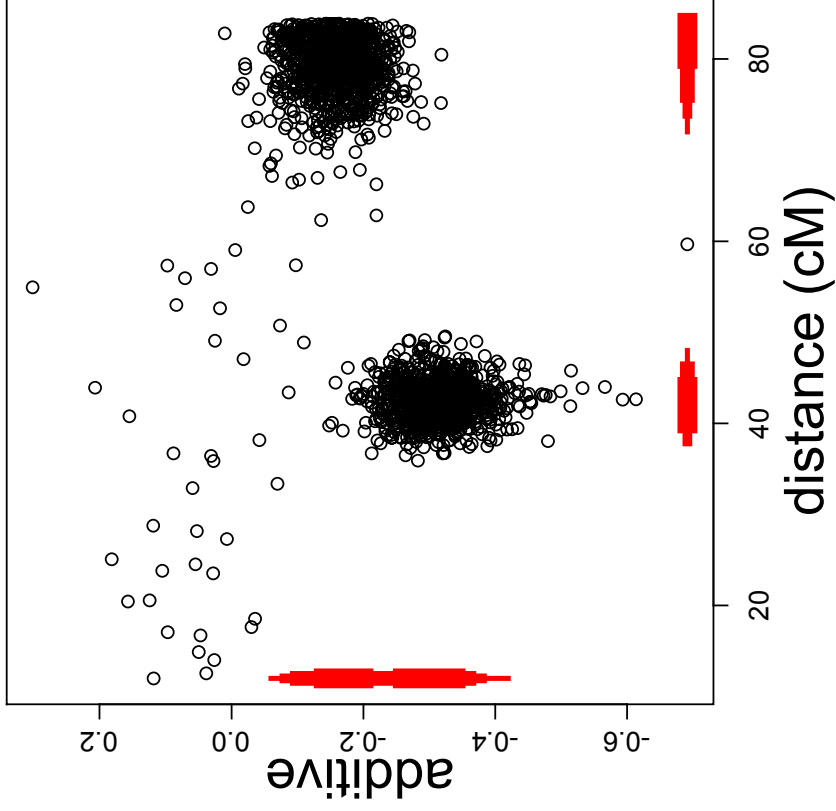
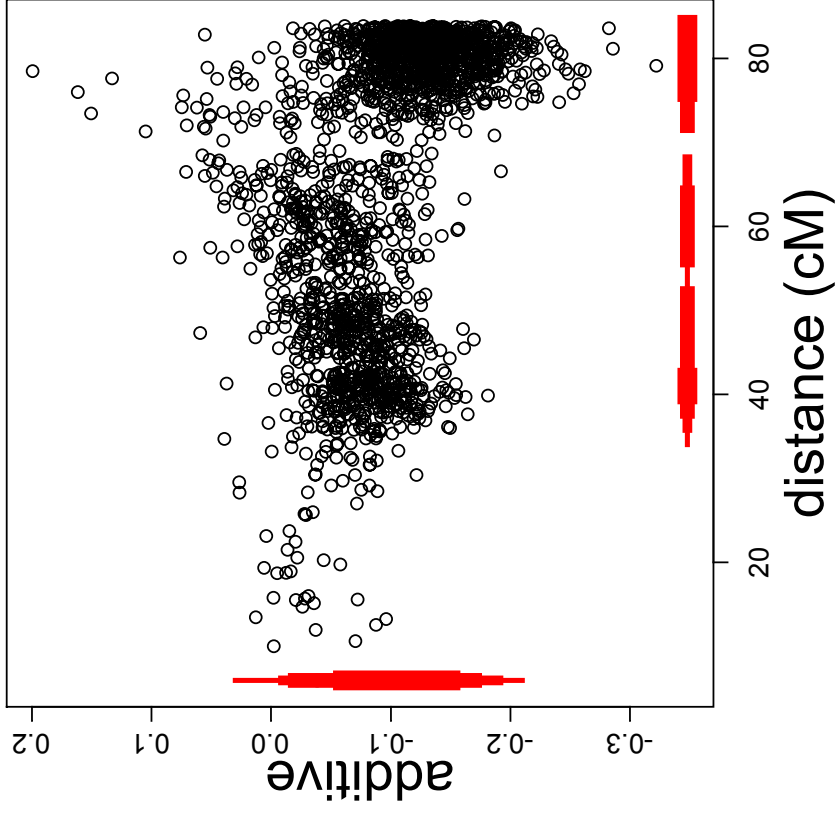


