

Figures S1-S7

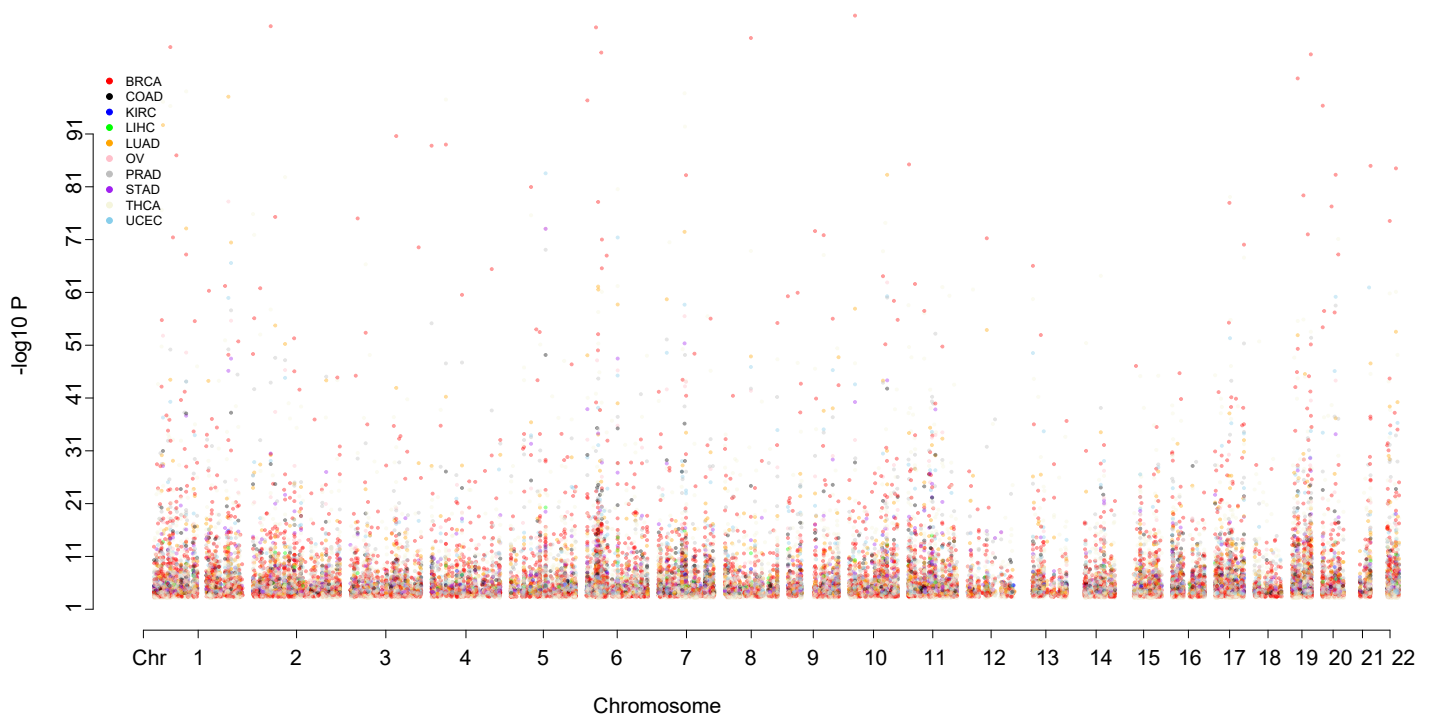


Figure S1 Manhattan plot of *cis*-eQTLs of mRNA in 10 cancer types

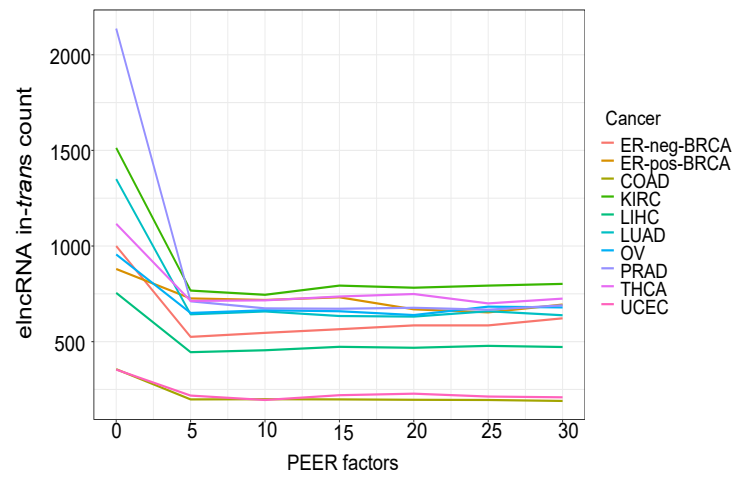
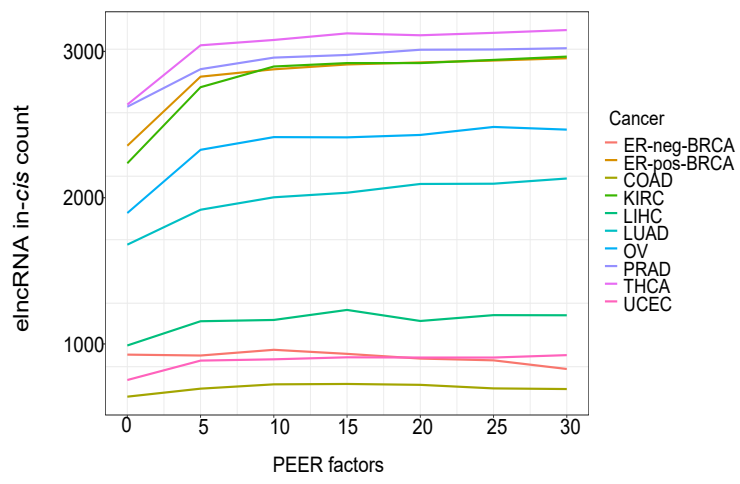


