



Figure S9. Number of shared 100 kb genomic windows in the top empirical 0.1% vs. mean F_{ST} for pairs of populations. Each point is a different population pair (some points are labeled, see key). 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 right corner: "NS": not significant, "**": < 0.05 , "***": < 0.01 , "****": < 0.001 .