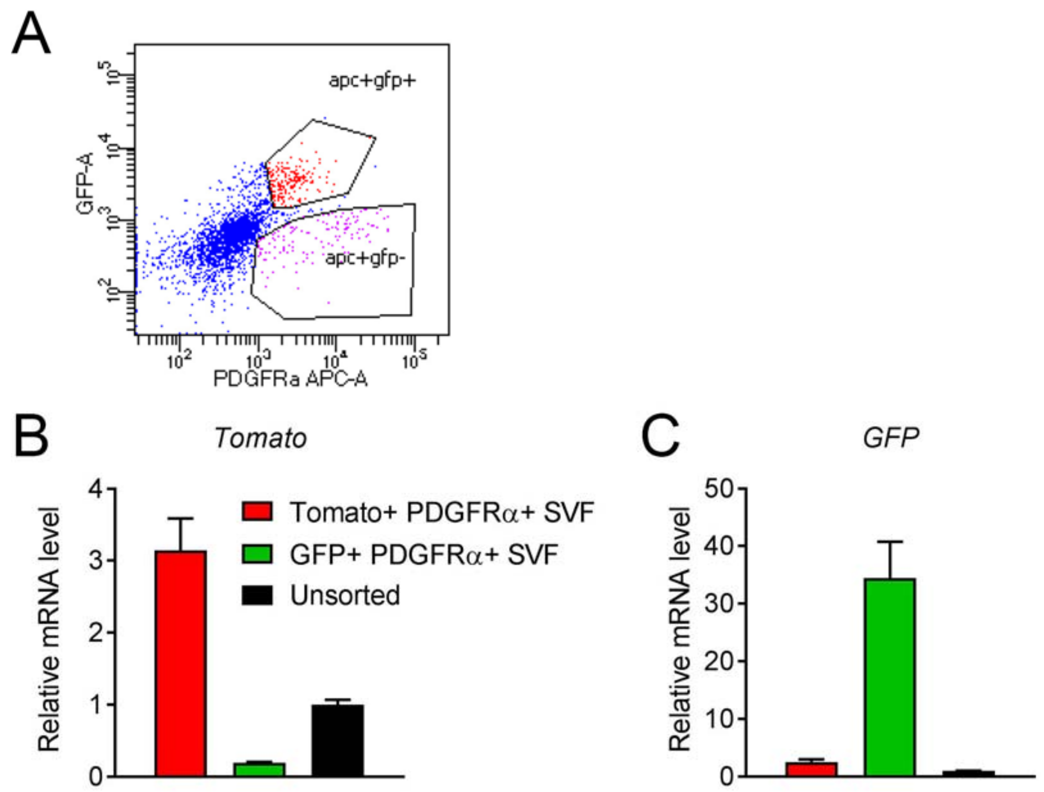
**Cell Metabolism, Volume *28***

## Supplemental Information

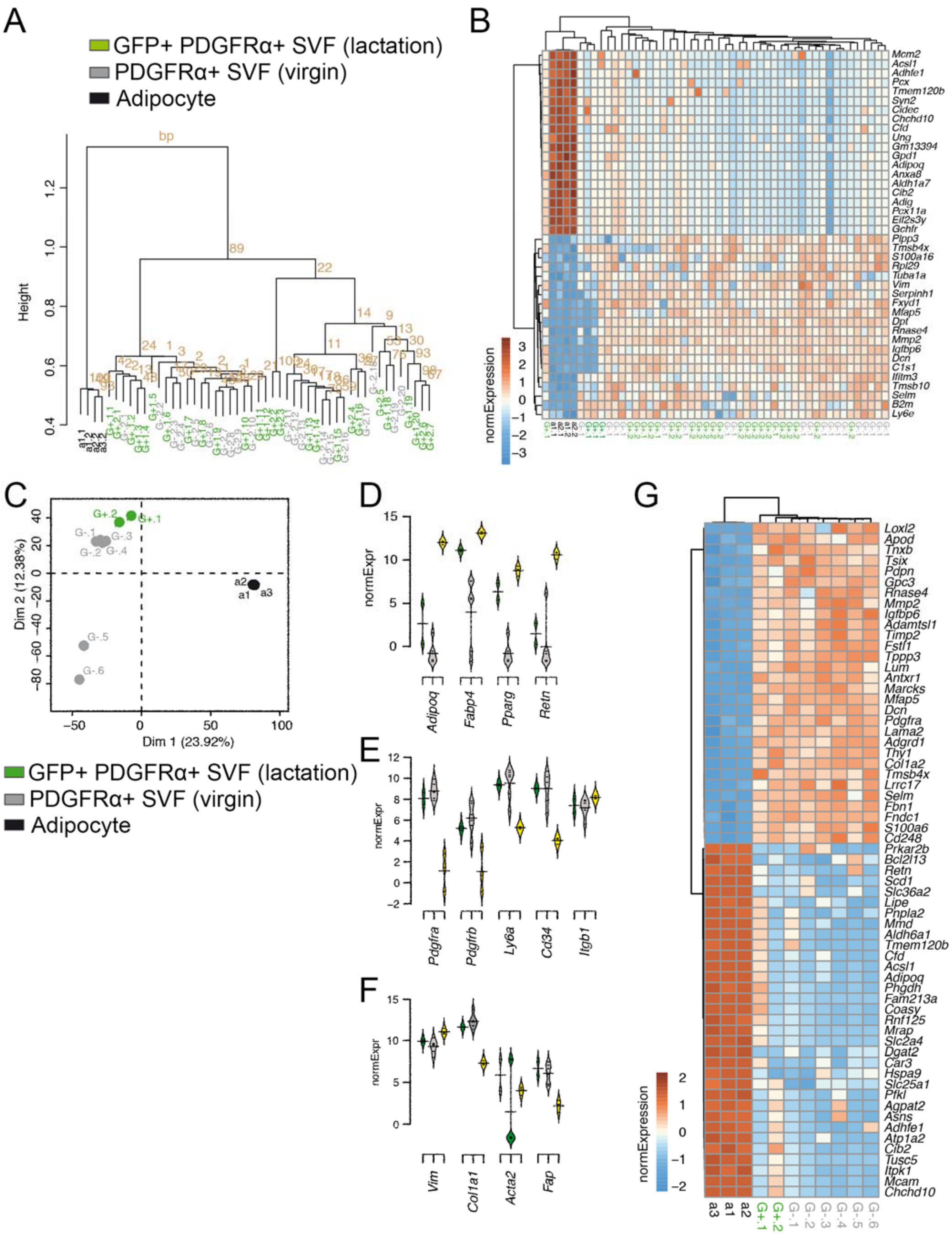
# Reversible De-differentiation of Mature White Adipocytes into Preadipocyte-like Precursors during Lactation

**Qiong A. Wang, Anying Song, Wanze Chen, Petra C. Schwalie, Fang Zhang, Lavanya Vishvanath, Lei Jiang, Risheng Ye, Mengle Shao, Caroline Tao, Rana K. Gupta, Bart Deplancke, and Philipp E. Scherer**



**Supplemental Figure 1. FACS sorting of the de-differentiated mammary adipocytes (related to Figure 4)**

(A) FACS sorting of the de-differentiated mammary adipocytes (CD31$^{-}$/CD45$^{-}$/PDGFRα$^{+}$/GFP$^{+}$ cells) from the mammary gland SVFs of lactating females. (B, C) qPCR analysis shows the mRNA expression levels of *Tomato* (B) and *GFP* (C) in the sorted CD31$^{-}$/CD45$^{-}$/PDGFRα$^{+}$/Tomato$^{+}$ and CD31$^{-}$/CD45$^{-}$/PDGFRα$^{+}$/GFP$^{+}$ cells from the mammary gland SVFs of lactating females. *n* = 2 sorted cell samples.


