Supplemental Material

Supplemental Figure 1.

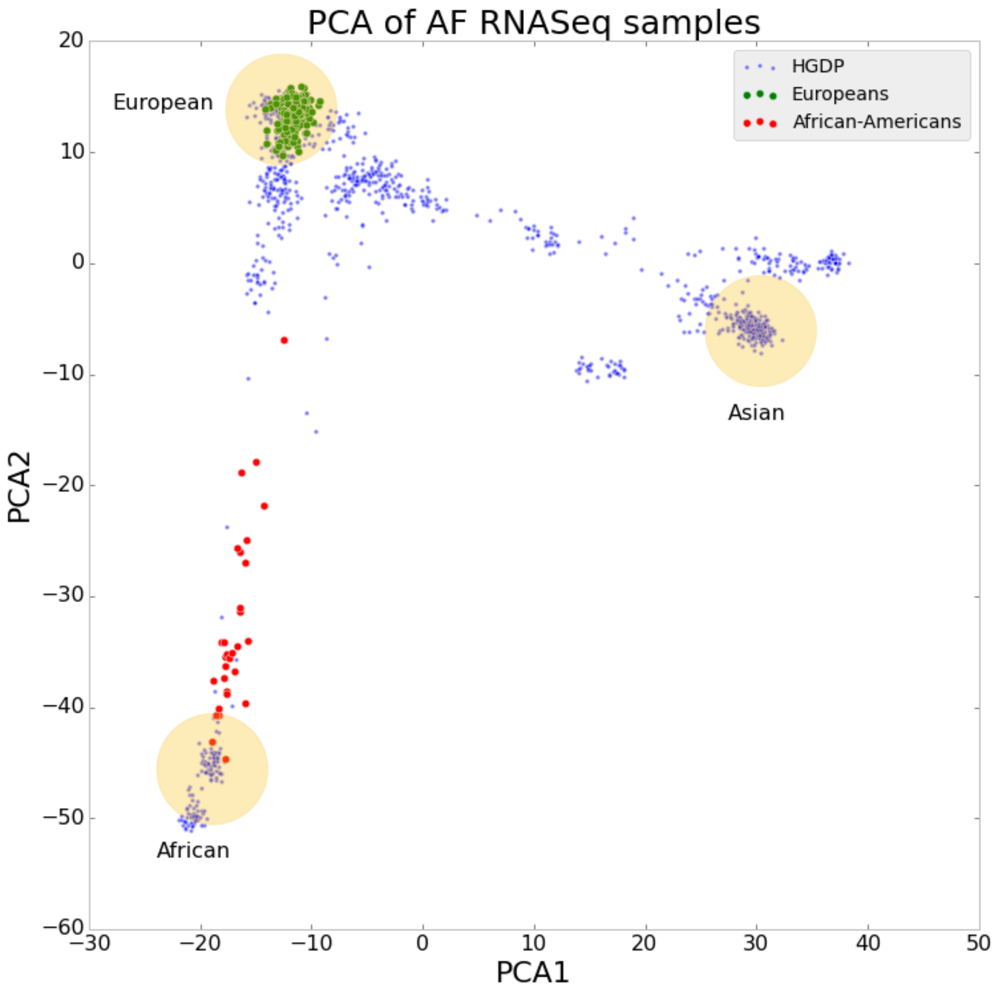

Figure S1. Genetic principal component analysis (PCA) of LA DNA samples compared with that of samples from the human genome diversity project (HGDP, small blue dots). 20,000 random SNPs from all autosomal chromosomes were used in the PCA calculation. Our samples clustered with European descent (green dots) and African or African-European admixture descent (red dots).

