**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 (r² ≥ 0.2).
(B) Distribution of RegulomeDB categories of cis-eQTLs of mRNA/lncRNA (r² ≥ 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.
(A) lincRNAs that are significantly overlapped for immune-related lncRNAs
(B) meta-analysis of corresponding normal tissues showing the enrichment of cis-eQTLs in different epigenetic markers.

Figure S5
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, R²>0)