Figure S8. Principal component analysis plot of the HapMap3 reference populations and the admixed AFR-EUR participants in the PNAT2+KIS3 clinical trials. Plotted principal components were computed from merging the HapMap3 reference populations and all samples from the PNAT2+KIS3 trials. The admixed participants (study sample; black N=68) were determined through ancestry clustering to the reference HapMap3 project based on lying on the cline between the CEU (Utah residents with European ancestry; red) and the ASW (African ancestry in Southwest USA; purple) or YRI (Yoruba in Ibadan, Nigeria; green) subpopulations. The following PC cut-points (represented by the black lines) were used to determine the admixed study sample: -.0.025<PC1<0.054 & PC2≤0.01.