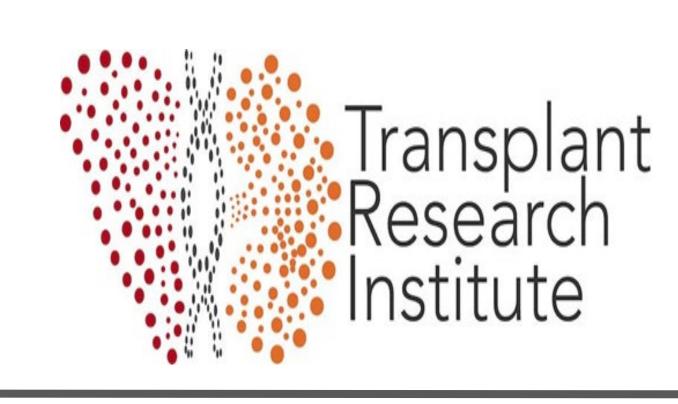
Using CRISPR Gene Editing to Prevent Accumulation of Lipids in Hepatocytes



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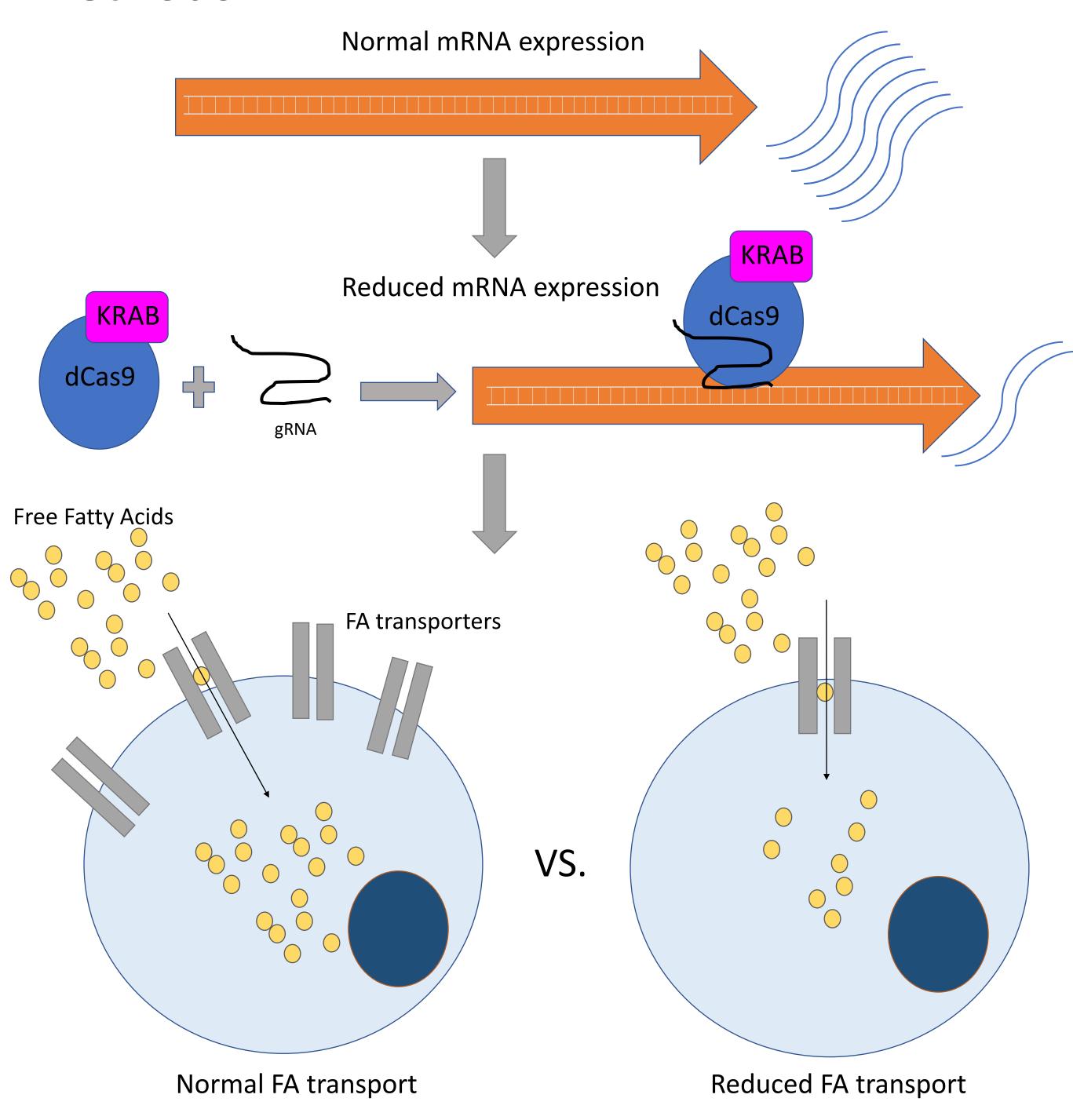
James D. Eason Transplant Institute

Background

CRISPR gene editing technology can be used to modify the expression of genes known to play a role in lipid accumulation in hepatocytes.

