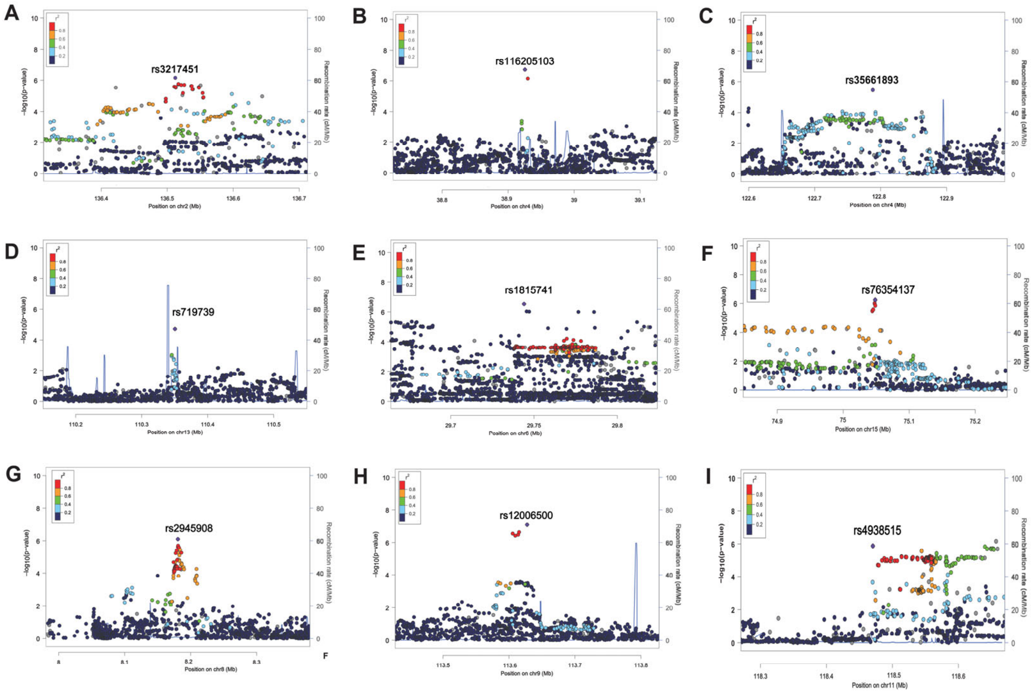
Supplementary Information

Qin N, Li Y, et al. Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma.

Supplementary Figures

Supplementary Figure 1. Regional plots for 9 risk loci with meta *P* values < 1×10^{-6}.

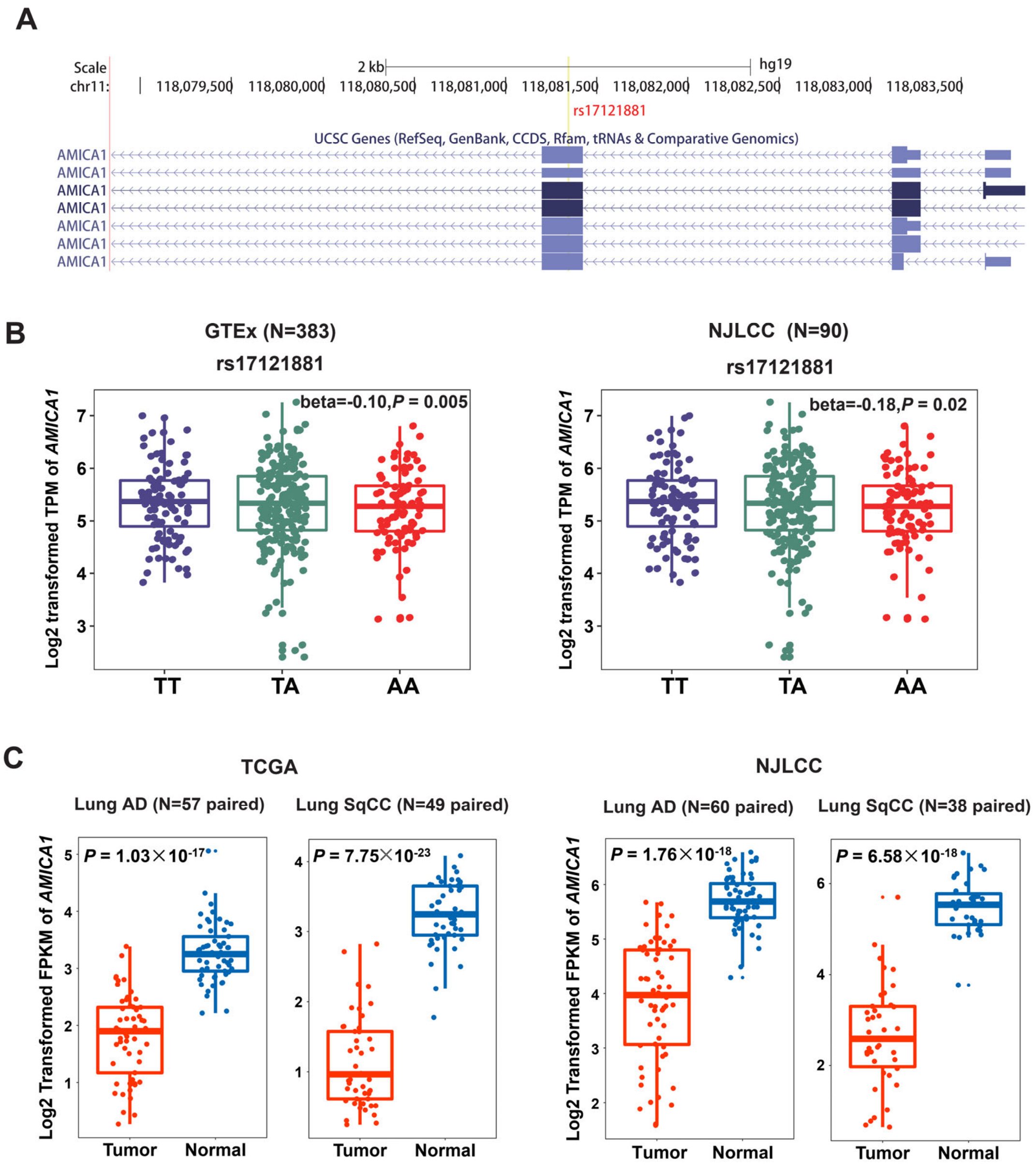


Supplementary Figure 2. Detailed functional annotation result for 11q23.3.

