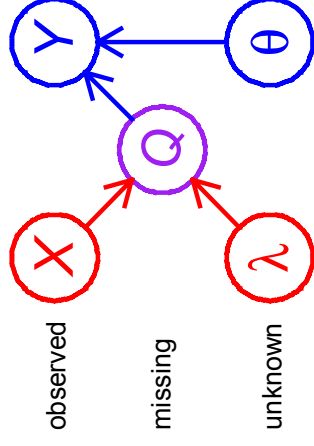


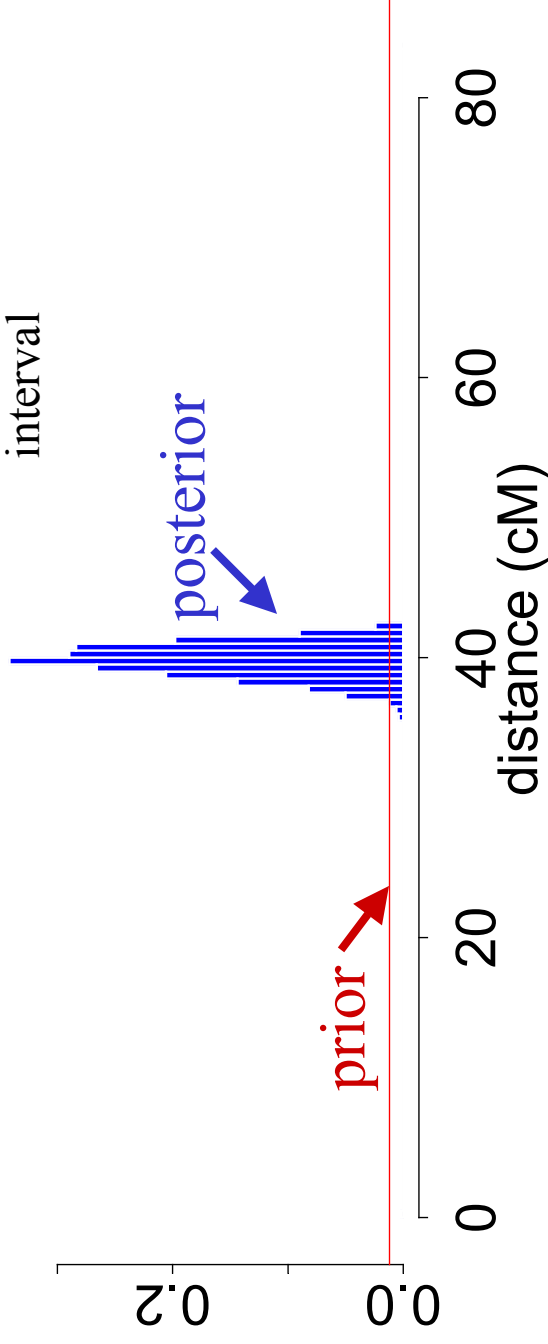
marginal posteriors

- joint posterior
 - $\text{pr}(\lambda, Q, \theta | Y, X) = \text{pr}(\theta) \text{pr}(\lambda) \text{pr}(Q | X, \lambda) \text{pr}(Y | Q, \theta) / \text{constant}$
- genetic effects
 - $\text{pr}(\theta | Y, X) = \text{sum}_Q \text{pr}(\theta | Y, Q) \text{pr}(Q | Y, X)$
- QTL locus
 - $\text{pr}(\lambda | Y, X) = \text{sum}_Q \text{pr}(\lambda | X, Q) \text{pr}(Q | Y, X)$
- QTL genotypes more complicated
 - $\text{pr}(Q | Y, X) = \text{sum}_{\lambda, \theta} \text{pr}(Q | Y, X, \lambda, \theta) \text{pr}(\lambda, \theta | Y, X)$
 - impossible to separate λ and θ in sum

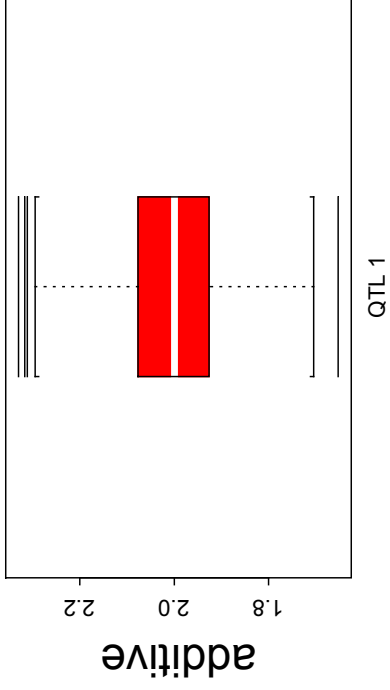
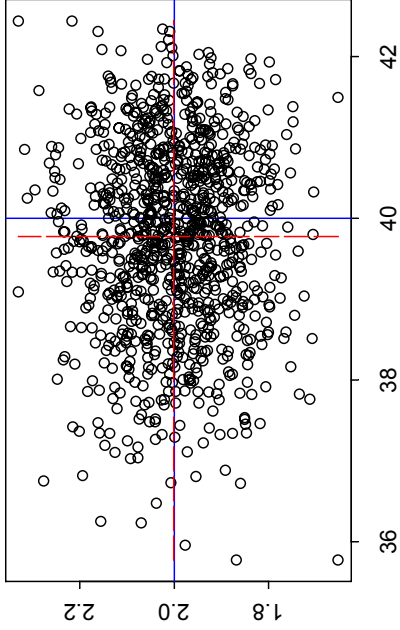


prior & posterior for QT locus

- prior information from other studies
 - concentrate on credible regions
 - use posterior of previous study as new prior
- no prior information on locus
 - uniform prior over genome
 - use framework map
 - choose interval proportional to length
 - then pick uniform position within interval

