Fig. S1

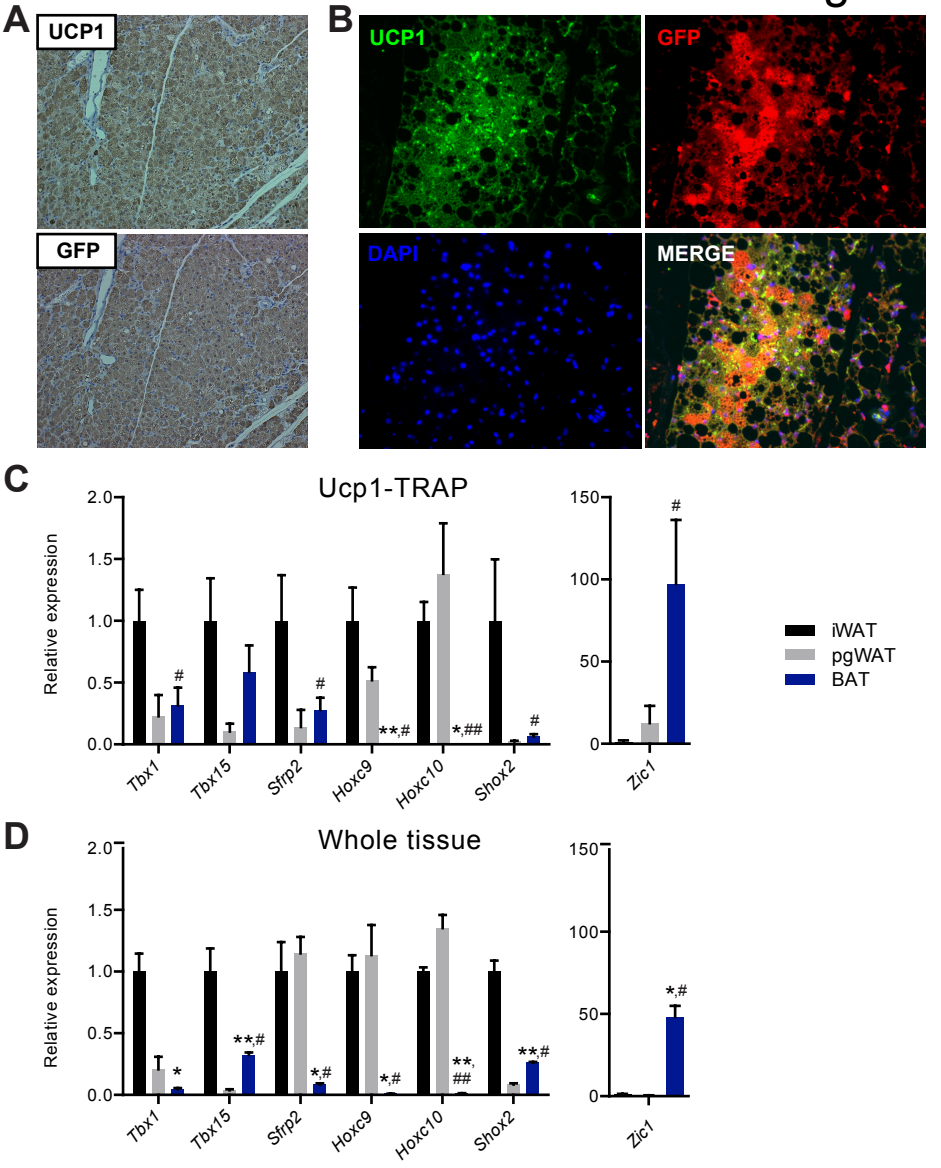
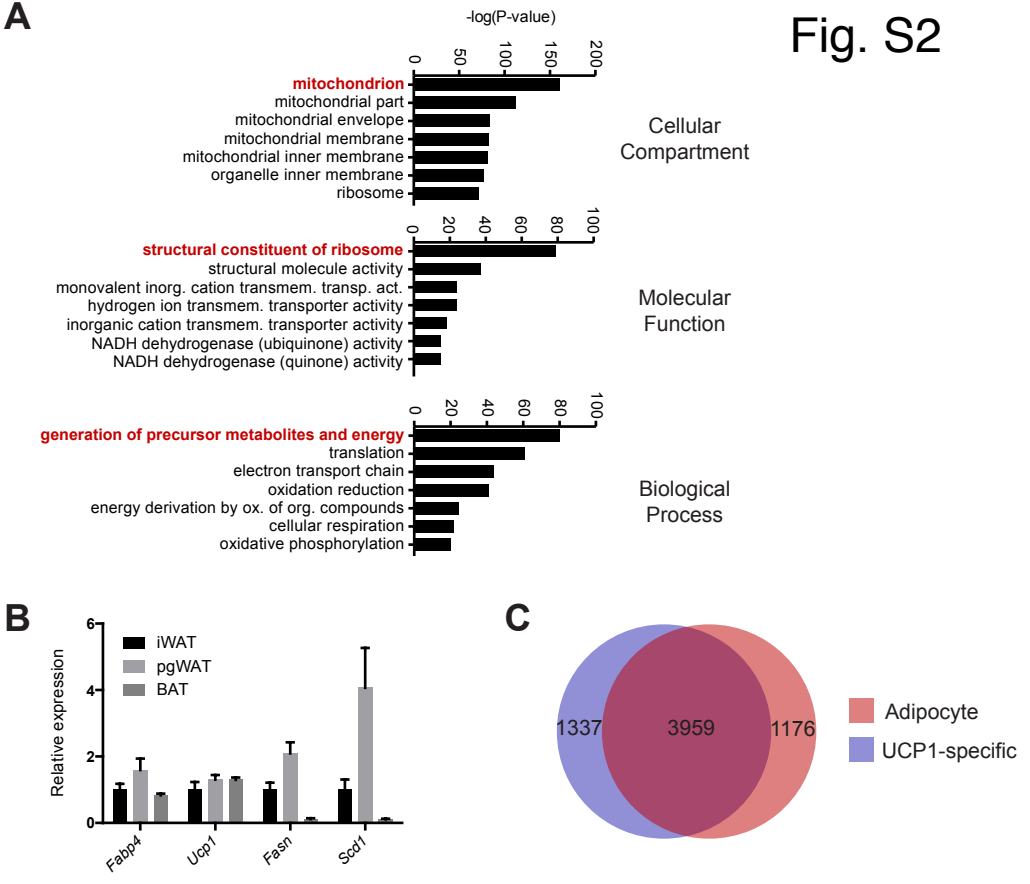

