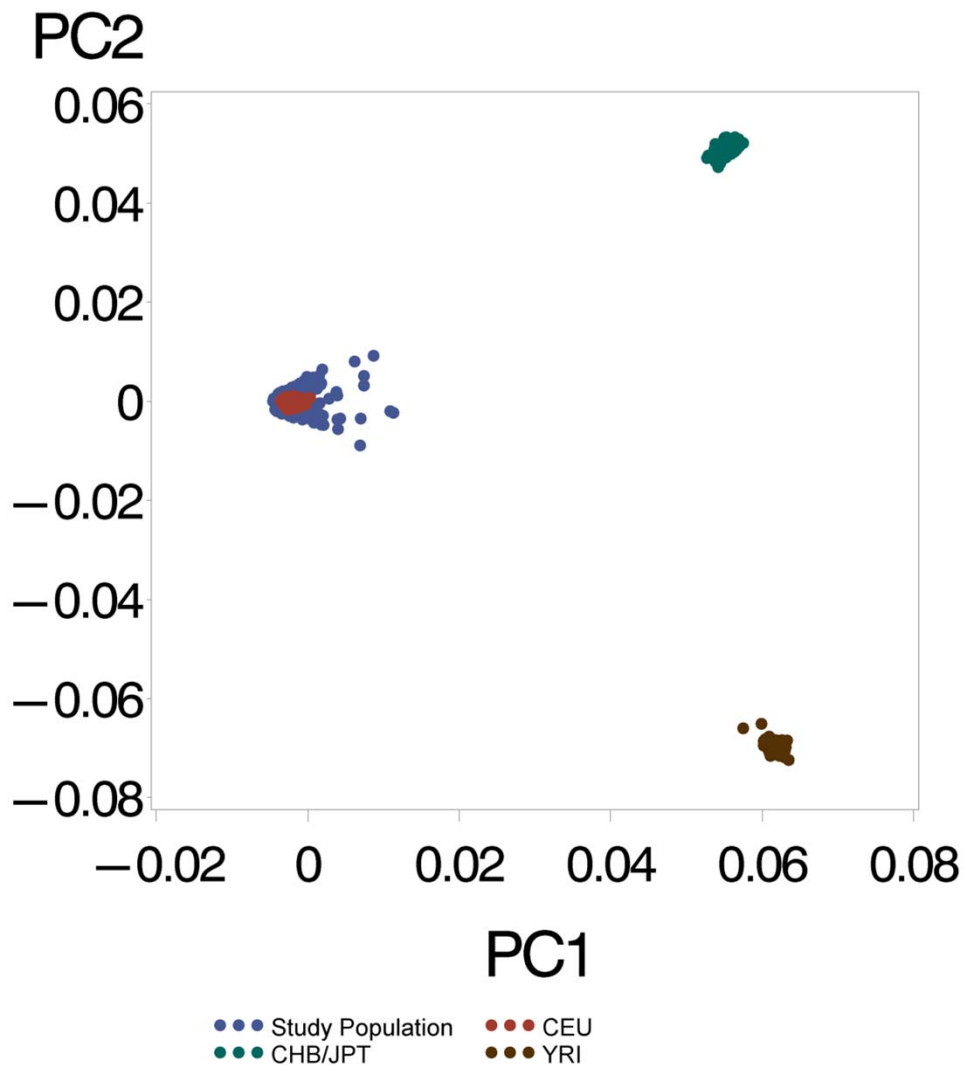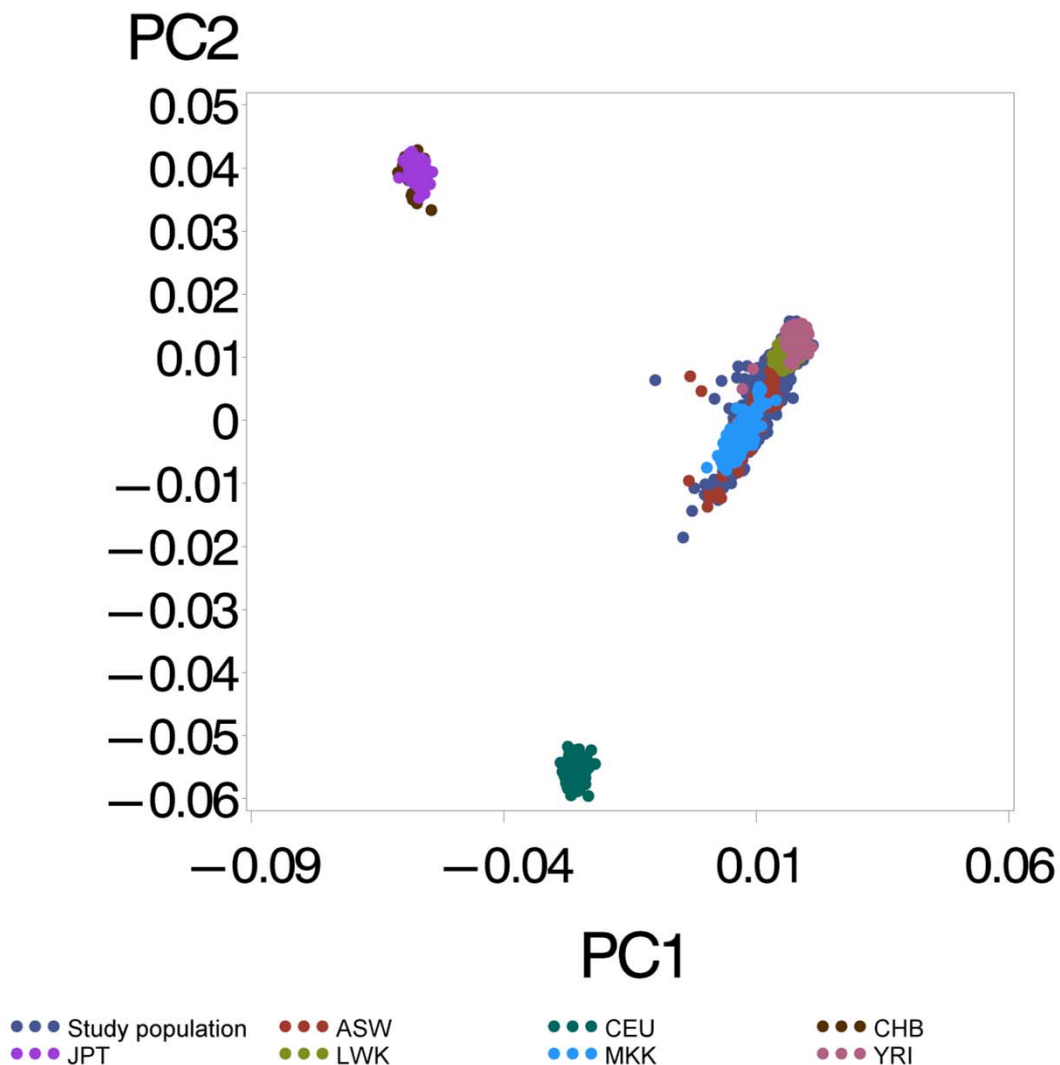# Supplemental figure 1

Supplemental Figure 1. Scatter plot for a principal component analysis comparing the STRUCTURE-defined EA study subjects with HAPMAP subjects. Principal components were fit for a data set that include eMERGE EA study population and the CEU, YRI and CHB/JPT HAPMAP populations. The graph shows the first 2 principal components. The eMERGE EAs are clustered tightly around the CEU population.