Brassica credible regions

4-week

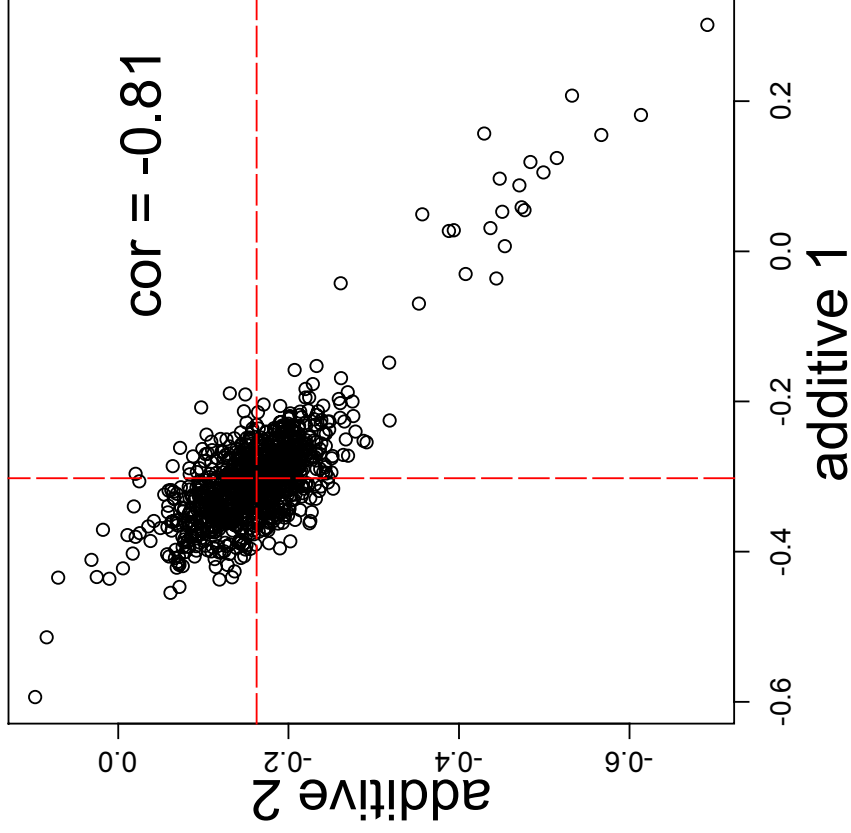


8-week

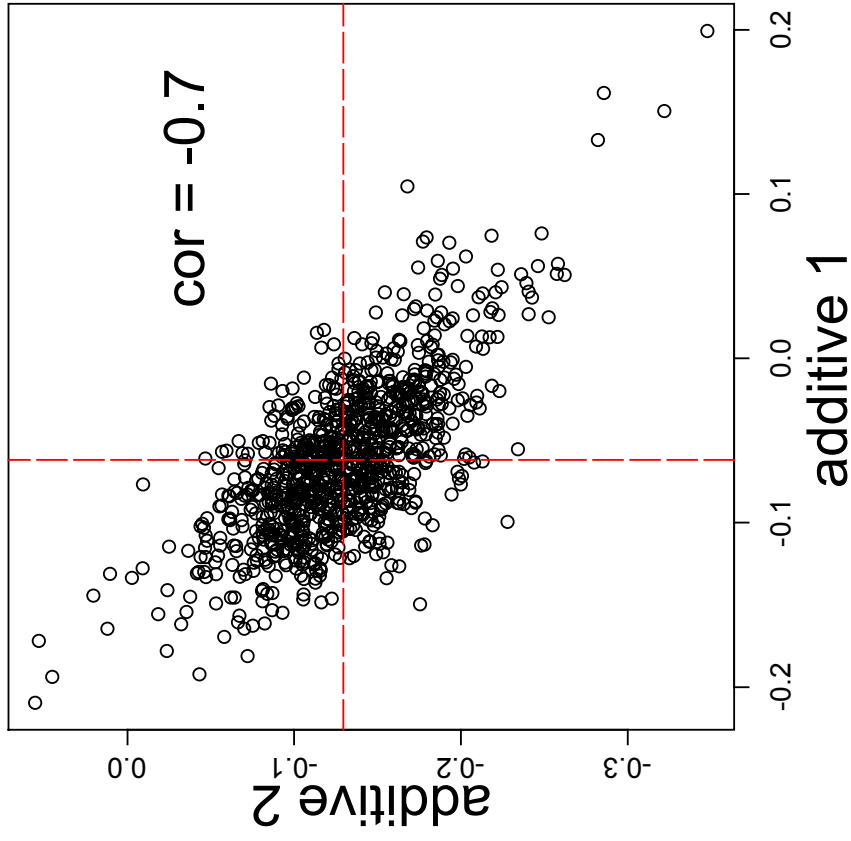