Figure S2 elncRNA *in-cis/trans* count using different PEER factors

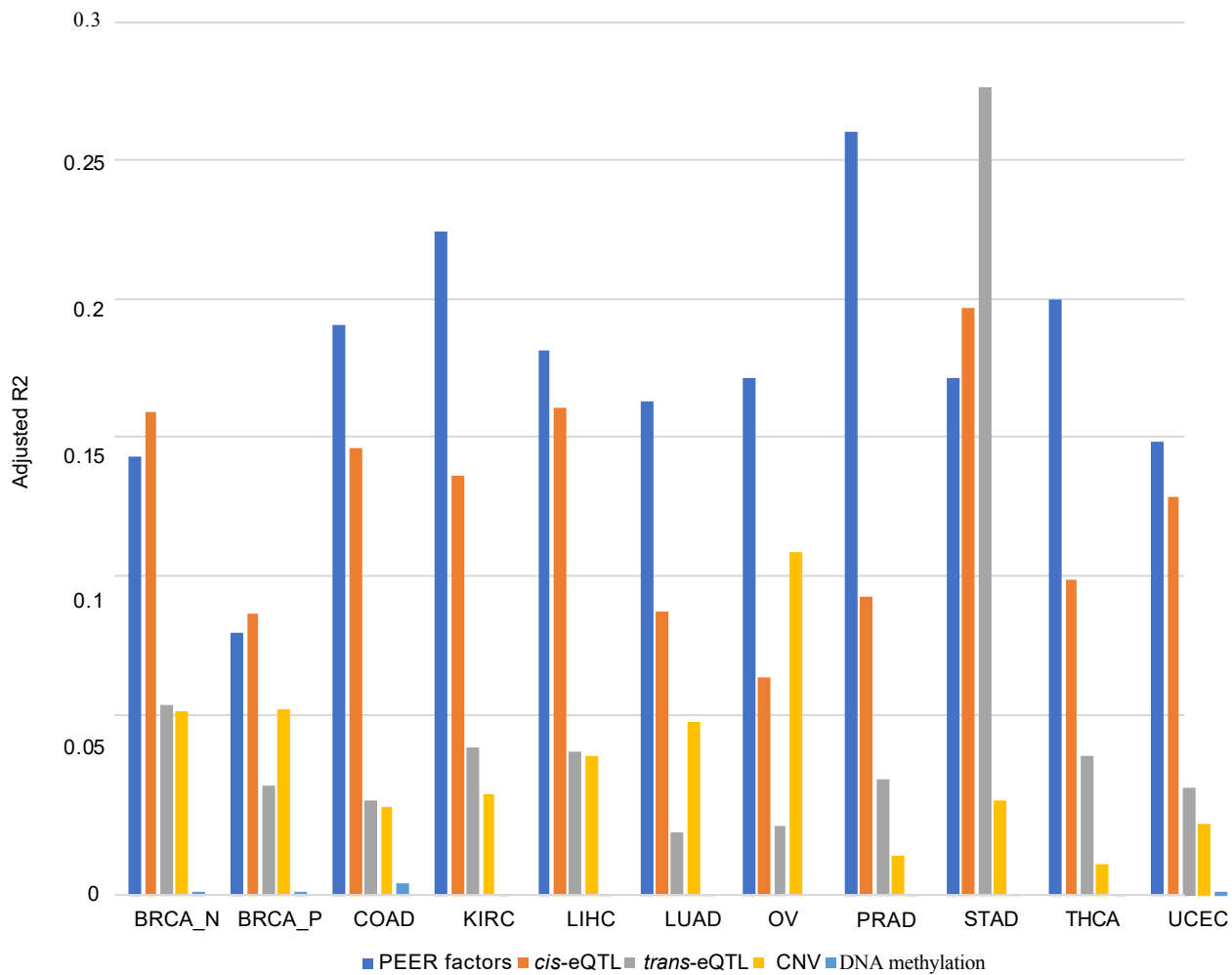


Figure S3 Comparison of the fractions of variation of lncRNA expression explained by the major factors