Supplemental Figure 2

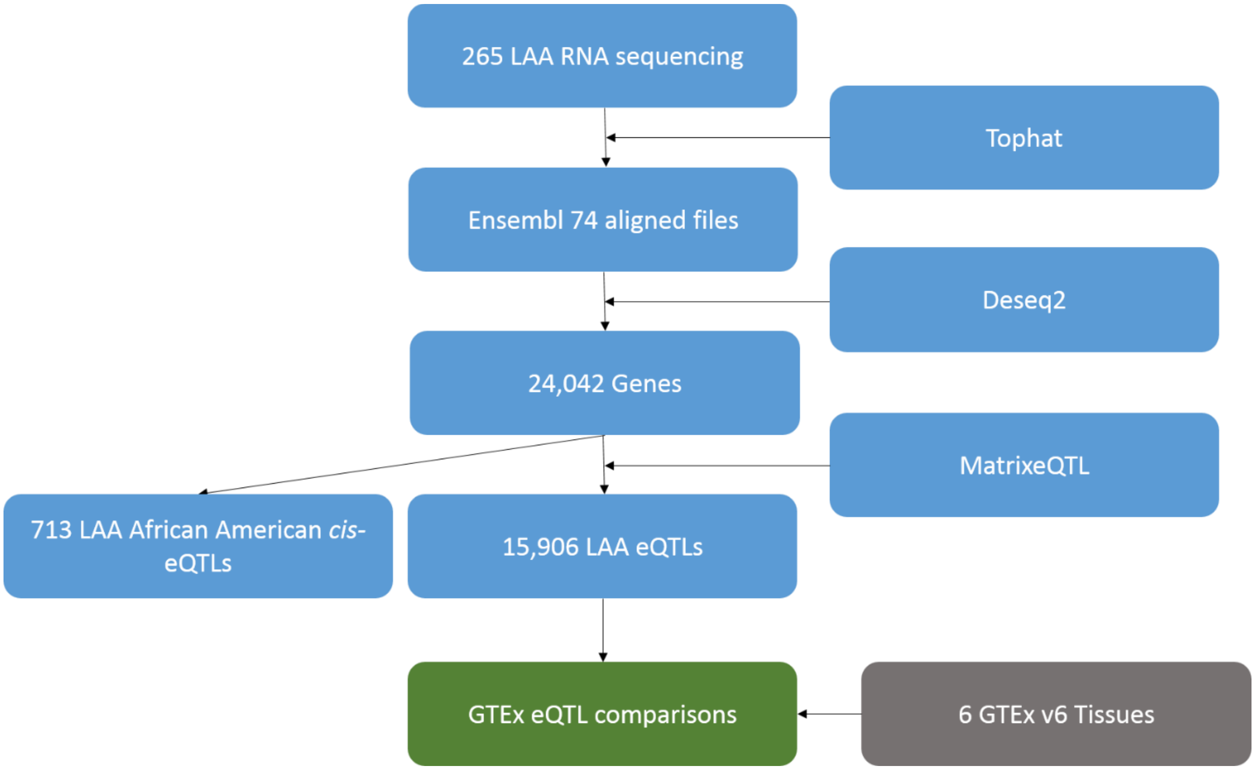

Figure S2. Diagram of LAA RNAseq and eQTL analysis.

Supplemental Figure 3.