Specifically, fatty acid transport proteins 2 and 5 (FATP2 & 5), located in the plasma membrane, are present at increased levels in people with non-alcoholic fatty liver disease¹. This experiment aimed to reduce expression of FATP2 & 5 by using a dead Cas9 with an appended inhibitory domain (KRAB) that acts on the promotor region of the gene. The mRNA expression, fatty acid assays, and flow cytometry were used to evaluate the efficiency of the CRISPR-Cas9 inhibitory system.

Methods



mRNA Expression

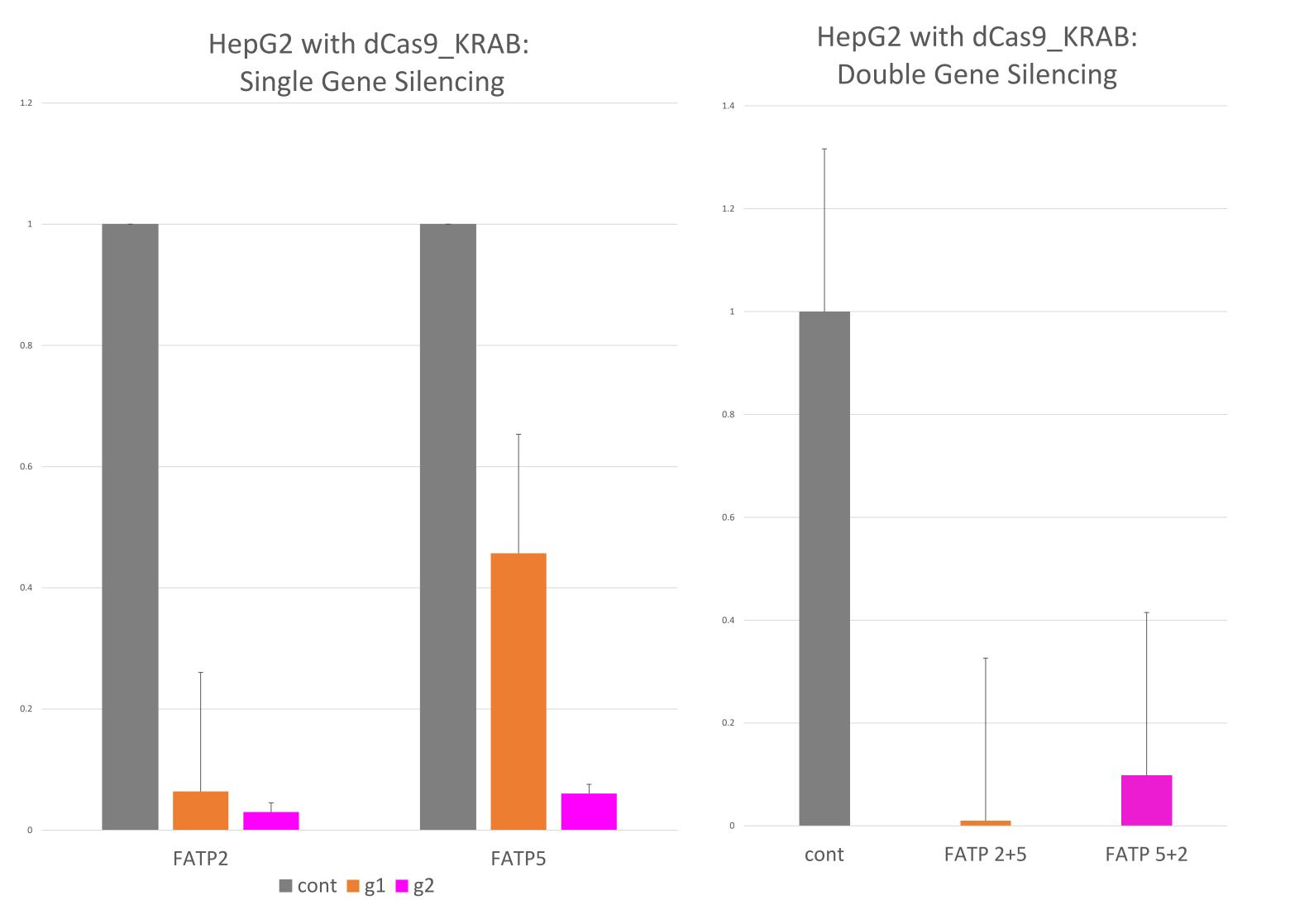
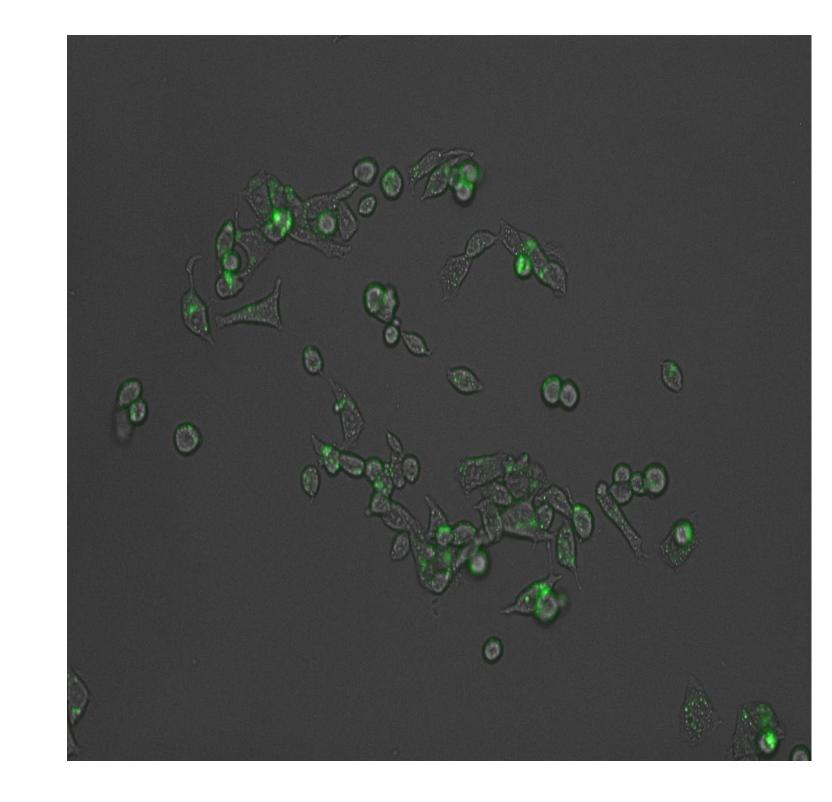


