



Figure S11. Correlations of window statistics over all 100 kb genomic windows vs. average Bantu ancestry for pairs of populations. Average proportion of Bantu ancestry is inferred from HENN *et al.* (2011), see Methods. Each point is a different population pair. Titles indicate the haplotype statistics for which the correlations are calculated. 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 or left corner: "NS": not significant, "**": < 0.05, "***": < 0.01, "****": < 0.001. Note that the Namibian San are not included, as Bantu ancestral proportions for all individuals are not available from HENN *et al.* (2011).