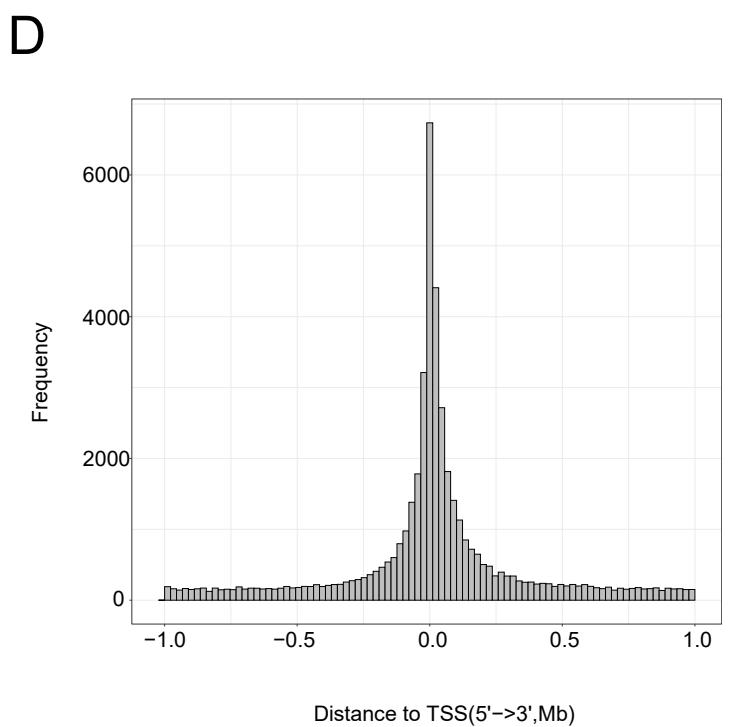
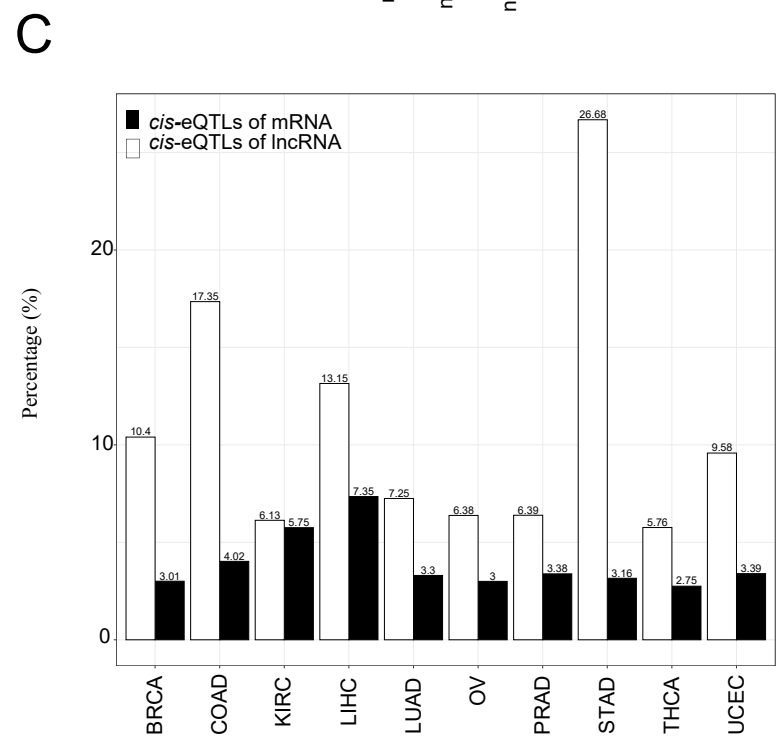