Figure 1: mRNA expression of FATP genes

Fatty Acid Assays

A mixture of palmitic and oleic acids in a 2:1 ratio (total concentration 200 μ M) was added to the cells and allowed to incubate. BODIPY stain was added to highlight lipid inside the cells.



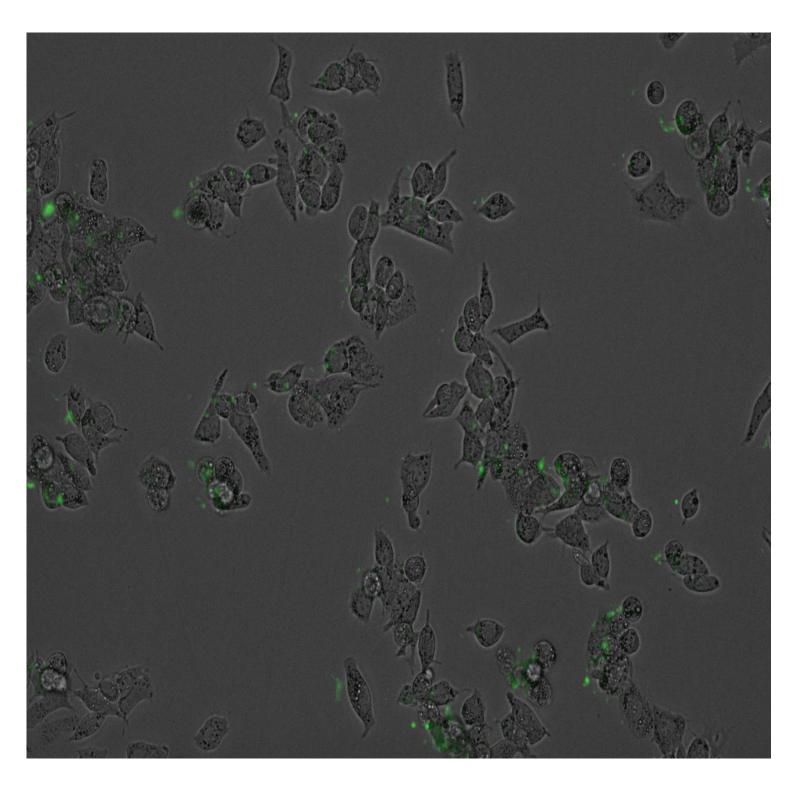


Figure 2: Left: control, Right: inhibition of FATP2 gRNA2

Flow Cytometry

Sample Name	Subset Name	Count
CK2021-10-20LFA Cont.0001.mqd	Single Cells	16603
CK2021-10-20LFA FATP2g2.0001.mqd	Single Cells	12293
CK2021-10-20LFA FATP5g2.0001.mqd	Single Cells	16378

