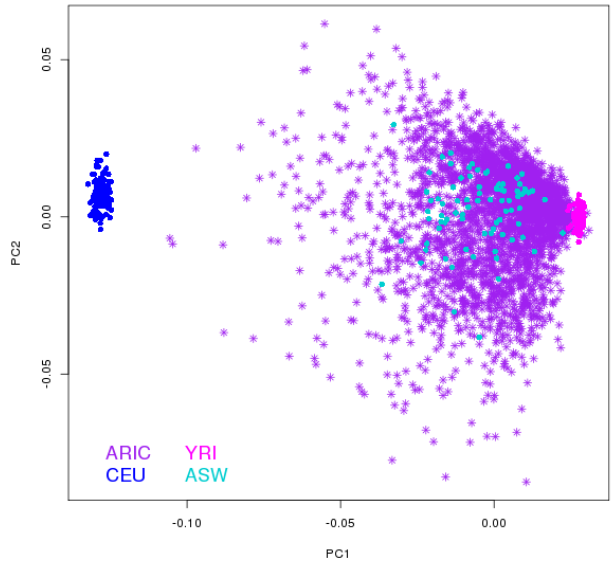
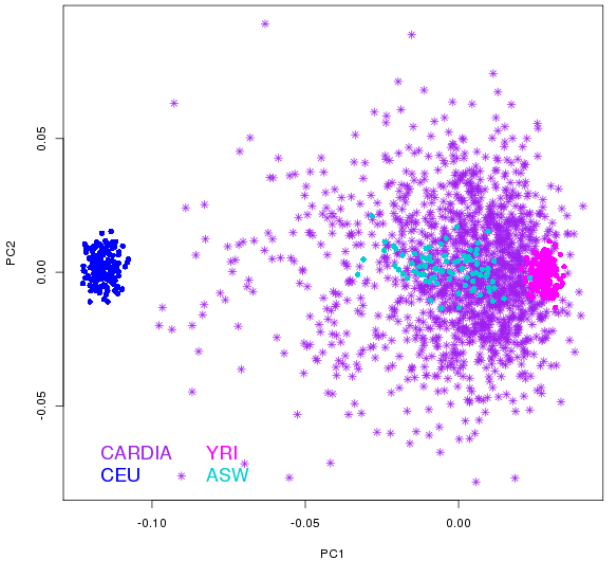
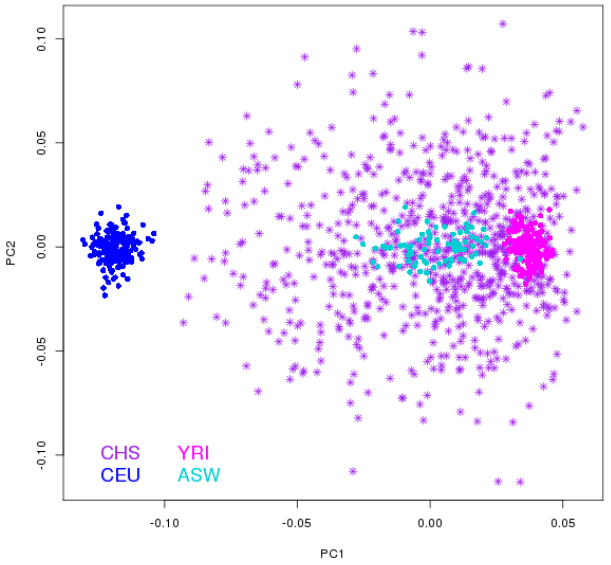
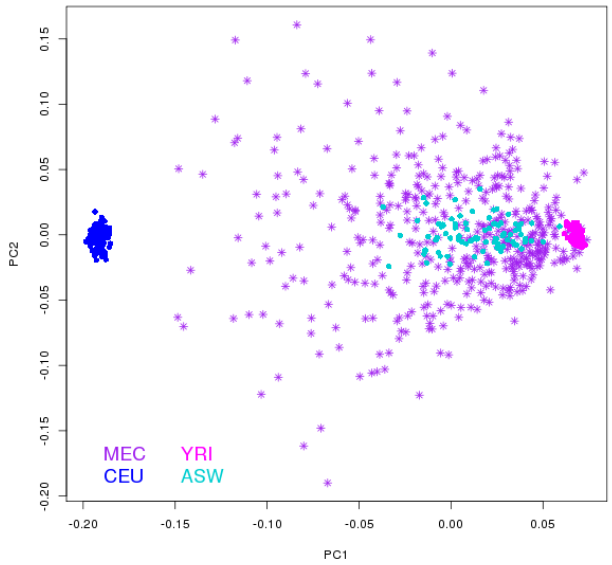
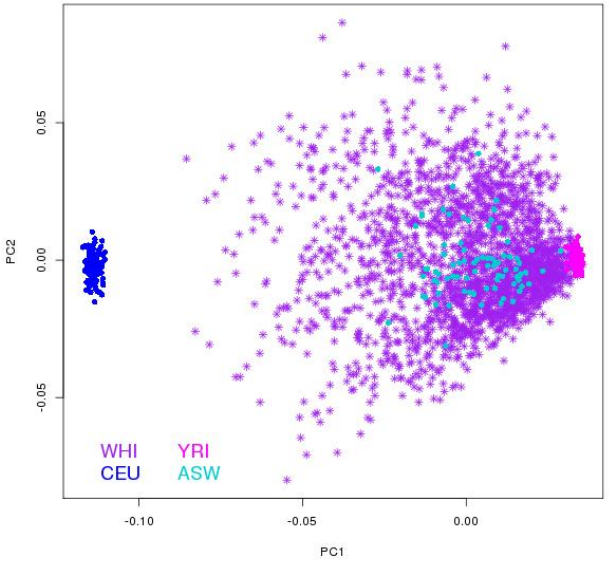