Brassica effect correlations

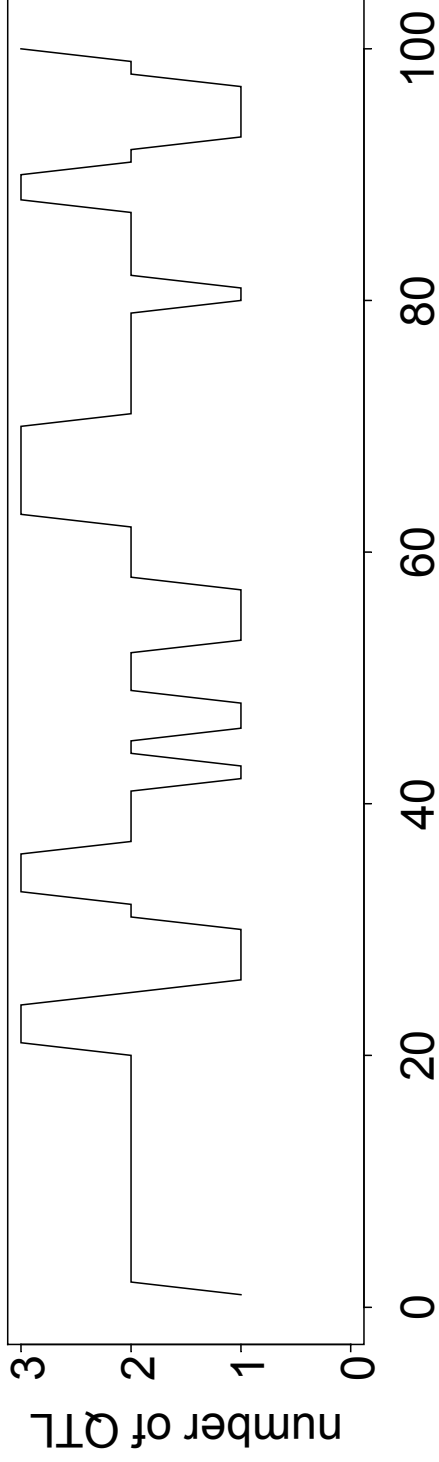
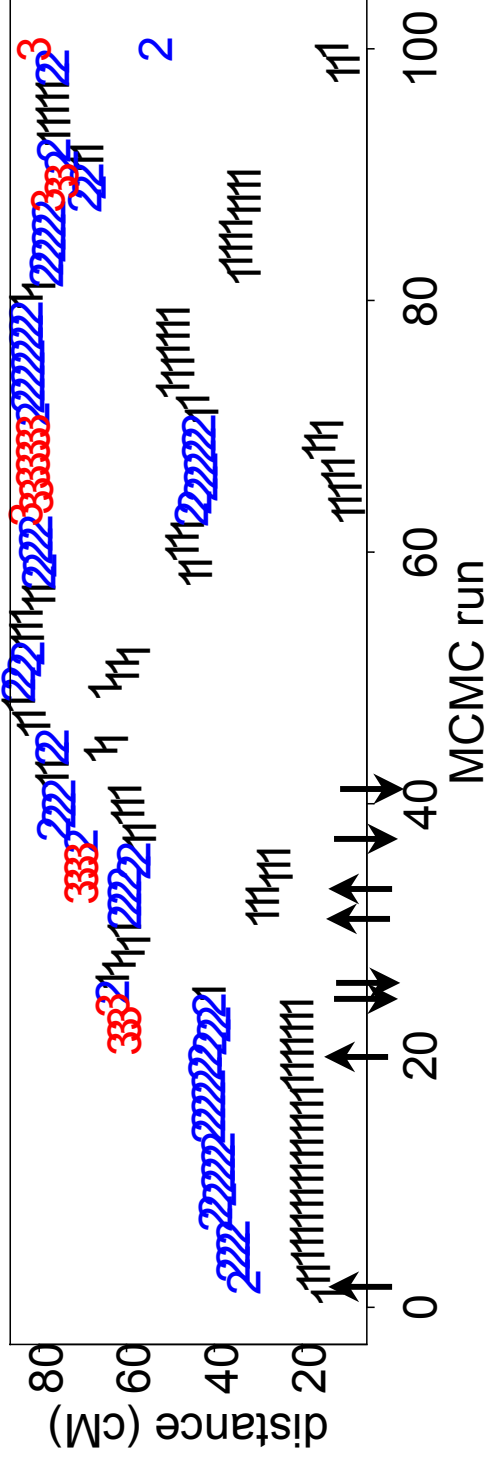
4-week