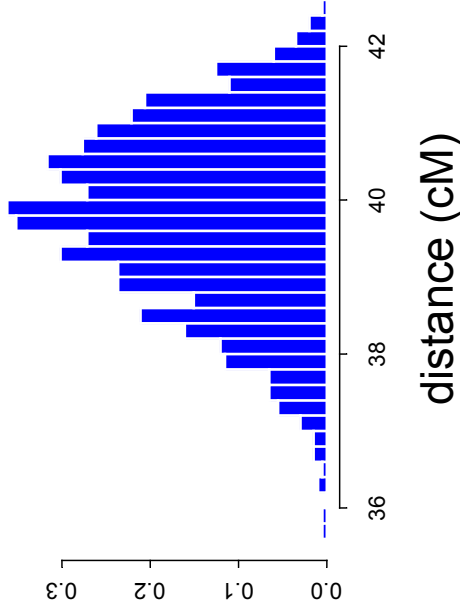


Posterior for locus & effect

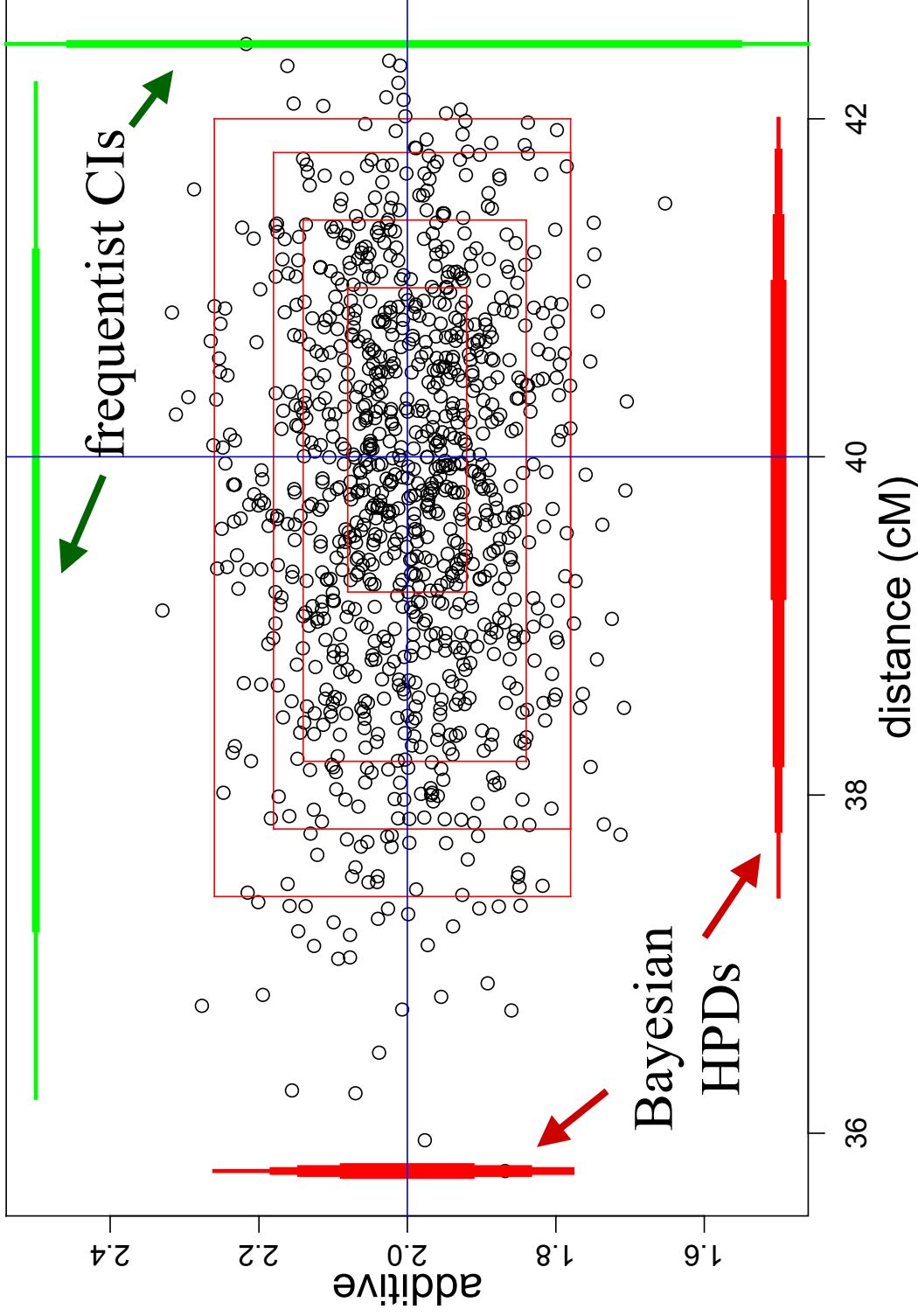


distance (cM)

summaries of MC samples
joint scatter plot
(lines for true, estimates)
marginal histogram
marginal box-plot