A. Genomic region of *AMICA1* (rs17121881) in 11q23.3.

B. eQTL analysis of rs17121881 and *AMICA1* expression in GTEx and NJLCC normal lung tissues.

C. Differential expression analysis of *AMICA1* in TCGA and NJLCC lung AD and SqCC tumor/adjacent pairs.

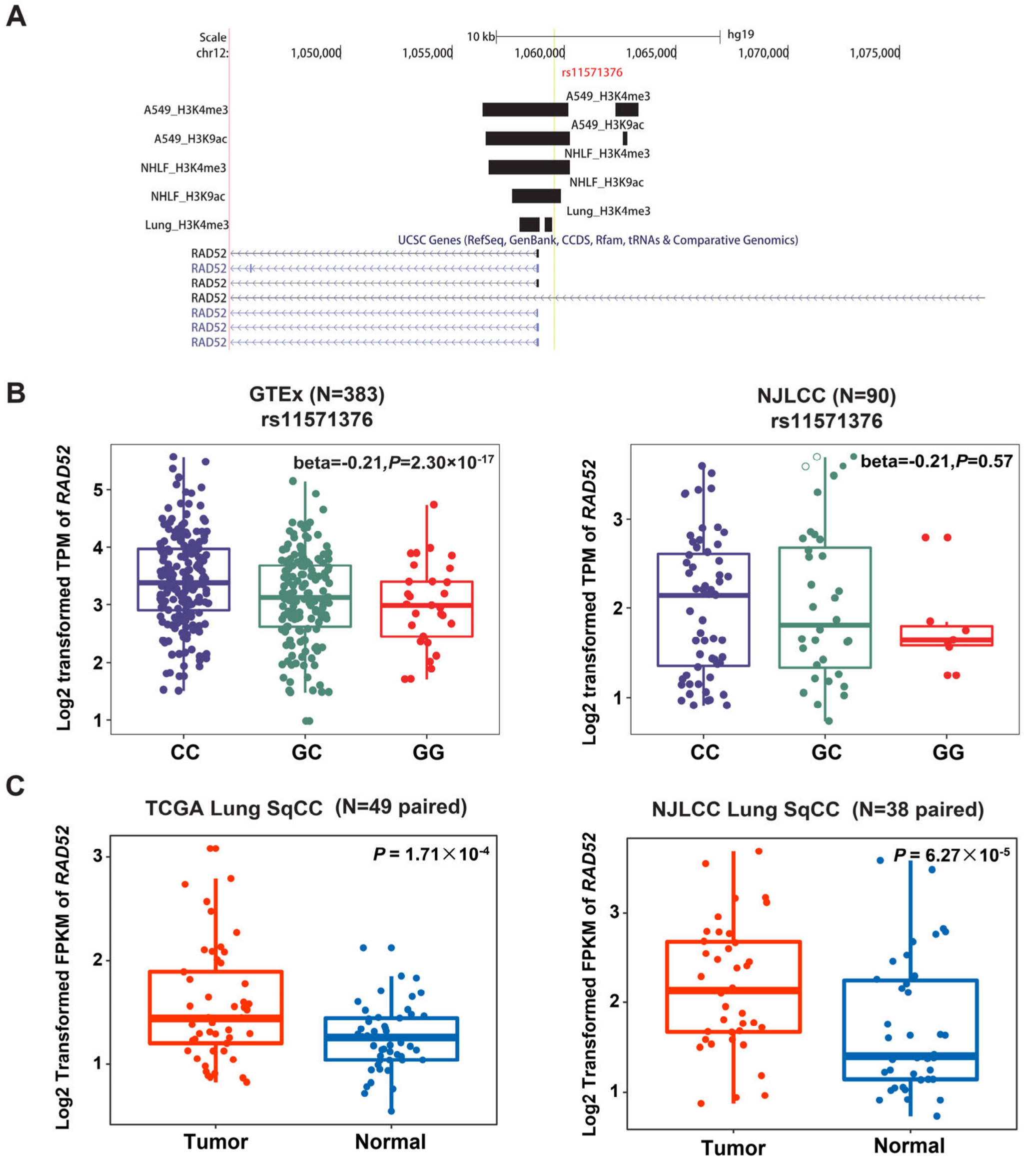


Supplementary Figure 3. Detailed functional annotation result for 12p13.33.

A. Genomic region of *RAD52* (rs11571376) in 12p13.33.

B. eQTL analysis of rs11571376 and *RAD52* expression in GTEx and NJLCC normal lung tissues.

C. Differential expression analysis of *RAD52* in TCGA and NJLCC lung SqCC tumor/adjacent pairs.



Supplementary Figure 4. Detailed functional annotation result for 20q13.3.

A. Genomic region of *LIME1* (rs6122147) in 20q13.3.

B. eQTL analysis of rs6122147 and *LIME1* expression in GTEx and NJLCC normal lung tissues.