Figure S2  Estimates of gene-conversion rate and tract length in 10 kb sequences simulated with conversion alone. Each figure represents the joint posterior distribution of population gene-conversion rate ($\gamma$) and mean tract length ($m$) for an independent simulated dataset with the population crossing-over rate ($\mu$) fixed at 0. The starting value of the parameters in the MCMC chain were set at the true values used in simulations.

a) $\gamma = 3000$, $m = 352$ bp, $\theta = 10.0$, Samples = 20
b) $\gamma = 3000, \ m = 352 \text{ bp}, \ \bar{\theta} = 10.0, \ \text{Samples} = 20$
c) $\gamma = 5000$, $m = 150$ bp, $\theta = 15.0$, Samples = 20
d) $\gamma = 2000$, $m = 500$ bp, $\theta = 15.0$, Samples = 20
e) $\gamma = 1000$, $m = 800$ bp, $\theta = 10.0$, Samples = 50