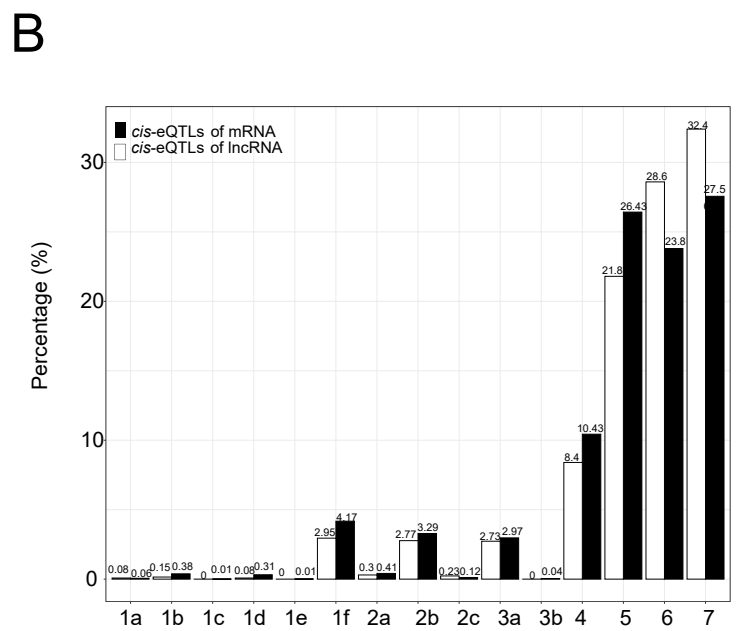
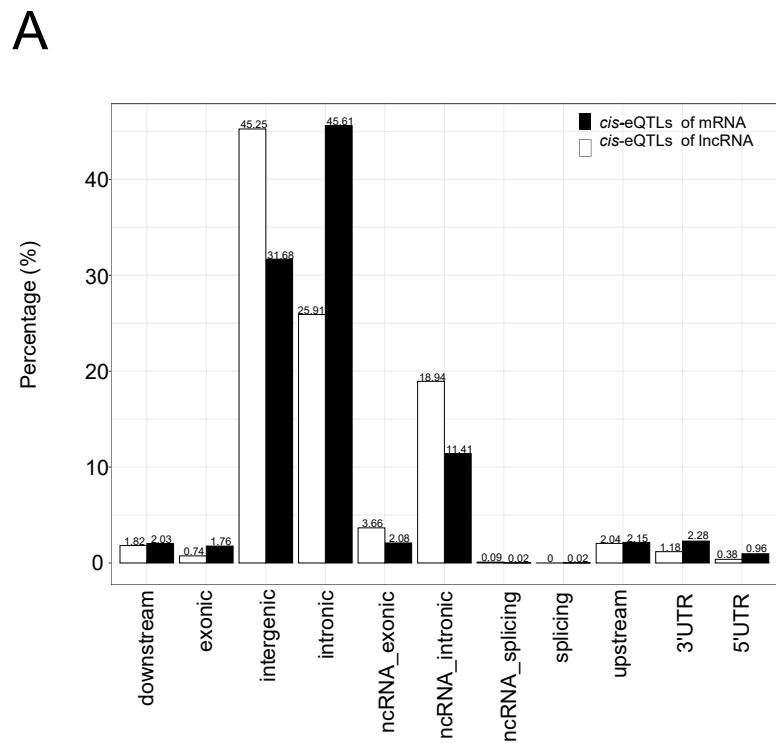


