



Figure S1: Linkage disequilibrium decay in largest contigs for all samples. Linkage disequilibrium measured by r^2 measured pairwise for each SNP within 100kb of each other (0-30kb shown in plot). 95% confidence shaded intervals displayed based on 100 bootstrap replicates. A 1% subsample of the r^2 values was used to fit the model of decay. **(A-E)** display results from contigs 1, 2, 3, 4, and 5-6, respectively, which span chromosomes X, 2, and 3, based on homology with *D. melanogaster*.