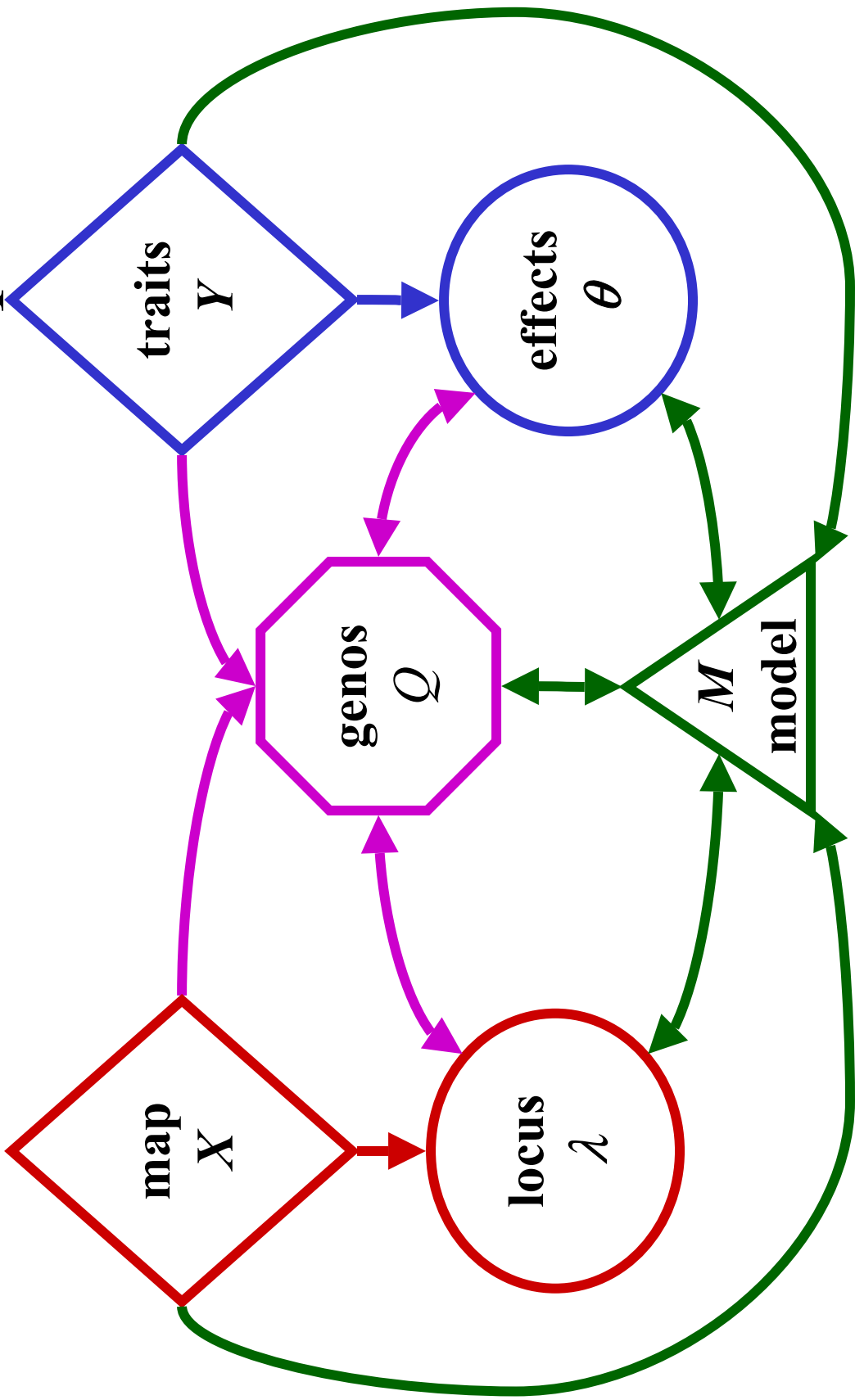
8-week



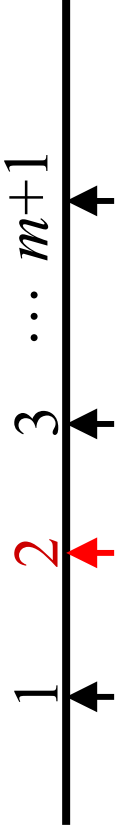
jumping QTL number and loci



RJ-MCMC full conditional updates



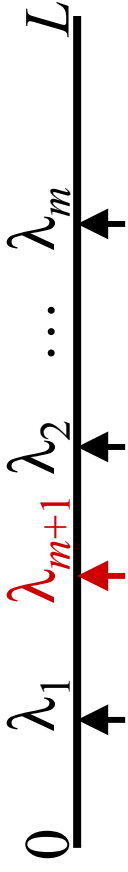
propose to drop a locus



$$q_d(r; m+1) = \frac{1}{m+1}$$

- choose an existing locus
 - equal weight for all loci ?
 - more weight to loci with small effects?
- “drop” effect & genotypes at old locus
 - adjust effects at other loci for collinearity
 - this is reverse jump of Green (1995)
- check acceptance ...
 - do not drop locus, effects & genotypes
 - until move is accepted

propose to add a locus

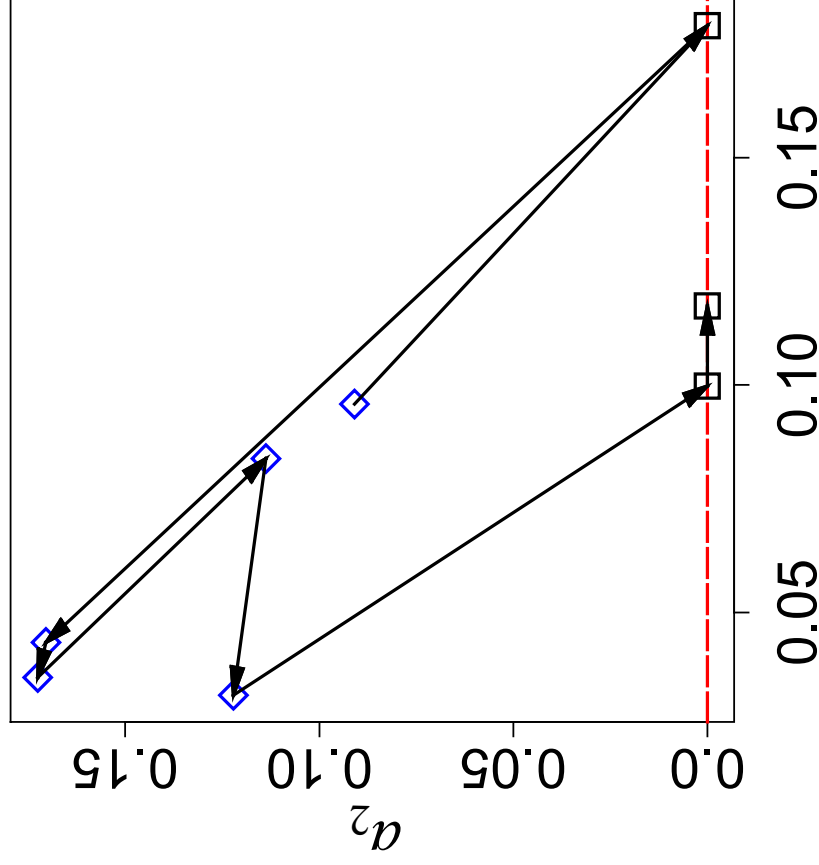


- propose a new locus
 - uniform chance over genome
 - actually need to be more careful (R van de Ven, pers. comm.)
 - choose interval between loci already in model (include $0, L$)
 - probability proportional to interval length $(\lambda_2 - \lambda_1)/L$
 - uniform chance within this interval $1/(\lambda_2 - \lambda_1)$
 - need genotypes at locus & model effect
- innovate effect & genotypes at new locus
 - draw genotypes based on recombination (prior)
 - no dependence on trait model yet
 - draw effect as in Green's reversible jump
 - adjust for collinearity: modify other parameters accordingly
- check acceptance ...

