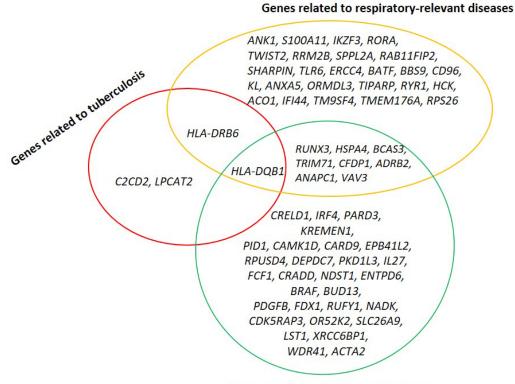
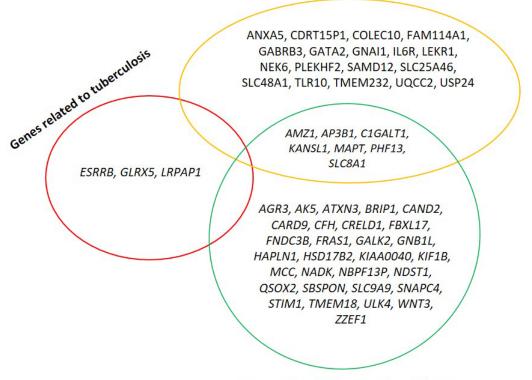
## SUPPLEMENTARY FIGURES



Genes related to lung-relevant diseases

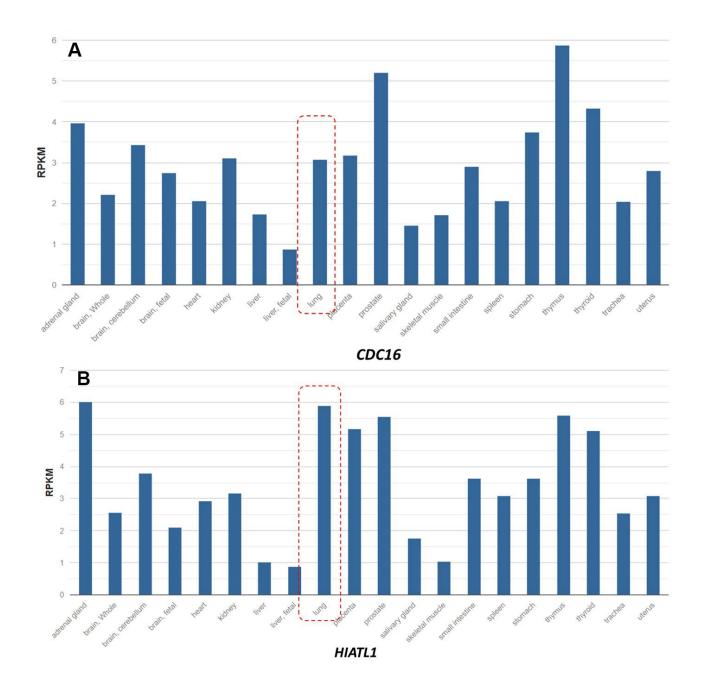
Supplementary Figure 1. Previous studies provide supportive evidence of these Sherlock-identified genes in the discovery stage.

