

Fig. S1 UMAP visualization of all samples in four normal lncRNAs transcriptome resources. Samples were coloured by resources.

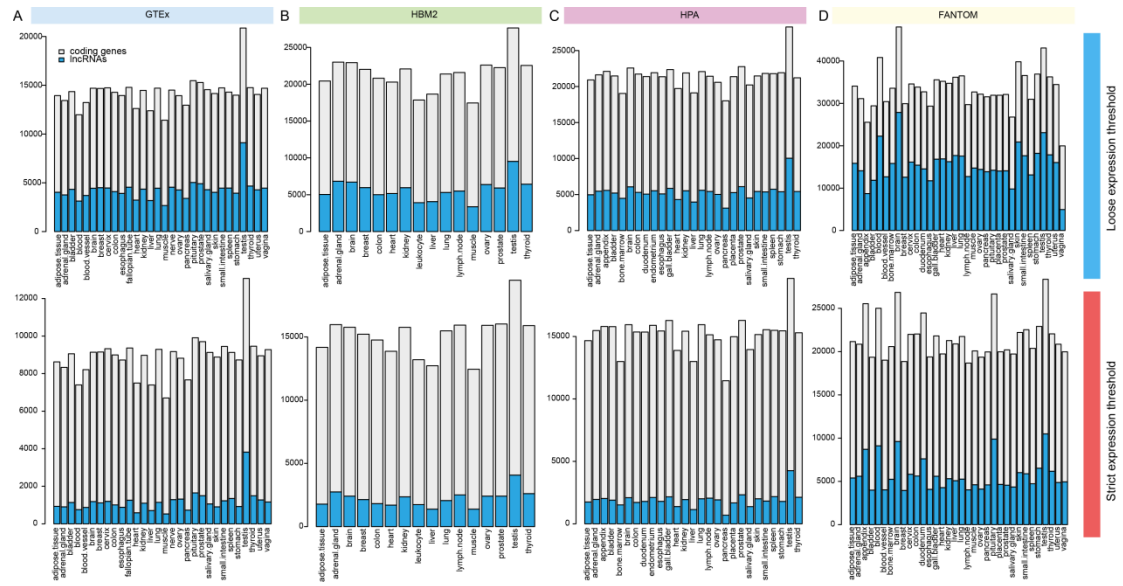


Fig. S2 Expressed lncRNAs and mRNA in each tissue of four resources (top, FPKM>0.1; bottom, FPKM>1). (A) GTEx. (B) HBM2. (C) HPA. (D) FANTOM.