Figure S4 Characterization and comparison of *cis*-eQTLs of mRNA and lncRNA

- (A) Functional effects of *cis*-eQTLs on mRNA/lncRNA ($r \geq 0.2$).
- (B) Distribution of RegulomeDB categories of *cis*-eQTLs of mRNA/lncRNA ($r \geq 0.2$).
- (C) Distribution of *cis*-eQTLs of mRNA/lncRNA associated with GWAS cancer-related risk loci.
- (D) Location distribution of significant *cis*-eQTLs relative to the mRNAs aggregated across all cancer types.

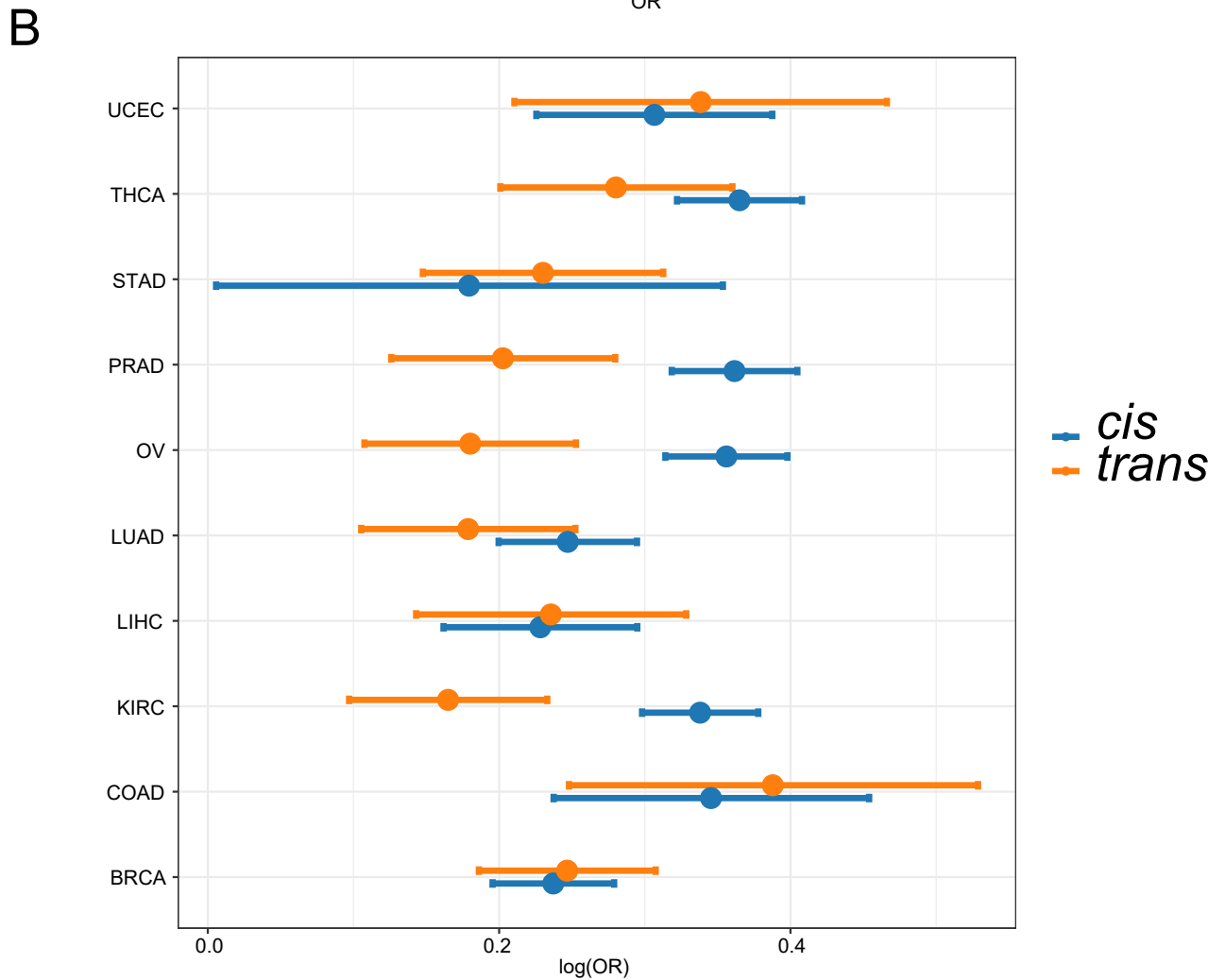
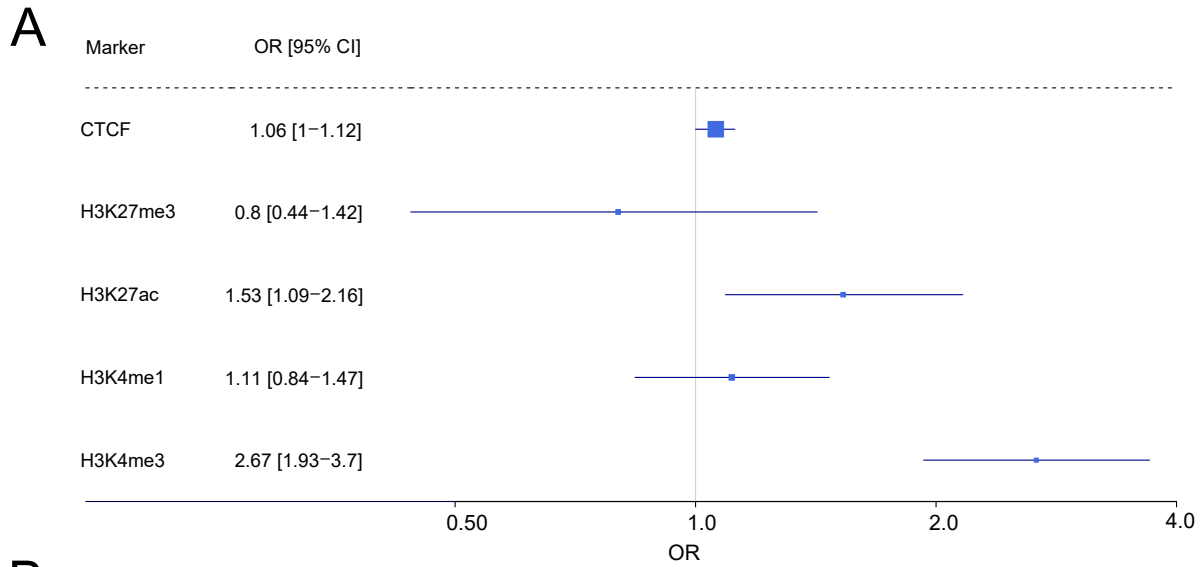


Figure S5

(A) lincRNAs that are significantly overlapped for immune-related lincRNAs

(B) meta-analysis of corresponding normal tissues showing the enrichment of *cis*-eQTLs in different epigenetic markers.