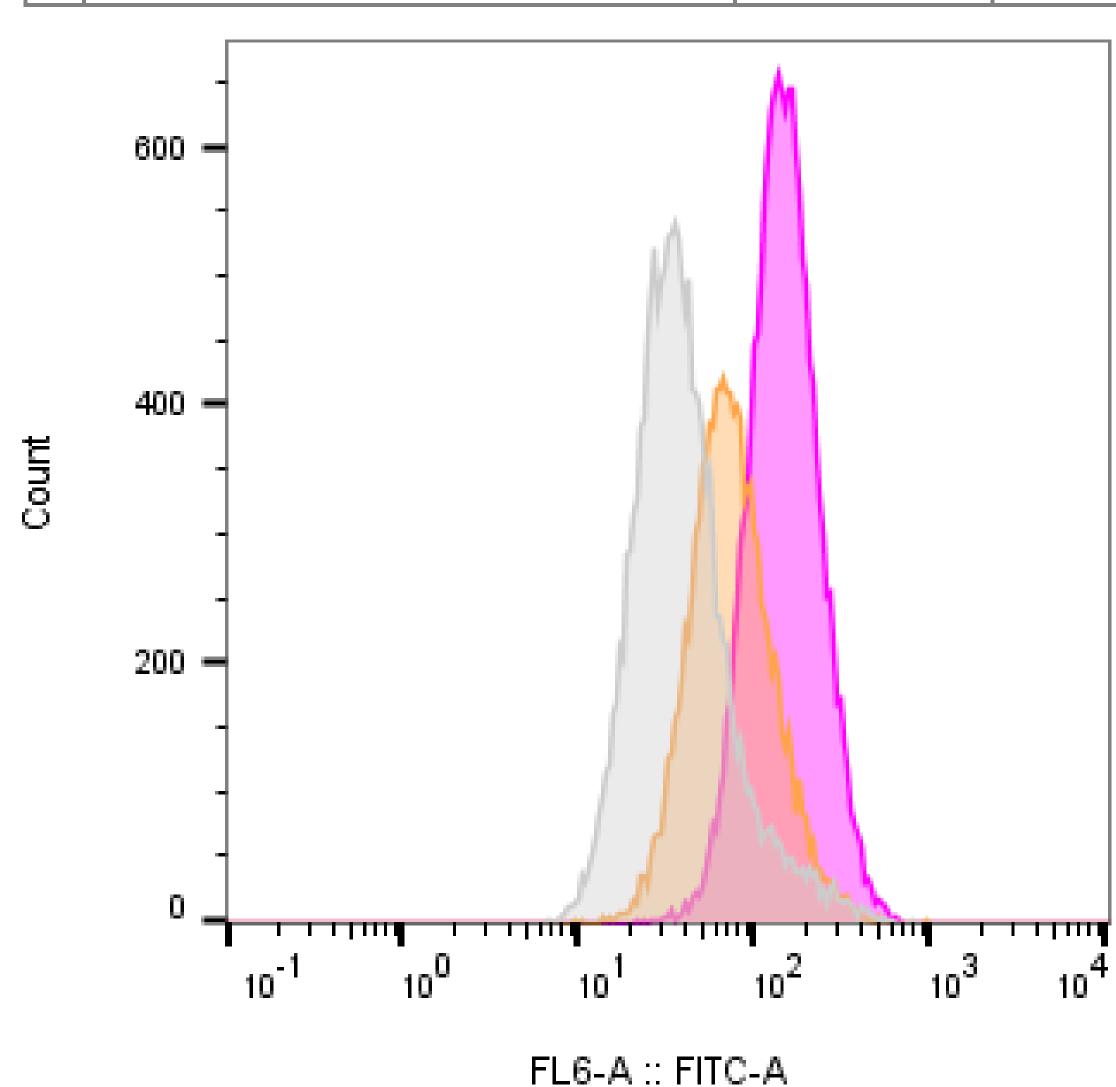


Figure 3: Flow cytometry results from BODIPY stained cells

Discussion

Although the results from mRNA expression levels and fatty acid assays were expected, the same level of inhibition does not seem to be observed in the flow cytometry. Current work is aimed at deciphering the mechanism behind why lipid accumulation is not inhibited to the same extent, such as possible upregulation of the uninhibited transporter. Consequently, targeting both FATP2 & 5 in the same cell line may produce the desired results. Additionally, other future projects include running Seahorse metabolic analysis.

References