## Genes related to respiratory-relevant diseases

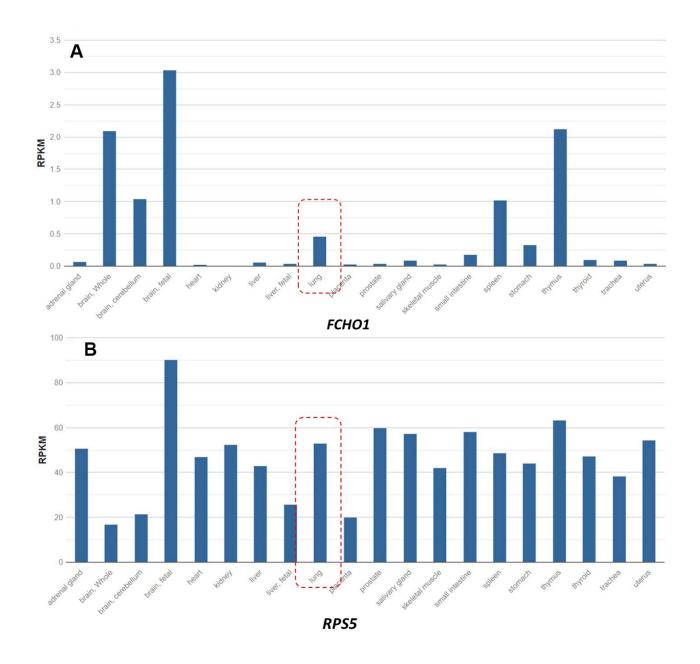


Genes related to lung-relevant diseases

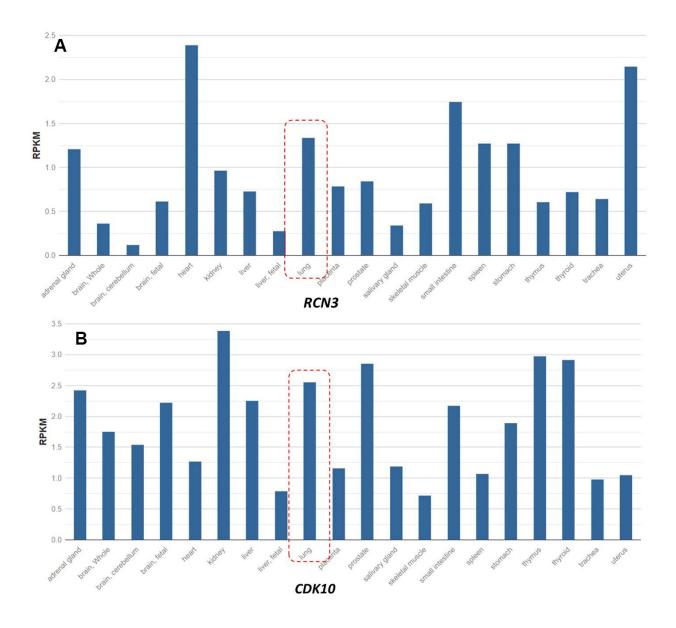
Supplementary Figure 2. Previous studies provide supportive evidence of these Sherlock-identified genes in the replication stage (based on both Dataset #4 and #5).



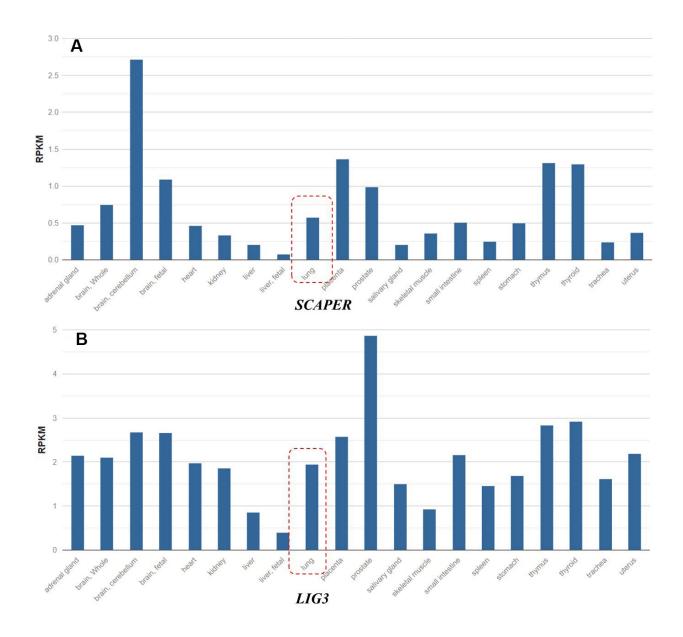
**Supplementary Figure 3. Expression abundance of** *CDC16* **and** *HIATL1* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



