SUPPLEMENTAL LEGENDS

Supplemental Figure 1. aP2-Cre Expression and Weights of Tissues in Control and A-BCA Mutant Mice

(A, B) X-gal staining (blue) of control (rosa26-flox-stop-flox-LacZ; R26R) or aP2-Cre; R26R (A) whole tissues and (B) subcutaneous adipose stromal vascular fraction (SVF). SVF counterstained with nuclear fast red. Note lack of X-gal staining in the SVF of aP2-Cre; R26R mice. IWAT = inguinal white adipose tissue (WAT), GWAT = perigonadal WAT, MWAT = mesenteric WAT.

(C) Kidney and heart weights of control (mixture of aP2-Cre and fBC mice) and A-BCA (aP2-Cre; fBC) siblings. $n \geq 8$ per cohort, $n \geq 3$ cohorts.

Error bars indicate standard error of the mean (SEM). Statistical significance assessed by two-tailed Student ’s t-test.

Supplemental Figure 2. Cre Expression in PPARγ-tTA System and Weights of Tissues in Control and P-BCA Mutant Mice

(A, B) X-gal staining (blue) of control (PPARγ-tTA; R26R) and PPARγ-tTA; TRE-Cre; R26R in (A) whole tissues and (B) subcutaneous adipose stromal vascular fraction (SVF). SVF counterstained with nuclear fast red. Note presence of X-gal staining (blue) in the SVF of PPARγ-tTA; TRE-Cre; R26R mice. IWAT = inguinal white adipose tissue (WAT), GWAT = perigonadal WAT, MWAT = mesenteric WAT.

(C) Comparison of Cre mRNA levels in adipocyte and stromal vascular (SV) cells of PPARγ-tTA; TRE-Cre mice.

(D) Comparison of Cre mRNA levels in aP2-Cre and PPARγ-tTA; TRE-Cre adipocytes.

(E) Kidney and heart weights of control (mixture of PPARγ-tTA; TRE-Cre and PPARγ-tTA; fBC) and P-BCA (PARγ-tTA; TRE-Cre; fBC) siblings. n ≥ 8 per cohort, n ≥ 3 cohorts

Error bars indicate SEM. Statistical significance assessed by two-tailed Student's t-test, *p<0.05

Supplemental Figure 3. Fibrotic and Genetic Changes as well as Lineage Tracing of BAT, Skin and Perigonadal Adipose Tissue of Control and P-BCA Mutant Mice

(A) Hematoxylin and eosin (H&E) stained histological sections of control and P-BCA brown adipose tissue (BAT).

(B) Trichrome stained histological sections of control and P-BCA skin.

(C) qCR of perigonadal adipose depots (PGW) of control and P-BCA siblings of the indicated adipogenic (PPARγ), fibroblast (Col-6a1, DDR2) and Wnt target (Wisp2) markers. n ≥ 6, repeated ≥ 3 cohorts

(D) Histological sections of X-gal stained P-BCA BAT and skin. Red arrows indicate lineage positive cells.

Error bars indicate SEM. Statistical significance assessed by two-tailed Student's t-test. **p<0.01

Genotypes: control = PPARγ-tTA; TRE-Cre, and PPARγ-tTA; fBC. P-BCA = PPARγ-tTA; TRE-Cre; fBC. For D, P-BCA = PPARγ-tTA; TRE-Cre; fBC; R26R.