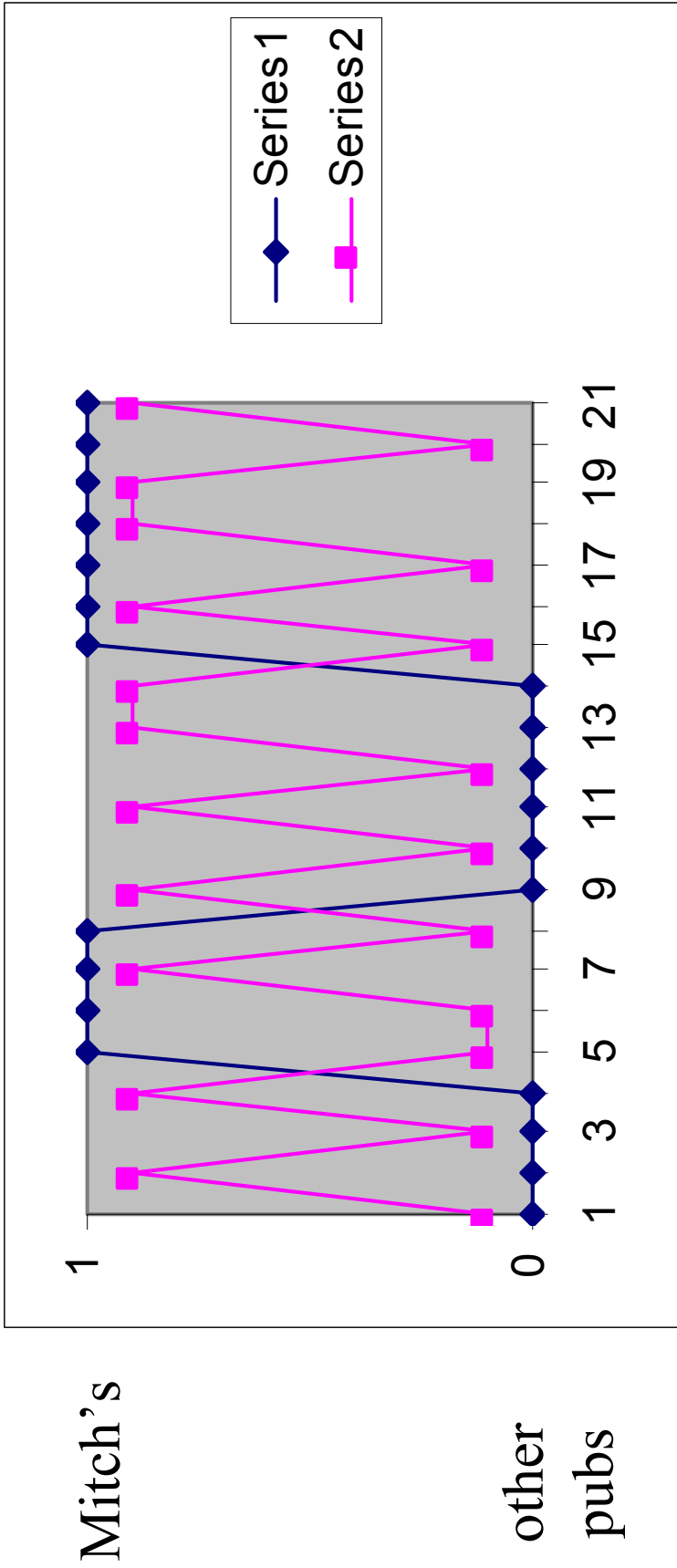
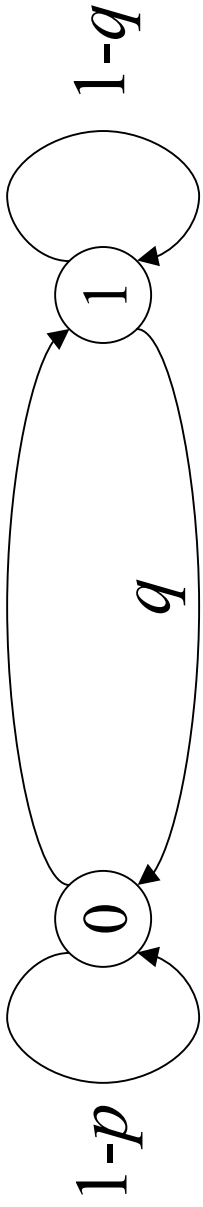