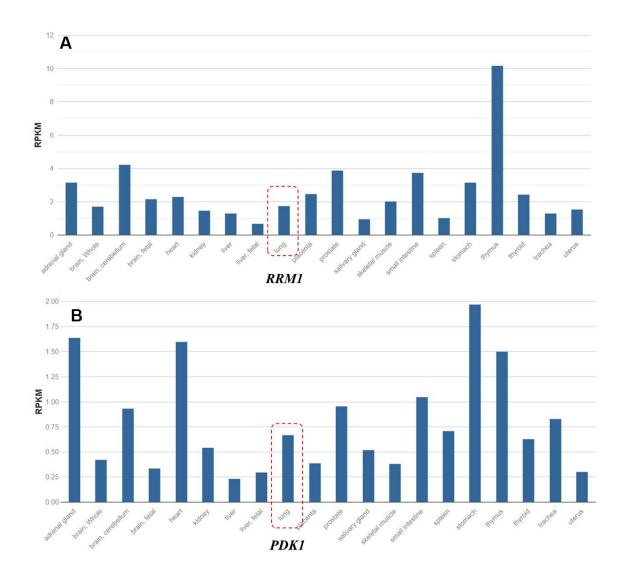
**Supplementary Figure 4. Expression abundance of FCHO1 and RPS5 based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



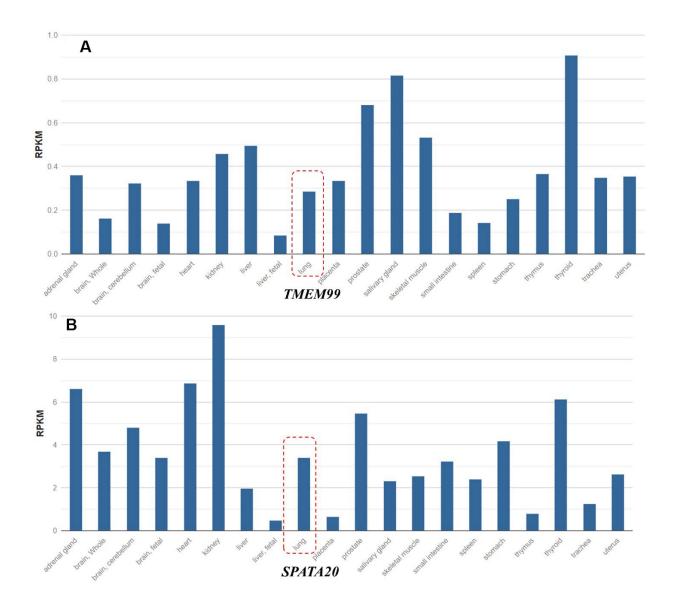
**Supplementary Figure 5. Expression abundance of** *RCN3* **and** *CDK10* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



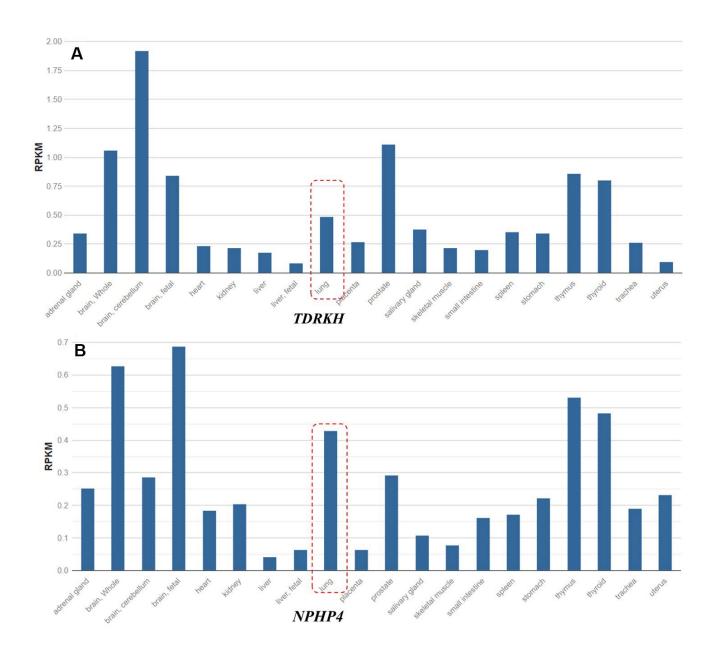
**Supplementary Figure 6. Expression abundance of** *SCAPER* **and** *LIG3* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