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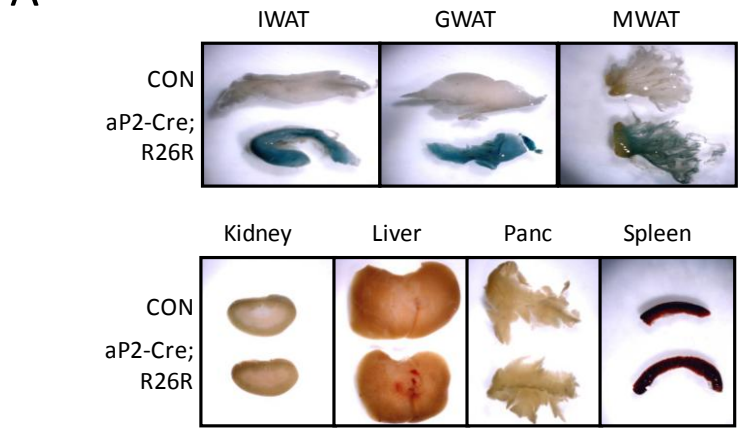
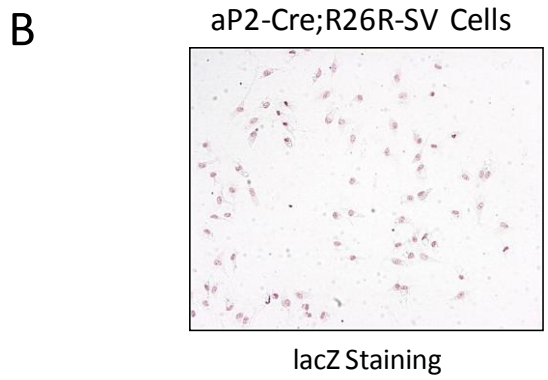
Serum insulin levels were quantified after two hours of insulin and glucose infusion in control (PPARγ-tTA; TRE-Cre and PPARγ-tTA; fBC) and P-BCA (PPARγ-tTA; TRE-Cre; fBC) siblings. $n \geq 8$ per cohort, repeated ≥ 3 cohorts

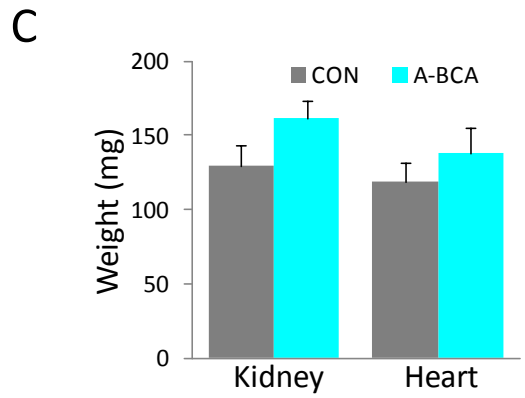
Error bars indicate SEM. Statistical significance was assessed by two-tailed Student's t-test**.**

Supplemental Information

Supplemental Figure 1







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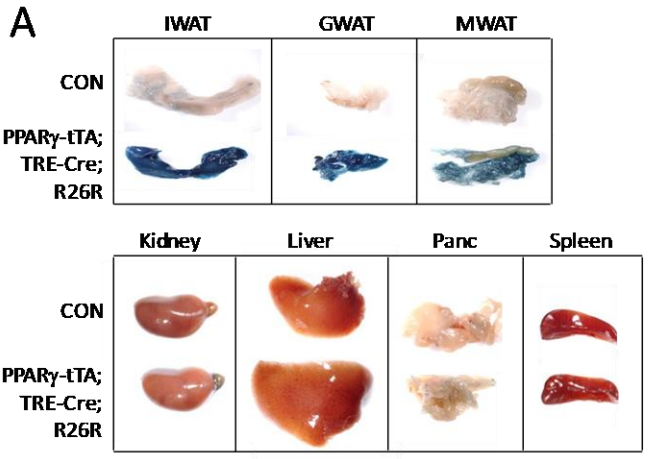