HPD region for locus & effect

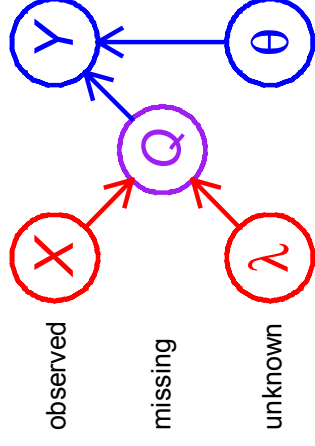


Markov chain idea

$$\text{pr}(1) = p / (p + q)$$

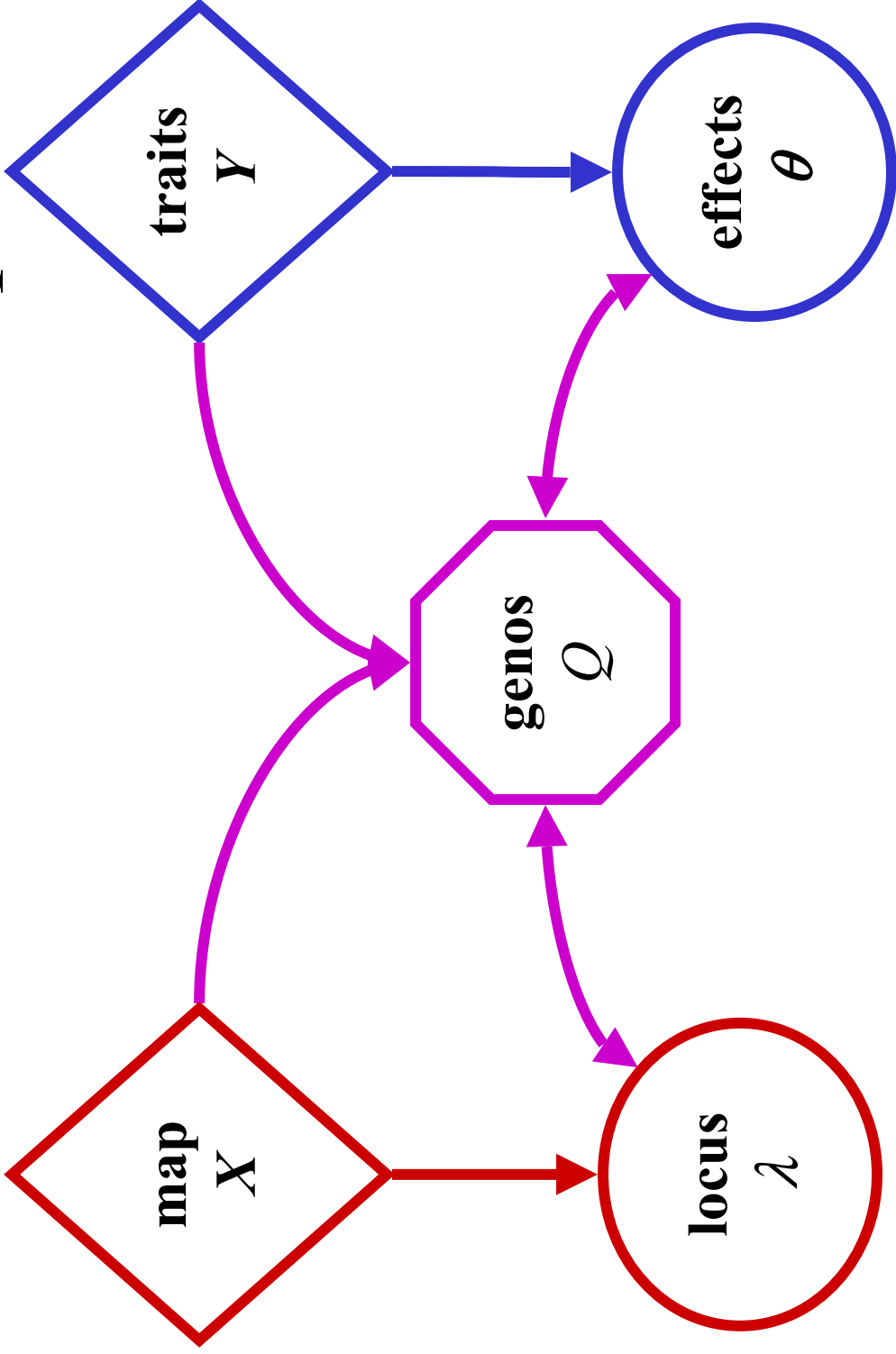


sample from full conditionals

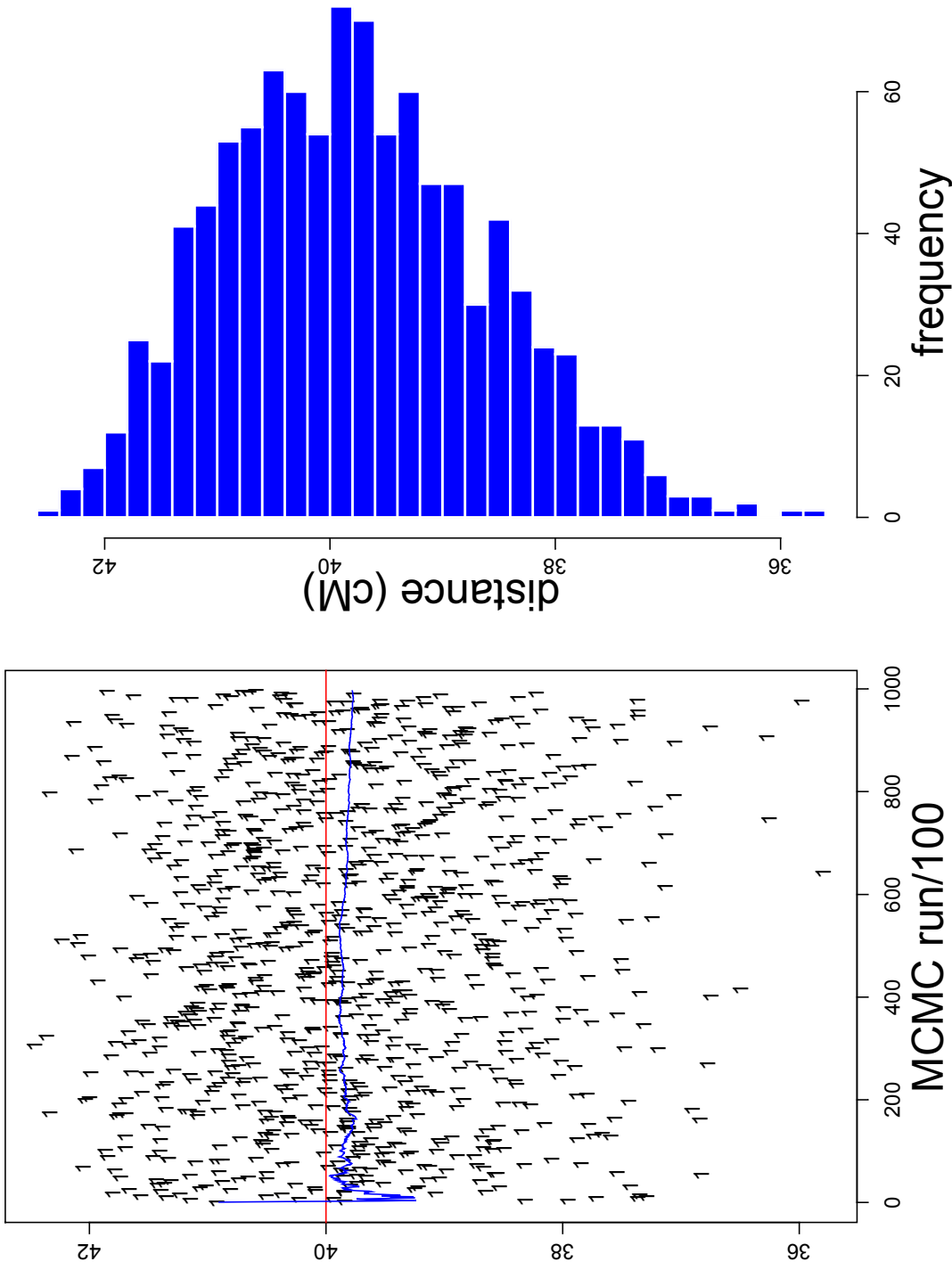


- hard to sample from joint posterior
 - $\text{pr}(\lambda, Q, \theta | Y, X) = \text{pr}(\theta) \text{pr}(\lambda) \text{pr}(Q | X, \lambda) \text{pr}(Y | Q, \theta) / \text{constant}$
- easy to sample parameters from full conditionals
 - full conditional for genetic effects
 - $\text{pr}(\theta | Y, X, \lambda, Q) = \text{pr}(\theta | Y, Q) = \text{pr}(\theta) \text{pr}(Y | Q, \theta) / \text{constant}$
 - full conditional for QTL locus
 - $\text{pr}(\lambda | Y, X, \theta, Q) = \text{pr}(\lambda | X, Q) = \text{pr}(\lambda) \text{pr}(Q | X, \lambda) / \text{constant}$
 - full conditional for QTL genotypes
 - $\text{pr}(Q | Y, X, \lambda, \theta) = \text{pr}(Q | X, \lambda) \text{pr}(Y | Q, \theta) / \text{constant}$

