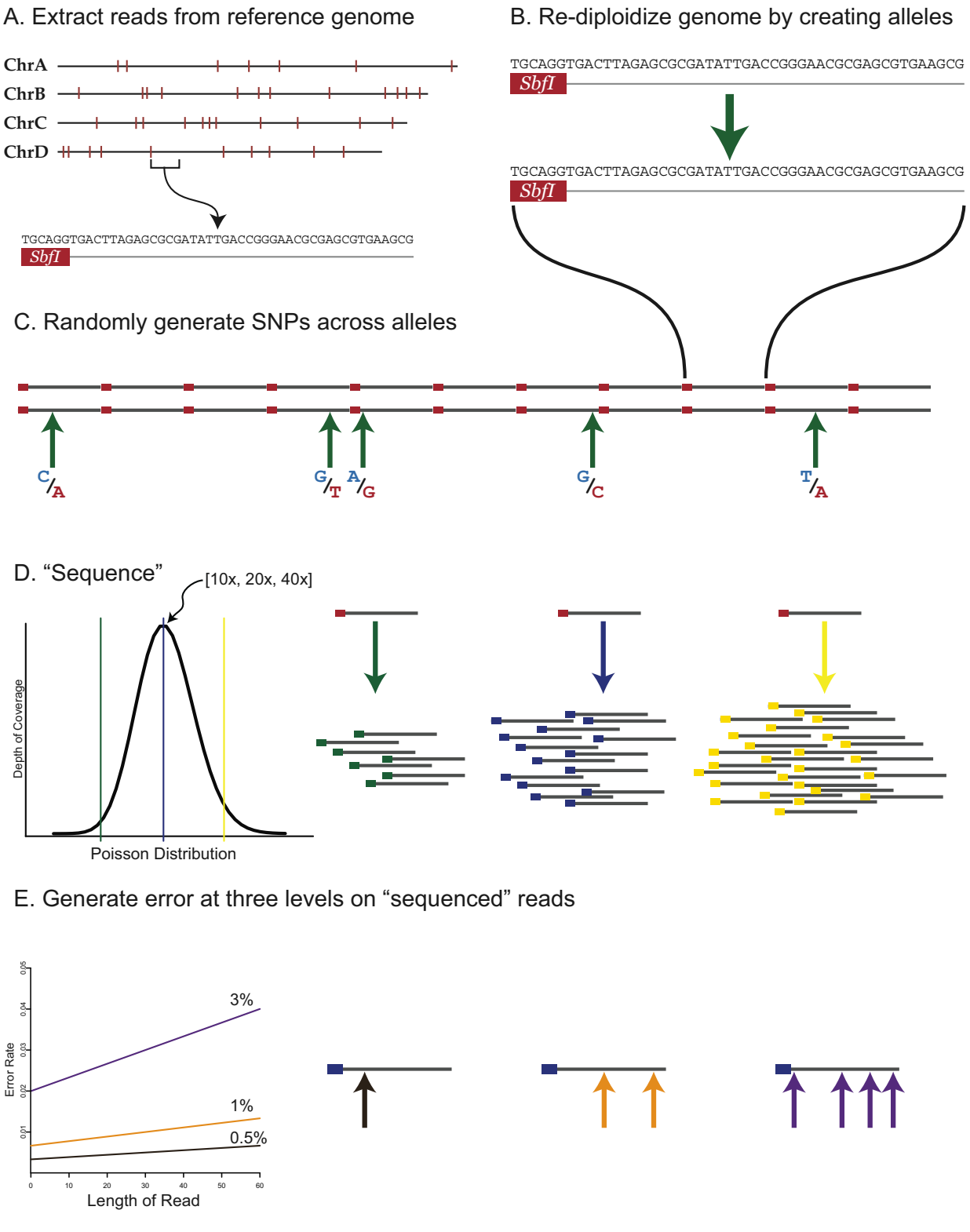

Figure S1 RAD-seq Simulation. (A) 60bp reads were extracted *in silico* from the stickleback reference genome at each occurrence of an *SbfI* restriction enzyme cut site. (B) Extracted reads were re-diplodized and (C) SNPs were added to the reads at a uniform rate of 0.5%. (D) The reads were "sequenced" 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%.