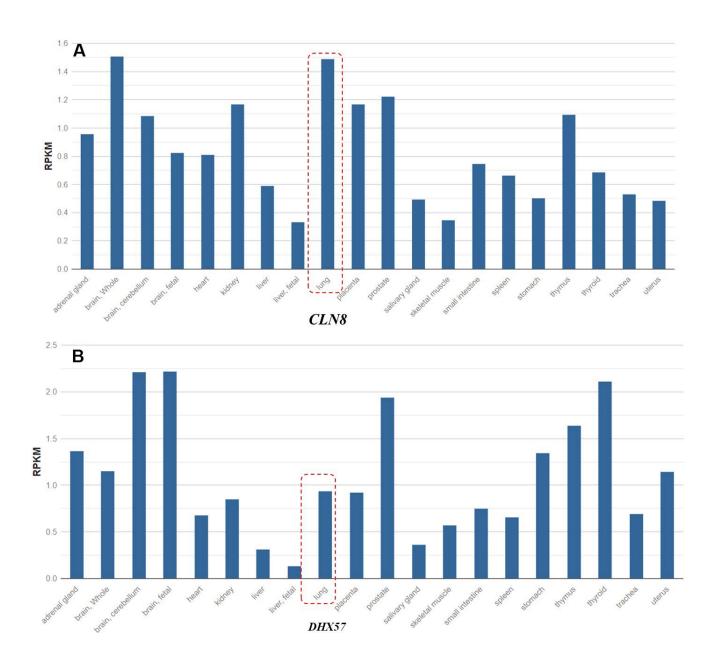
**Supplementary Figure 7. Expression abundance of** *RRM1* **and** *PDK1* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



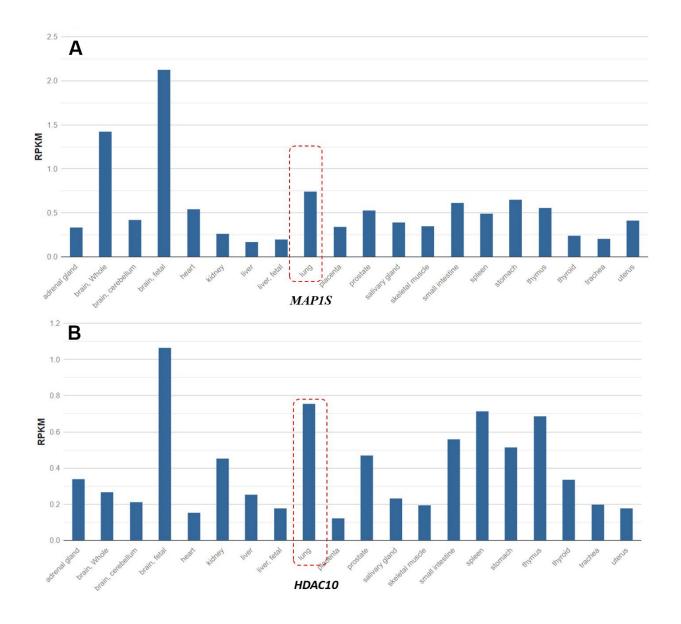
**Supplementary Figure 8. Expression abundance of** *TMEM99* **and** *SPATA20* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



