



Figure 2 – Supplementary Figure 1. Principal Components Analysis of Kalinago and comparison populations. PCA analysis was performed on HGDP sample (940 individuals), with 458 Kalinago individuals projected on the same axes. **A**, PC1 and PC2; **B**, PC1 and PC3. In both panels, HGDP individuals are colored to indicate cluster membership (AFR, African; nAFR/ME, Northern Africa and Middle East; EUR, Europe; CSA, Central and Southern Asia; EAS, East Asia; OCE, Oceania; NAM, Native American). Ancestry was represented by the first 10 principal components because AFR and NAM ancestries are not independent of each other. The first PC correlated strongly with AFR or NAM ancestry (r^2 0.94 and 0.97, respectively), but also with EUR ancestry (r^2 = 0.32). Several other principal components displayed considerably lower levels of correlation with ancestry (r^2 < 0.1 for EUR and r^2 < 0.05 for EAS). Individuals homozygous for the albino variant were excluded from association analyses. Association analysis did not reveal any novel variants that reached genome-wide significance, after correction for statistic inflation. The inflation factor (lambda) for the full genotyped sample excluding the albinos (n=444) sample was 1.349. Values of lambda for the nine N=50 subsets ranged from 1.001 to 1.184 (median 1.075), suggesting that the elimination of second order relatives did not remove all effects of relatedness.