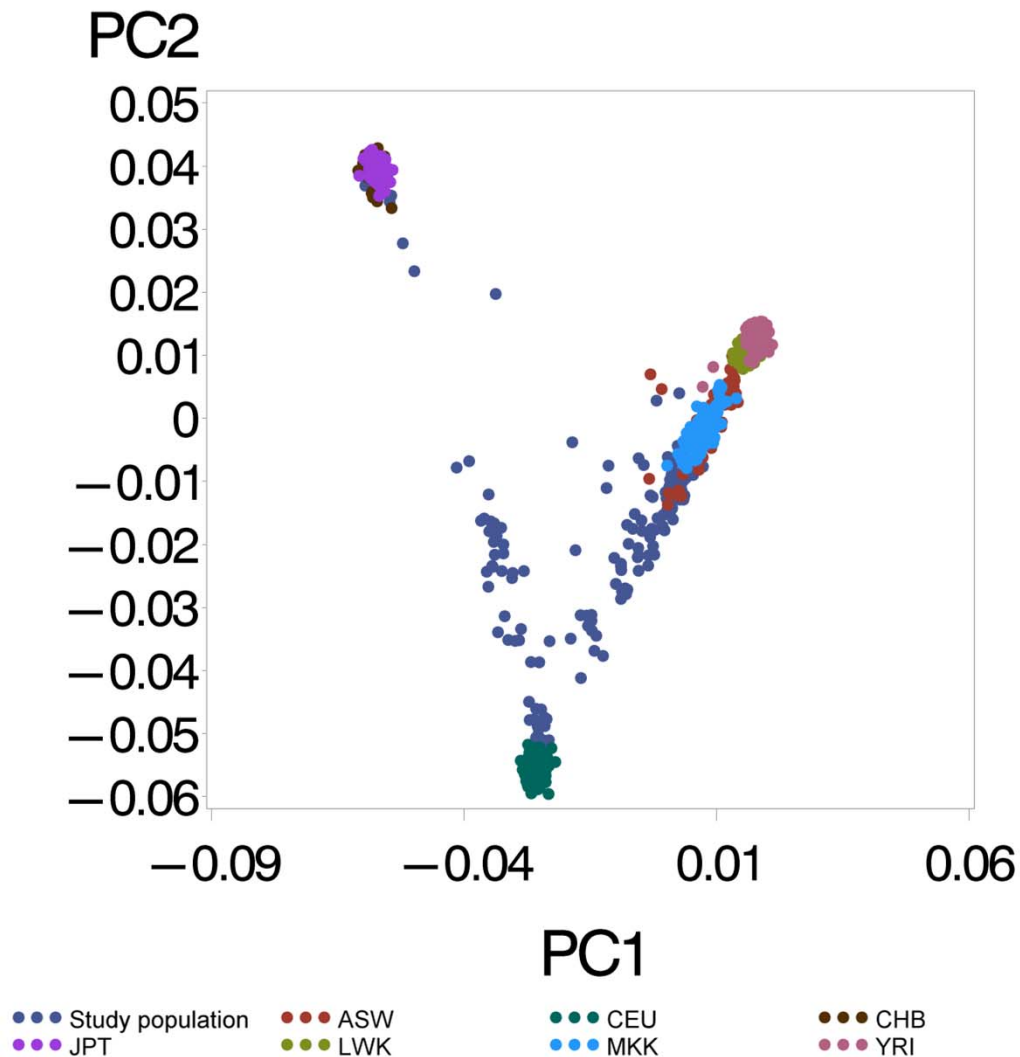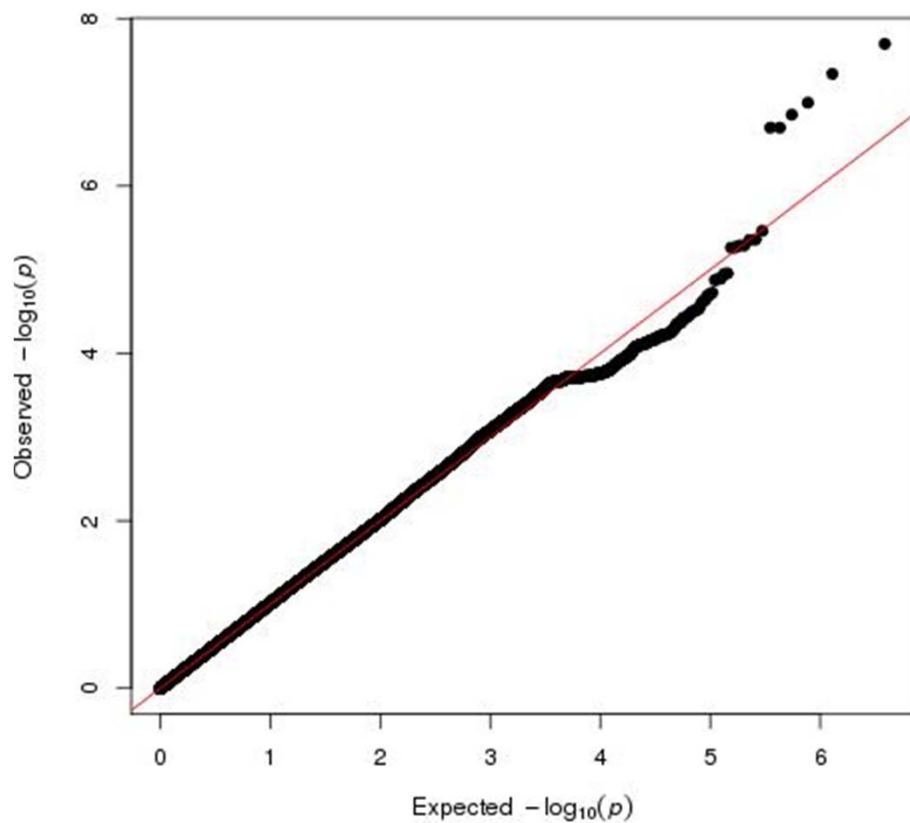
Supplemental figure 2

Supplemental Figure 2. Scatter plot for a principal component analysis comparing the STRUCTURE-defined AA study subjects with HAPMAP subjects. Principal components were fit for a data set that include eMERGE AA study population and the ASW, LWK, MKK, CEU, YRI and CHB/JPT HAPMAP populations. The