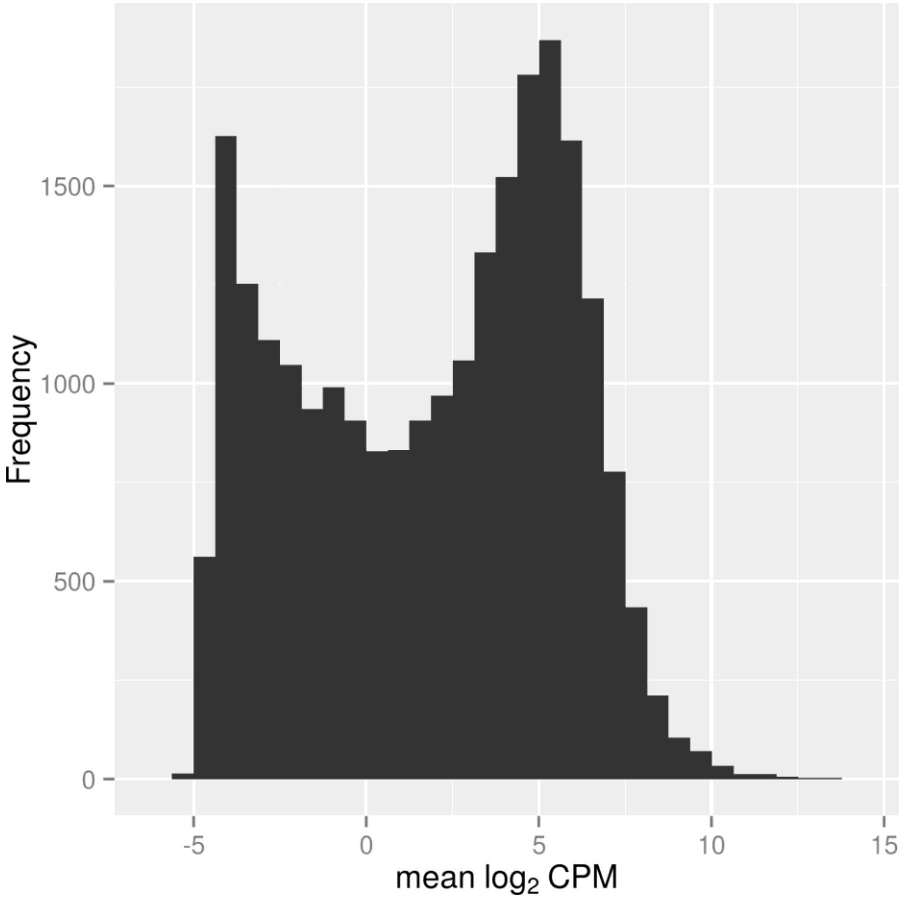

Figure S3. The distribution of the average log2 counts per million (CPM) of each gene across 24,042 expressed genes that met our minimum count threshold of 1000 variance stabilized counts summed from all 235 European-descent samples.

