**Figure 1.** **Sampling locations of marine and freshwater stickleback populations from southcentral Alaska.** Inset: Geography of Cook Inlet near Anchorage, AK. Marine stickleback were sampled from Rabbit Slough (RS, red). Freshwater stickleback were sampled from Boot Lake (BT, dark blue) and Bear Paw Lake (BP, light blue). All areas in the inset were glaciated during the Late Wisconsin glaciation until ~10 kya.

**Figure 1.** **The structure of simulations to test the effects of population structure on genetic variation in a model of local adaptation.** **A:** Habitat H1 (red) (: red, H2: blue) consists of a single deme while habitat H2 (blue) consists of *k* demes. We adjust the size of each deme in H2 so that the total census size of each habitat is constant across simulations. Diamonds represent a single locus with locally adaptive alleles. **B:** We assessed genetic diversity at the locally adaptive locus and in non-overlapping windows. We used the pattern of reciprocal monophyly (outlined in gold) to classify RAD loci as ‘divergent’ in the threespine stickleback population genomic dataset. (See Methods and Nelson and Cresko [2018]). **C:** Genetic diversity within and among allelic classes in a simulation where *k*H2 = 1. Shown are 95% confidence intervals of nucleotide diversity (π) and Watterson’s θ after 10N generations of selection. Because patterns of variation are symmetrical about the locus under selection, we present ‘folded’ curves (panel C, right) throughout this work.

**Figure 3. Patterns of sequence variation differ on marine and freshwater stickleback chromosomes.** **A-C:** Genome-wide sequence diversity (π) as a function of the distance from a RAD locus with reciprocally monophyly of marine and freshwater haplotypes. Diamonds show average sequence diversity among reciprocally monophyletic RAD loci. Density of RAD loci at x distance from the nearest reciprocally monophyletic locus with y level of diversity is shown in shades of gray. Bold lines are smoothed splines, dashed lines are genome-wide means. **A:** Sequence diversity in the combined dataset (marine [Rabbit Slough] + freshwater [Boot Lake and Bear Paw Lake]). **B:** Sequence diversity on chromosomes carrying marine haplotypes. **C:** Sequence diversity on chromosomes carrying freshwater haplotypes. **D:** Smoothed splines as in A-C. **E:** Sequence diversity of RAD loci within 1 Mb of a reciprocally monophyletic RAD locus and on chromosomes not carrying a reciprocally monophyletic locus (‘unlinked’). Data are means ± 1 SD. \*\*\* p < 0.001. **F:** Splines as in **A-D** of Watterson’s θ.

**Figure 4. Asymmetric population structure generates asymmetric patterns of linked variation on simulated chromosomes.** Simulations were performed as described in Methods and **Figure 1**. Bands are 95% confidence intervals of Watterson’s θ at a given distance from a locally adaptive locus (red: θ1, blue: θ2). Columns show the effect of increasing population structure (*k*) in habitat H2. Rows show the effect of increasing the length of the selection phase of the simulations. Rows 1-3 show results under strong selection (*s* = 0.20). Row 4 shows results for simulations identical to row 3 but with moderate selection (*s* = 0.02). All simulations were performed using a migration rate, *m*, of one migrant per generation between habitat H1 and each population of habitat H2. Total diversity(see Fig. **X**) is not shown.

**Figure 5.** **The recombination landscape varies within and among genetic maps of freshwater (BT) and F1 hybrid threespine stickleback.** Each point represents a RADseq-based marker segregating within a mapping family. Blue: BT, black: F1 hybrid. The inset on chromosome 21 shows suppression of recombination due to inversion heterozygosity in the F1 hybrid. Genetic maps for all chromosomes and for the marine (RS) map are given in supplemental figures **SX-X**.

**Figure 6. The recombination landscape extends to genomic reach of divergent selection.** **A-B:** FST scans were performed on the physical map (top, scale bars = 5 Mb) and imputed onto the freshwater and F1 hybrid genetic maps (middle and bottom, scale bars = 10 cM) for chromosomes 4 and 7. Lines connect evenly-spaced windows on the physical map to the imputed positions on each genetic map and are colored by the kernel-averaged FST for that window. Positions of divergent RAD loci are shown in gold. **C-D:** physical positions of all RAD loci within 0.2 cM from a divergent locus on the freshwater map (blue lines) and the F1 hybrid map (black lines).

**Figure SX. Genetic divergence comprises a smaller proportion of the genetic map than the physical map.** Each line represents the proportion of the overall map length (Mb or cM) taken up by windows of genetic divergence (FST or dXY) greater than or equal to a given value. Black: physical map (reference genome), red: RS genetic map, blue: BT genetic map, purple: F1 hybrid genetic map.