graph shows the first 2 principal components. The eMERGE AAs are clustered around the ASW, LWK, MKK, and YRI populations.
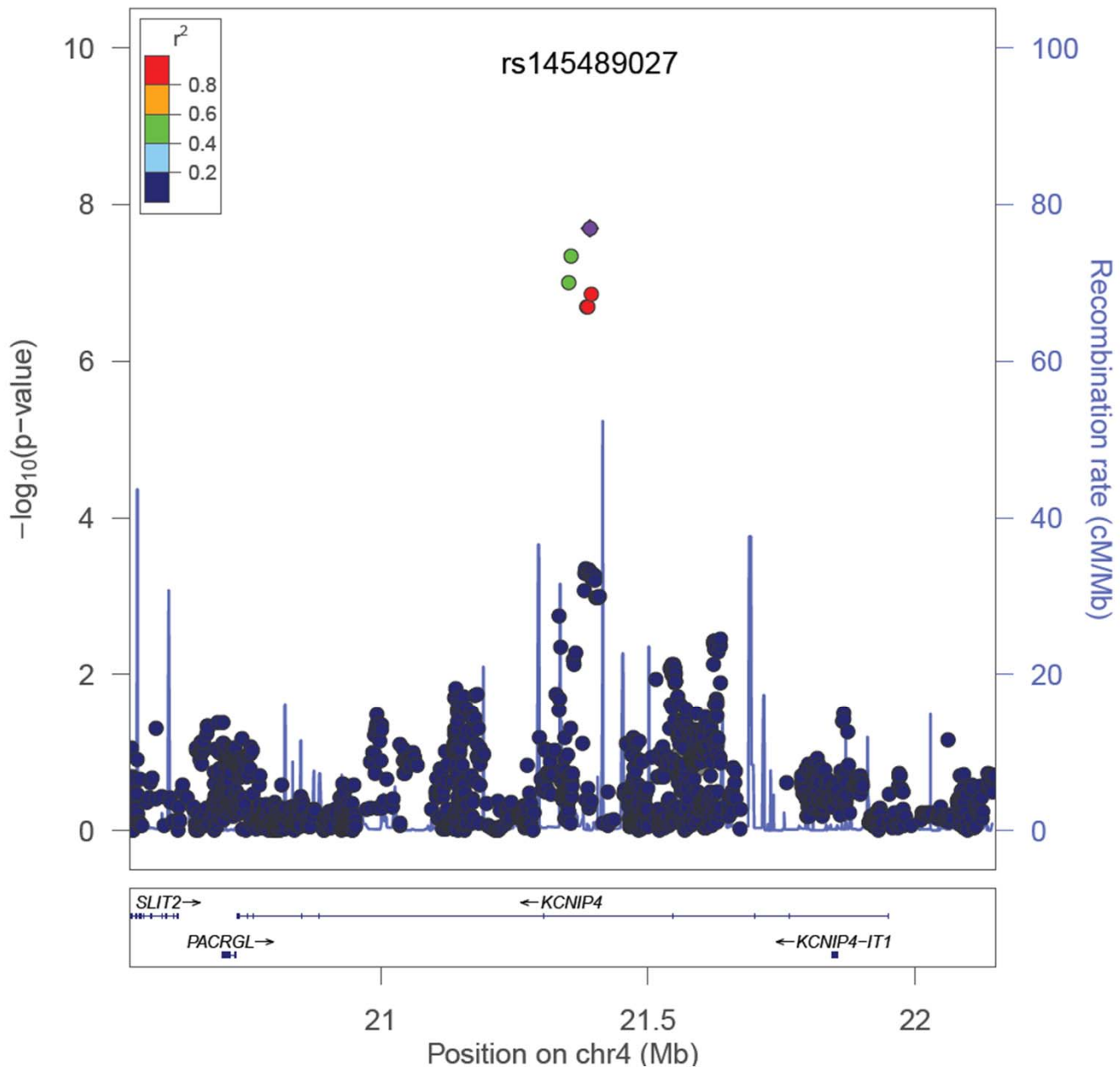
Supplemental figure 3

Supplemental Figure 3. Scatter plot for a principal component analysis comparing the study subjects who did not fall into the EA or AA STRUCTURE-defined clusters with HAPMAP subjects. Principal components