Supplemental Figure 4

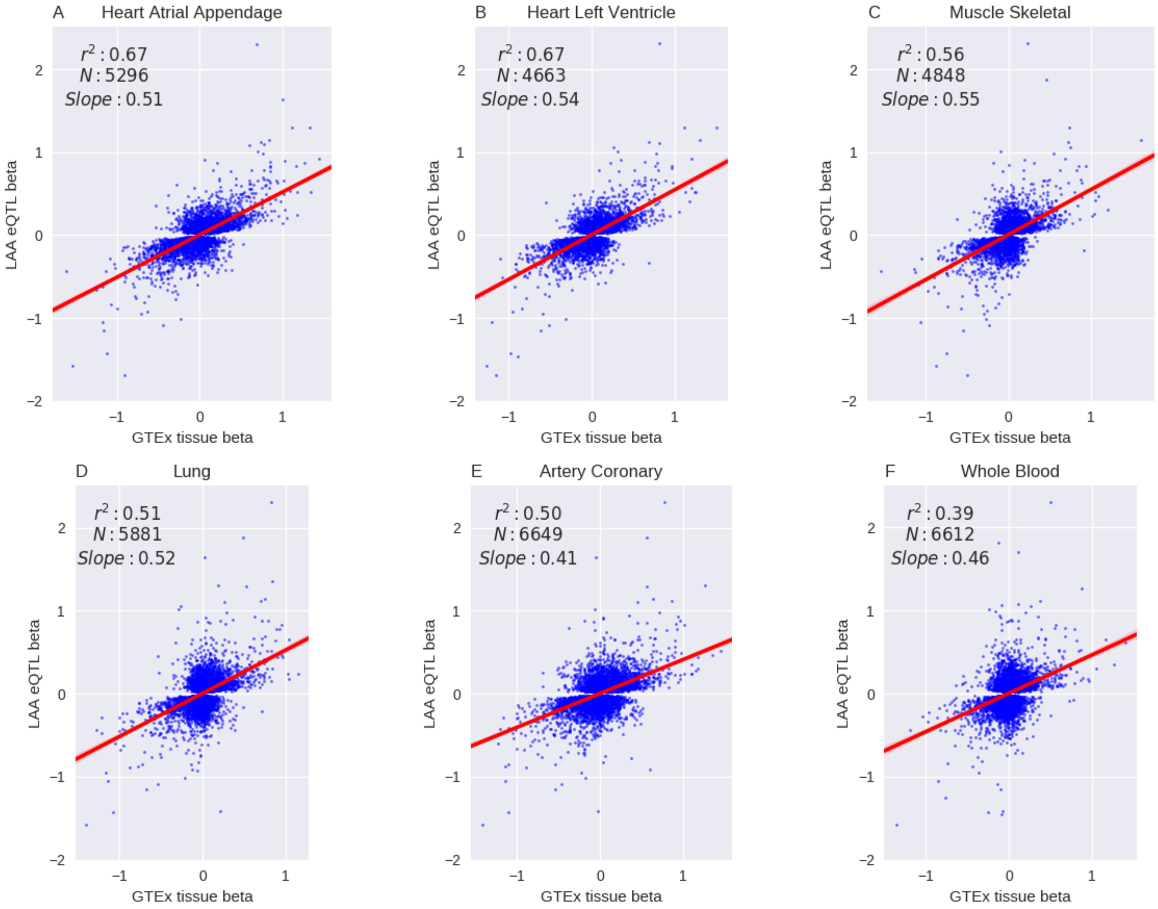

Figure S4. Conservation of the LA cis-eQTLs (SNP-gene pairs) effect size and direction on gene expression (beta coefficients) with cis-eQTL beta coefficients derived from the V6p analysis of the GTEx project for A) right atrial appendage, B) left ventricle, C) skeletal muscle, D) lung, E) coronary artery, and F) whole blood. The GTEx beta coefficient was defined using the top cis-eQTL SNP identified in our LAA study.

Supplemental Figure 5.

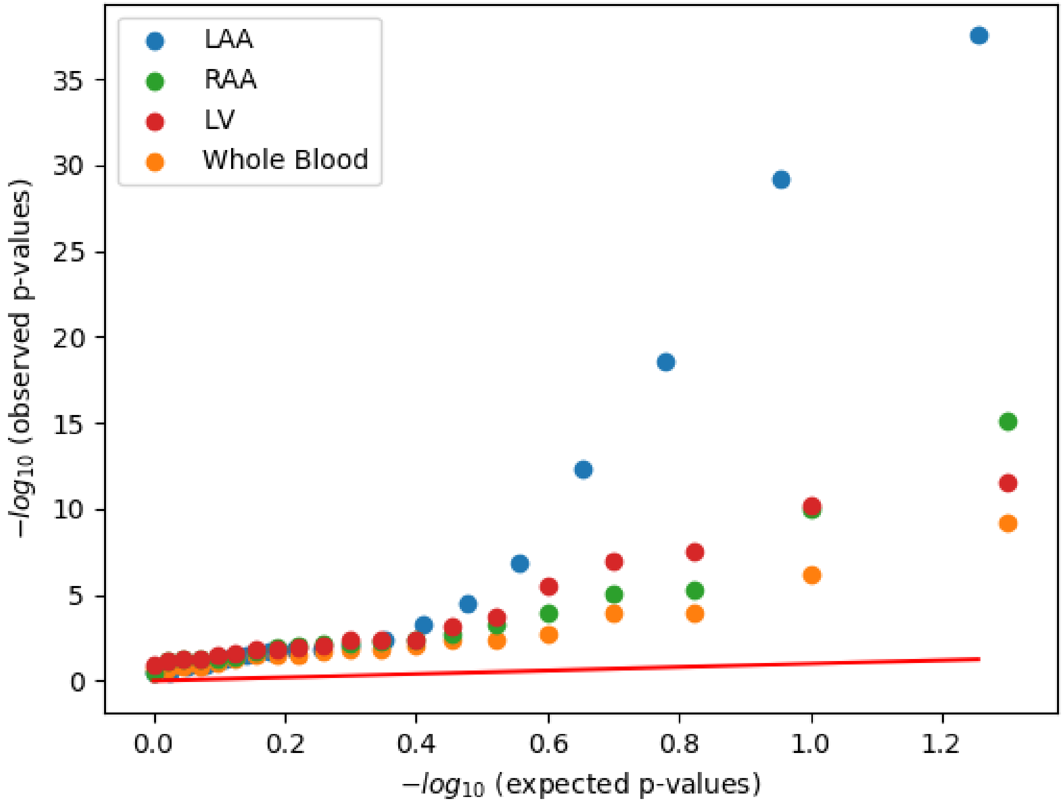

Figure S5: Q-Q plots showing eQTL p-values for the AF GWAS SNPs listed in Table 1 in the LAA samples (blue circles) compared to those observed in right atrial appendage (RAA, green circles), left ventricle (LV, red circles), and whole blood (orange circles) from GTEx. The red line shows the default expected eQTL p-values due to chance.

