

SUPPLEMENTAL INFORMATION:

**Development of an Optimized Clearing Protocol to Examine Adipocyte Subpopulations in
White Adipose Tissue**

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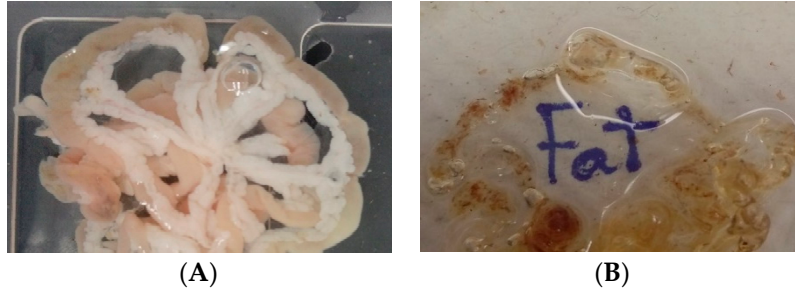


Figure S1. BABB-D4 clearing of mesenteric fat. Gross histology: (A) pre-clearing image; (B) post-clearing image. A part of the intestines has been flipped to the right of the image to show the transparency of the adipose tissue.

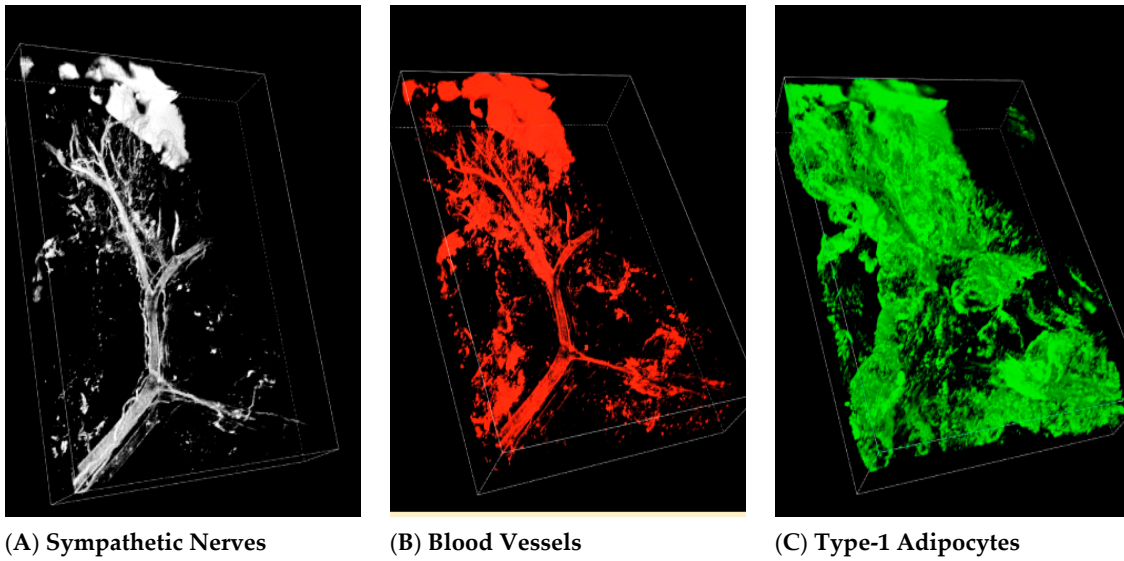


Figure S2. BABB-based clearing without DCM delipidation successfully labelled sympathetic nerves and blood vessels. (A) sympathetic nerves (anti-tyrosine kinase), (B) blood vessels (isolectin B4), and (C) Type 1 adipocytes. All pictures were taken at 100x magnification. Scale bar = 100 μ m.