A
UCP1
GFP
B
UCP1
GFP
DAPI
MERGE
C
Ucp1-TRAP
Relative expression
2.0
1.5
1.0
0.5
0.0
150
100
50
0
Tbx1
Tbx15
Sfrp2
Hoxc9
Hoxc10
Shox2
Zic1
iWAT
pgWAT
BAT
D
Whole tissue
Relative expression
2.0
1.5
1.0
0.5
0.0
150
100
50
0
Tbx1
Tbx15
Sfrp2
Hoxc9
Hoxc10
Shox2
Zic1

Fig. S2


A
-log(P-value)
0
50
100
150
200
mitochondrion
mitochondrial part
mitochondrial envelope
mitochondrial membrane
mitochondrial inner membrane
organelle inner membrane
ribosome
Cellular Compartment
0
20
40
60
80
100
structural constituent of ribosome
structural molecule activity
monovalent inorg. cation transmem. transp. act.
hydrogen ion transmem. transporter activity
inorganic cation transmem. transporter activity
NADH dehydrogenase (ubiquinone) activity
NADH dehydrogenase (quinone) activity
Molecular Function
generation of precursor metabolites and energy
translation
electron transport chain
oxidation reduction
energy derivation by ox. of org. compounds
cellular respiration
oxidative phosphorylation
Biological Process
B
Relative expression
0
2
4
6
iWAT
pgWAT
BAT
Fabp4
Ucp1
Fasn
Scd1
C
1337
3959
1176
Adipocyte
UCP1-specific