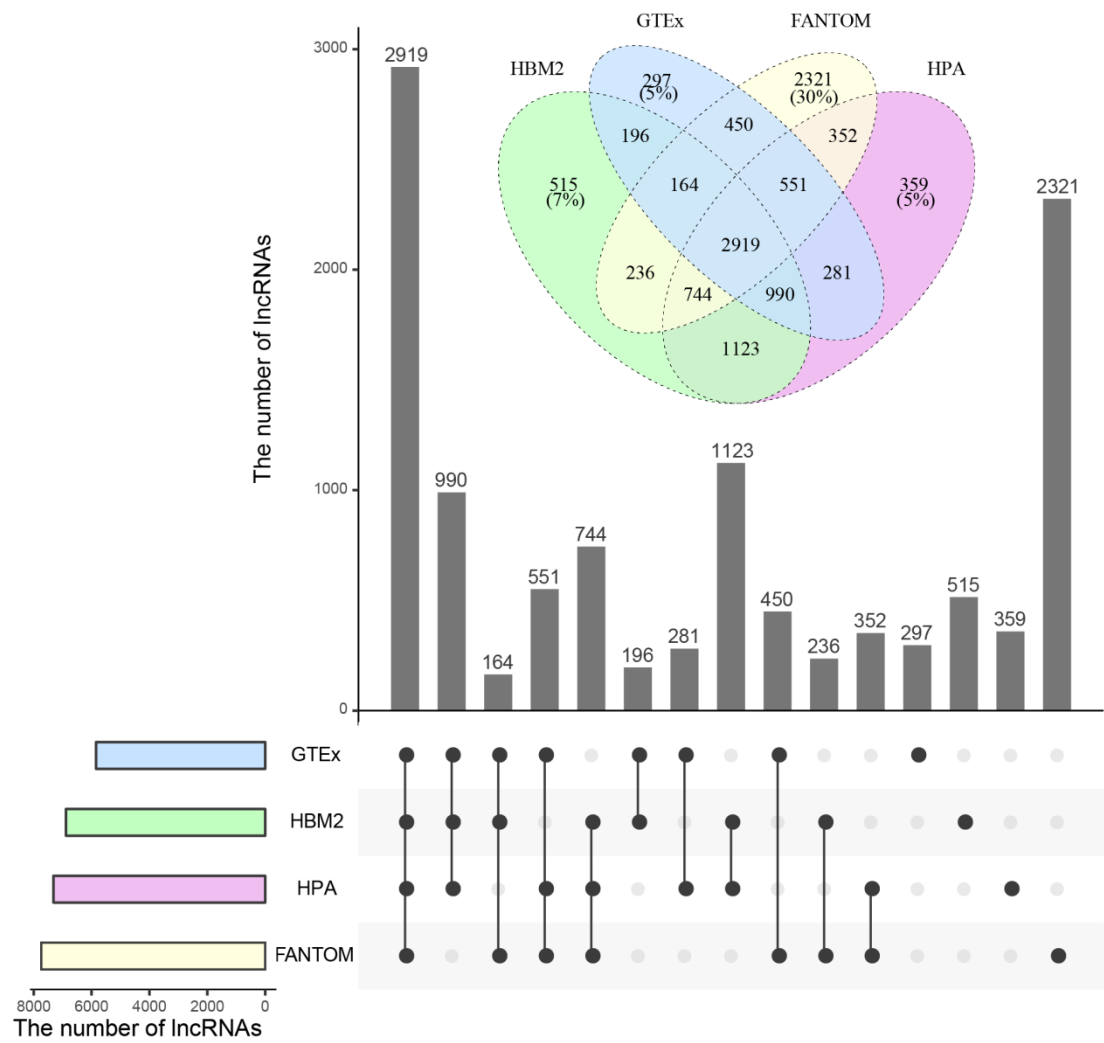


Fig. S3 Number of lncRNAs at the relatively strict expression threshold in GTEx, HPA, HBM2, and FANTOM.