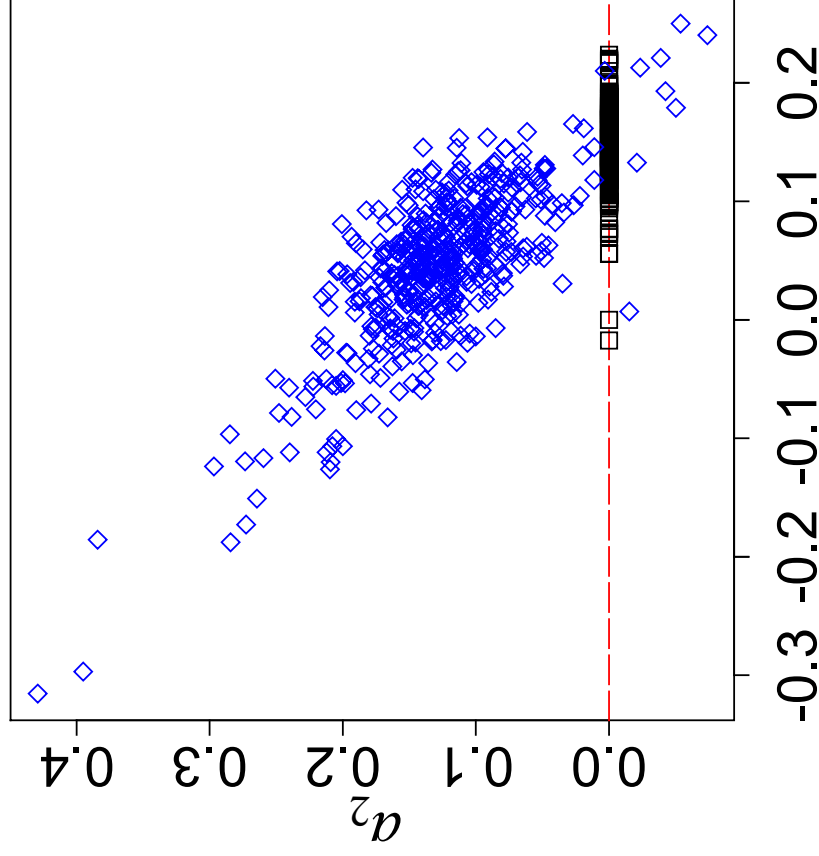
$$q_b(\lambda) = 1/L$$

QT additive reversible jump

a short sequence



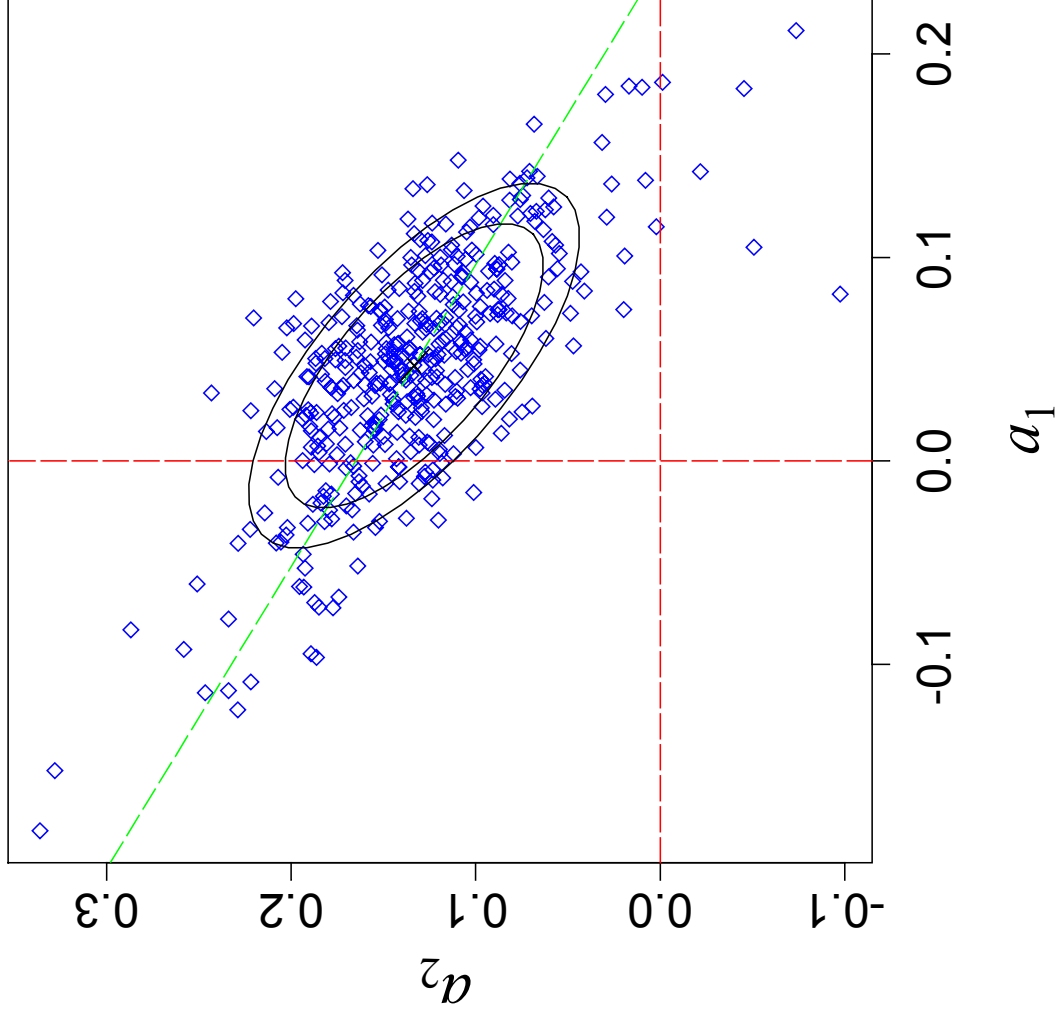