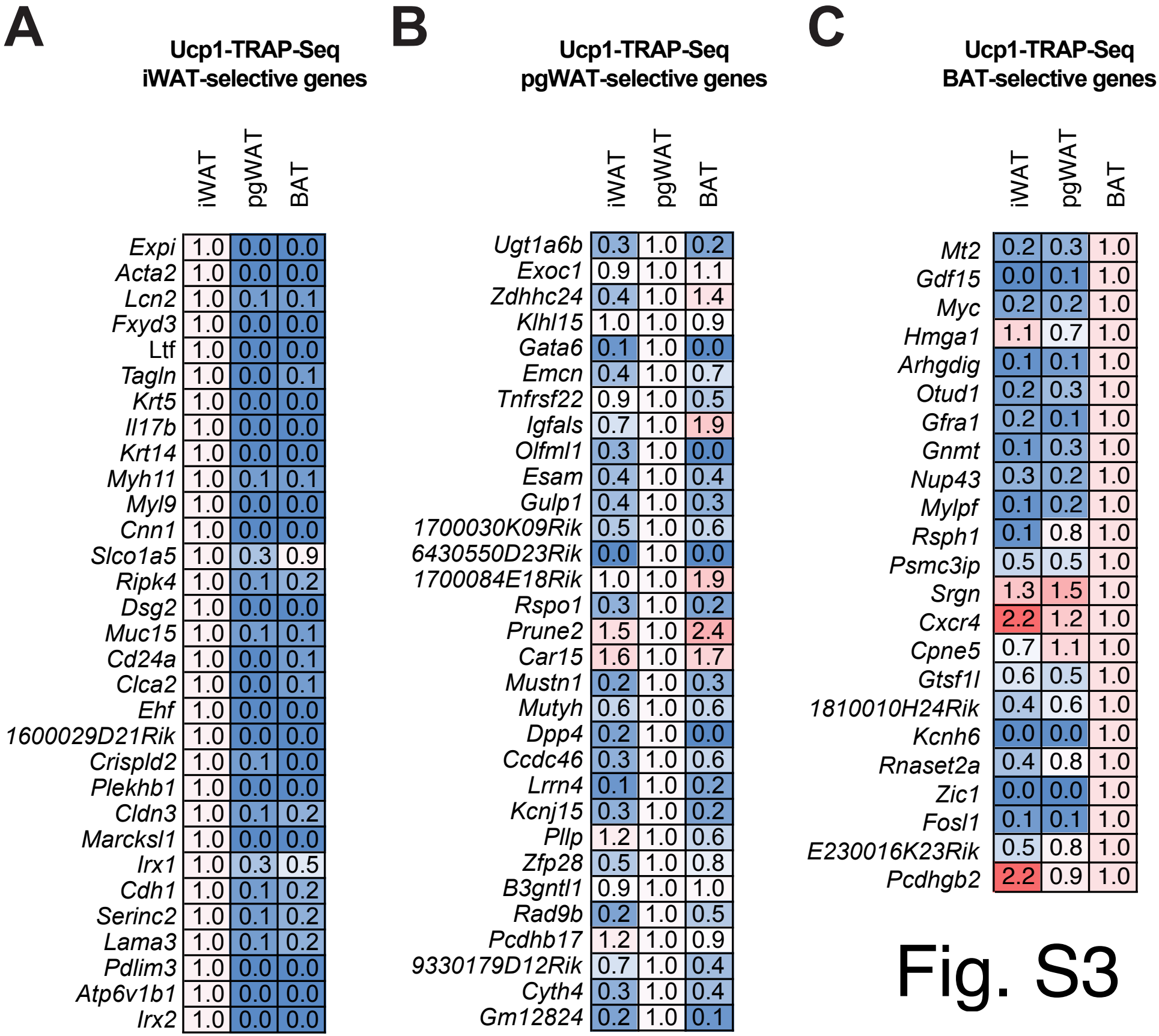

A
Ucp1-TRAP-Seq
iWAT-selective genes
iWAT pgWAT BAT
Expi 1.0 0.0 0.0
Acta2 1.0 0.0 0.0
Lcn2 1.0 0.1 0.1
Fxyd3 1.0 0.0 0.0
Ltf 1.0 0.0 0.0
Tagln 1.0 0.0 0.1
Krt5 1.0 0.0 0.0
Il17b 1.0 0.0 0.0
Krt14 1.0 0.0 0.0
Myh11 1.0 0.1 0.1
Myl9 1.0 0.0 0.0
Cnn1 1.0 0.0 0.0
Slco1a5 1.0 0.3 0.9
Ripk4 1.0 0.1 0.2
Dsg2 1.0 0.0 0.0
Muc15 1.0 0.1 0.1
Cd24a 1.0 0.0 0.1
Clca2 1.0 0.0 0.1
Ehf 1.0 0.0 0.0
1600029D21Rik 1.0 0.0 0.0
Crispld2 1.0 0.1 0.0
Plekhb1 1.0 0.0 0.0
Cldn3 1.0 0.1 0.2
Marcksl1 1.0 0.0 0.0
Irx1 1.0 0.3 0.5
Cdh1 1.0 0.1 0.2
Serinc2 1.0 0.1 0.2
Lama3 1.0 0.1 0.2
Pdlim3 1.0 0.0 0.0
Atp6v1b1 1.0 0.0 0.0
Irx2 1.0 0.0 0.0
B
Ucp1-TRAP-Seq
pgWAT-selective genes
iWAT pgWAT BAT
Ugt1a6b 0.3 1.0 0.2
Exoc1 0.9 1.0 1.1
Zdhhc24 0.4 1.0 1.4
Klhl15 1.0 1.0 0.9
Gata6 0.1 1.0 0.0
Emcn 0.4 1.0 0.7
Tnfrsf22 0.9 1.0 0.5
Igfals 0.7 1.0 1.9
Olfml1 0.3 1.0 0.0
Esam 0.4 1.0 0.4