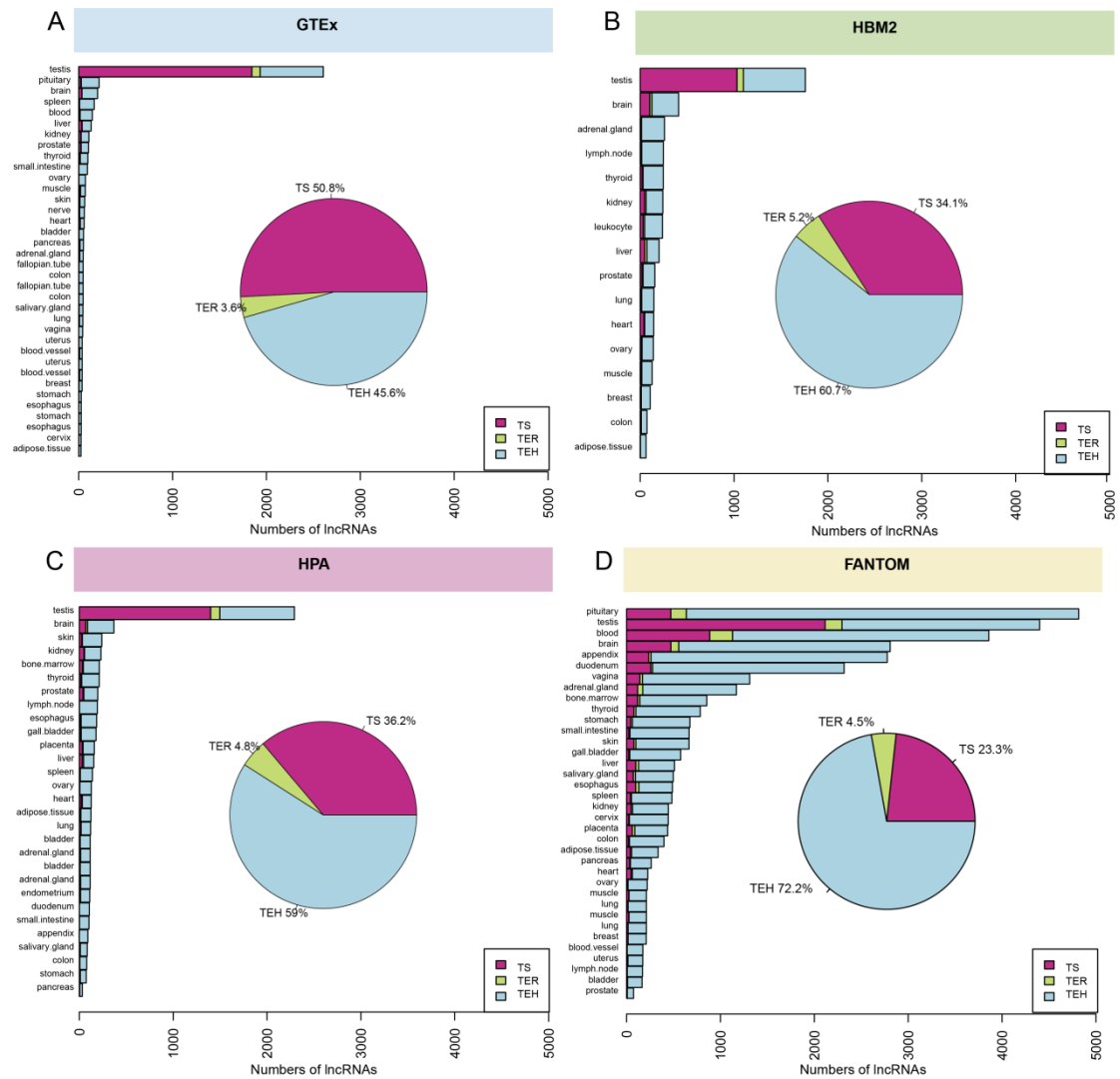


Fig. S4 Number of TE lncRNAs of each tissue in transcriptome source when using strict threshold (GTEx、HPA、HBM2 is 1, FANTOM is 0.4). The histogram, TE lncRNAs in each tissue. TE lncRNAs in each tissue of GTEx, HPA, HBM2 and FANTOM. Purple represents tissue specific lncRNAs (TS), green represents tissue enriched lncRNAs (TER), light blue represents tissue enhanced lncRNAs (TEH). The pie, proportion of each type TE lncRNAs in four transcriptome resources. (A) GTEx. (B) HBM2. (C) HPA. (D) FANTOM.

