

Supplemental data

Maternal Retinoids Increase PDGFR α ⁺ Progenitor Population and Beige Adipogenesis in Progeny by Stimulating Vascular Development

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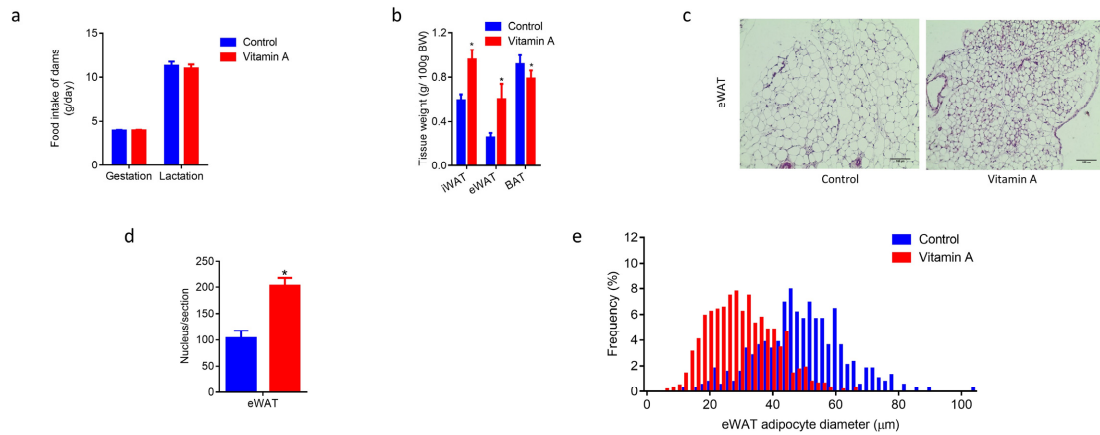


Figure S1. Maternal vitamin A supplementation affects adipose tissue deposition and morphology. For the MVA offspring, (a) Adipose tissue weight was calculated as the ratio to body weight. (b) Representative images of H&E stained eWAT. (c) Average number of nucleus per section. (d) Distribution of adipocytes size in eWAT. (e) Food intake of mother mice during pregnancy and lactation. Data presented are mean \pm SEM, $n = 6$, unpaired two-tail t-test, $*p < 0.05$.