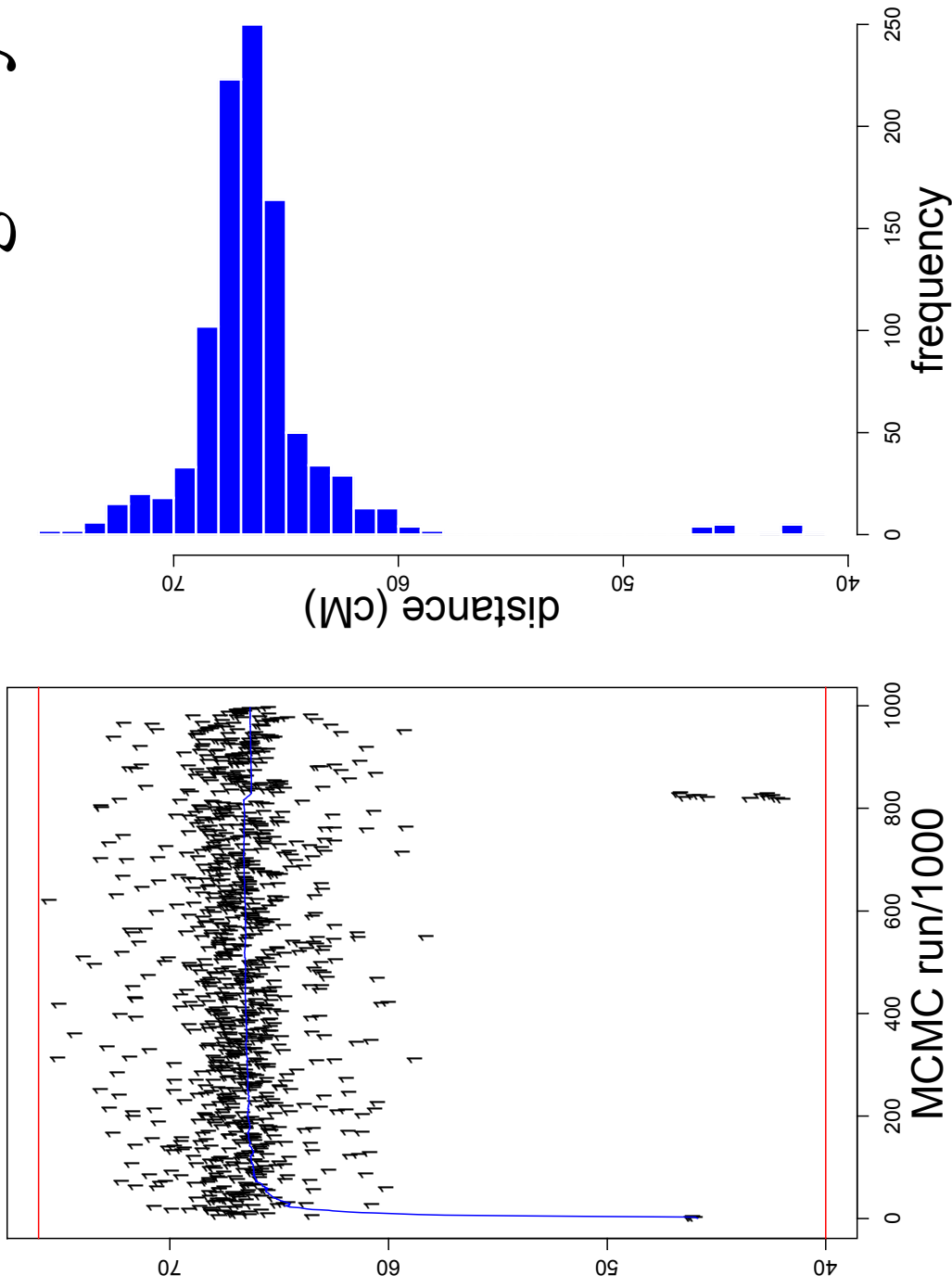
MCMC full conditional updates



MCMC Run for 1 locus at 40cM

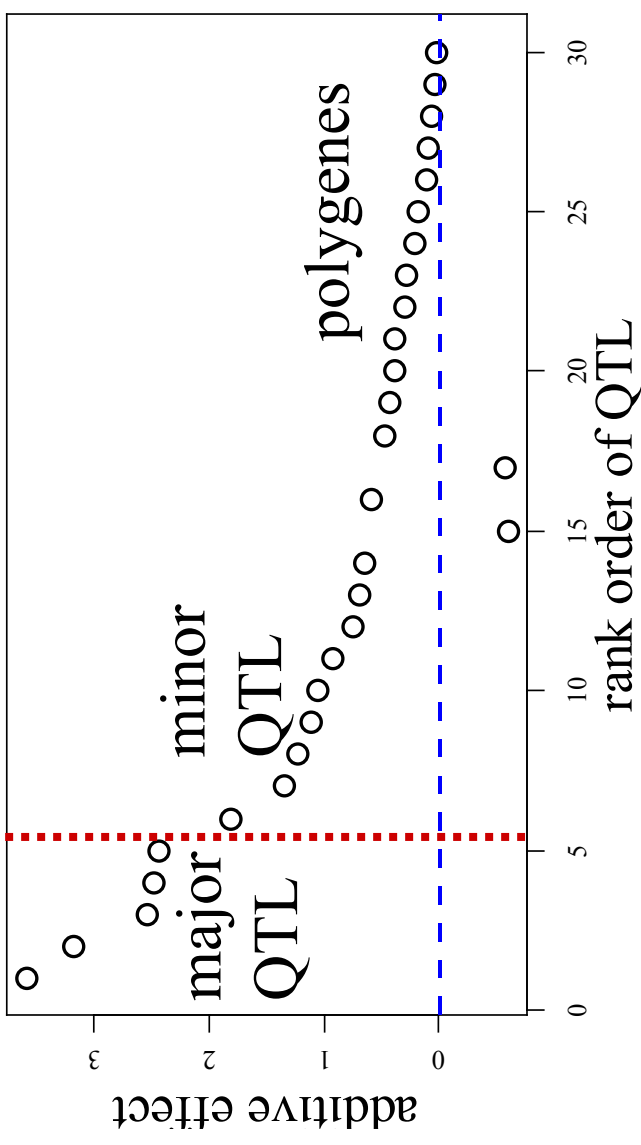
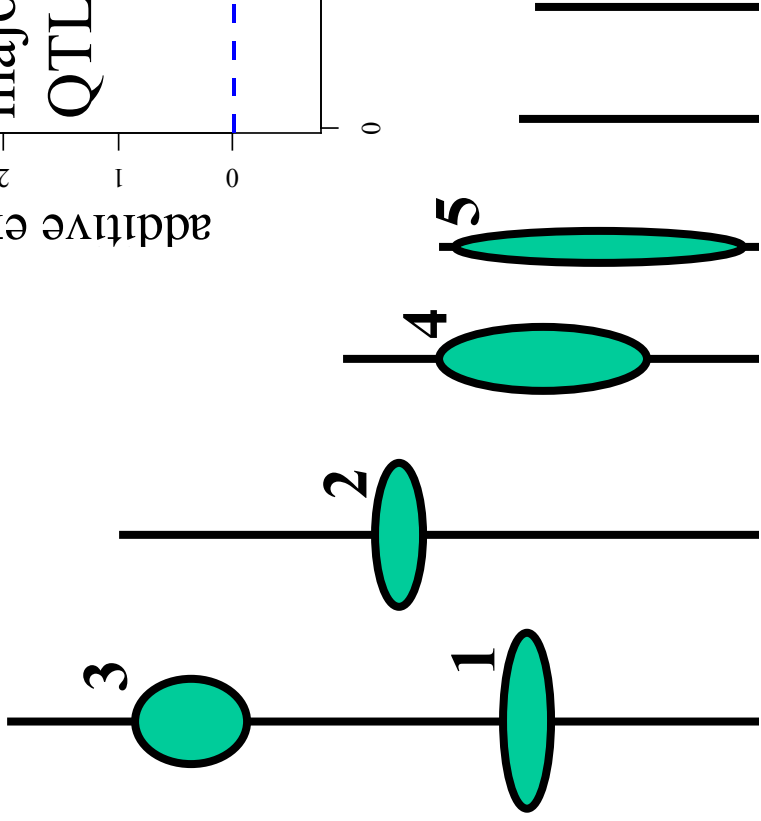