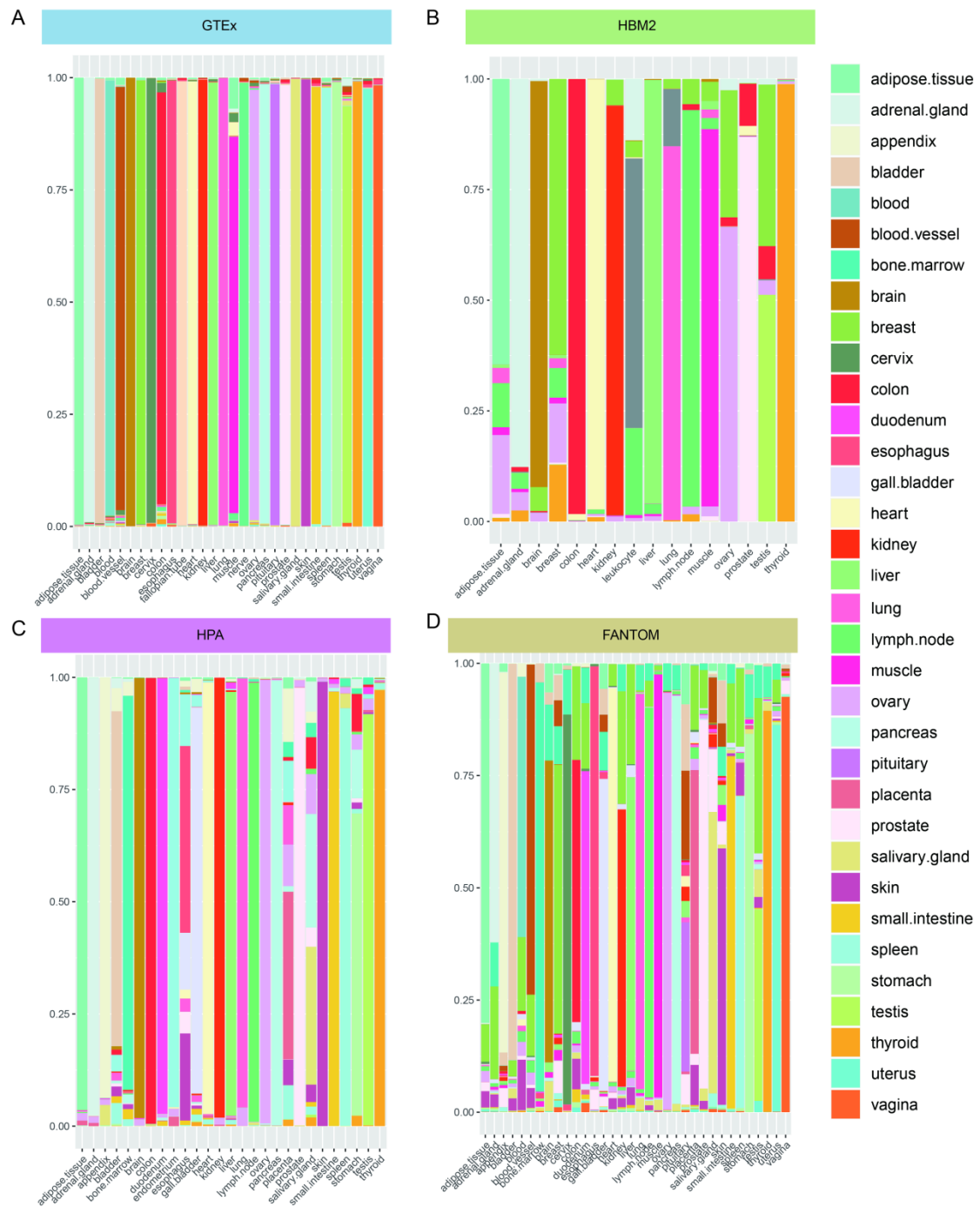


Fig. S5 Robust TE lncRNAs as a feature set to characterize each tissues. (A) GTEx; (B) HBM2; (C) HPA; (D) FANTOM.

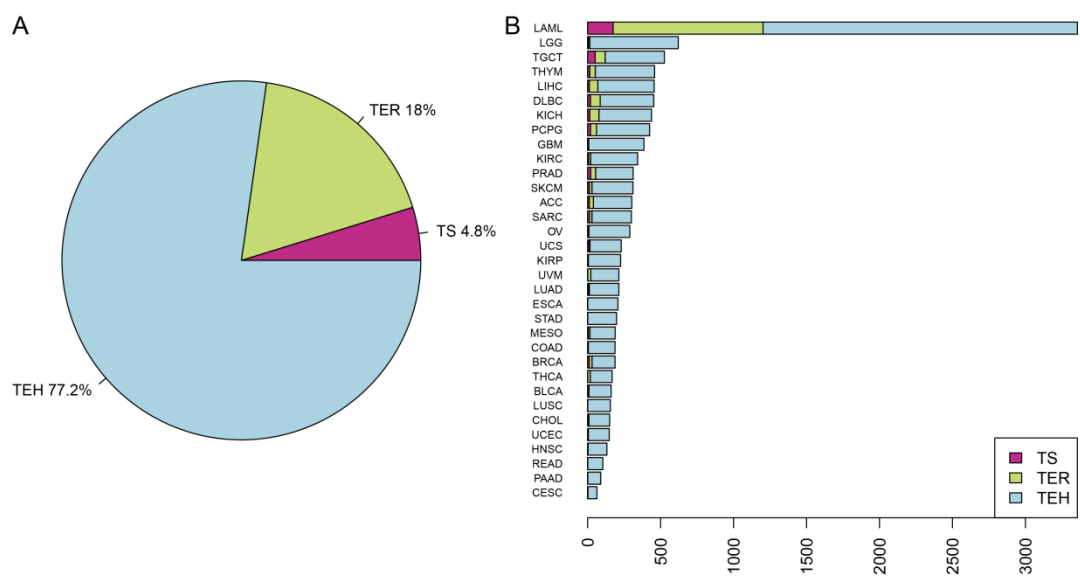


Fig. S6 Comparison of TE lncRNAs in TCGA projects. (A) The pie showing proportion of each type of TE lncRNAs in TCGA projects. (B) TE lncRNAs in each cancer of TCGA projects.