first 1000 with $m < 3$



credible set for additive

90% & 95% sets
based on normal

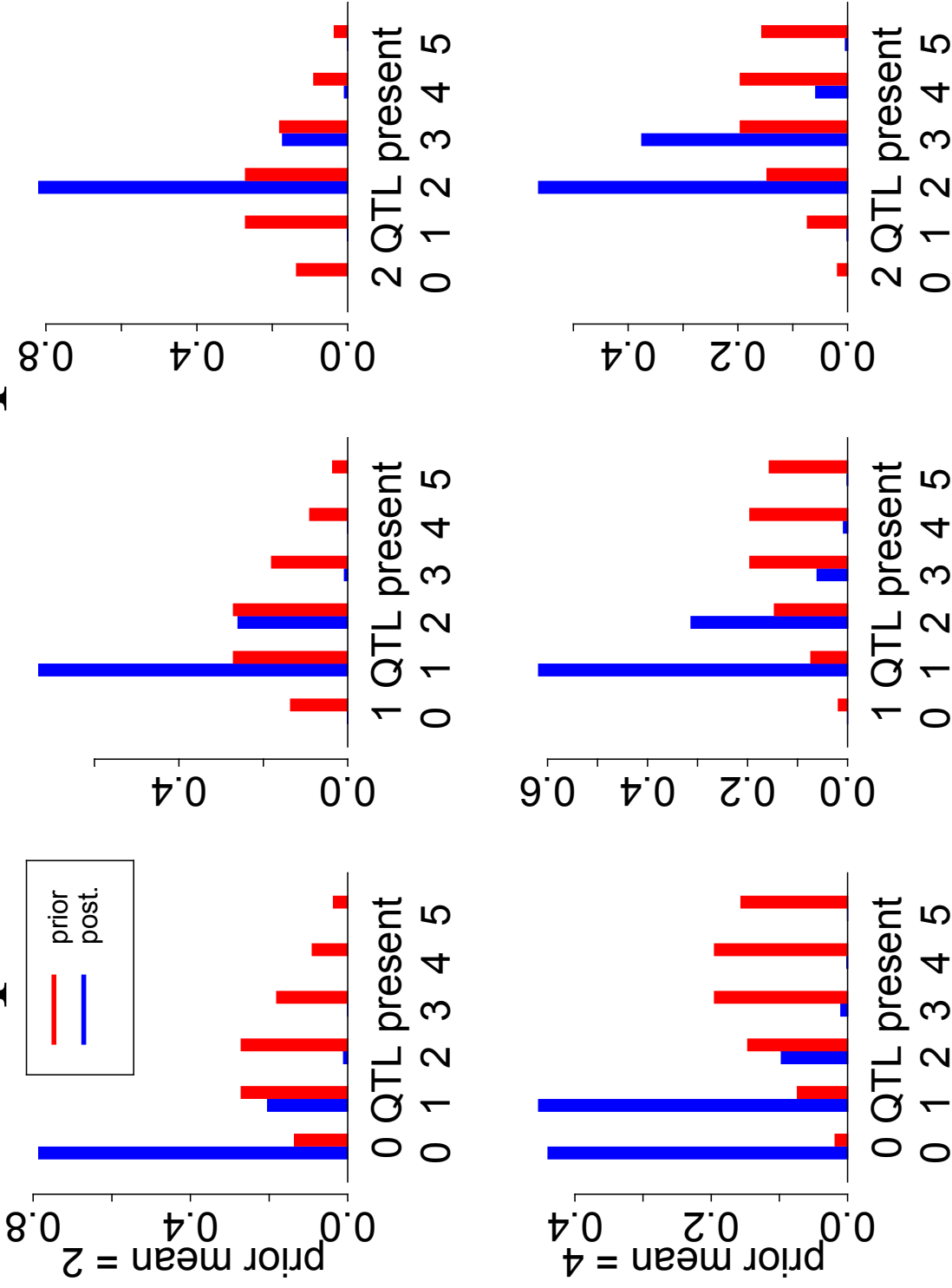
regression line
corresponds to
slope of updates



