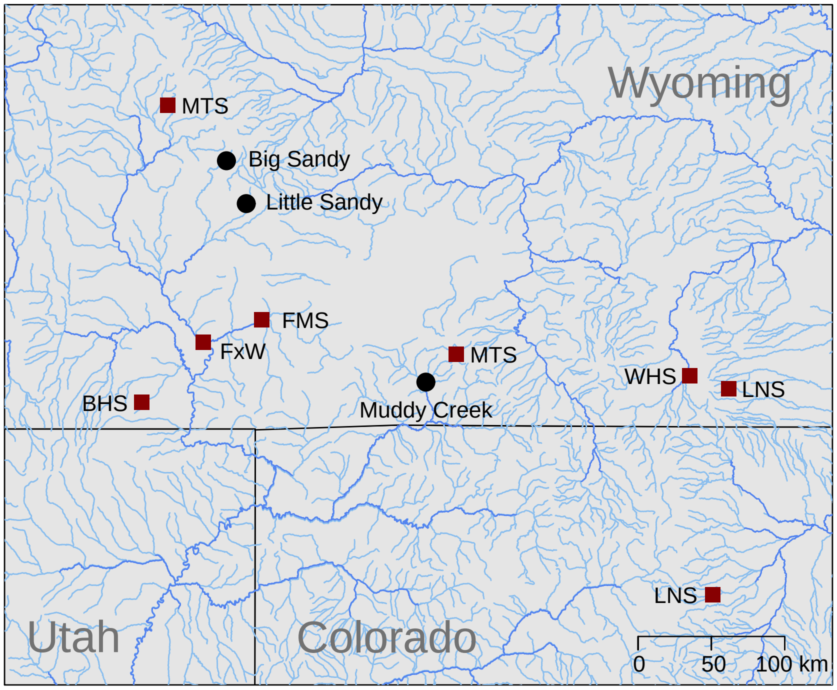

Figure S1: Map of sampling sites in the Upper Colorado River basin and east of the Continental Divide. The three focal drainages were Big Sandy, Little Sandy, and Muddy Creek (marked with black circles on the map). The other populations (marked with red squares) were included for reference, and only one species or hybrid cross was sampled from each of the reference sites.