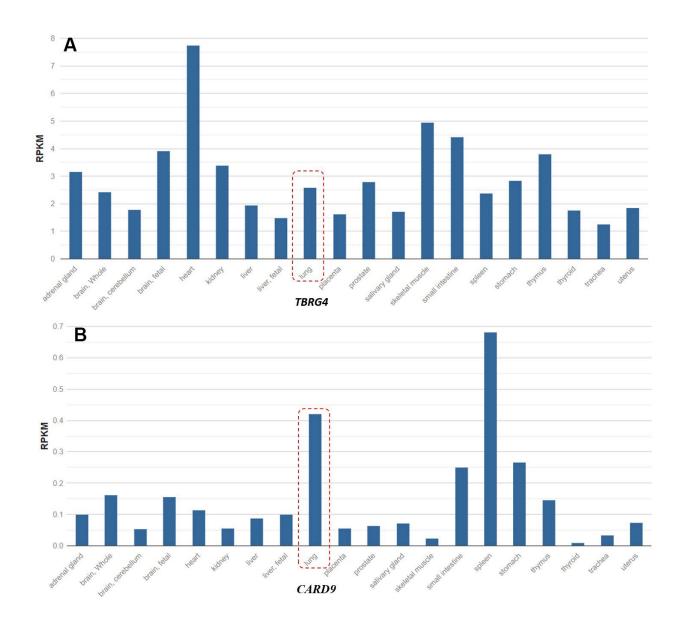
**Supplementary Figure 9. Expression abundance of** *TDRKH* **and** *NPHP4* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



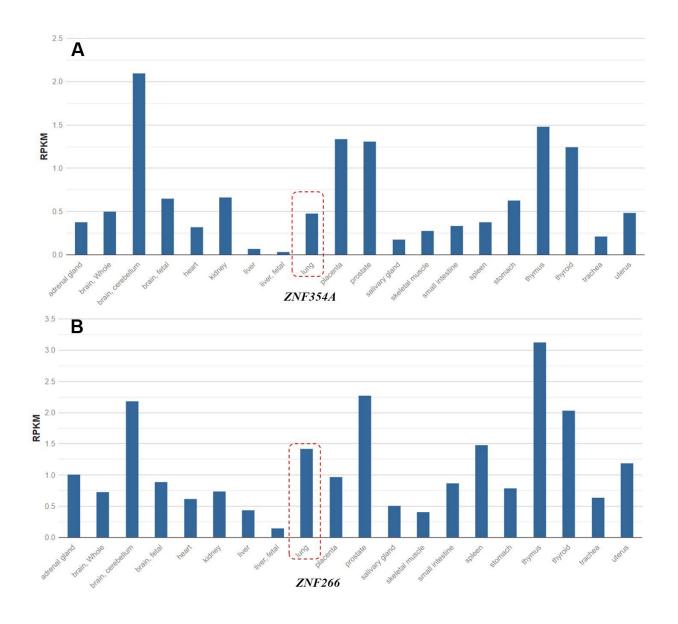
**Supplementary Figure 10. Expression abundance of** *CLN8* **and** *DHX57* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



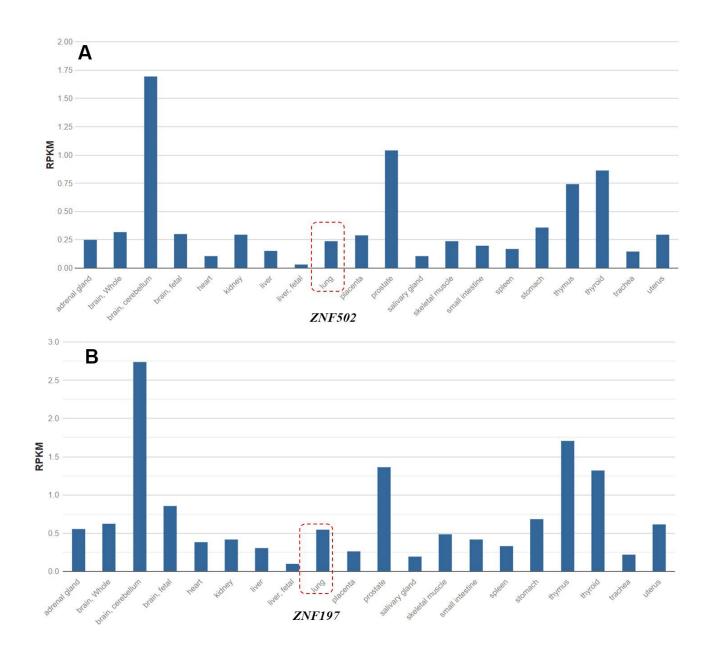
**Supplementary Figure 11. Expression abundance of** *MAP1S* **and** *HDAC10* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