Gulp1 0.4 1.0 0.3
1700030K09Rik 0.5 1.0 0.6
6430550D23Rik 0.0 1.0 0.0
1700084E18Rik 1.0 1.0 1.9
Rspo1 0.3 1.0 0.2
Prune2 1.5 1.0 2.4
Car15 1.6 1.0 1.7
Mustn1 0.2 1.0 0.3
Mutyh 0.6 1.0 0.6
Dpp4 0.2 1.0 0.0
Ccdc46 0.3 1.0 0.6
Lrrn4 0.1 1.0 0.2
Kcnj15 0.3 1.0 0.2
Pllp 1.2 1.0 0.6
Zfp28 0.5 1.0 0.8
B3gntl1 0.9 1.0 1.0
Rad9b 0.2 1.0 0.5
Pcdhb17 1.2 1.0 0.9
9330179D12Rik 0.7 1.0 0.4
Cyth4 0.3 1.0 0.4
Gm12824 0.2 1.0 0.1
C
Ucp1-TRAP-Seq
BAT-selective genes
iWAT pgWAT BAT
Mt2 0.2 0.3 1.0
Gdf15 0.0 0.1 1.0
Myc 0.2 0.2 1.0
Hmga1 1.1 0.7 1.0
Arhgdig 0.1 0.1 1.0
Otud1 0.2 0.3 1.0
Gfra1 0.2 0.1 1.0
Gnmt 0.1 0.3 1.0
Nup43 0.3 0.2 1.0
Mylpf 0.1 0.2 1.0
Rsph1 0.1 0.8 1.0
Psmc3ip 0.5 0.5 1.0
Srgn 1.3 1.5 1.0
Cxcr4 2.2 1.2 1.0
Cpne5 0.7 1.1 1.0
Gtsf1l 0.6 0.5 1.0
1810010H24Rik 0.4 0.6 1.0
Kcnh6 0.0 0.0 1.0
Rnaset2a 0.4 0.8 1.0
Zic1 0.0 0.0 1.0
Fosl1 0.1 0.1 1.0
E230016K23Rik 0.5 0.8 1.0
Pcdhgb2 2.2 0.9 1.0
Fig. S3

