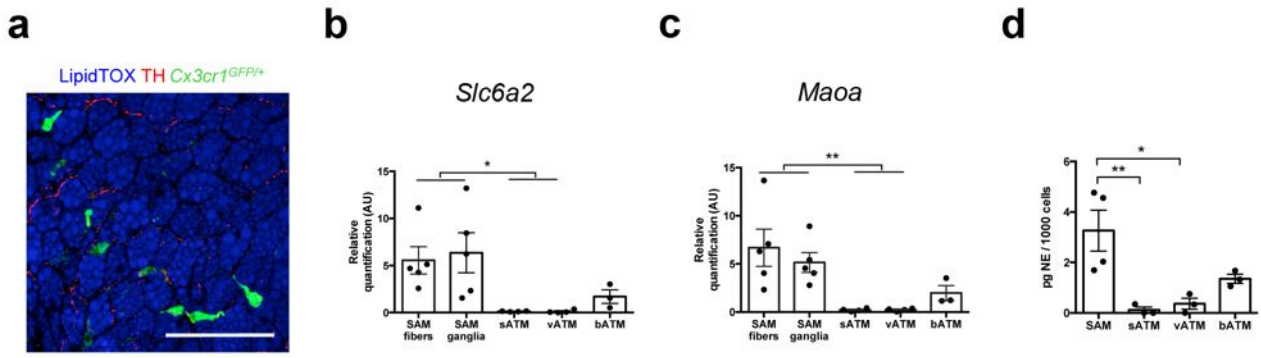
Supplementary Figure 10



Supplementary Figure 10. Macrophages in brown adipose tissue have intermediate phenotype between ATMs and SAMs.
(a) Confocal image of BAT isolated from *Cx3cr1*$^{GFP/+}$ mice and stained using lipid stain LipidTOX (blue), anti-TH (red) and anti-GFP (green) antibodies. Micrograph is representative of 2 experiments. Scale bar, 100 μm. **(b)** Expression of mRNA for *Slc6a2* determined by qRT-PCR relative to *Gapdh* expression. Each data point represents tissues pooled from 10 mice. n = 5 experiments for SAM fibers and SAM ganglia, n = 4 experiments for vATM, sATM, n = 3 experiments for bATM, $^{*}P < 0.05$. **(c)** Expression of mRNA for *Maoa* determined by qRT-PCR relative to *Gapdh* expression. Each data point represents tissues pooled from 10 mice. n = 5 experiments for SAM fibers and SAM ganglia, n = 4 experiments for vATM, sATM and n = 3 experiments for bATM, $^{**}P < 0.01$. **(d)** NE content in sorted CD45.2-PE, F4/80-Alexa Fluor 647 – double positive cells measured by NE ELISA. Number of cells used in NE assays were as follows: 858 ± 258 for SAMs (n = 4 experiments), 1000 cells for sATM and vATM (n = 3 experiments), 1494 ± 172 for bATM (n = 3 experiments). $^{*}P < 0.05$, $^{**}P < 0.01$. Data in panels **b**,**c**,**d** were analyzed by one-way ANOVA followed by Tukey's multiple comparison test and are shown as average ± SEM. Data for SAM, sATM and vATM in panels **b, c**, and **d** are also shown in **Figure 2 g, h,** and **i.**