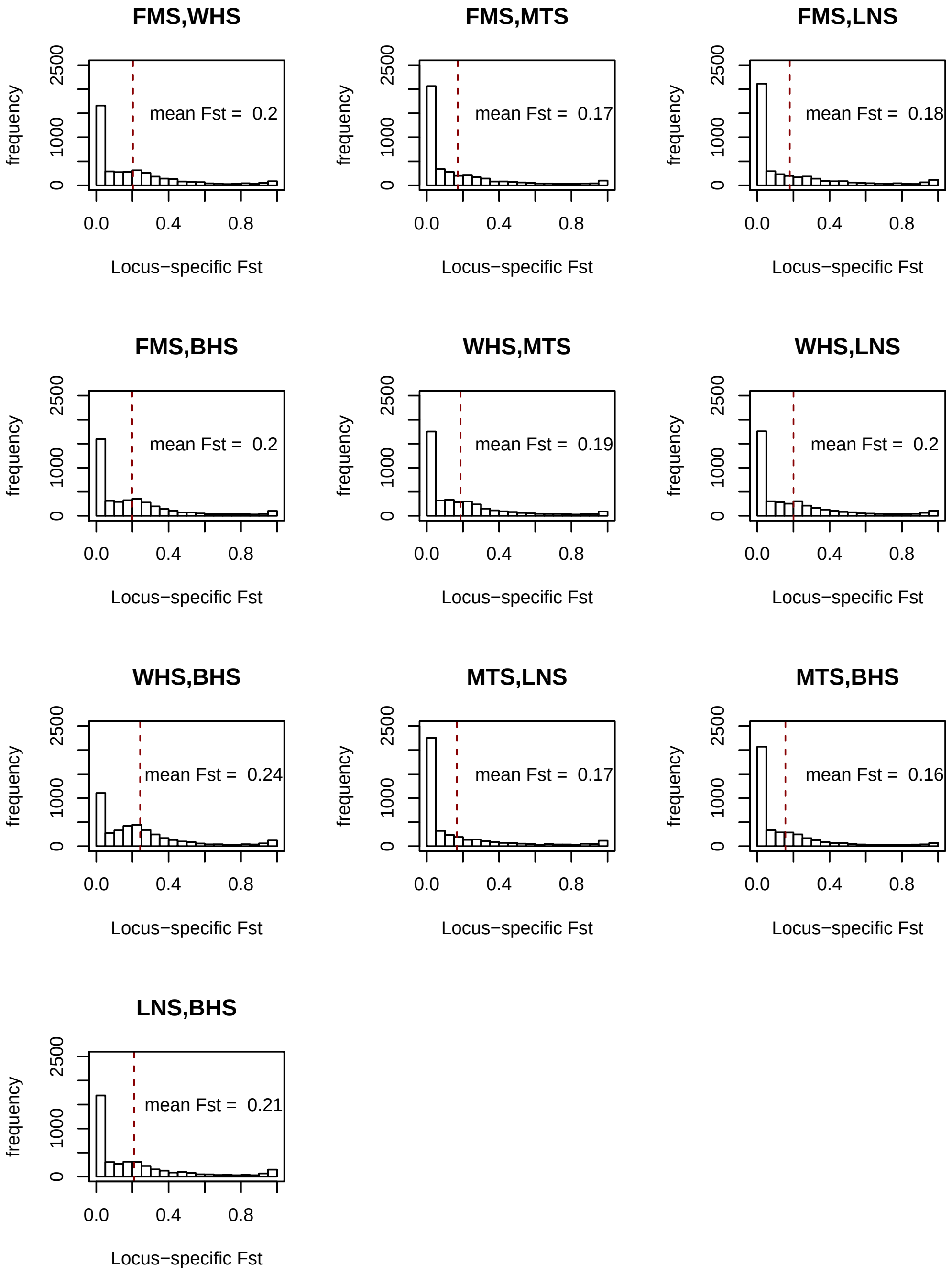

Figure S2: Distribution of locus-specific F_{ST} (Hudson's F_{ST}; Hudson *et al.* 1992), pairwise between all species, for all 4,095 SNPs used in analyses in this study. Each histogram is labeled with abbreviations for the two species being compared. For each pair of species, the mean locus-specific F_{ST} suggests that these loci are sufficiently informative to differentiate between species.

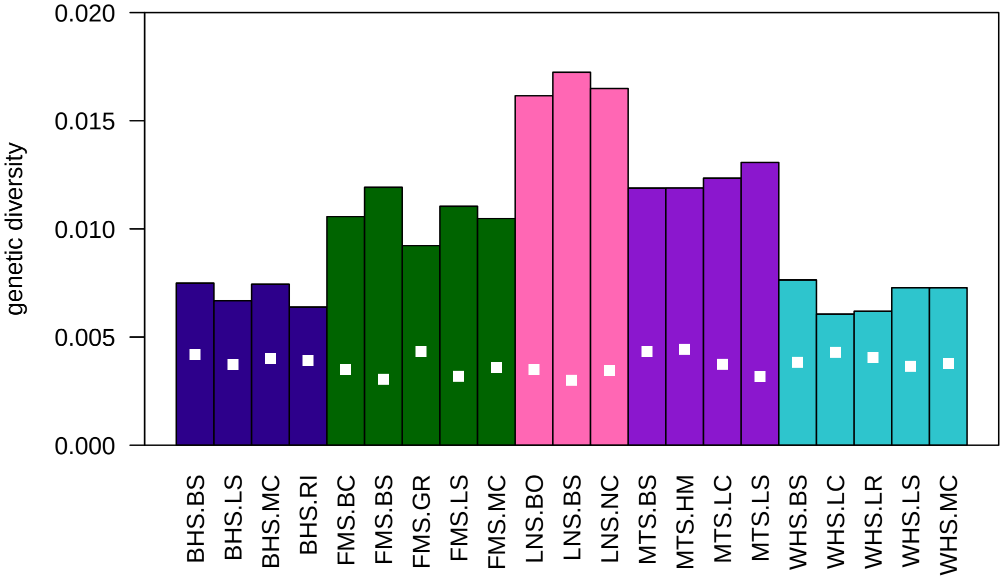

Figure S3: Genetic diversity for each population of each species. Estimates of Waterson's theta are shown by bars, while estimates of expected heterozygosity are denoted by white squares. Colors and labels are consistent with Fig. 3.

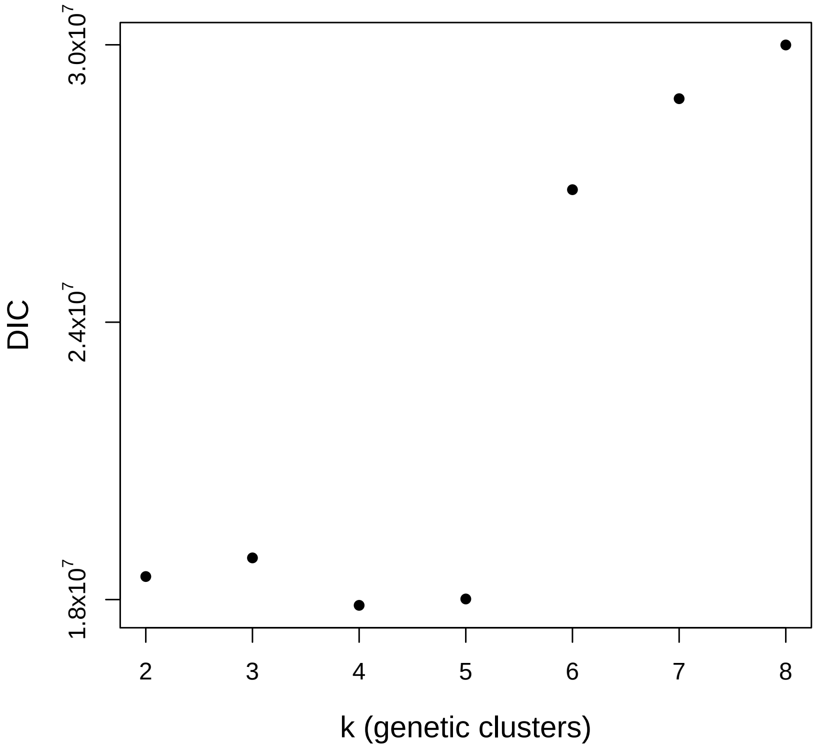

Figure S4: DIC (deviance information criterion, a model-choice criterion) for `entropy` models with $k = 2$ to $k = 8$ clusters. Lower values of DIC correspond to better model fit. We interpreted our results using the $k = 5$ model.