Fig. S4

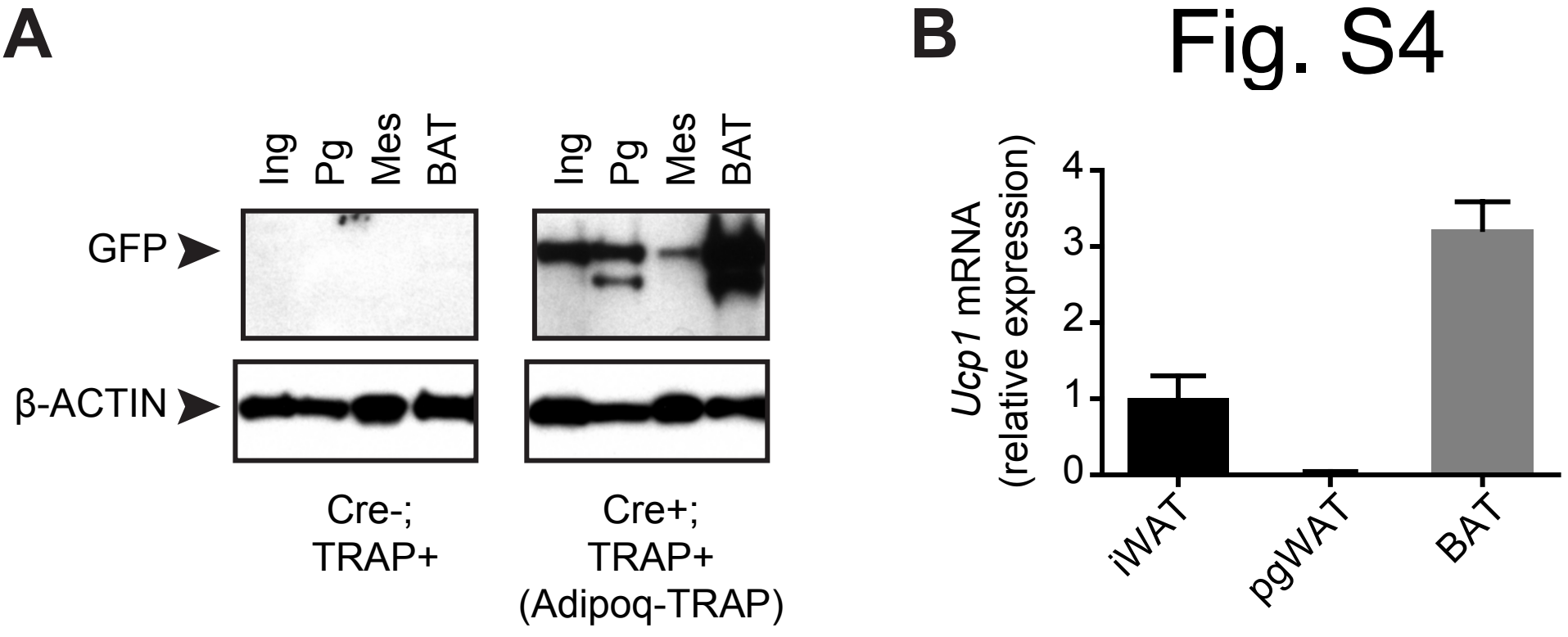
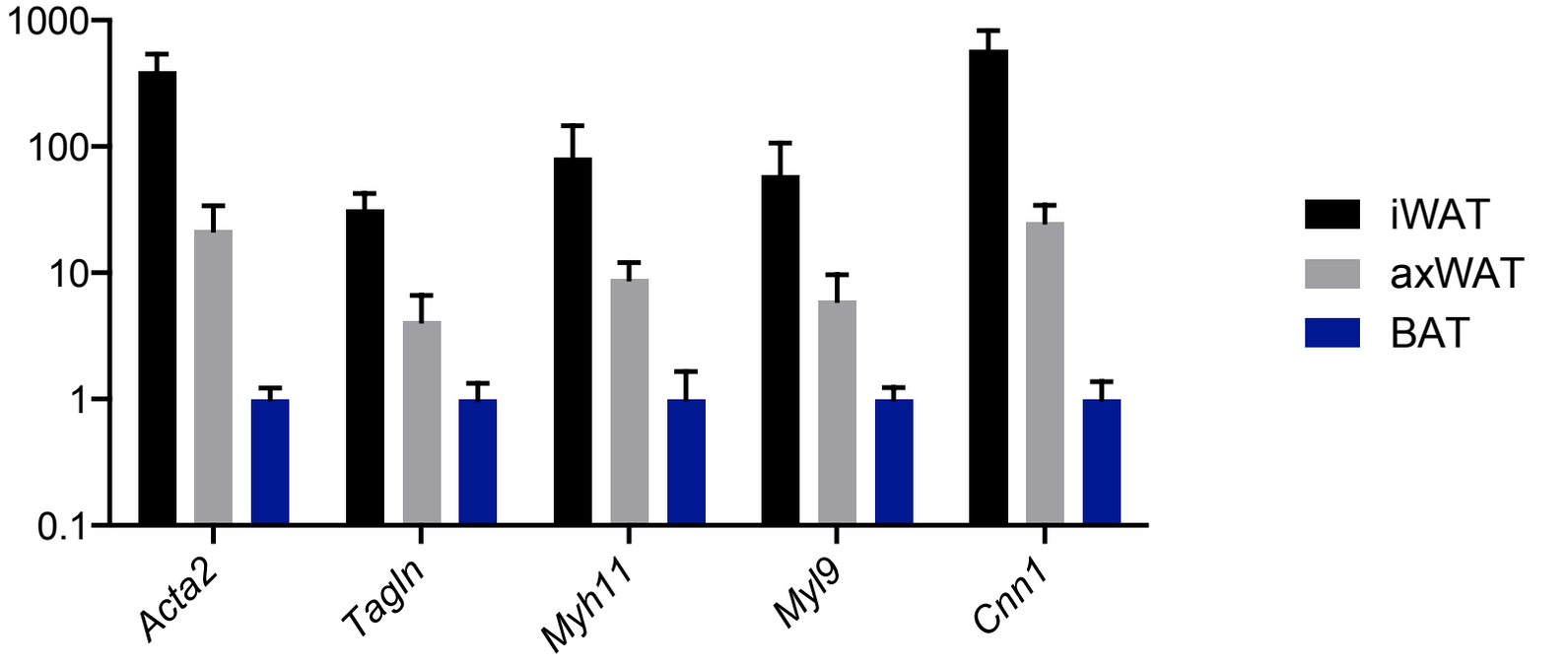