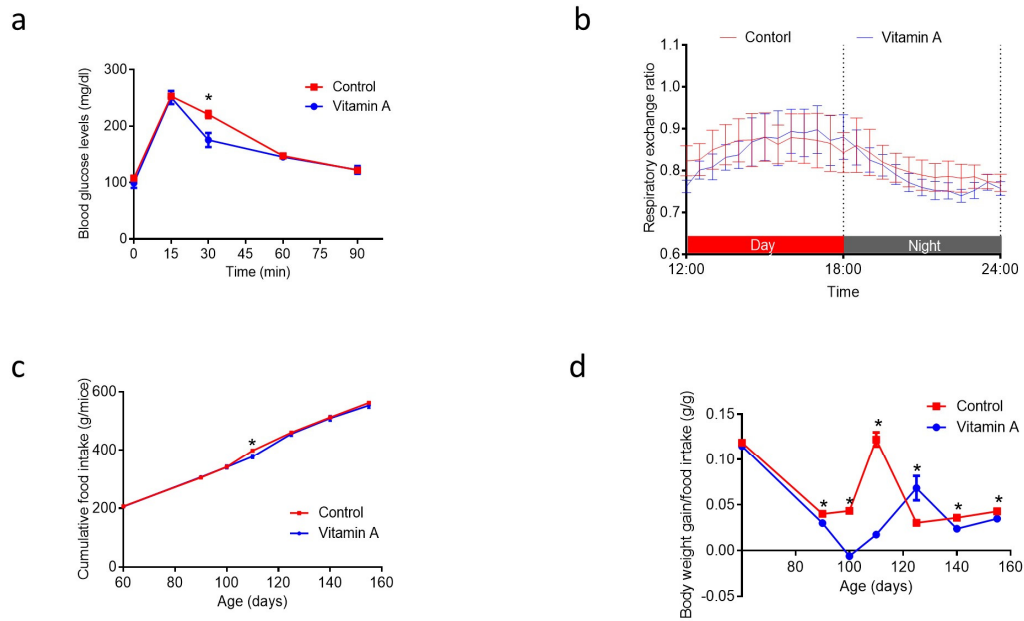


Figure S2. Maternal vitamin A supplementation prevents offspring obesity development induced by high fat diet. MVA offspring were fed a high fat diet (HFD, 45% energy from fat) from 30 days to 155 days old. **(a)** Glucose tolerance test at the beginning of HFD feeding ($n = 3$). **(b)** Respiratory exchange ratio after HFD feeding ($n = 4$). **(c)** Food intake during HFD feeding ($n = 3$). **(d)** Ratio of body weight gain/food intake ($n = 3$). Data presented are mean \pm SEM, unpaired two-tail t-test, $*p < 0.05$.

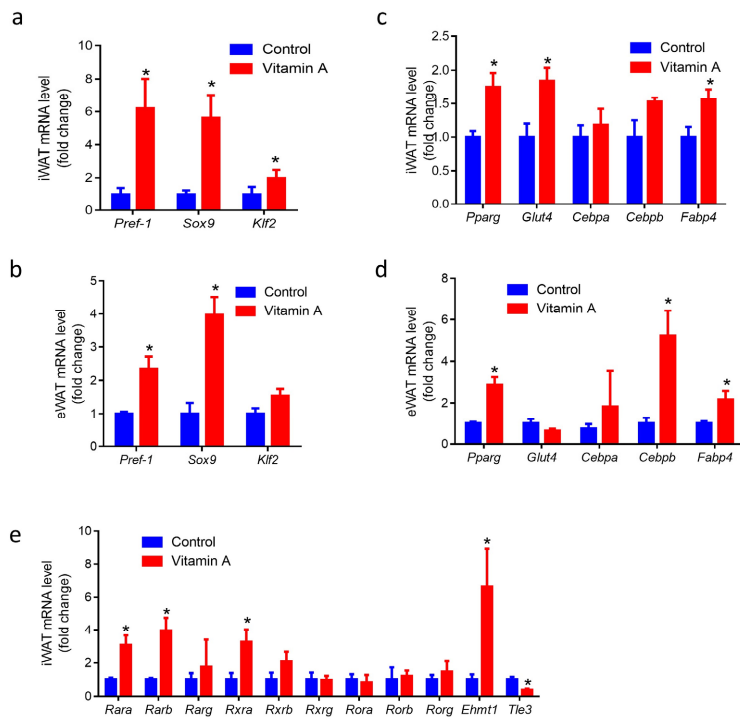


Figure S3. Maternal vitamin A supplementation promotes brown/beige adipogenesis in both white and brown adipose tissue. (a-b) mRNA levels of preadipose marker genes in iWAT (a) and eWAT (b). **(c-d)** mRNA levels of adipocyte markers in iWAT (c) and eWAT (d). **(e)** mRNA levels of RARs, RORs and other adipose related genes in iWAT. Data presented are mean \pm SEM, n = 6, unpaired two-tail t-test, * $p < 0.05$.

