# README for Cancer Research journal: CFL1 and HIF1A Analysis

This R script generates the figures included in the supplementary data of the manuscript

"**IL-9 induces metastatic migration of malignant T-cells by activating a downstream HIF-1-Cofilin-1 axis in cutaneous T-cell lymphoma**."

## Dependencies:

- R (version 3.4.1)

- Required packages: dplyr, tidyr, ggplot2, ggrepel

## Instructions:

1. Set the working directory to the folder containing the data files.

2. Install the required R packages (if not already installed).

3. Run the script in R or RStudio.

## Generated Figures:

- \*\*Figure S3A\*\*: HIF1A CRISPR KO Gene Effect vs Expression.

- \*\*Figure S3B\*\*: CFL1 CRISPR KO Gene Effect vs Expression.

- \*\*Figure S3C\*\*: Density plot for CFL1 Gene Effect.

## Data Files:

- "CFL1 CRISPR.csv": DepMap gene effect data for CFL1:

Link: https://depmap.org/portal/partials/entity\_summary/download?entity\_id=4505&dep\_enum\_name=Chronos\_Combined&size\_biom\_enum\_name=expression&color=mutations\_prioritized

- "HIF1A CRISPR.csv": DepMap gene effect data for HIF1A.

Link:

https://depmap.org/portal/partials/entity\_summary/download?entity\_id=11600&dep\_enum\_name=Chronos\_Combined&size\_biom\_enum\_name=expression&color=mutations\_prioritized

- "OmicsExpression.csv": Omics expression data.

Link:

https://depmap.org/portal/partials/entity\_summary/download?entity\_id=11600&dep\_enum\_name=Chronos\_Combined&size\_biom\_enum\_name=expression&color=mutations\_prioritized

- "T cell cancers.csv": Metadata for T cell cancer lines.

See file: T cell cancers.csv