A
GFP+ PDGFRα+ SVF (lactation)
PDGFRα+ SVF (virgin)
Adipocyte
bp
Height
0.4
0.6
0.8
1.0
1.2
89
22
14
9
13
30
93
11
24
1
3
2
a1.1
a1.2
a2.2
a3.2
B
Mcm2
Acsl1
Adhfe1
Pcx
Tmem120b
Syn2
Cidec
Chchd10
Cfd
Ung
Gm13394
Gpd1
Adipoq
Anxa8
Aldh1a7
Cib2
Adig
Pcx11a
Eif2s3y
Gchfr
Plpp3
Tmsb4x
S100a16
Rpl29
Tuba1a
Vim
Serpinh1
Fxyd1
Mfap5
Dpt
Rnase4
Mmp2
Igfbp6
Dcn
C1s1
Ifitm3
Tmsb10
Selm
B2m
Ly6e
normExpression
3
2
1
0
−1
−2
−3
C
G+.2
G+.1
G−.1
G−.3
G−.2
G−.4
a2
a1
a3
G−.5
G−.6
Dim 1 (23.92%)
Dim 2 (12.38%)
40
20
0
−20
−40
−60
−80
−50
0
50
100
GFP+ PDGFRα+ SVF (lactation)
PDGFRα+ SVF (virgin)
Adipocyte
D
normExpr
15
10
5
0
Adipoq
Fabp4
Pparg
Retn
E
normExpr
12
10
8
6
4
2
0
−2
Pdgfra
Pdgfrb
Ly6a
Cd34
Itgb1
F
normExpr
15
10
5
0
Vim
Col1a1
Acta2
Fap
G
Loxl2
Apod
Tnxb
Tsix
Pdpn
Gpc3
Rnase4
Mmp2
Igfbp6
Adamtsl1
Timp2
Fstl1
Tppp3
Lum
Antxr1
Marcks
Mfap5
Dcn
Pdgfra
Lama2
Adgrd1
Thy1
Col1a2
Tmsb4x
Lrrc17
Selm
Fbn1
Fndc1
S100a6
Cd248
Prkar2b
Bcl2l13
Retn
Scd1
Slc36a2
Lipe
Pnpla2
Mmd
Aldh6a1
Tmem120b
Cfd
Acsl1
Adipoq
Phgdh
Fam213a
Coasy
Rnf125
Mrap
Slc2a4
Dgat2
Car3
Hspa9
Slc25a1
Pfkl
Agpat2
Asns
Adhfe1
Atp1a2
Cib2
Tusc5
Itpk1
Mcam
Chchd10
normExpression
2
1
0
−1
−2
a3
a1
a2
G+.1
G+.2
G−.1
G−.2
G−.3
G−.4
G−.5
G−.6

**Supplemental Figure 2. Sample clustering and expression overview of GFP positive, negative, and mature adipocyte control samples from single-cell and population RNA-seq analysis (related to Figure 4)**

(A) Overview of single-cell clustering of 26 de-differentiated mammary adipocytes (CD31$^-$/CD45$^-$/PDGFRα$^+$/GFP$^+$ cells) from the mammary gland SVFs of lactating females, 20 classic preadipocytes (CD31$^-$/CD45$^-$/PDGFRα$^+$ cells) from the mammary gland SVFs of virgin females, and 4 brown adipocytes by hierarchical clustering. BP – bootstrap probability value (a, black). (B) Heat map of the expression (row-wise z-scores of log_cpm, blue to red) of top 20 genes significantly up- and downregulated, respectively (FDR 0.05, FC 2) in both GFP+, and GFP- versus mature adipocytes, as assessed by single-cell RNA-seq. (C) Overview of sample grouping by principal component analysis (population GFP+, GFP- and mature adipocyte samples, normExpr). (D-F) Beanplots showing the distribution of normalized expression values across samples that belong to one of these three categories of common adipocyte markers (D), common preadipocyte markers (E) and common fibroblast markers (F). (G) Heat map of the expression (row-wise z-scores of log_cpm, normExpr, blue to red) of top 20 genes significantly up- and down-regulated, respectively (FDR 0.1, FC 2) in both GFP+ and GFP- versus mature adipocytes, as assessed by both population and single-cell RNA-seq (intersection).