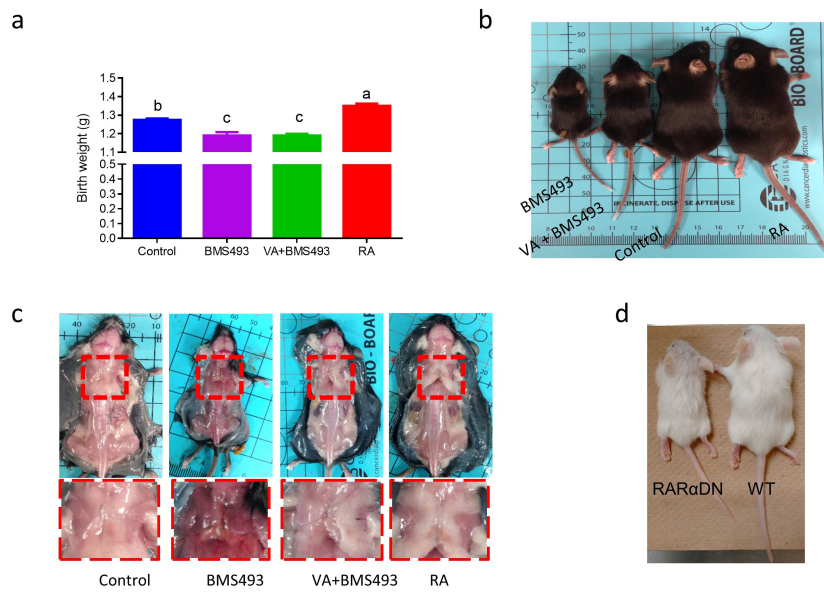


Figure S4. Retinoic acid signaling is required for fetal adipose tissue development. Pregnant mice were injected with BMS493 or RA at E10.5 and 13.5, and one BMS493 treated group was supplemented with vitamin A during gestation. **(a)** Birth weight. **(b)** Representative images of offspring at weaning **(c)** Representative images of subcutaneous fat tissue at weaning. **(d)** Representative images of weaning *Pdgfra-cre/ER/RARαDN* offspring. Data presented are mean \pm SEM, n = 6, ANOVA, bars with different letters differ significantly.

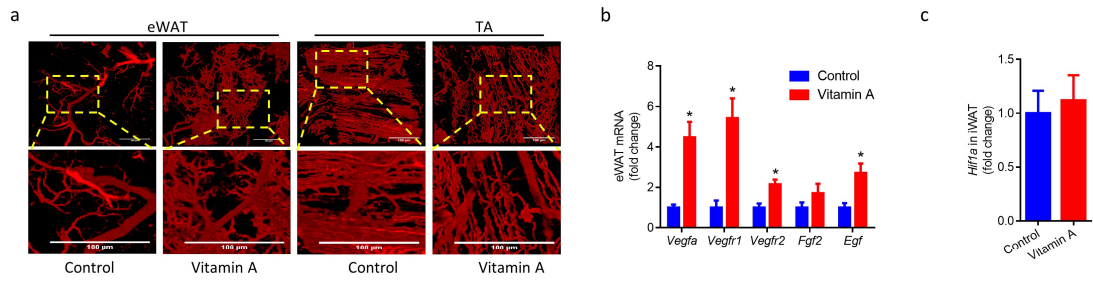


Figure S5. Maternal retinoic acid promotes vasculature in adipose tissues. For the MVA weaning offspring, **(a)** Blood vessels in eWAT and *Tibialis anterior* (TA) muscle stained by Dil. **(b)** mRNA levels of angiogenic genes in eWAT. **(c)** Expression of *Hif1a* in iWAT. $n = 6$. Data presented are mean \pm SEM, unpaired two-tail t-test, $*p < 0.05$.