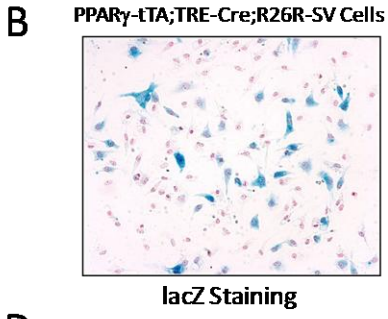

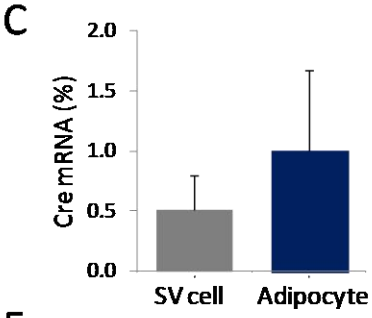

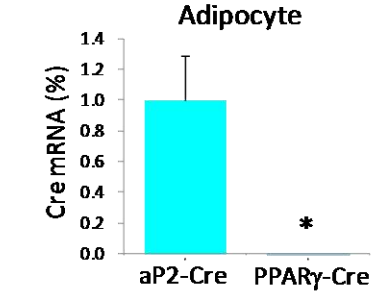

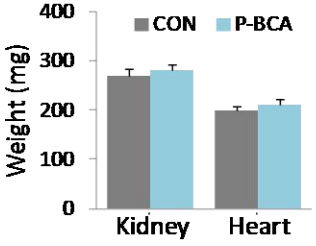

Supplemental Figure 3

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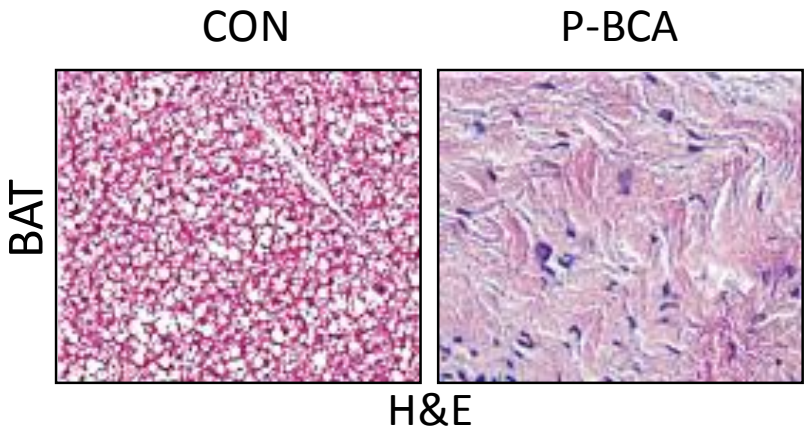

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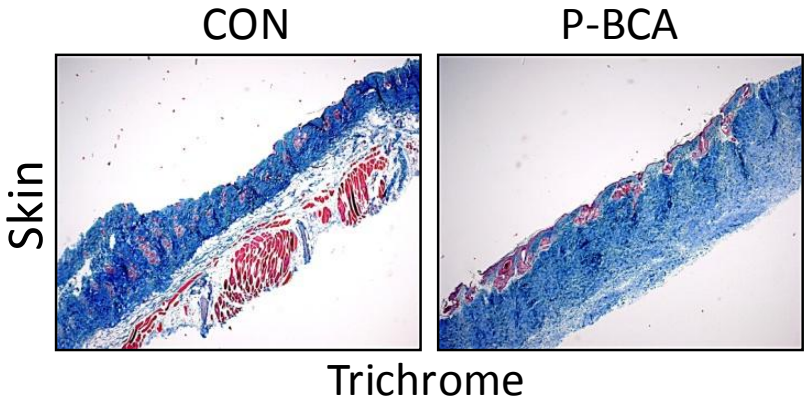

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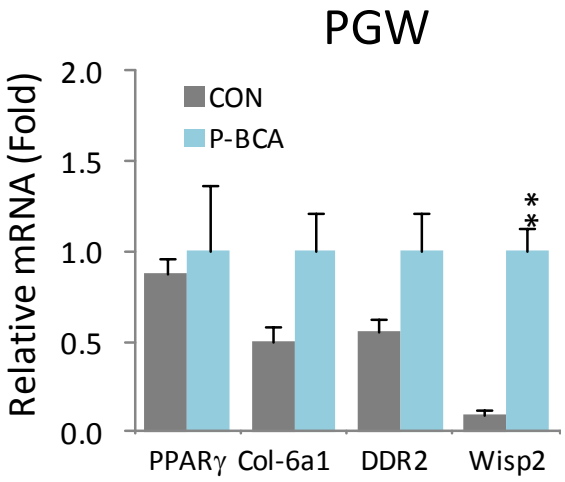

