This list contains the meta-analysis of 302,951 eRNA loci in multiple datasets.

1. eRNA loci annotation: the genomic location of 302,951 eRNA loci is provided in the file TCGA_300k_peaks_all.bed, while eRNA loci for each specific TCGA cancer type are provided in peaks_XXXX.bed where XXXX stands for the cancer type. These files are in the UCSC bed format.
2. eRNA expression in TCGA samples (9,284 tumor samples and 720 normal samples of 32 cancer types). The file RPKM_300k_peaks_XXXX.tsv.gz provides the RPKMs of 302,951 eRNAs in TCGA samples of the XXXX cancer type. The first row contains the sample_id and each of the other rows contains an eRNA locus and the RPKMs of samples in the first row.
3. eRNA expression in GTEx samples (9,664 samples). The file GTEx_RPKM_300k_peaks_XXXX.tsv.gz provides the RPKMs of 302,951 eRNAs in GTEx samples of the XXXX tissue type. The first row contains the sample_id and each of the other rows contains an eRNA locus and the RPKMs of samples in the first row.
4. eRNA expression in CCLE samples (925 cell lines). The file CCLE_eRNA_300k_peak.tsv.gz provides the RPKMs of 302,951 eRNAs in 925 CCLE cell lines. The first row contains the sample_id and each of the other rows contains an eRNA locus and the RPKMs of samples in the first row.
5. Pan-Cancer analysis of the eRNAs: the association between 49,849 eRNAs and patient survival times can be found in the file Association_between_patient_survial_and_eRNA_expression.tsv; the list of 4,725 non-coding focal copy-number changes affecting eRNA loci can be found in the file eRNA_loci_in_TCGA_focal_CNV.tsv; the level of 3,919 CpG methylation within eRNA loci can be found here.
6. The 164 eRNA and 36 target genes associated with immunotherapy response can be found here.
7. The 32,298 Hi-C interactions between eRNA loci and gene promoters can be found in the file Hi-C_interaction_between_promoter_and_eRNA_loci.tsv. Each eRNA/gene pair shows consistence co-expression in at least three TCGA cancer types. The Spearman's *Rho* and adjusted p-values of co-expression are also provided. The TF

binding signal from cistrome database in each eRNA locus can be find in the file [cistrome_TF_binding_in_eRNA_loci.tsv.gz].

8. **The information of all samples included in this dataset can be found in the file Sample_info.xlsx.**
9. **For questions about the data, please contact hliang1@mdanderson.org**