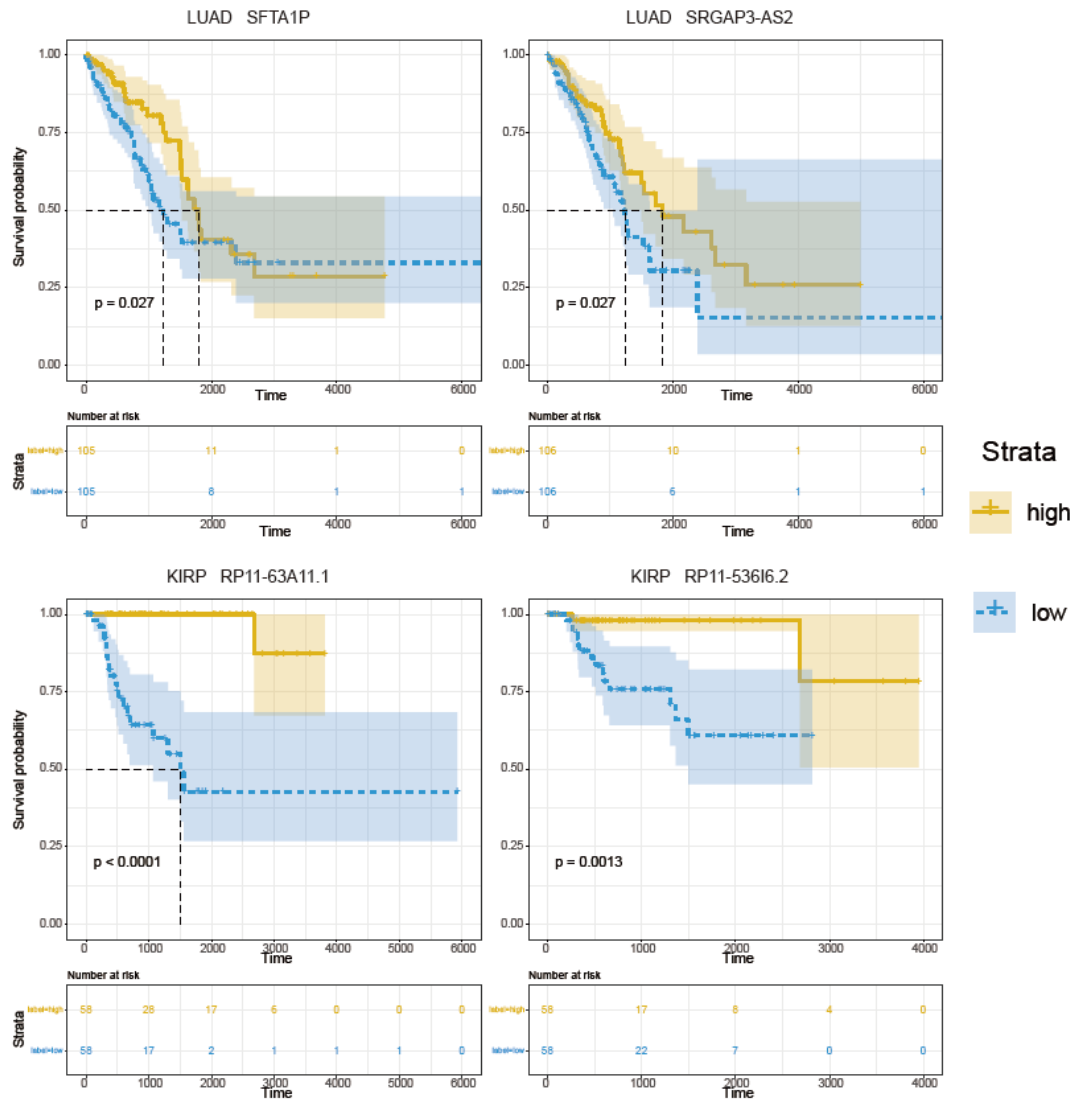


Fig. S7 Kaplan-Meier survival analysis of patients stratified by the expression levels of lncRNAs.