Supplement Figure 4

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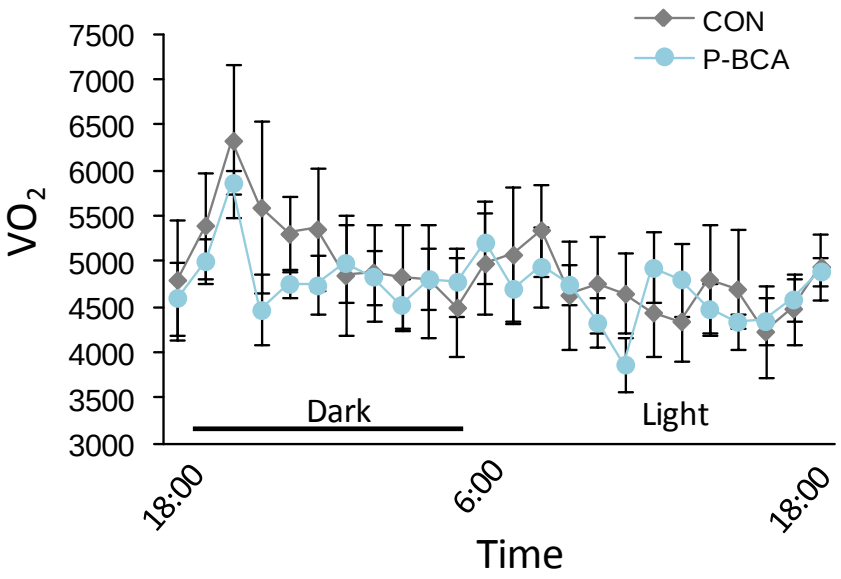

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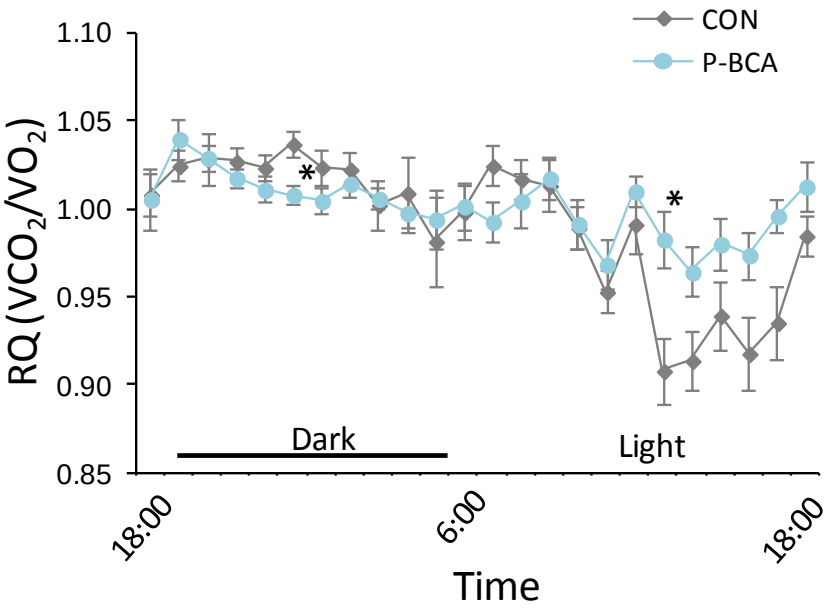

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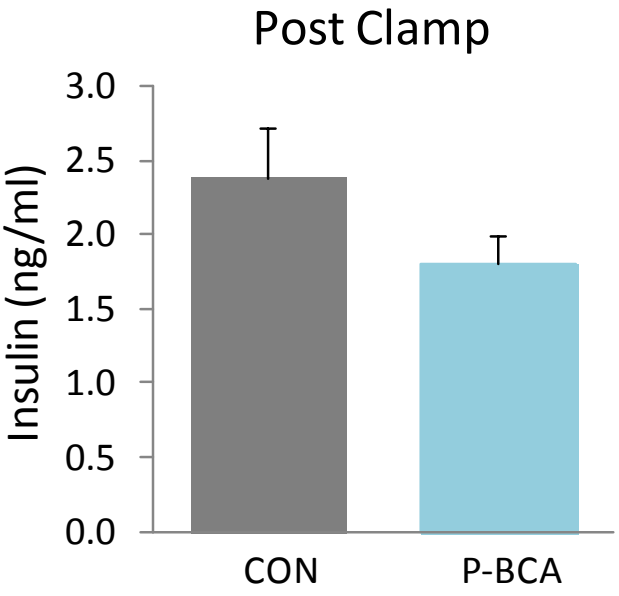

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