were fit for a data set that included the study subjects and the ASW, LWK, MKK, CEU, YRI and CHB/JPT HAPMAP populations. The graph shows the first 2 principal components.
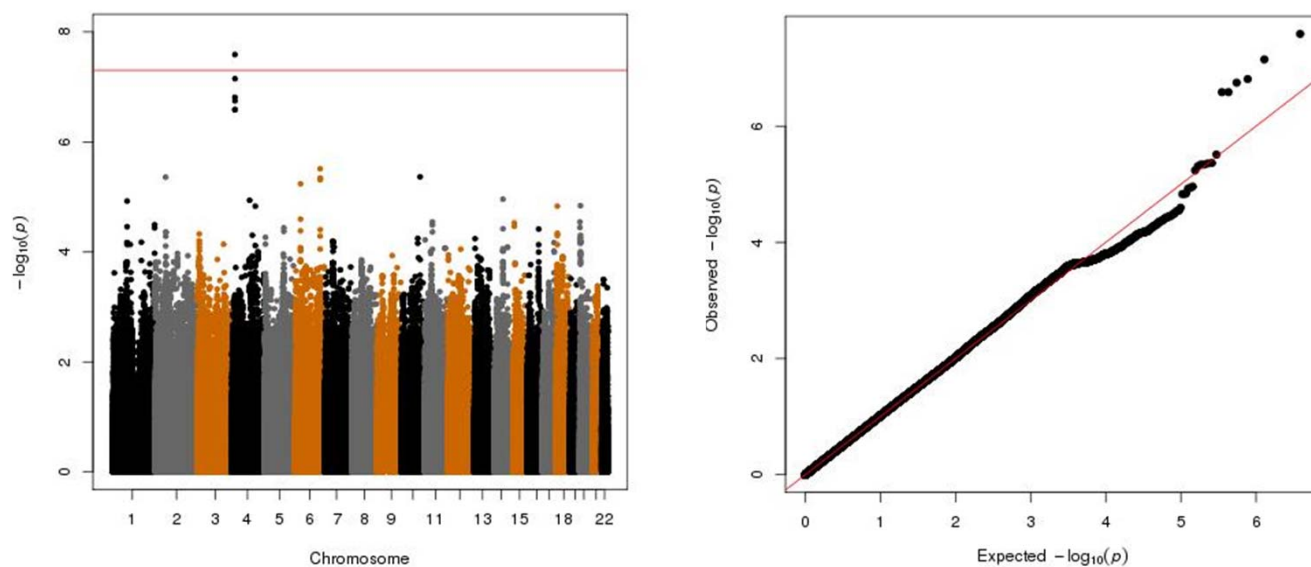
Supplemental figure 4

Supplemental Figure 4. A QQ plot for SNP associations from a GWAS of ACE-inhibitor induced cough using an additive model adjusted for 10 PCs, birth year and sex.