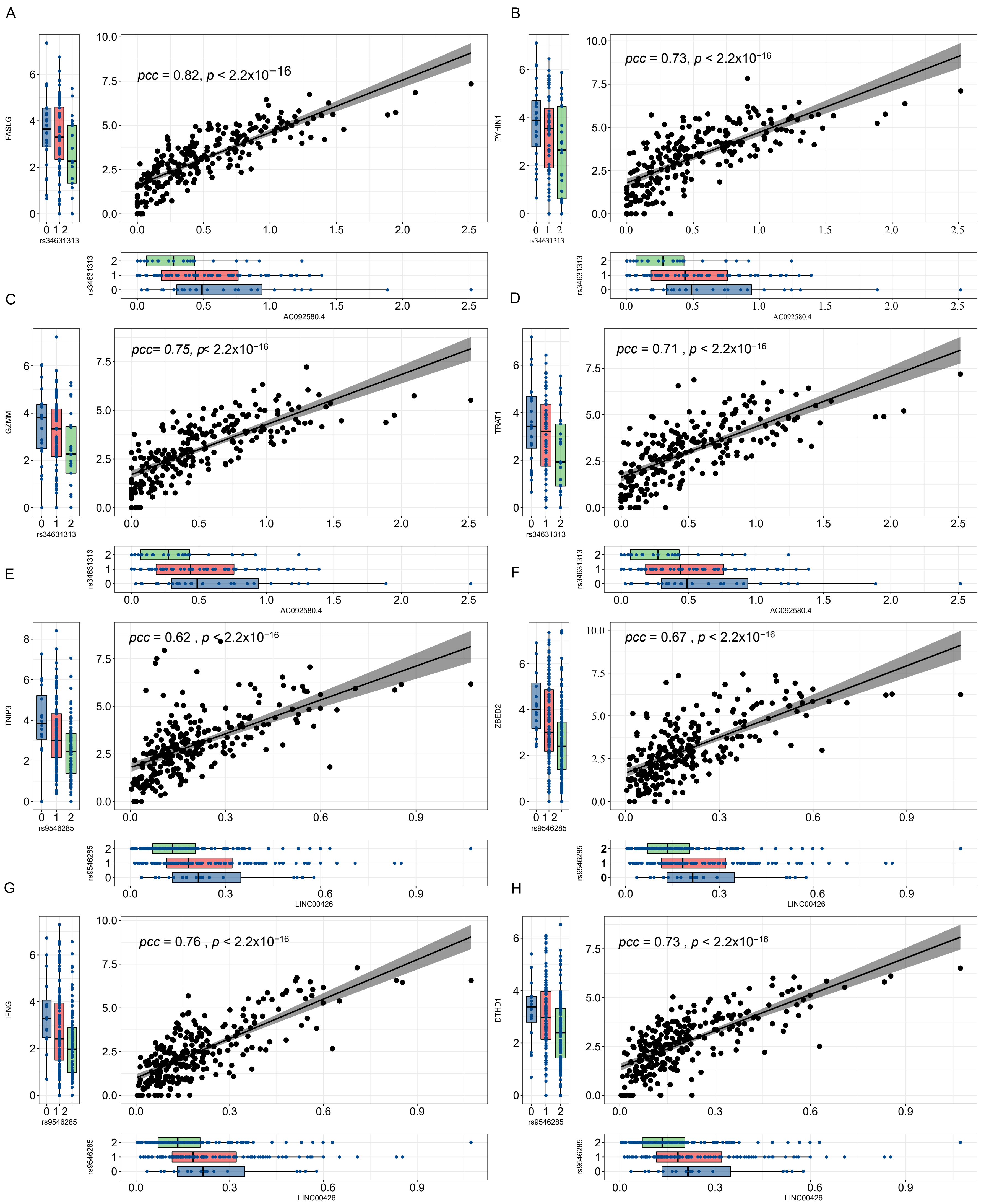


Figure S6 (A-D) Correlations among rs34631313(2p25.2)-AC092580.4-FASLG/GZMM/PYHIN1/TRAT1 regulatory axis in ovarian cancer (OV). **(E-H)** Correlations among rs9546285(13q12.3)-LINC00426-TNIP3/ZBED2/PYHIN1/DTHD1 regulatory axis in Kidney Renal Clear Cell Carcinoma (KIRC).