MCMC run: 2 loci assuming only 1

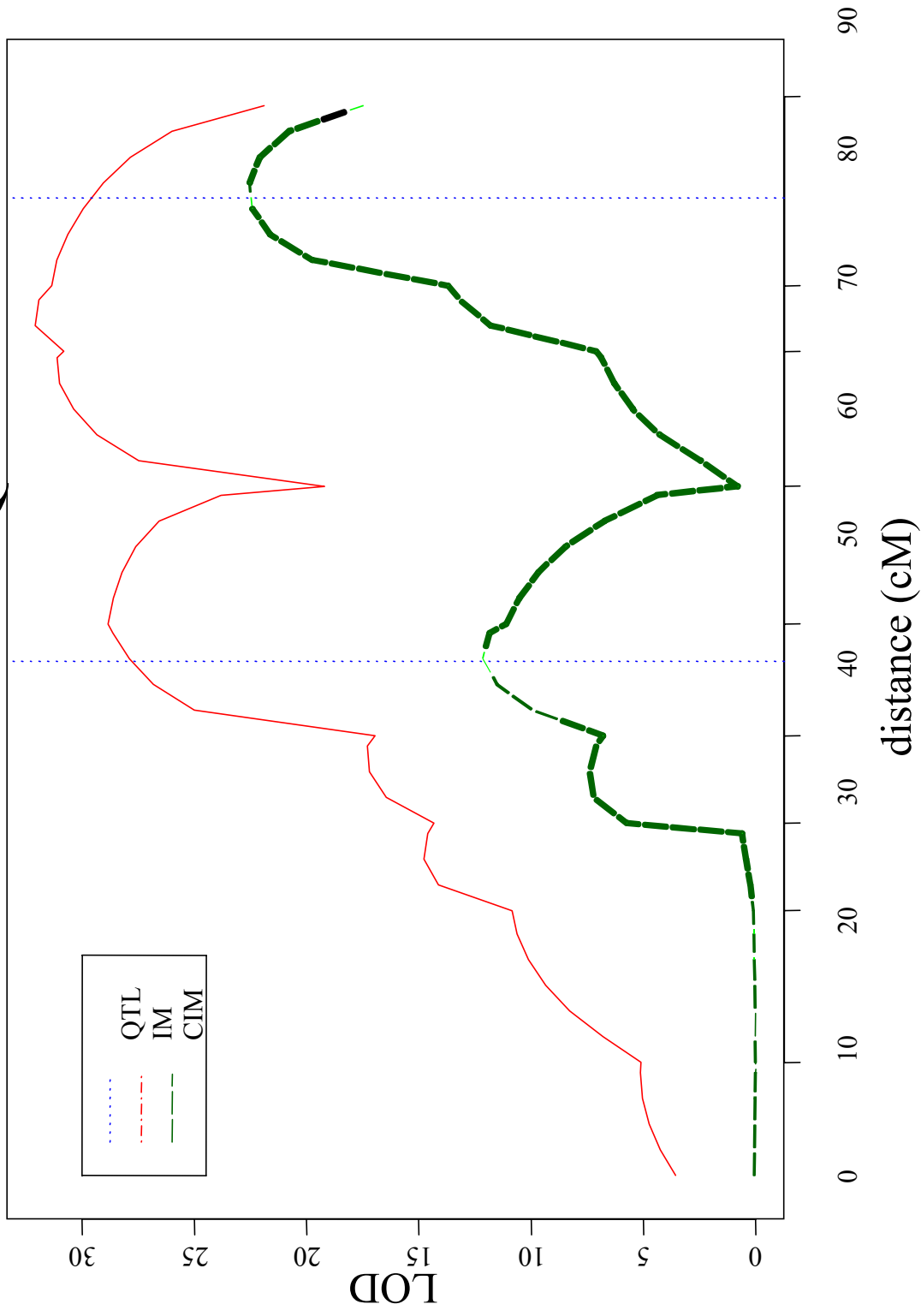


Pareto diagram of QTL effects

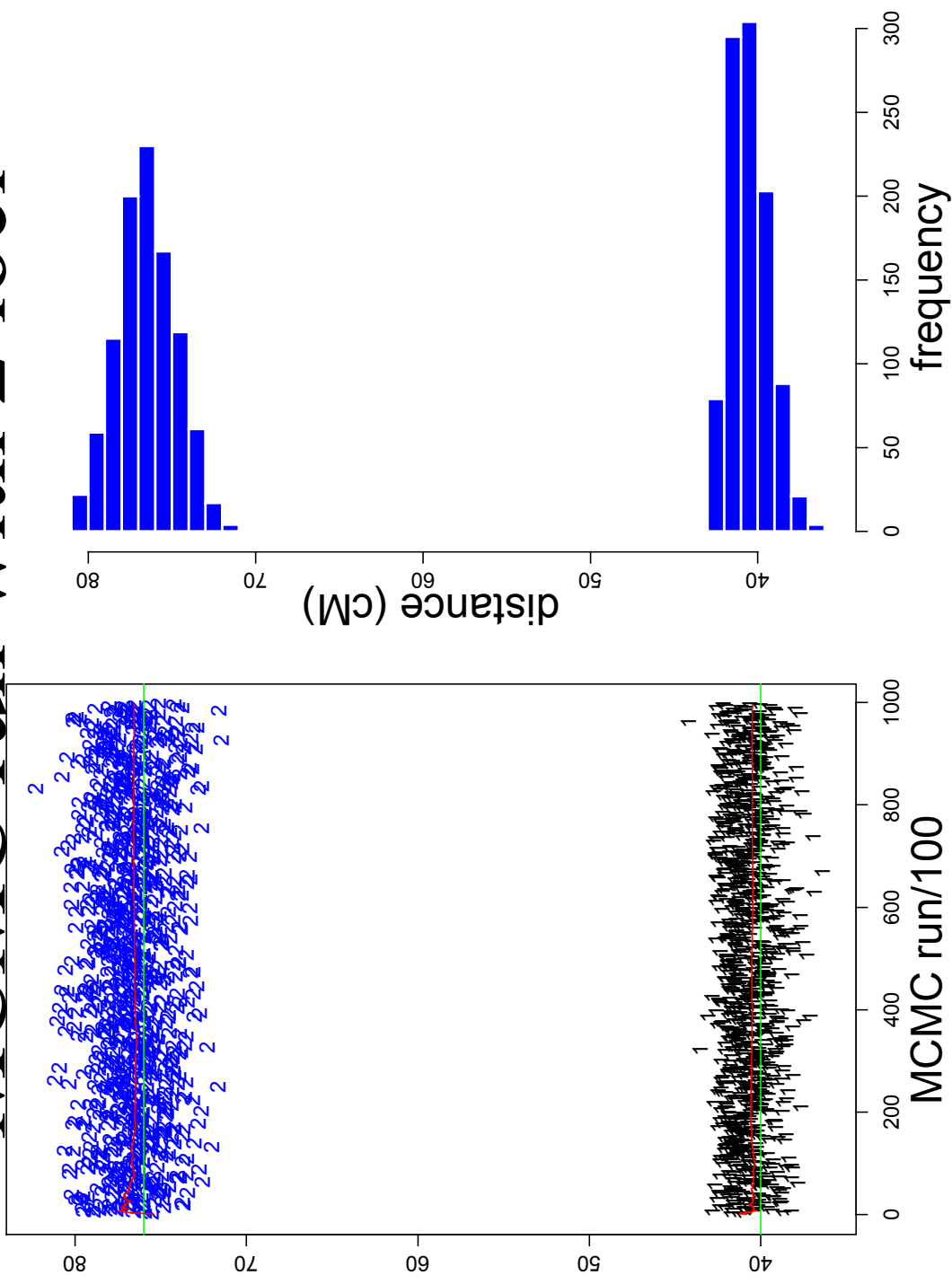
