**System requirements**

All source codes were tested on the Linux(Ubuntu 18.04), R(3.6.3), and Python(3.8.8)

To run the R script, it requires the library listed below.

DESeq2(1,26.0), stringr(1.4.0), readr, tximportData, readxl, dplyr(2.1.1), pheatmap, ggplot2(3.3.5), xlsx, pvclust, dendextend, EnsDb.Hsapiens.v86, org.Hs.eg.db

To run the Python script, it requires the library listed below.

matplotlib, pandas, numpy, PIL

**Installation guide**

All scripts are not required specific installation step.

**Demo**

Simply run the each script to get results.

All scripts are completed less than an hour with 100 number of samples

Expected outputs

1. DrawRectangleColor\_Empty\_withcolor  
   Multiple circles that indicate the isolated region on the tissue image
2. Spatial\_A\_to\_I  
   A-to-I editing heatmap (columns – samples, rows – genes)
3. Target\_gene  
   Gene expression heatmap of target gene set (columns – sample, rows – target gene set)
4. DE\_AtoI\_A  
   Volcano plot of differential analysis based-on the A-to-I editing status of two groups

**Instructions for use**

1. DrawRectangleColor\_Empty\_withcolor  
   This script requires the tissue image file, isolated position information, and metadata of each isolated sample.
2. Spatial\_A\_to\_I  
   This script requires the gene expression count, isolated position information, and A-to-I information of each isolated sample
3. Target\_gene  
   This script requires the gene expression count, target gene sets, and metadata of each isolated sample
4. DE\_AtoI\_A  
   This script requires the AtoI mutation information, and gene expression count of each isolated sample