals")
```

Corolla Traits

```
cor.dia.h <- scanone(jal_cross, pheno.col=12, method="em", addcovar=h_morph) plot(cor.dia.h,  
main="Corolla Diameter (H)")
```

```
cor.dep.h <- scanone(jal_cross, pheno.col=14, method="em", addcovar=h_morph) plot(cor.dep.h,  
main="Corolla Depth (H)")
```

```
cor.fus.h <- scanone(jal_cross, pheno.col=16, method="em", addcovar=h_morph) plot(cor.fus.h,  
main="Corolla Fusion (H)")
```

```
log.cor.fus.h <- scanone(jal_cross, pheno.col=17, method="em", addcovar=h_morph) plot(log.cor.fus.h,  
main="Log Corolla Fusion (H)")
```

```
prop.cor.fus.h <- scanone(jal_cross, pheno.col=19, method="em", addcovar=h_morph) plot(prop.cor.fus.h,  
main = "Proportion(?) Corolla Fusion (H)")
```

Petals

```
pet.h <- scanone(jal_cross, pheno.col=21, method="em", addcovar=h_morph) plot(pet.h, main="Petals  
(H)")
```

```
log.pet.h <- scanone(jal_cross, pheno.col=22, method="em", addcovar=h_morph) plot(log.pet.h, main="Log  
Petals (H)") #““
```