A. Extract reads from reference genome

ChrA

ChrB

ChrC

ChrD

B. Re-diploidize genome by creating alleles

\[ \text{SbfI} \]

\[ \text{TGCAGGTGACTTAGAGCGCGATATTGACCGGGAACGCGAGCGTGAAGCG} \]

\[ \text{SbfI} \]

\[ \text{TGCAGGTGACTTAGACGCGATATTGACCGGGAACGCGAGCGTGAAGCG} \]

C. Randomly generate SNPs across alleles

D. “Sequence”

\[ 3\% \]

\[ 1\% \]

\[ 0.5\% \]

E. Generate error at three levels on “sequenced” reads

**Figure S1** RAD-seq Simulation. (A) 60bp reads were extracted *in silico* from the stickleback reference genome at each occurrence of an *SbfI* restriction enzyme cut site. (B) Extracted reads were re-diploidized and (C) SNPs were added to the reads at a uniform rate of 0.5%. (D) The reads were “sequenced” at per-allele mean depths of 10x, 20x, and 40x by drawing numbers from a Poisson distribution. (E) Errors were added to the “sequenced” reads at three rates, 0.5%, 1%, and 3%.