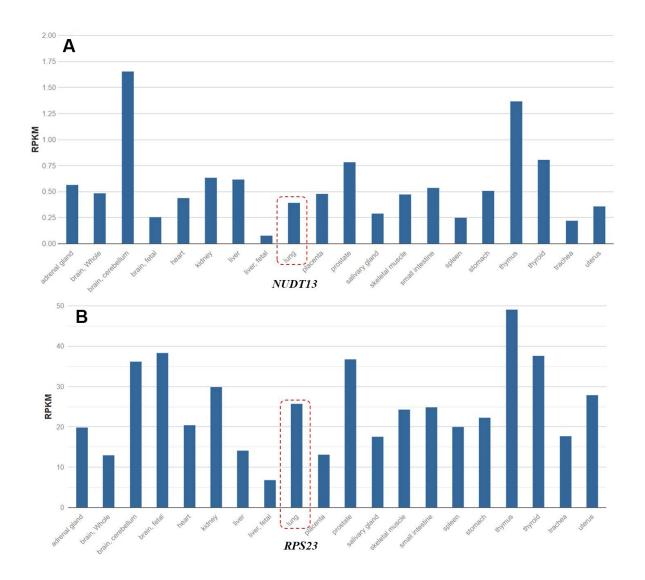
**Supplementary Figure 12. Expression abundance of TBRG4 and CARD9 based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



**Supplementary Figure 13. Expression abundance of** *ZNF354A* **and** *ZNF266* **based on RNA sequencing from 20 human tissues.** The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).



**Supplementary Figure 14. Expression abundance of** *ZNF502* and *ZNF197* based on RNA sequencing from 20 human tissues. The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).

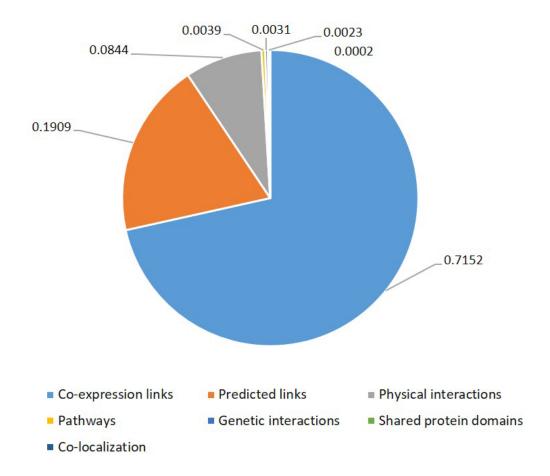


**Supplementary Figure 15. Expression abundance of** *NUDT13* and *RPS23* based on RNA sequencing from 20 human tissues. The expression data were obtained from BioProject (Accession No. PRJNA280600). Expression values are shown in Reads Per Kilobase per Million mapped reads (RPKM).