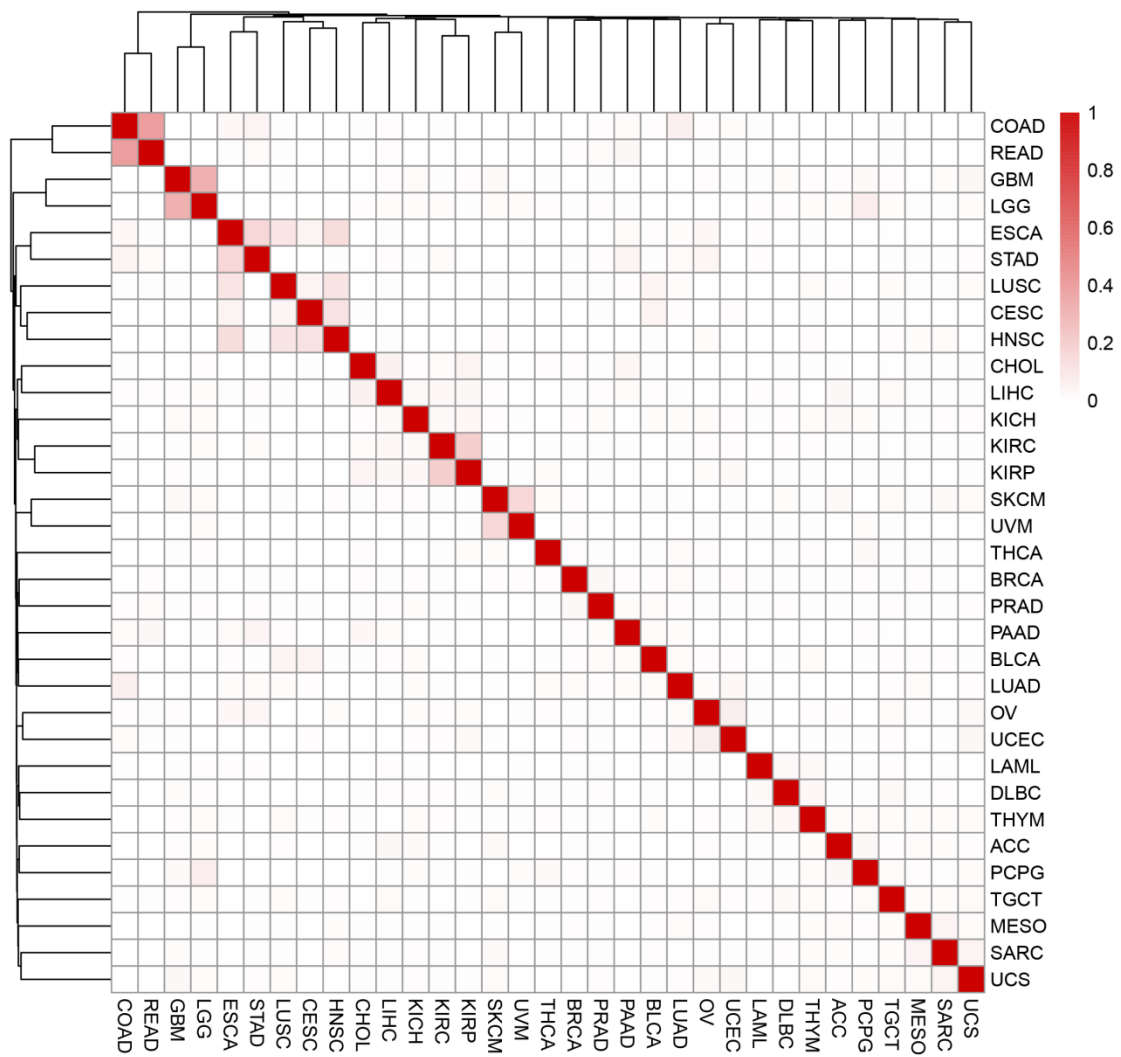


Fig. S8 Overlapping of TE lncRNAs based on the Jaccard index in cancer types.