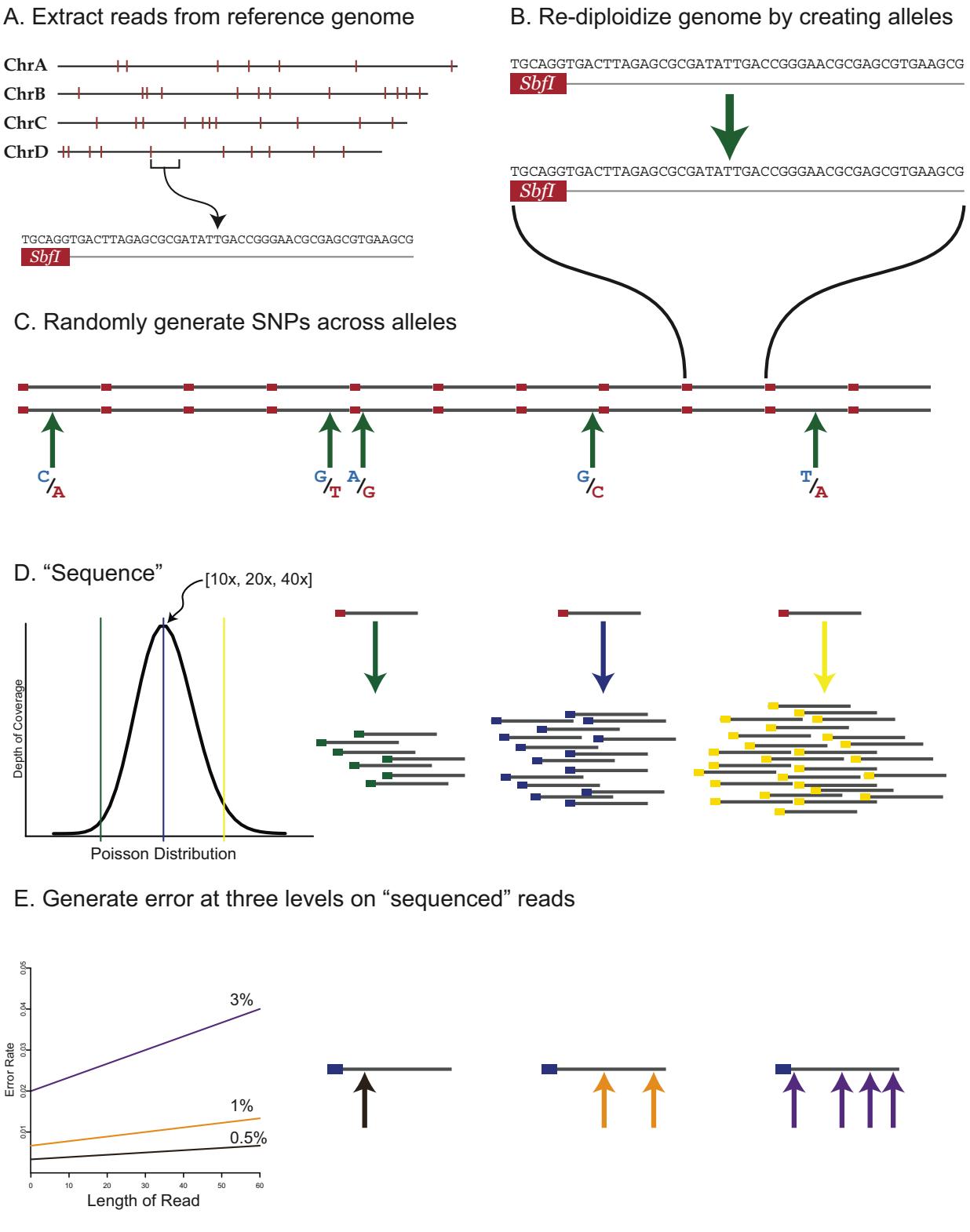
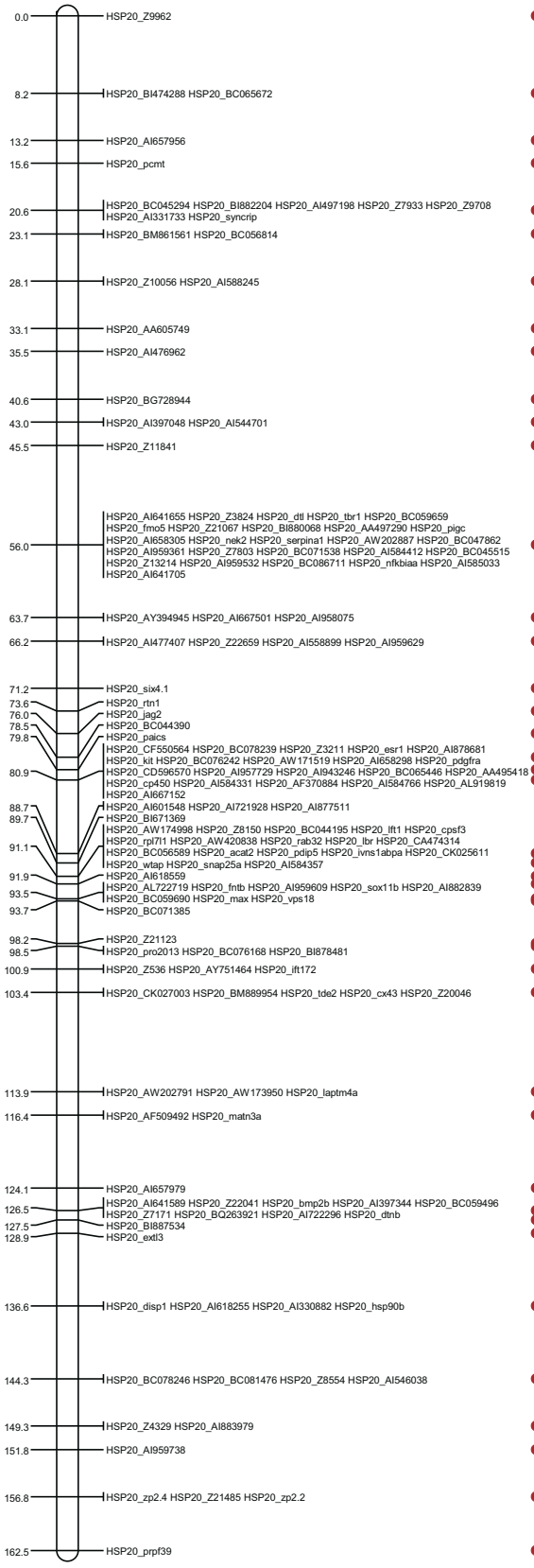



