**Readme File for JCAP-Intron-Exon Visualization and Guide Table Using Isoviz.**

**Main point of the application (app)-**

This app provides a user interface for the newly created R package Isoviz. The full documentation for the package can be found at <https://github.com/daklab/isoviz>. In particular, this app lets you create a Junction to Isoform map and download it as a .png file as well as create a guide table showing your junction gRNA efficiency predictions (TIGER model) that can be downloaded as a .csv file.

**Mechanics/How to Use**

**Getting Started**

You can run this app on a server. However, to run this app locally, (as with all Shiny apps), you must put the app.R file and the .css file in one folder before running the app.R file in R/R Studio.

**Initial File Inputs**

The first 4 buttons on the sidebar upload the required files to generate the Junction to Isoform map and guide table. From the top to the bottom of the side bar there are the following file browse buttons:

1. “Upload Genome .psl File” - This button uploads your .psl file of expressed isoforms.
2. “Upload Gene-Transcript Conversion .txt File”- This button uploads your gene to transcript conversion data.
3. “Upload Junction File (.junc.txt)” - This button uploads your leafcutter junctions.
4. “Upload Intron Annotations .rda File” -This button uploads your intron annotations.

**Text inputs**

The next two elements (going from top to bottom ) on the sidebar are text inputs needed for the Junction to Isoform map.

1. “Enter Gene Name:” -This text input allows you to provide the name (HGNC symbol) of your gene of interest.
2. “Enter Gene Ensembl ID:” - This text input allows you to provide the Ensembl ID of your gene of interest.

**Last three inputs**

a) “Upload Junctions List (.txt)”- This file browse button allows you to upload a list of junctions (as a text file ) that you would like the guide table to focus on.

b) “Enter Cell Type:”- This text input allows you to tell the app what type of cells your samples are. The default is custom.

c) Minimum Junction Usage:” - This numerical input tells the app the minimum usage events that occur at a potential junction for the app to consider it a proper junction.

**Generate/Action Buttons**

a) “Generate Plot” -This button creates and displays your Junction to Isoform map which is shown in a “Plot” tab. The tab is labeled with “Your exon-intron visualization will appear here.” This label will be under your map when it is displayed. Also, you will get a notification on the screen when this process begins and is completed.

b) “Generate Guide Table” -This button will create a guide table showing your junction gRNA efficiency predictions (TIGER model). The table will appear in the “Guide Table” tab. Before the button is clicked, the tab will contain the text, “Your guide table will appear here.” After the table is generated, that text will be shown beneath the table. Also, you will get a notification on the screen when this process begins and is completed.

**Download Buttons**

The last two buttons going down the sidebar allow you to download the map as a .png file and the guide table as a .csv file. They are labeled as “Download Plot” and “Download Table” respectively.