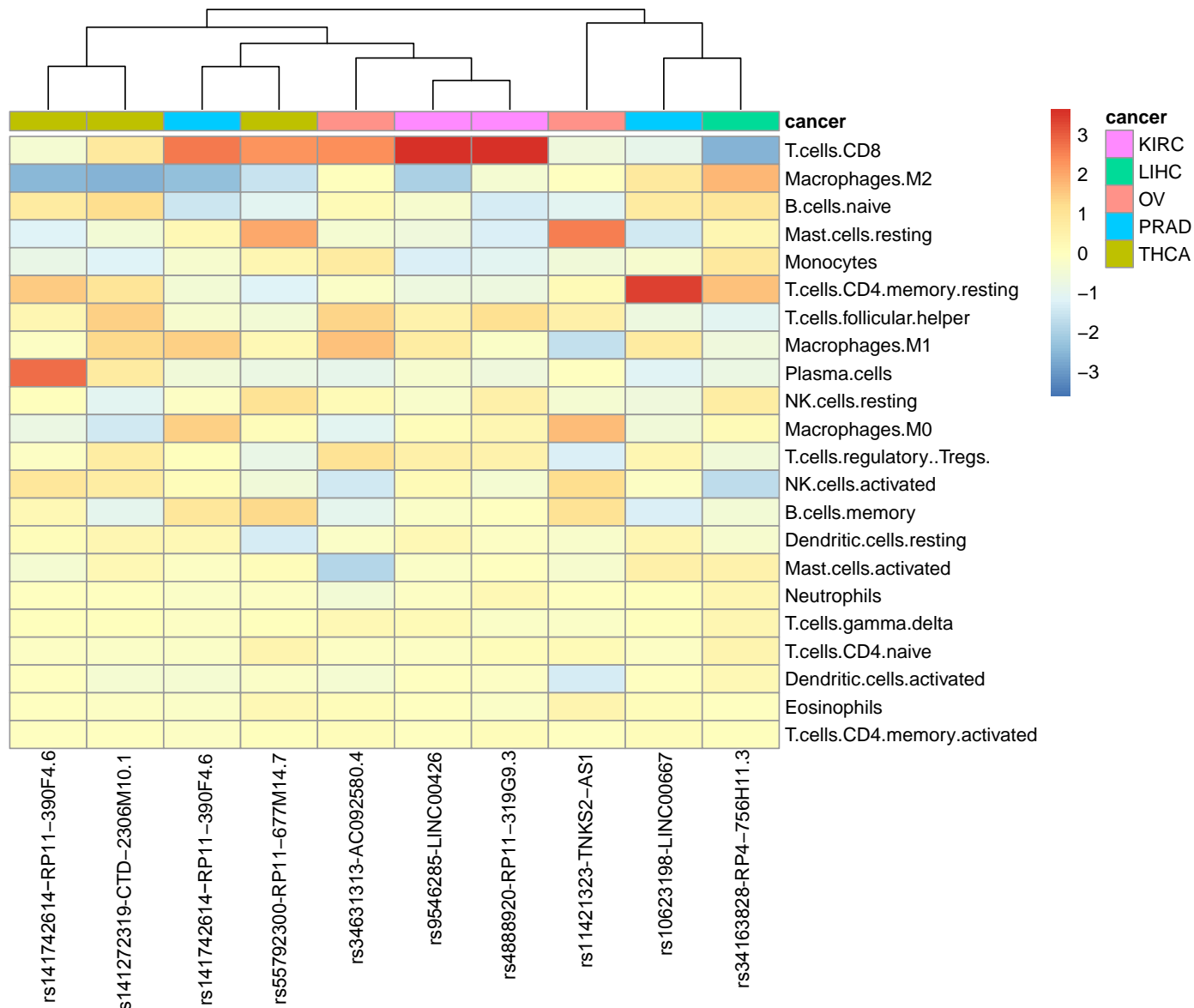


Figure S7 elncRNAs that are significant associated with tumor infiltrating immune cell fractions from IV analysis ($P < 0.05$, $R^2 > 0$)