



Figure S10. Number of shared 100 kb genomic windows in the top empirical 1% vs. correlations of window statistics over all genomic windows for pairs of populations. Each point is a different population pair. Titles indicate the haplotype statistics for which the shared windows occur. Line is a best-fit *lowess* curve through the points. Significance of the p-value for the Mantel correlation between the *x* and *y* variables is indicated in the upper left corner: "NS": not significant, "***": < 0.05, "****": < 0.01, "*****": < 0.001.