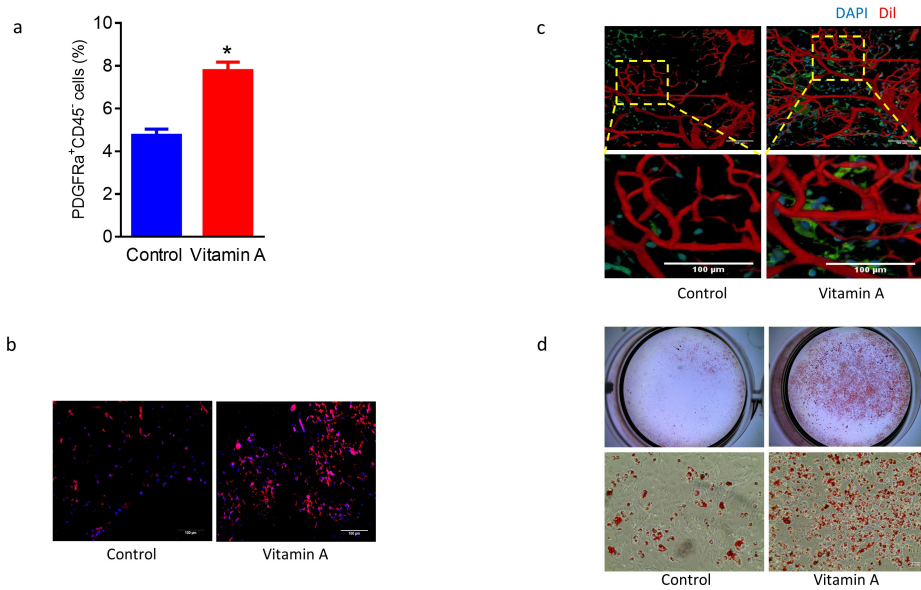


Figure S6. Maternal vitamin A increases PDGFR α ⁺ population in adipose tissue of weanling offspring. (a) Quantification of PDGFR α ⁺CD45⁻ cells in iWAT analyzed by flow cytometry. (b) Images of IHC staining of eWAT section using anti-PDGFR α antibody. (c) Representative images showing blood vessels and PDGFR α ⁺ cells in iWAT. (d) iWAT derived SVCs differentiated for 6 days in brown adipogenic medium, and adipocytes were stained by Oil-Red O. Data presented are mean \pm SEM, unpaired two-tail t-test, n = 4, * p < 0.05.

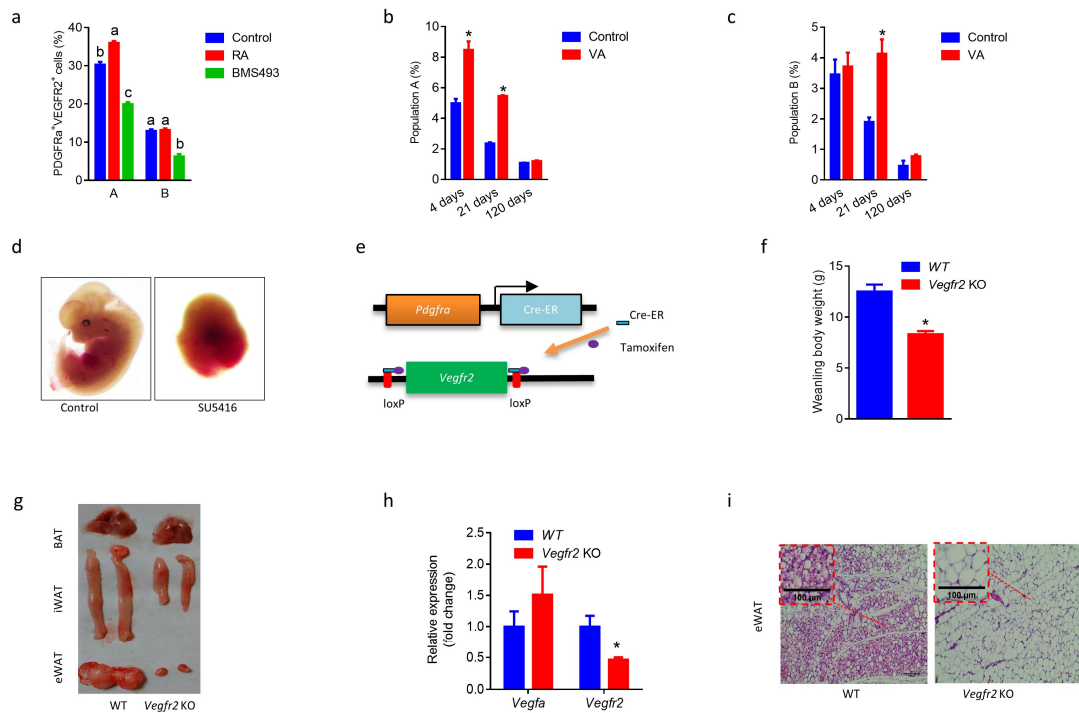


Figure S7. VEGF signaling plays an important role in RA regulation of adipogenesis. (a-c) Quantification of PDGFR α ⁺VEGFR2⁺ cells in iWAT of RA, BMS493 injected (a) or MVA offspring at different ages (b and c) (n = 4). (d) Representative images showing E12.5 embryos which were prenatally treated with 10 mg/kg BW SU5416 at E10.5. (e-i) *Vegfr2* was knocked out in PDGFR α ⁺ cells at E10.5 by an injection of 20 mg/kg BW tamoxifen to the pregnant mothers (e). Body weight was measured at weaning (f, n = 6). Representative images of adipose tissue mass were showed (g). mRNA expression of *Vegfa* and *Vegfr2* was measured by qRT-PCR (h, n =6). eWAT sections were stained by H&E (i). Data presented are mean \pm SEM, unpaired two-tail t-test (b-c, f and h) * p < 0.05 or ANOVA (a), bars with different letters differ significantly.