Supplemental Figure 6

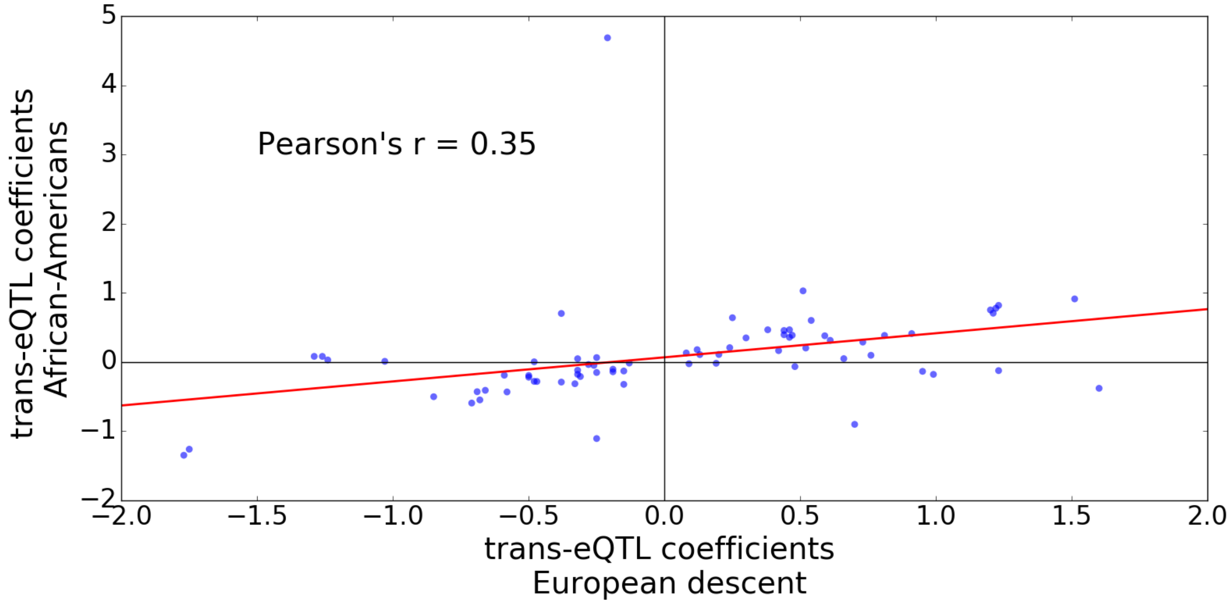

Figure S6. Conservation of trans-eQTL beta coefficients between the European and African decent subjects (r=0.35, p=1.91E-3). Full data for these trans-eQTLs is supplied in Supplemental Table 4.