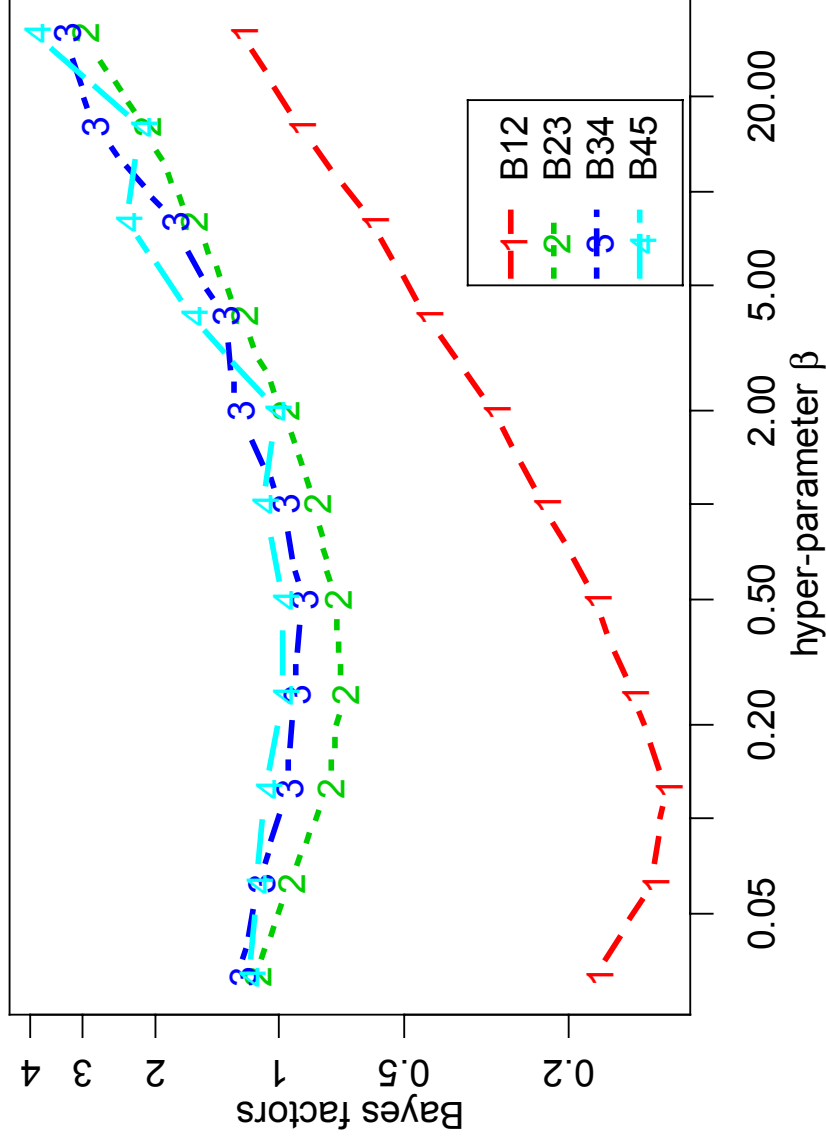
posterior genetic architecture

| | Chromosome count vector | | | | | | | | | | Count |
|----------|-------------------------|---|---|---|---|---|---|---|---|----|-------|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | |
| <i>m</i> | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | Count |
| 8 | 2 | 0 | 1 | 0 | 0 | 2 | 0 | 2 | 1 | 0 | 3371 |
| 9 | 3 | 0 | 1 | 0 | 0 | 2 | 0 | 2 | 1 | 0 | 751 |
| 7 | 2 | 0 | 1 | 0 | 0 | 2 | 0 | 1 | 1 | 0 | 377 |
| 9 | 2 | 0 | 1 | 0 | 0 | 3 | 0 | 2 | 1 | 0 | 218 |
| 9 | 2 | 0 | 1 | 0 | 0 | 2 | 0 | 2 | 2 | 0 | 198 |

effect of prior mean on posterior m

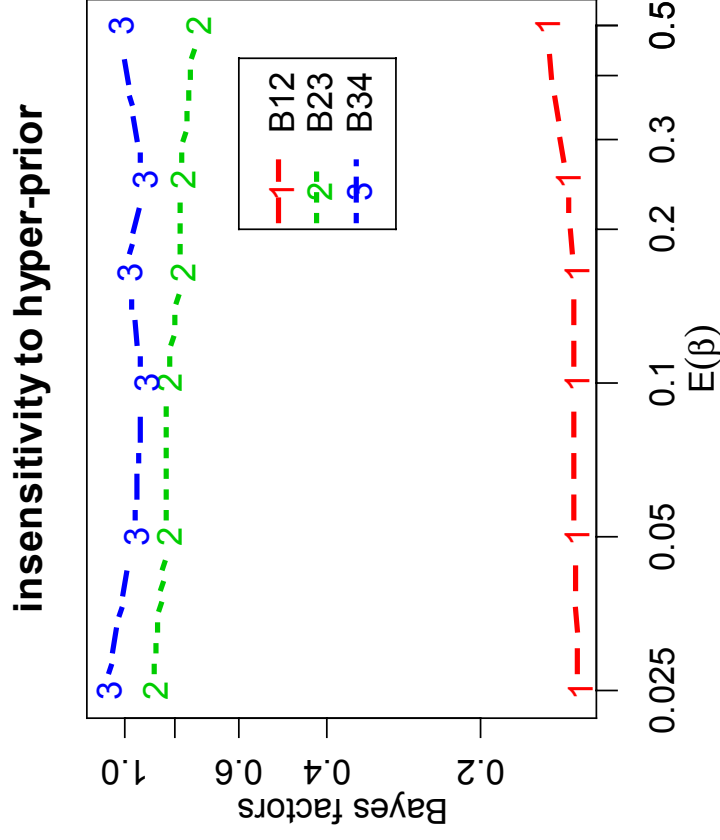
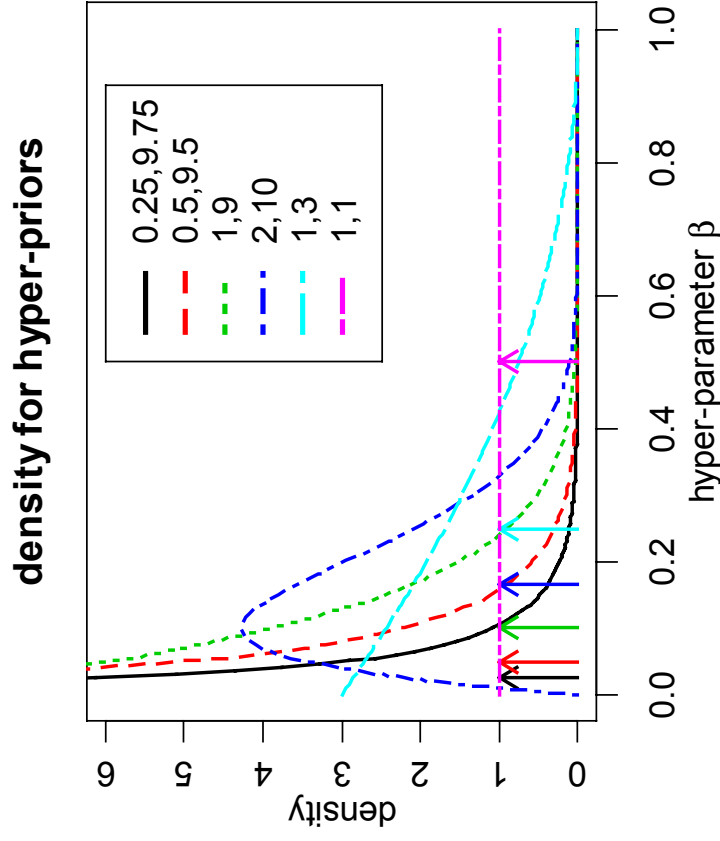