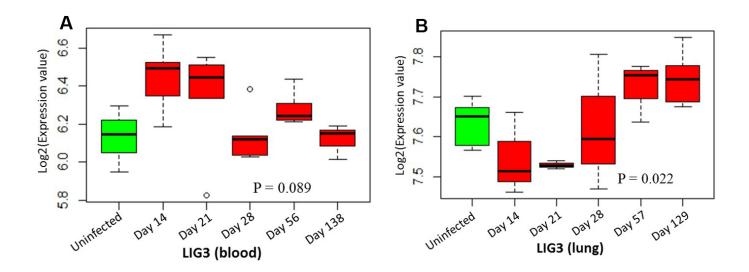
## Genes related to respiratory-relevant diseases PDZD2, RAB18, GTF2B, BATF, PKN2, CDH17, GLDC, SLC30A1, CDH4, STH, GRB10, PCDH9, Genes leaved to tiperculosis GATA2, PRR5L, PTCHD3, SLC25A46, APOBEC3C, TLN1, SPPL2C, PLEKHG4B, RUNX1, RORC, CACNG3, P2RX7, TNPO1, ERBB2, ZNF665, IL6R, KIAA1109, APOBEC3B, EFHD1 HLA-DRB5 AMZ1, AP3B1, C1GALT1, KANSL1, MAPT, PHF13, HLA-DRA, HLA-DQA1, SLC8A1 BTNL2 TNR, TNFRSF1B, SLC25A48, GLRX5, MAP3K1, MYO1F, MICAL2, SBSPON, **ZNF540** KIAA0040, TENM4, TRAF3IP1, CABLES1 ZNF263, CPVL, ARHGAP26, CPA1, MICALCL, CADPS, PER1, SORL1, DDIT4L, ADAMTS10, TBX4, C5AR1, TEAD1, GALK2, HOXB1, ITGAV, ST5, CAND2, BRIP1, ZSWIM2, UBR2, RUFY1, CALD1, PAPD5, TRIM26, CTTNBP2NL, RANBP3, DEPDC7, SMG6, BPTF, SMARCD2, AQP7, ZZZ3, ARHGAP31, NOP14, RIOK3, SHROOM3, PITX2, RBM20, NDUFC1, ACTR2, KSR2, CLDN18, HLX, TSEN2, KIF1B, SLX4IP, ASPSCR1, EIF4E2, RALGPS2, SLC1A2, SLC14A2, USP34, CAMK1D, EPB41L2

Genes related to lung-relevant diseases

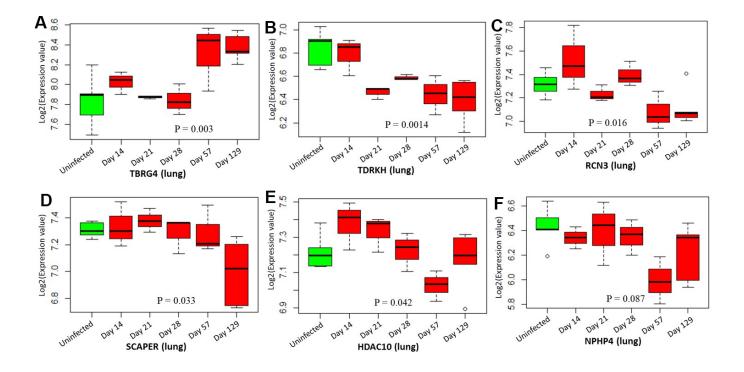
Supplementary Figure 16. Previous studies provides supportive evidence of these MAGMA-identified genes in the replication stage (based on Dataset #1).



