



Figure S6: MDS visualizations of the results of individual-based simulations using SLiM (see Appendix B.2 for details). All simulations incorporate linked selection by allowing selected mutations to appear in the same two regions of the genome: the one-sixth of the genome immediately before the halfway point, and the last one-sixth of the genome. **(top)** Constant recombination rate. **(top middle)** Stepwise varying recombination rate (as described in Figure S5). **(bottom middle)** Constant recombination rate with spatially varying effects of selection. **(bottom)** PCA plots corresponding to the highlighted corners of the last MDS visualization, showing how spatially varying linked selection has affected patterns of relatedness. The **(inset)** provides a key to the locations of the individuals on the spatial landscape.