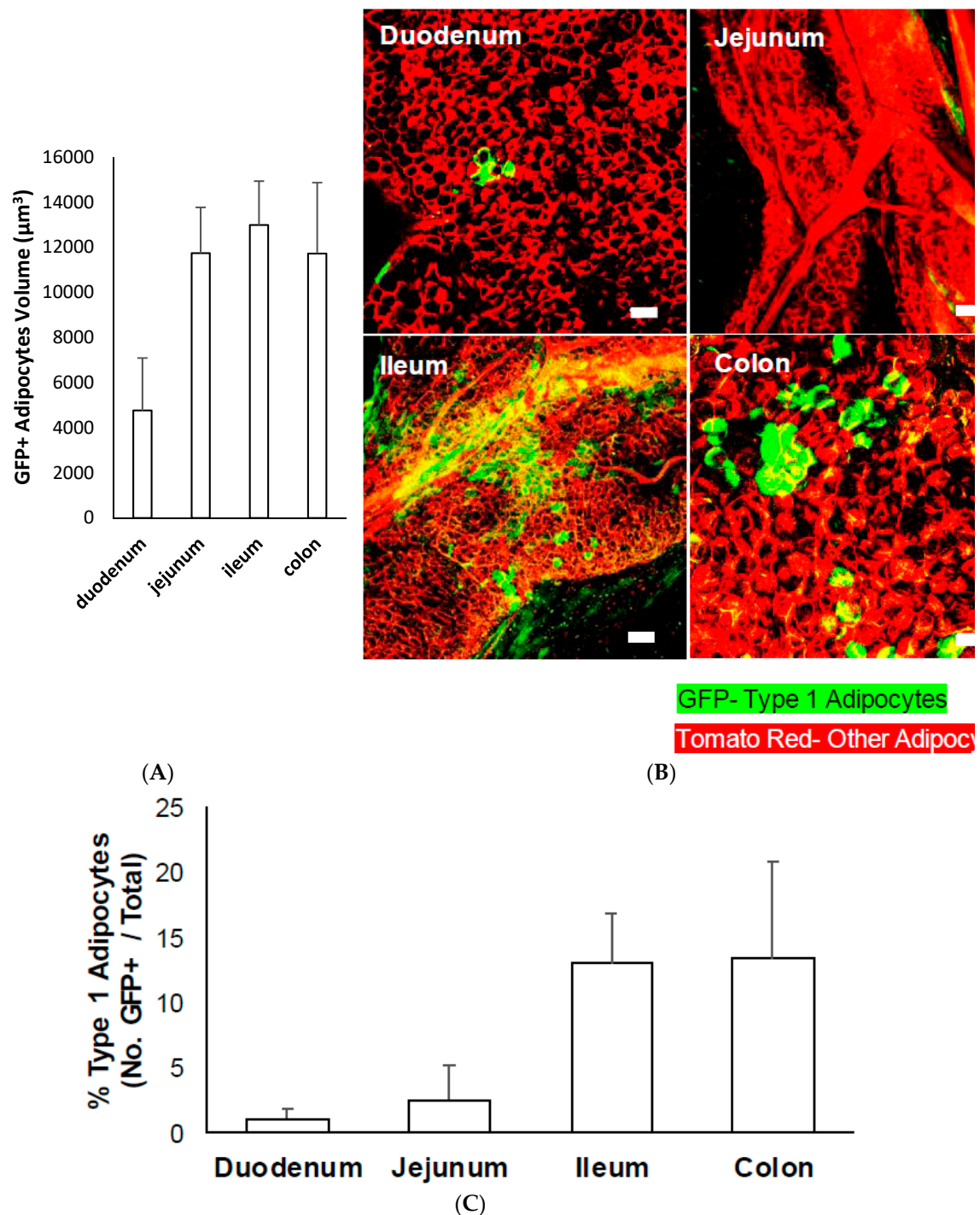


Figure S3. Confocal whole mount fluorescent imaging of mesenteric fat confirms findings of the tissue clearing technique as Type-1 adipocytes are associated with the ileum and colon. A)

Average calculated volumes of GFP+ adipocytes in mesenteric fat associated with different intestinal regions; B) Representative confocal images of whole mount fluorescence of mesenteric fat from two 6-week-old *Wt1-cre^{ERT2}/ROSA26^{mTmG}* mice associated with the duodenum, jejunum, ileum, and colon; C) Quantitation of GFP+ adipocytes in each region. All pictures were taken at 100x magnification. Scale bar = 100 μm .