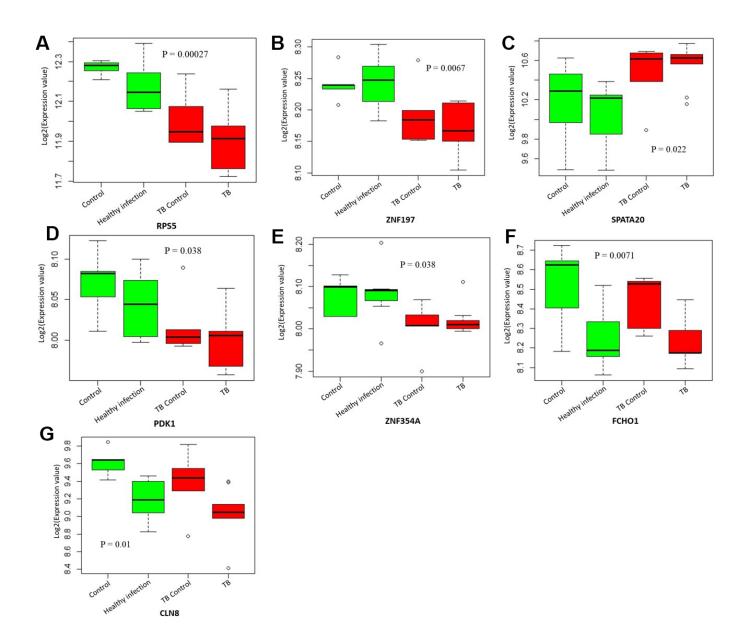
Supplementary Figure 17. The proportion of multiple layers of evidence in constructed GGI network using the GeneMANIA tool.



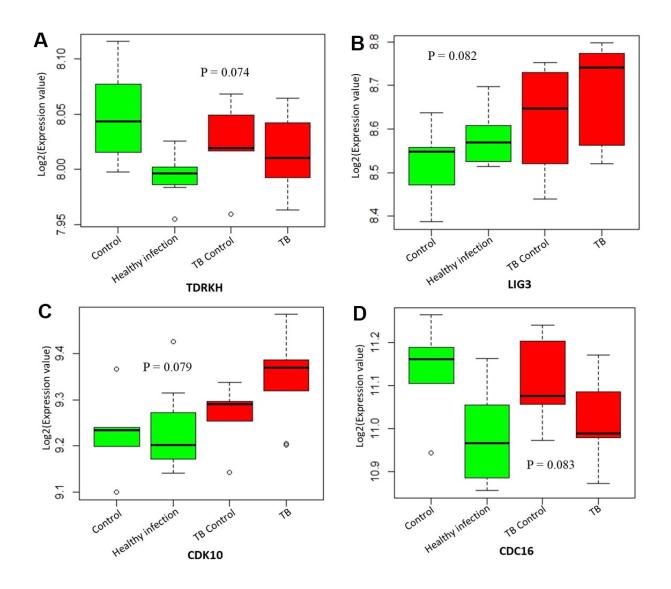
Supplementary Figure 18. Boxplots show the differential expression levels of tuberculosis-genes between uninfected mice and infected mice with 5 distinct time points based on two GSE1440943 (blood) and GSE1440944 (lung) datasets. (A) *LIG3* for blood; (B) *LIG3* for lung. P values were generated by Anova test.



Supplementary Figure 19. Boxplots show the differential expression levels of tuberculosis-genes between uninfected mice and infected mice with 5 distinct time points based on the GSE1440944 (lung) dataset. (A) *TBRG4* for lung; (B) *TDRKH* for lung; (C) *RCN3* for lung; (D) *SCAPER* for lung; (E) *HDAC10* for lung; (F) *NPHP4* for lung. P values were generated by Anova test.



Supplementary Figure 20. Boxplots show the significantly differential expression levels of tuberculosis-genes in alveolar macrophages with four groups of TB infection, TB control, healthy infection, and healthy control based on the GSE139825 dataset. (A) *RPS5*; (B) *ZNF197*; (C) *SPATA20*; (D) *PDK1*; (E) *ZNF354A*; (F) *FCH01*; (G) *CLN8*. P values were generated by Anova test.



Supplementary Figure 21. Boxplots show the suggestively differential expression levels of tuberculosis-genes in alveolar macrophages with four groups of TB infection, TB control, healthy infection, and healthy control based on the GSE139825 dataset. (A) *RPS5*; (B) *ZNF197*; (C) *SPATA20*; (D) *PDK1*; (E) *ZNF354A*; (F) *FCH01*; (G) *CLN8*. P values were generated by Anova test.