**Pre-processing pipeline for RNAmappe.R**

It is required that conda be installed on the computer being used to perform the RNAmappe.R pipeline. The download and installation information can be found at the link below.

<https://docs.conda.io/projects/conda/en/latest/user-guide/install/macos.html>

*Data files and folders:*

1) Start with a single empty folder called RNAmappe.R  
2) Place the RNA-Seq fasta reads for wildtype and mutant in this folder.  
3) A reference genome (FASTA) and gene model (GTF) are required:

Create environmental variables for the reference genome fasta and gtf files:

refGenome=/path/to/referenceGenome.Fa

gtfFile=/path/to/gtfFile.gtf

A conda environment should be created in this folder and should contain all of the package dependencies to run the pipeline.

Installed packages-version:

Package Version

fastqc 0.12.1

cutadapt 3.5

trimmomatic 0.39

hisat2 2.2.1

samtools 1.18

bcftools 1.17

cufflinks 2.2.1

ensembl-vep 13.0

To create this environment: ```conda create --name RNAmappe.R ```

To activate environment: ```conda activate RNAmappe.R```

To install packages: ```conda install <pkg>=<version>```

The environment should be activated before running any part of the pipeline.