**Figure S1** RAD-seq Simulation. (A) 60bp reads were extracted *in silico* from the stickleback reference genome at each occurrence of an *SbfI* restriction enzyme cut site. (B) Extracted reads were re-diplodized and (C) SNPs were added to the reads at a uniform rate of 0.5%. (D) The reads were "sequenced"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


**Figure S2** *Danio rerio* RADmap. We mapped 7,861 markers generated from a doubled haploid mapping panel; analysis by *Stacks* recapitulated the 25 zebrafish linkage groups. A c. We reconstructed the HSmap from its original set of markers and combined the HSmap markers with the new, RAD-seq markers and built a second map. LG20 shows very close agreement between markers in both maps, as indicated by red lines that connect identical markers in the two maps.

## DreLG20

## 157 EST markers




## DreLG20

## 311 RAD markers

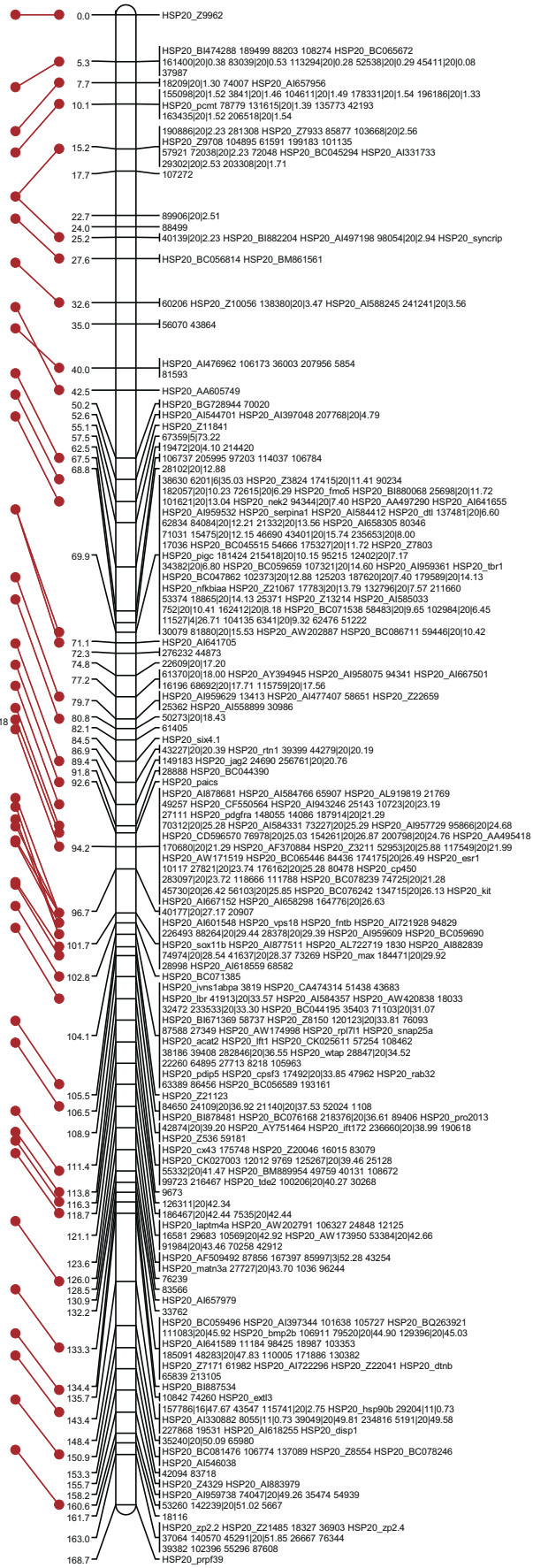


**Figure S3** HSmap versus RADmap. We reconstructed the HSmap from its original set of markers and combined the HSmap markers with the new, RAD-seq markers and built a second map. LG20, shown here, and all other linkage groups, shows very close agreement between markers in both maps, as indicated by red lines that connect identical markers in the two maps.