

Supplementary Tables and Figures

Supplementary Table 1. Genotype data from all 41 markers used for mice collected from the Saxon transect. Detailed marker positions are as listed in Teeter et al. 2008.

Supplementary Table 2. Two-parameter cline estimates generated in ClineFit for each marker used for the Saxon transect sample.

Supplementary Figure 1. Scatterplots for data from the Saxon and Bavarian transects for all 41 markers used. The center of a geographic cline estimated using a 6-parameter model was set to 0 km for each transect, and this was used to superimpose the data from the two transects.

Supplementary Figure 2. Comparison of genomic clines for the Bavaria and Saxony hybrid zones. Each pair of panels reports the results from a given locus in each hybrid zone. Each panel shows the 95% CI for the homozygous *M. domesticus* (dark green) and heterozygous (light green) genotypes as well as the clines for the observed genotype data for the homozygous *M. domesticus* (solid line) and heterozygous (dashed line) genotypes for a given locus. High hybrid index values correspond to individuals of primarily *M. musculus* ancestry, while low hybrid index values correspond to individuals of primarily *M. domesticus* ancestry. The locus name (chromosome number followed by map location) and *P*-value is displayed in each panel. The log ratio of the likelihood of the data from the Saxony hybrid zone given the Saxony hybrid zone model to the likelihood of the data from the Saxony hybrid zone given the Bavaria hybrid zone model is shown between each pair of panels.

Supplementary Figure 3. Plot of pairwise epistatic interaction for the two hybrid zone transects. The value in each box corresponds to the difference in model AIC between genomic cline models for a focal marker with and without the inclusion of genotype data from a predictor marker. Positive values suggest that the genomic region surrounding the predictor marker has an epistatic effect on the fitness of genotypes in the genomic region surrounding the focal marker. Boxes are shaded to denote the strength of evidence for epistatic interaction (i.e. darker green colors denote higher differences in AIC). A. Bavaria. B. Saxony.

Supplementary Figure 4. Plots of 2-parameter estimates of cline width vs. 2-parameter estimates of cline center. Plots and analyses are for autosomal data only. Marker 13.029 was excluded from these correlations, as the estimated cline width was 342.8 km in Bavaria, longer than the actual transect. Cline center was significantly correlated with cline width in both transects (Bavaria: Spearman's $\rho = 0.618$; $p < 0.001$; Saxony: Spearman's $\rho = 0.812$; $p < 0.001$). A. Bavaria. B. Saxony.