



Figure S5: MDS visualizations of the results of individual-based simulations using SLiM (see Appendix B.2 for details). All simulations are neutral, and recombination is: **(top)** constant; **(top middle)** varies stepwise by factors of two in seven equal-length segments, with highest rates on the ends, so the middle segment has a recombination rate 64 times lower than the ends; **(bottom middle)** according to the HapMap human female chromosome 7 map. The **bottom** figure shows PCA maps corresponding to the three colored windows of the last (HapMap) situation; the outlying regions are long regions of low recombination rate, so that region can be dominated by a few correlated trees, similar to an inversion. The **(inset)** provides a key to the locations of the individuals on the spatial landscape.