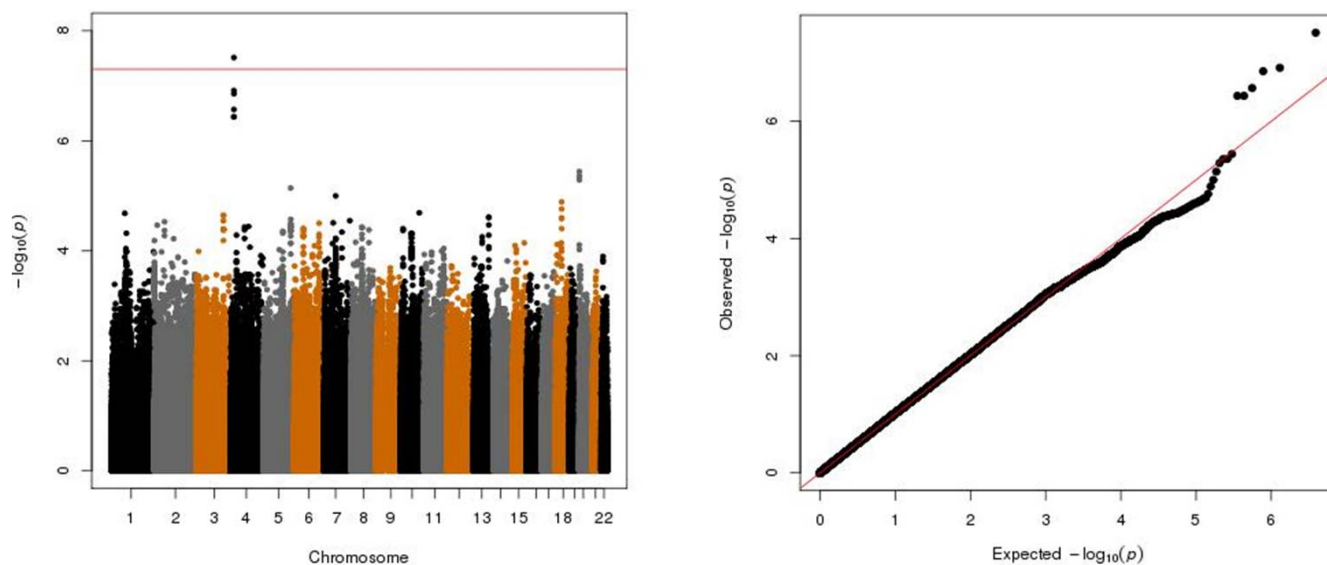
Supplemental figure 5

Supplemental Figure 5. LocusZoom plot of most strongly associated SNPs from GWAS located in the region of *KCNIP4* (chr4:20330238−22350374), centered around SNP rs145489027 (shown in purple). Linkage disequilibrium (based on r^2 values) with respect to rs145489027 are based on a 1000 Genomes African reference population. Imputed SNPs are denoted by squares and genotyped SNPs by circles.

Supplemental figure 6

Supplemental Figure 6. Manhattan and QQ plots for SNP associations from a GWAS of ACE-inhibitor induced cough using an additive model adjusted for 10 PCs, birth year, sex, smoking status and cough risk factors.

Supplemental figure 7

Supplemental Figure 7. Manhattan and QQ plots for SNP associations from a GWAS of ACE-inhibitor induced cough using an additive model that excludes subjects with lung disease and is adjusted for 10 PCs, birth year, sex, smoking status and cough risk factors.