major QTL on
linkage map



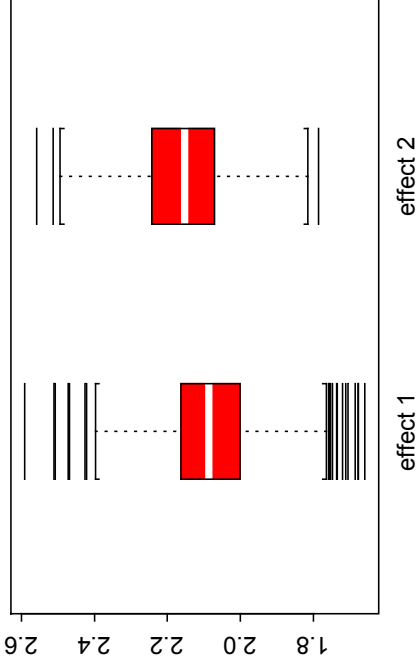
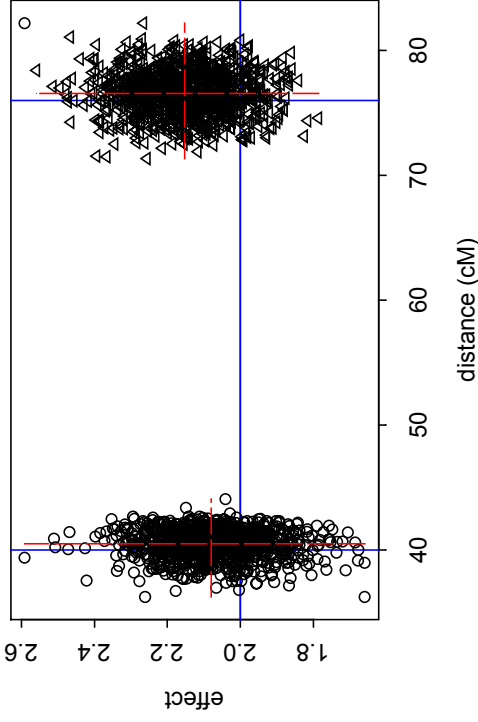
LOD for 2 QTL