Kernel Density Estimation Script

The following is the Kernel density estimation script written in R Studio.

```
#Loading Perl packages
```

```
library(imager)
```

```
library(ggplot2)
```

```
#loading images
```

```
Image <-load.image("")
```

```
Control <-load.image("")
```

```
#image processing into numerical values
```

```
fat <-as.data.frame(Image)
```

```
ctrl <-as.data.frame(Control)
```

```
#because individual image is a combination of three colors (Red, Green, and Blue), blue is extracted because it does not interfere with the existing green and red fluorescence colors in the image.
```

```
cells <- fat[which(fat$cc=='3'),]
```

```
cellsctrl<-ctrl[which(ctrl$cc=='3'),]
```

```
#convert those data point back to image format using cimg
```

```
cells <- points %>% as.cimg
```

```
cellsctrl<-pointsctrl %>% as.cimg
```

```
#convert it to grayscale for easier manipulation later on
```

```
c <-grayscale(cells)
```

```
cctrl<-grayscale(cellsctrl)
```

```
#blur out the image
```

```
c <- isoblur(c,10)
```

```
cctrl<-isoblur(cctrl,2)
```

```
#convert those data point back to image format using cimg
```

```
cells <- cells %>% as.cimg
```

```
cellsctrl<-cellsctrl %>% as.cimg
```

#Mathematically speaking, local maxima and minima can be found using second order derivatives. Because an image had both x and y variables, a second order partial derivative, $f''(x)$, such as the Hessian matrix was used. Hessian matrix is a square matrix of second-order partial derivatives function. The following equation described the Hessian matrix, where I_{xx} and I_{yy} are second partial derivatives of x and y, respectively.

$$\det(H) = I_{xx} \times I_{yy} - I_{xy}^2$$

```
Hdet<-with(imhessian(c),(xx*yy-xy^2))
Hdetctrl<-with(imhessian(cctrl),(xx*yy-xy^2))
plot(Hdet)
```

```
#set threshold to allow only points greater than 99.5% intensity to show up and stored as lab and
labctrl for experimental and control, respectively.
lab <- threshold(Hdet,"99.5%")>%label
labctrl <- threshold(Hdetctrl,"99.5%")>%label
plot(lab) #check to see if the points detected were only the GFP+ adipocytes initially present in the
image.
```

```
#convert to data frame and retrieve any data with value greater than 0 (non-background)
df<-as.data.frame(lab)%>%subset(value>0)
dfctrl<-as.data.frame(labctrl)%>%subset(value>0)
unique(df$value)
unique(dfctrl$value)
```

```
#finding center points (local maxima)
centers <- ddply(df,.(value),summarize, x=mean(x),y=mean(y))
centersctrl <- ddply(dfctrl,.(value),summarize, x=mean(x),y=mean(y))
```

```
#plot center points with original blob plots
plot(c)
with(centers,points(x,y,col="red"))
plot(cctrl)
with(centersctrl,points(x,y,col="red"))
```

```
#pixels for those center points for KDE analysis were retrieved; retrieve columns 2 and 3 from the
previous data
xypixels <- centers[,c(2,3)] #GFP+ adipocytes collected
xyctrl<-centersctrl[,c(2,3)] #control points
```

```
#Statistical test
library(ks)
```

```
#GFP+ cells vs all control cells and rounding to three digits of significant digits
w<-signif(kde.test(x1=xypixels,x2=xyctrl)$pvalue,digits=3)
```

```
#plotting images
m = ggplot(xypixels, aes(x=x,y=y)) +
  stat_density2d(aes(alpha=..level..,fill=..level..), size=2,bins=20, geom="polygon")+
  scale_fill_gradient(low = "yellow", high = "red") +
  scale_alpha(range = c(0.01, 0.8), guide = FALSE)+
```

```
geom_density2d(colour="blue", bins=10)+  
geom_point(data=xypixels)+  
guides(alpha=FALSE) + xlim(0, 1900) + ylim(0, 1400)+  
ggtitle("Mesenteric fat")+  
annotate("text",x=1500,y=200, label='p-value=')+  
annotate("text",x=1500,y=100,label=w)  
plot(m)
```