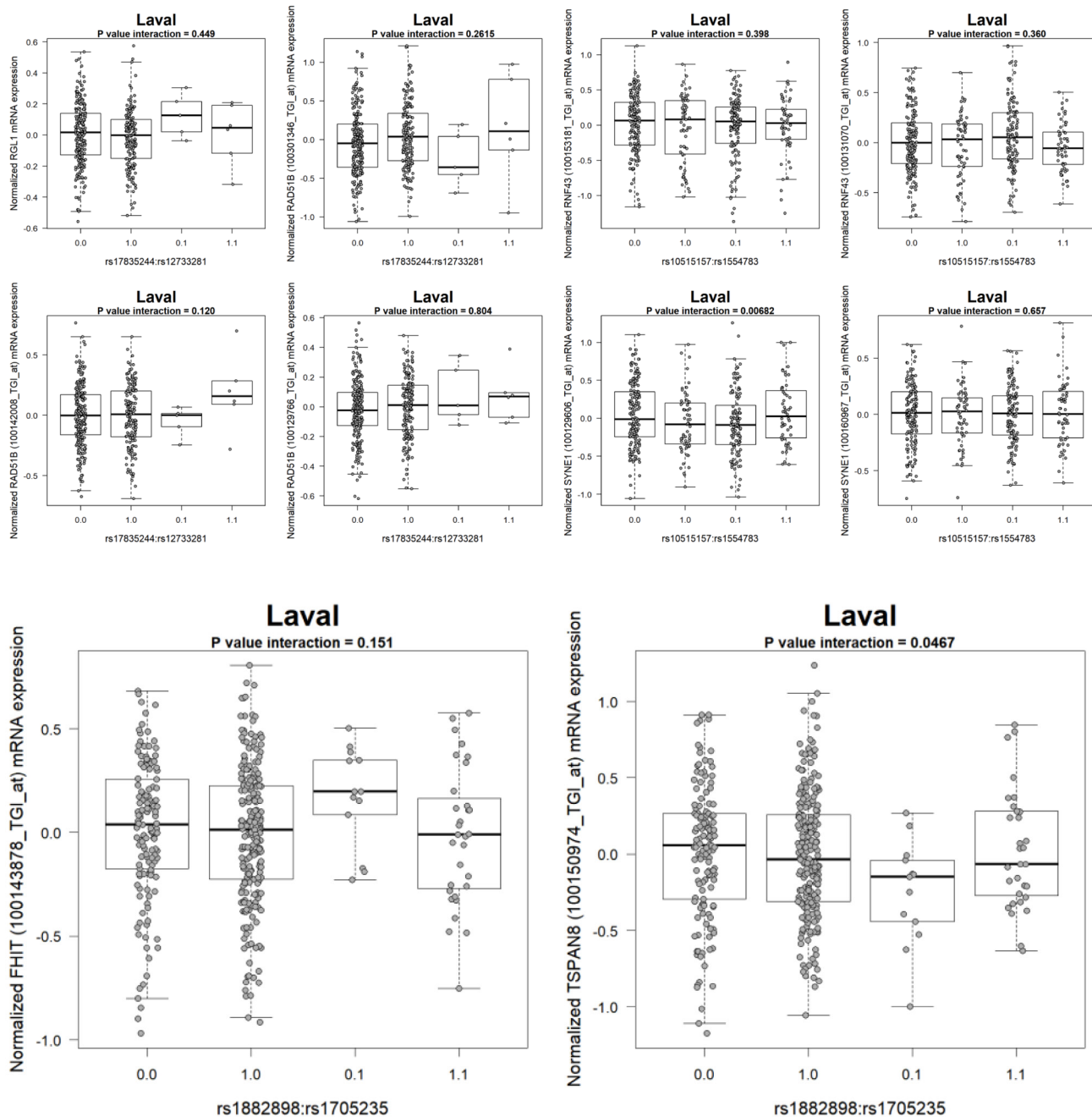
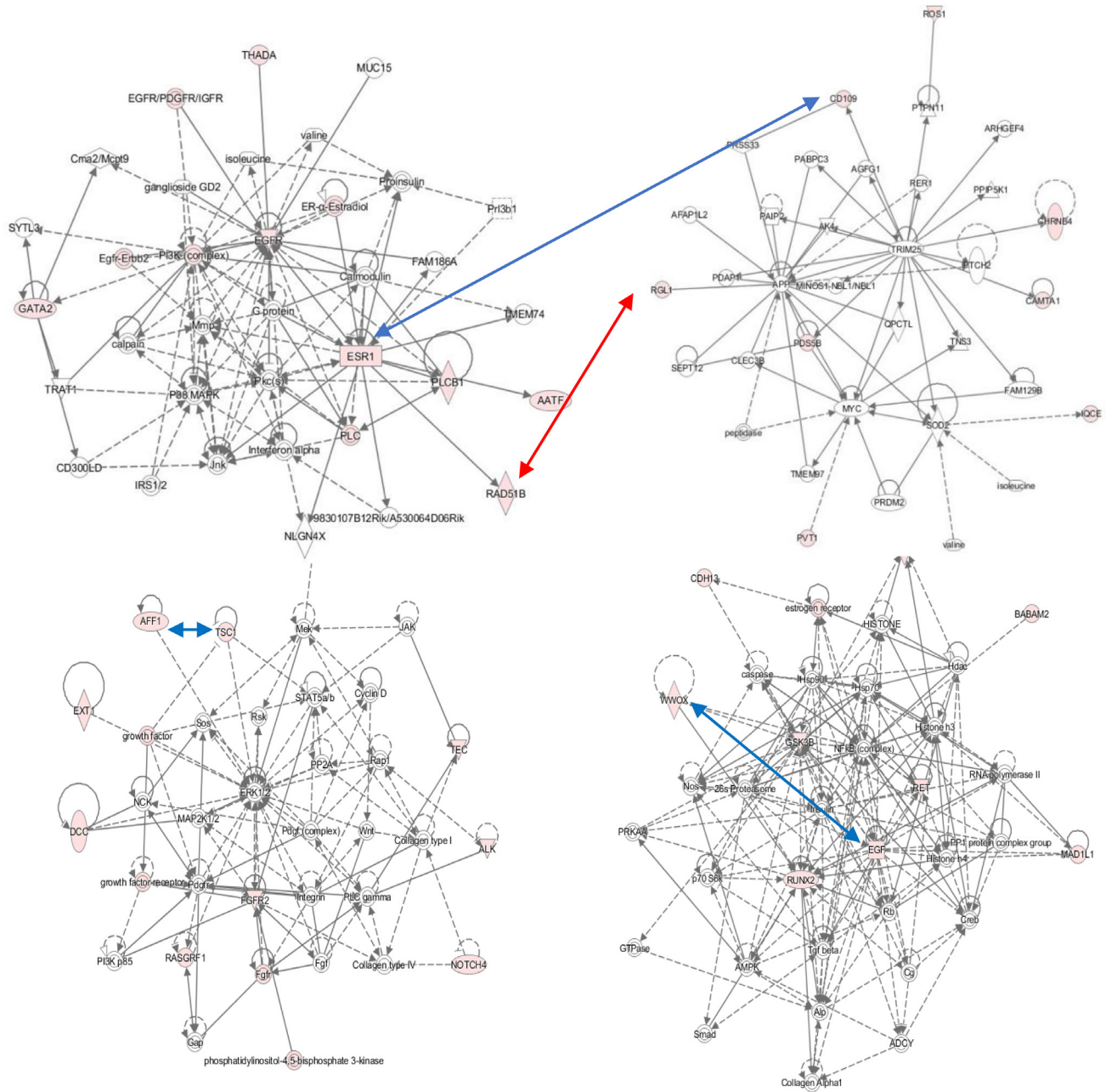


# Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development

## SUPPLEMENTARY MATERIALS



**Supplementary Figure 1: Analysis of genetic interaction effect on gene expression in human lung tissues.** Probe sets and SNPs implicated in the identified genetic interactions for lung cancer risk were selected including *RGL1:RAD51B* (S2-1), *RNF43:SYNE1* (S2-2), and *FHIT:TSPAN8* (S2-3). The interaction effects of SNP pairs on gene expression levels were evaluated using linear models. The evaluated genes and selected probes were labeled at Y-axes. The boxplots of gene expression level were plotted for each joint genotype group to display the genetic interaction effect on gene expression. Genotypes were coded in a dominant mode, i.e. 0 or 1 for absence or presence of the minor allele, respectively.



**Supplementary Figure 2: Top gene networks created by IPA program for ALL lung cancer cohort.**

**Supplementary Table 1: Number of SNP pairs with different p value cutoff in Z-score test at discovery stage**

| Study | $1 \times 10^{-7}$ | $1 \times 10^{-6}$ | $1 \times 10^{-5}$ | $1 \times 10^{-4}$ |
|-------|--------------------|--------------------|--------------------|--------------------|
| ALL   | 102                | 734                | 7113               | 70145              |
| NSCLC | 87                 | 717                | 7137               | 69089              |
| ADE   | 138                | 971                | 7459               | 70170              |
| SQC   | 161                | 1118               | 7860               | 69089              |