**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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/5_Super_enhancer_annotation/)**, while eRNA loci for each specific TCGA cancer type are provided in** [**peaks\_XXXX.bed**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/1_eRNA_expression/1_TCGA/) **where XXXX stands for the cancer type. These files are in the UCSC** [**bed format**](https://genome.ucsc.edu/FAQ/FAQformat.html#format1)**.**
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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/1_eRNA_expression/1_TCGA/) **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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/1_eRNA_expression/2_GTEx/) **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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/1_eRNA_expression/3_CCLE/) **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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/2_PanCancer_analysis/)**; 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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/2_PanCancer_analysis/)**; the level of 3,919 CpG methylation within eRNA loci can be found** [**here**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/2_PanCancer_analysis/CpG_methylation_in_eRNA_loci/)**.**
6. **The 164 eRNA and 36 target genes associated with immunotherapy response can be found** [**here**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/3_eRNA_differential_immunotherapy/)**.**
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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/4_eRNA_locus_gene_interaction/)**. 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**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/4_eRNA_locus_gene_interaction/)**.**
8. **The information of all samples included in this dataset can be found in the file** [**Sample\_info.xlsx**](https://bioinformatics.mdanderson.org/Supplements/Super_Enhancer/6_Sample_ID/)**.**
9. **For questions about the data, please contact hliang1@mdanderson.org**