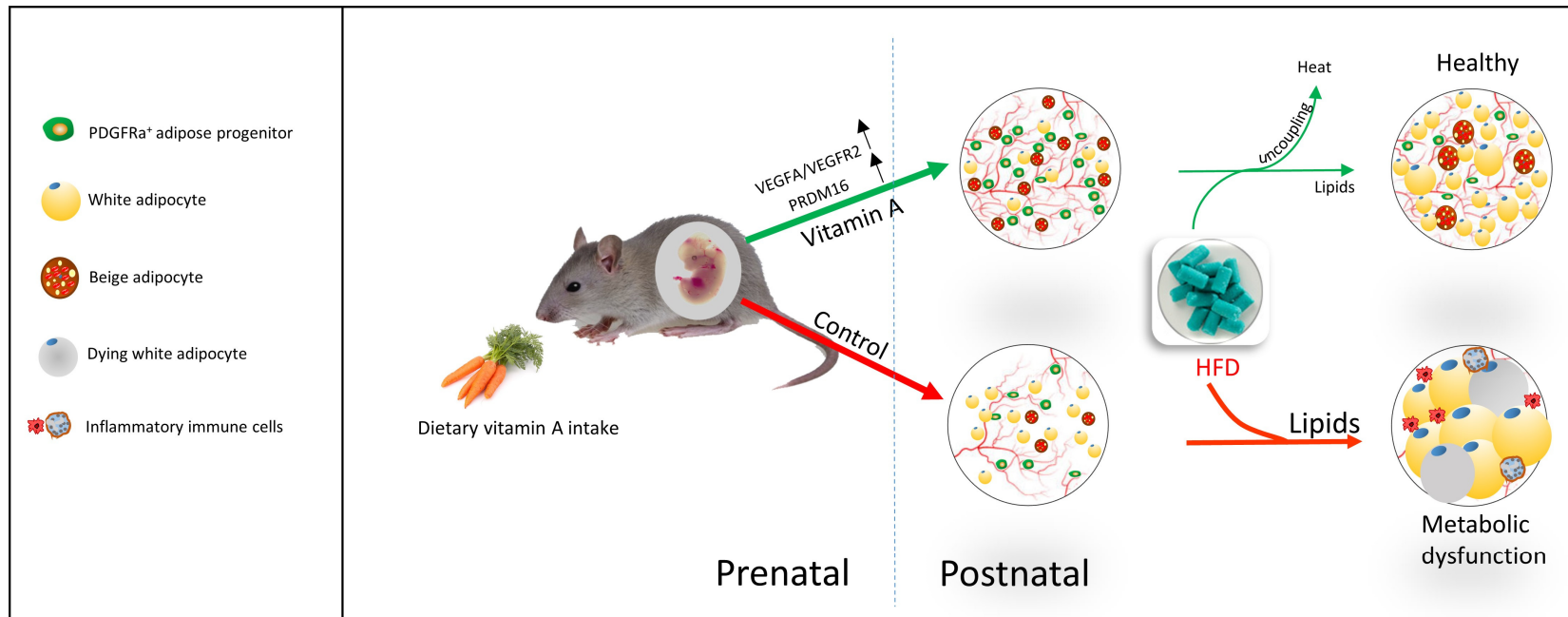


Figure S8. Diagram showing that maternal supplementation of vitamin A promotes angiogenesis and beige adipogenesis, which protects offspring from high fat-induced obesity.

Supplemental Table 1. qPCR primer sequences.