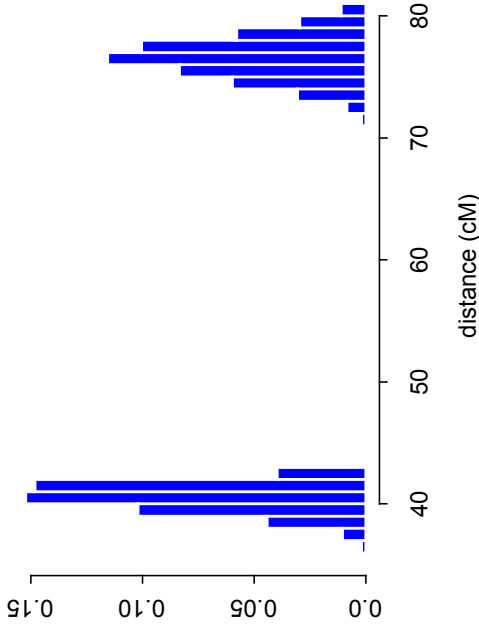
MCMC run with 2 loci



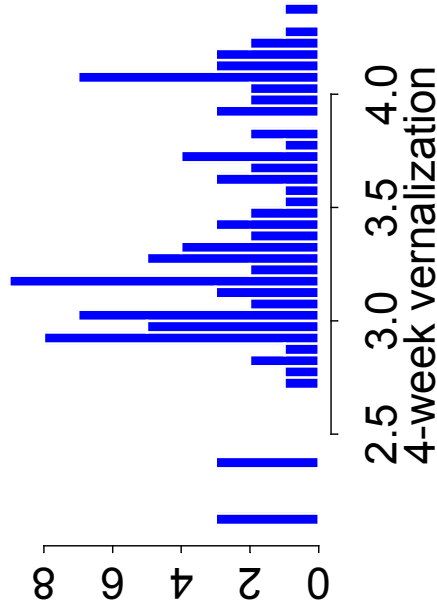
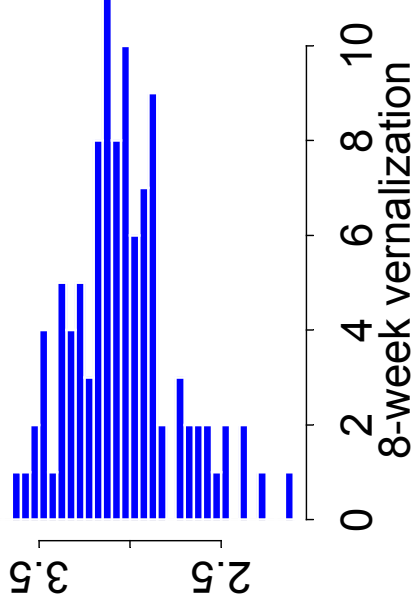
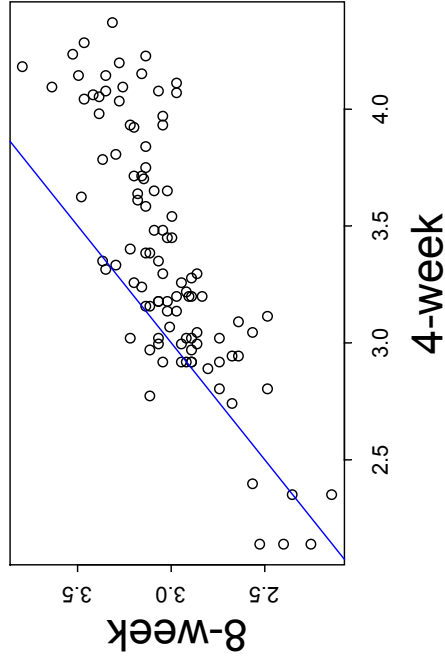
effects for 2 simulated QTL



summaries of MC samples
joint scatter plots by loci
(lines for true, estimates)
marginal histograms
marginal box-plots

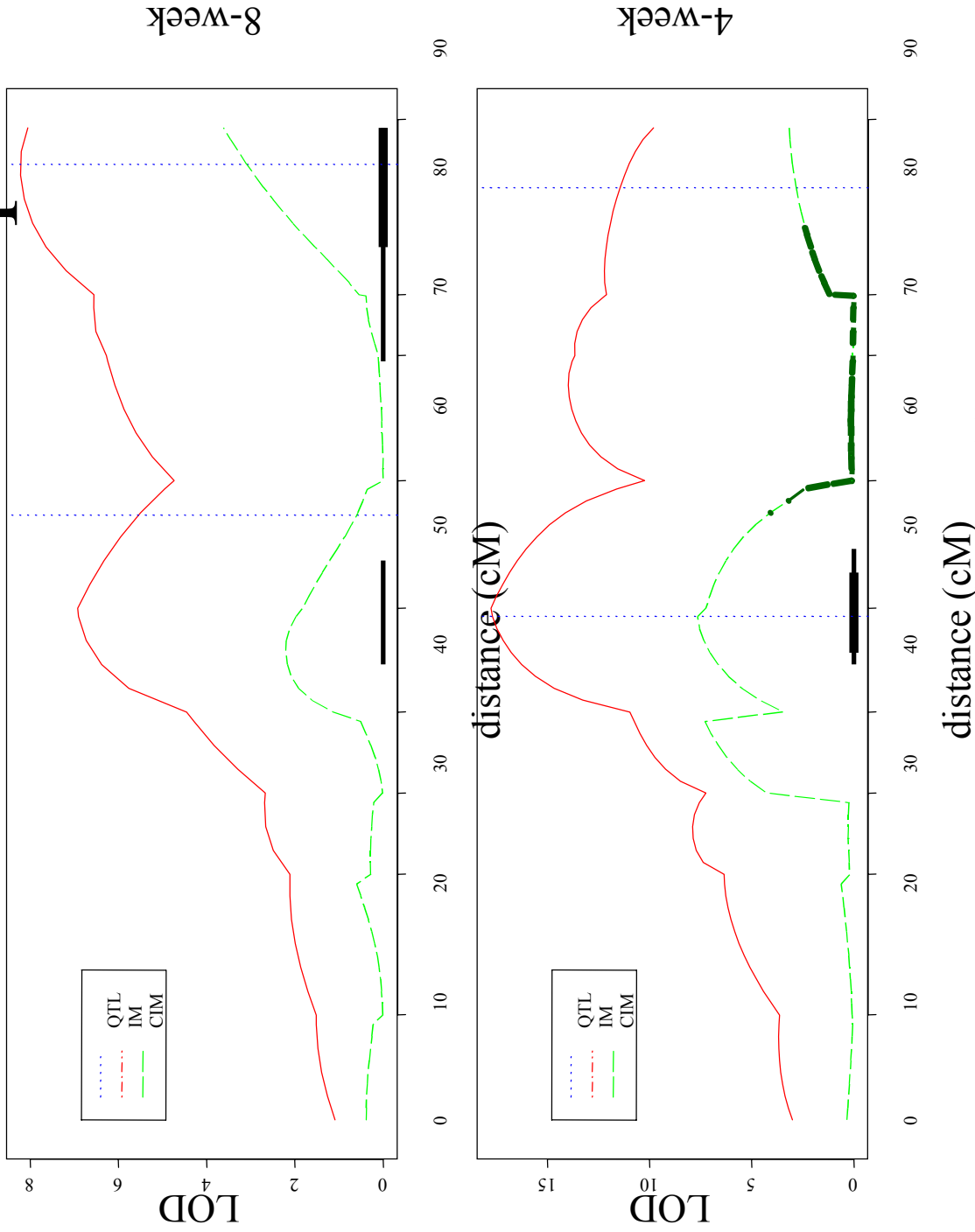


Brassica 4- & 8-week data



summaries of raw data
joint scatter plots
(identity line)
separate histograms

Brassica data LOD maps



Brassica 8-week data locus MCMC with $m=2$