A
Ing
Pg
Mes
BAT
Ing
Pg
Mes
BAT
GFP
β-ACTIN
Cre-;
TRAP+
Cre+;
TRAP+
(Adipoq-TRAP)
B
Ucp1 mRNA
(relative expression)
4
3
2
1
0
iWAT
pgWAT
BAT

Fig. S5

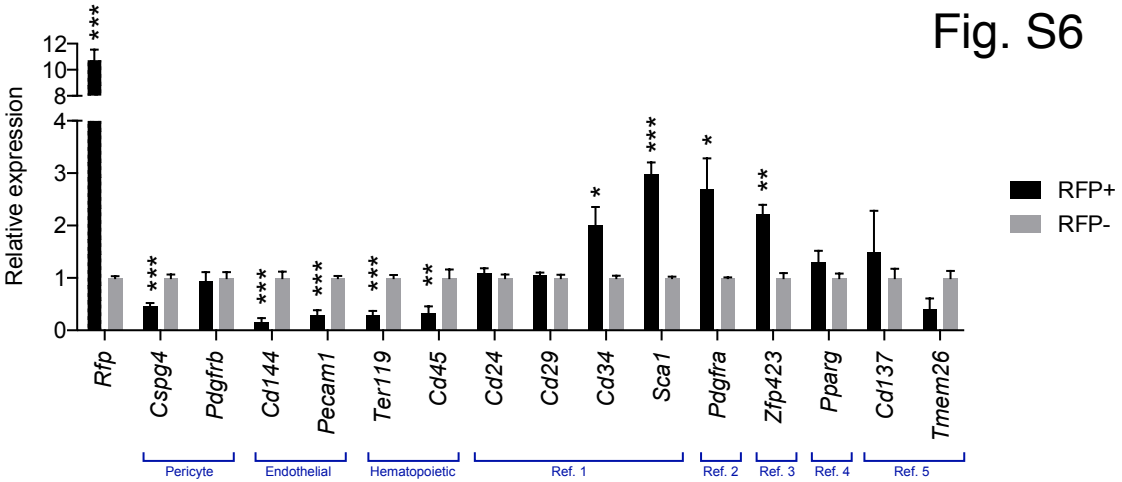
A



B

	iWAT			pgWAT		BAT			
Cspg4	2.9	3.7	2.0	6.4	4.4	1.7	1.9	1.2	Pericyte markers
Pdgfrb	0.5	0.5	0.1	0.7	0.4	0.0	0.0	0.3	
Pecam1	0.2	1.0	0.2	2.6	0.8	0.7	0.7	0.7	
Cdh5	0.6	0.8	0.3	2.1	0.5	0.1	0.0	0.1	endothelial cell markers
Thbd	0.0	0.0	0.0	2.9	0.1	0.2	0.0	0.0	
Vwf	0.0	0.2	0.0	0.3	0.2	0.1	0.1	0.1	
Acta2	90.0	38.4	25.7	2.2	0.9	0.0	0.0	0.6	SMC markers
Myh11	7.8	5.4	3.0	0.4	0.3	0.1	0.0	0.0	
Myl9	9.0	2.6	3.5	1.4	0.4	0.0	0.0	0.0	
Cnn1	7.8	3.5	2.9	0.5	0.0	0.0	0.2	0.2	
Tagln	21.7	8.8	7.2	1.3	0.8	0.0	0.0	0.0	

Fig. S6


Relative expression
12
10
8
4
3
2
1
0
***
***
***
***
***
**
*
***
*
**
RFP+
RFP-
Rfp
Cspg4
Pdgfrb
Cd144
Pecam1
Ter119
Cd45
Cd24
Cd29
Cd34
Sca1
Pdgfra
Zfp423
Pparg
Cd137
Tmem26
Pericyte
Endothelial
Hematopoietic
Ref. 1
Ref. 2
Ref. 3
Ref. 4
Ref. 5