

Table S3. Mantel correlations between matrices of the indicated variables for each haplotype statistic.

| Haplotype Statistic | F_{ST} and | | Correlation of Window Statistics and | | Average Bantu Ancestry and | |
|---------------------|---------------------------|--------------------------|--------------------------------------|--------------------------|----------------------------------|---------------------------|
| | Overlap Top 1% | Overlap Top 0.1% | Overlap Top 1% | Overlap Top 0.1% | Correlation of Window Statistics | Overlap Top 1% |
| iHS | -0.626 (0.0002) | -0.116 (0.212) | 0.833 (0.002) | 0.223 (0.057) | 0.300 (0.175) | 0.468 (0.029) |
| XP-EHH CEU | -0.885 (0) | -0.664 (0) | 0.894 (0.0002) | 0.637 (0.0004) | 0.400 (0.123) | 0.490 (0.043) |
| XP-EHH YRI | -0.200 (0.137) | -0.096 (0.346) | 0.834 (0.0002) | 0.310 (0.066) | -0.643 (0.008) | -0.531 (0.0004) |
| XP-EHH MKK | -0.500 (0) | -0.341 (0.001) | 0.866 (0.0002) | 0.514 (0.007) | 0.455 (0.043) | 0.443 (0.023) |
| XP-EHH KHB | -0.500 (0) | -0.647 (0) | 0.869 (0.0002) | 0.655 (0.0002) | 0.495 (0.063) | 0.527 (0.021) |

The indicated variables are calculated between all pairs of populations (creating matrices for which Mantel correlations can be calculated). P-values for the Mantel correlations, assessed by 5,000 randomizations, are indicated in parentheses and in bold if significant (p-value < 0.05). F_{ST} : mean F_{ST} over all SNPs between pairs of populations; Correlations of Window Statistics: correlations of window statistics across all genomic windows between pairs of populations; Overlap Top 1%: number of shared windows in the empirical top 1% between pairs of populations; Overlap Top 0.1%: number of shared windows in the empirical top 0.1% between pairs of populations.