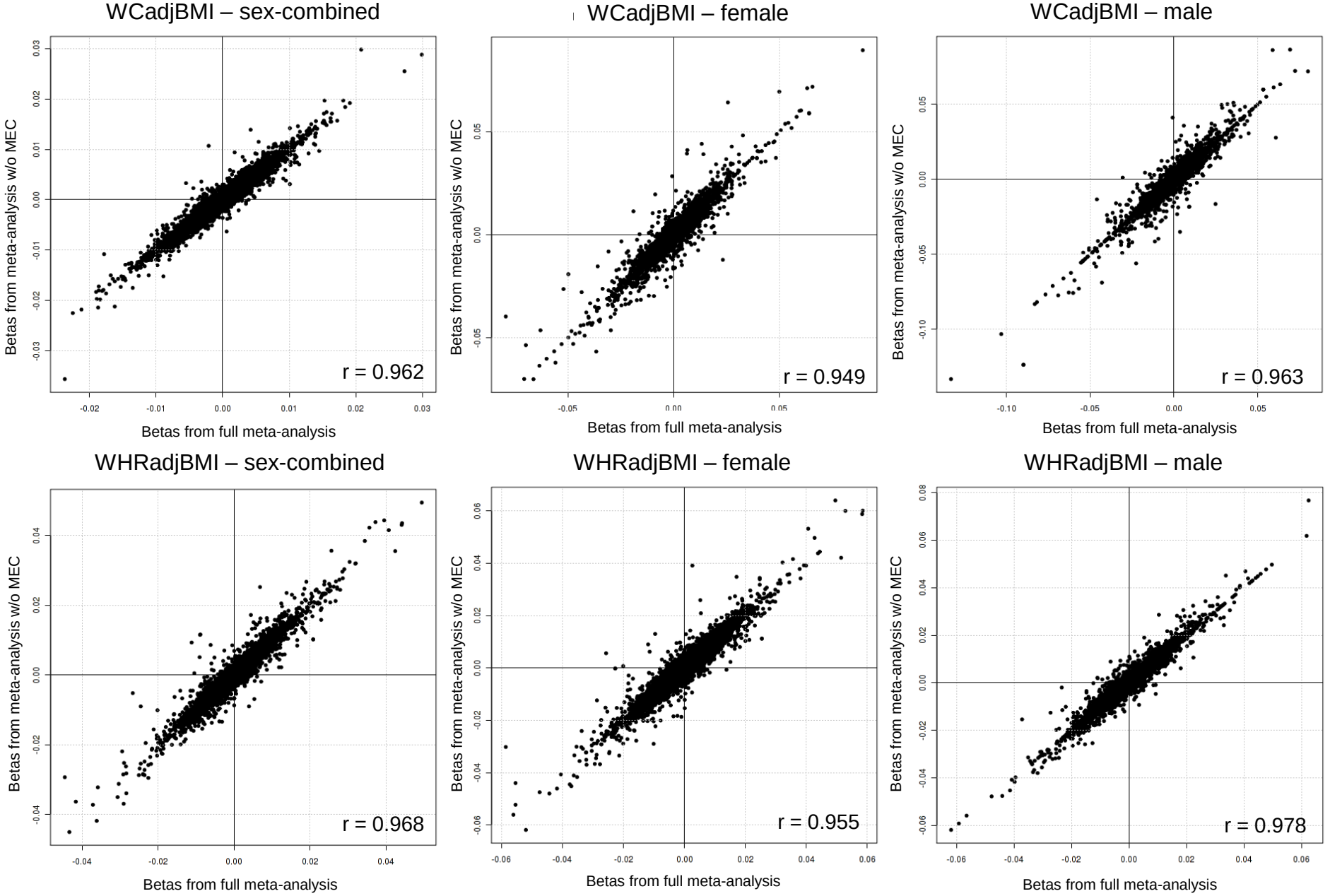




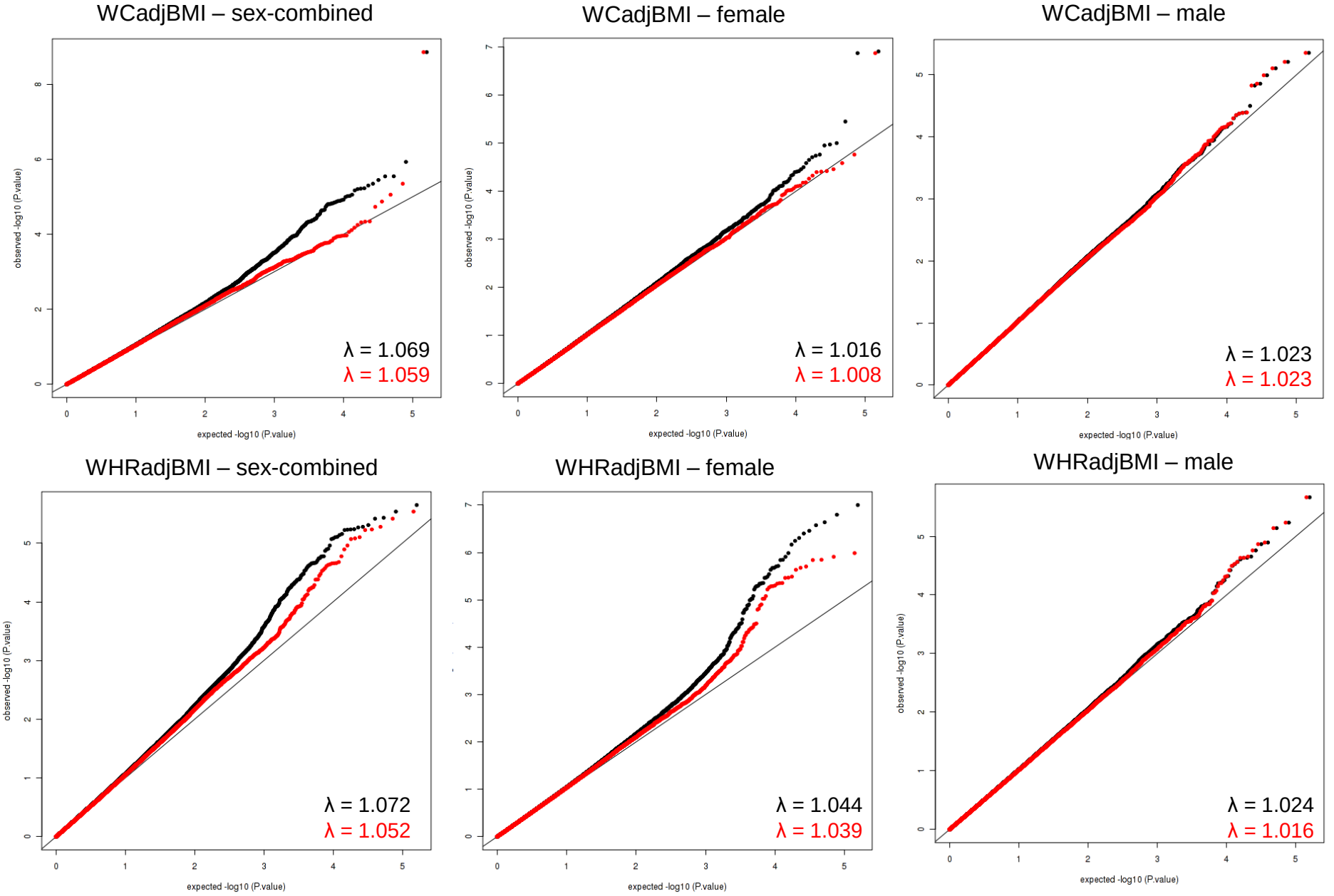




Supplementary Figure 1. Principal component (PC) analyses. Principal components from study participants (purple stars) were plotted and used 1000 Genome populations as references. Participants mostly cluster near the YRI reference population and largely overlap with the 1000 Genomes African American reference population (light blue), as expected for the admixed African American populations in our study. ASW: Americans of African Ancestry in SW USA (light blue); CEU: Utah Residents - CEPH with Northern and Western Ancestry (blue),; YRI: Yoruba in Ibadan, Nigeria (pink). Unfortunately, we did not collect raw data from our study collaborators (MESA, HyperGen, GenNet). Therefore, we asked our colleagues to adjust for PCs as part of the analysis plan, but did not ask for their PC plots.



Supplementary Figure 2. Sensitivity analysis of meta-analysis without the MEC study. The MEC study was the only study with self-reported/measured anthropometric values. To estimate whether MEC values unduly affect the meta-analysis spearman correlation (r) comparing the effect estimates (beta) of SNPs from the full meta-analysis against the effect estimate from the meta-analysis excluding the MEC study were calculated. High correlation (r > 0.95) indicate little undue influence from MEC and none of the top SNPs identified in the four significant WHR loci changed with the exclusion of MEC.



Supplementary Figure 3. QQ plots of all SNPs included in each of the six meta-analysis (black dots). Due to the custom design of the Metabochip consisting of majority SNPs previously identified as associated with cardiovascular and metabolic traits, we expect slightly inflated λ. Therefore, to remove some of the bias from the high content of cardiovascular associated SNPs, we also conducted QQ plots with the removal of previously known WHR or WC associated SNPs and recalculated the λ (red dots). In both instances of λ calculation, the resulting values were low (λ < 1.1) indicating sufficient genomic control.