Gene name	Forward	Reverse	Product size (bp)
<i>Zfp423</i>	GTCACCAGTGCCAGGAAGAAGAC	AACATCTGGTTGCACAGTTTACACTCAT	144
<i>Pref1</i>	TGACAATGTCTGCAGGTGCCAT	TATTTTCGAGAATTTCCCGTCC	145
<i>Sox9</i>	GGAAGTCGGTGAAGAACGGA	GGACCCTGAGATTGCCCAGA	166
<i>Klf2</i>	TAGTGGTGTGGCTGGGGATA	TTATGGCTCAAAGTAGCAGACT	178
<i>Pparg</i>	AGCTCCAAGAATACCAAAGTGCAT	AGGTTCTTCATGAGGCCTGTTGTAGA	98
<i>Cebpa</i>	ATGAGAGAAGGAGGGGAGCAGG	AGGTGGGAGAGGCGTGGAECTA	203
<i>Fabp4</i>	CGACAGGAAGGTGAAGAGCATCATA	CATAAACTCTTGTGGAAATCACGCCT	158
<i>Glut4</i>	CTCTCAGGCATCAATGCTGTTTTCTA	CGAGACCAACGTGAAGACCGTATT	123
<i>Prdm16</i>	CAGCACGGTGAAGCCATTC	GCGTGCATCCGCTTGTG	87
<i>Ucp1</i>	ACTGCCACACTCCAGTCATT	CTTTGCCTCACTCAGGATTGG	123
<i>Pdgfra</i>	GGACTTACCCTGGAGAAGTGAGAA	ACACCAGTTTGATGGATGGGA	78
<i>Vegfa</i>	TGGACCCTGGCTTACTGCT	GCAGTAGCTTCGCTGGTAGA	126
<i>Vegfr1</i>	GGCCCGGATATTTATAAAGAAC	CCATCCATTTTAGGGGAAGTC	71
<i>Vegfr2</i>	CAGTGGGATGGTCTTGTCAT	ACGGTGGTCTGTGTCATC	177
<i>Egf</i>	GTTAGCACCATCCCTCATCC	TCTGAGTGCAGCCGAAAG	246
<i>Fgf2</i>	GGCTGCTGGCTTCTAAGTGT	GTCCCGTTTTGGATCCGAGT	153
<i>Pgc1a</i>	CCCTGCCATTGTTAAGACC	TGCTGCTGTTCTGTTTTTC	161
<i>Cidea</i>	ATCACAACTGGCCTGGTTACG	TACTACCCGGTGCCATTCT	136
<i>Elovl3</i>	GATGGTTCTGGCACCATCTT	CGTTGTTGTGGCATCCTT	73
<i>Cox7a1</i>	CAGCGTCATGGTCAGTCTGT	AGAAAACCGTGTGGCAGAGA	112
<i>Rxra</i>	TGGGGCTTGTGAGGTGTATTC	CACCTGGGTAGAGAAGTCGAAA	96
<i>Rxrb</i>	GCGTCCTTCTCCATCGGTC	CAAAGATGGCTCCCACGCCT	109
<i>Rxrg</i>	GAACCACGCGCAACAGAAC	CTGCGTCTCCGTGACTAACA	81
<i>Rara</i>	TGGGGCGAGATGTACGAGA	CTCGATGGAGTGGTTTGAGC	186
<i>Rarb</i>	CAGTGCCATACTGGTGTCT	AGGGCTGTTAATCCAGGAGG	186
<i>Rarg</i>	CTGCATGGAATCGTTTGCC	TCTCCACCGATTGTAGACTGG	152
<i>Rora</i>	CGCGGCGTAAAGGATGTATT	CCGACCAAACCTGACAGCATC	286
<i>Rorb</i>	TCTCACAGCATTTGCCAGT	AAGGTGGTGAGTGTGTGCAA	299
<i>Rorg</i>	TGCTGTCCTGGGCTACCCTAC	CAAACCTGACAGCATCTCGGGAC	298
<i>Tle3</i>	CGGGCAAACCTCCAGGCAT	AGCTGGTGAGGGGTGATGGGT	75
<i>Ehmt1</i>	GGCACCTTTGTCTGCGAATAC	AGAACCAGCGTCAATGCAG	130
<i>Hif1a</i>	AGGATGAGTCTGAACGTCGAA	AAACCATGTCGCGCTCATCT	298
<i>18s</i>	TTGTACACACCGCCCGTCGC	CTTCTCAGCGCTCCGCCAGG	102