Supplemental Figure 7

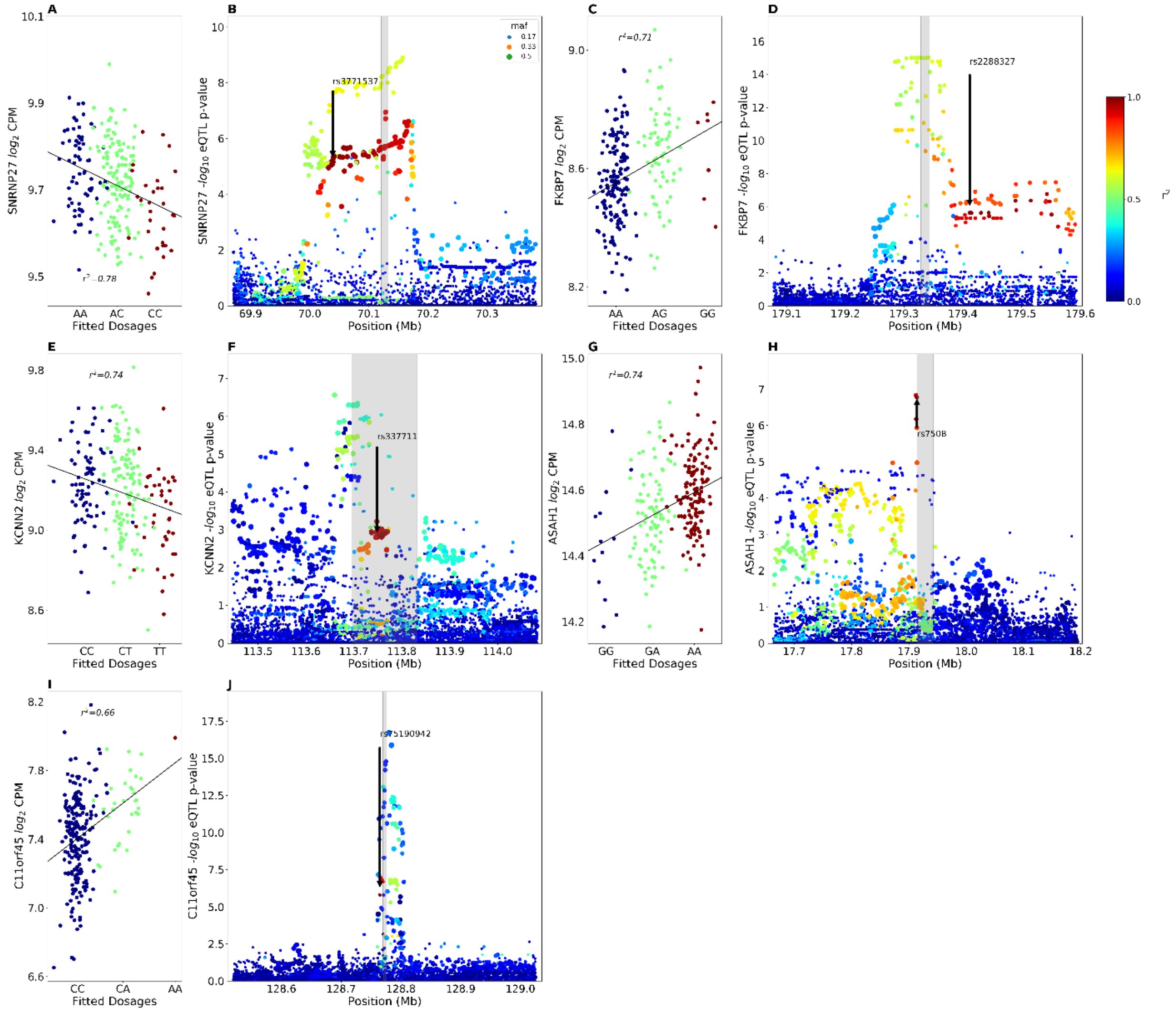

Figure S7. Top *cis*-eQTLs for additional AF GWAS SNPs. (A, C, E, G, I) Partial regression plot showing the effect of the AF GWAS SNPs rs3771537, rs2288327, rs337711, rs7508, rs75190942 on the LA expression of the *SNRNP27, FKBP7, KCNN2, ASAH1,* and *C11orf45* genes in European descent subjects after adjusting for genetic MDS, transcription SVAs, and gender. Blue dots are subjects homozygous for the reference allele (GRCh37 build), green dots are heterozygotes, and red dots are homozygous for the variant allele. (B, D, F, H, J) eQTL p-values and LD relationship (color scale) with the GWAS SNP (arrow) in the 0.5 Mb region around the TSS of the *SNRNP27, FKBP7, KCNN2, ASAH1,* and *C11orf45* genes in European subjects.

Supplemental Tables 1-6 are presented as separate Excel files.

Supplemental Table 1 – Significant left atrial cis-eQTLs in European descent (euro) subjects and their associated significance in African American (aa) subjects.

Supplemental Table 2 – Significant left atrial cis-eQTLs in African American (aa) subjects and their associated significance in European descent (euro) subjects.

Supplemental Table 3 – LAA unique eQTLs

Supplemental Table 4 – Trans eQTLs

Supplemental Table 5 – cis-eQTLs at AF GWAS loci

Supplemental Table 6 – cis-AEI SNP evaluated as cis-eQTL and compared to top cis-eQTL SNP.