BF sensitivity to fixed prior for effects



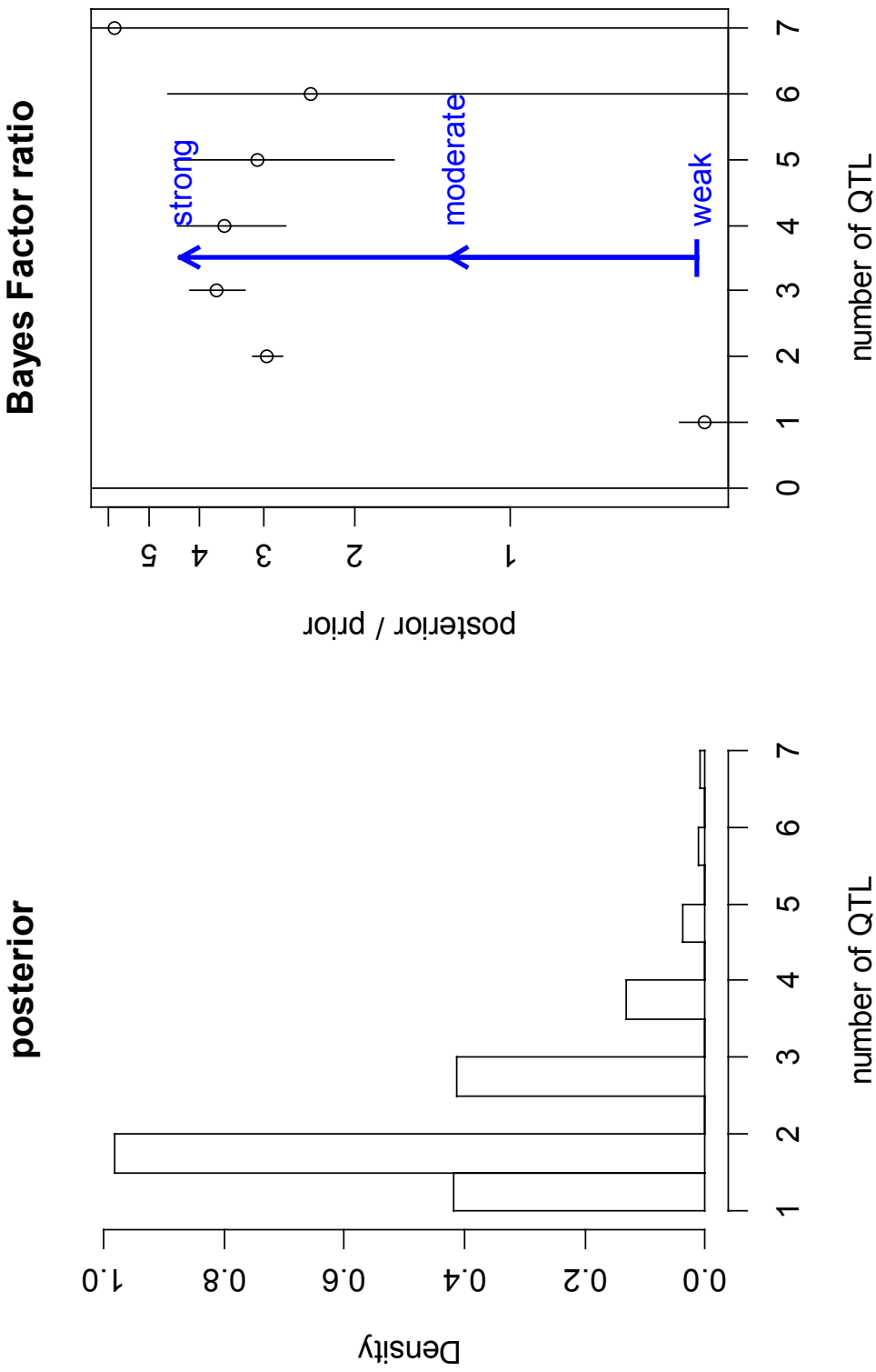
Bayes factors for 8-week vernalization data

BF insensitivity to random effects prior



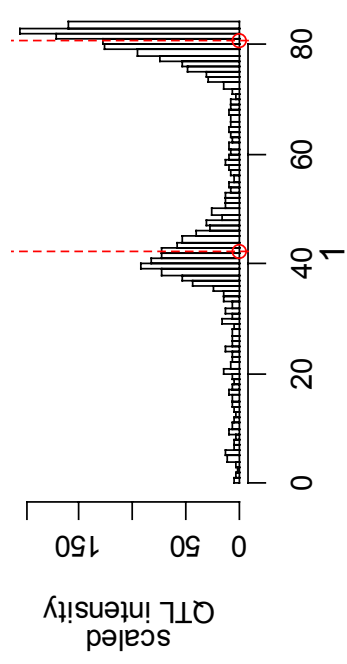
$$a_r \sim N(0, 2\beta s^2 / m), \beta \sim \text{Beta}(?, ?)$$

Bmapqtl.nqtl(data, prior)



Bmapqtl.loci(data, nqtl)

marginal summaries



conditional on m >= 2

