Supplementary figure and table

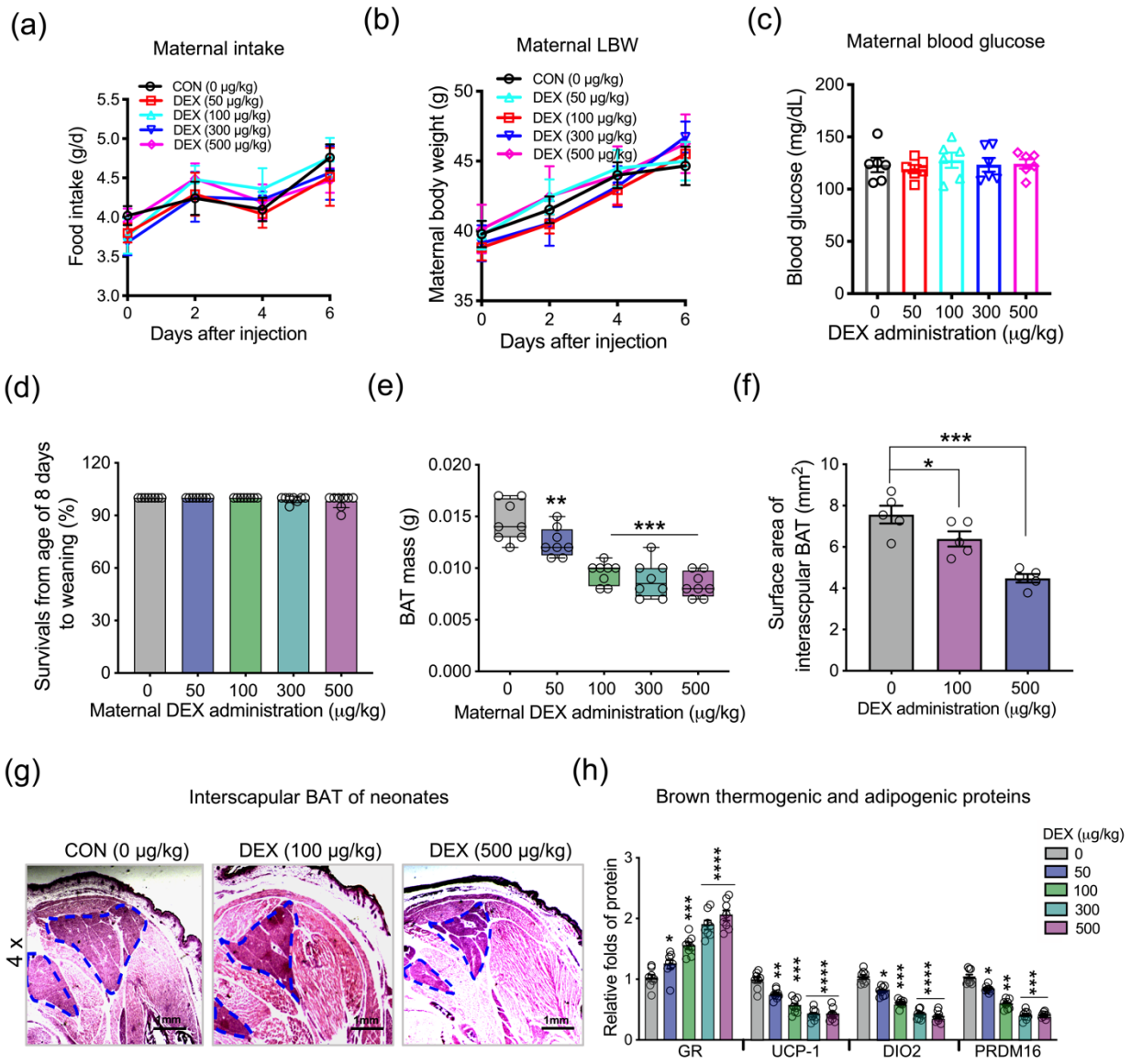

Fig. S1. (a–c) Food intake (a), body mass (b) and blood glucose (c) of pregnant mice administrated with dosed synthetic glucocorticoids dexamethasone (DEX) in the last trimester (*n* = 8 in each group). (d) Neonatal survival percentage from age of 7 days to weaning (*n* = 8 in each group). (e) Neonatal BAT mass on postnatal day 1 (P1). (f and g) H&E staining measurement of surface area of interscapular BAT in neonates at P1. Surface area of BAT in blue dash line was quantified by ImageJ (*n* = 5 in each group). (h) Quantified protein contents of

glucocorticoid receptor (GR), UCP-1, DIO2 and PRDM16 in neonatal BAT. β-actin was used as a loading control (n = 8 in each group). Data are mean ± SEM and each dot represents one replicate (each pregnancy); *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001; unpaired one-way ANOVA multiple test was used in analyses.

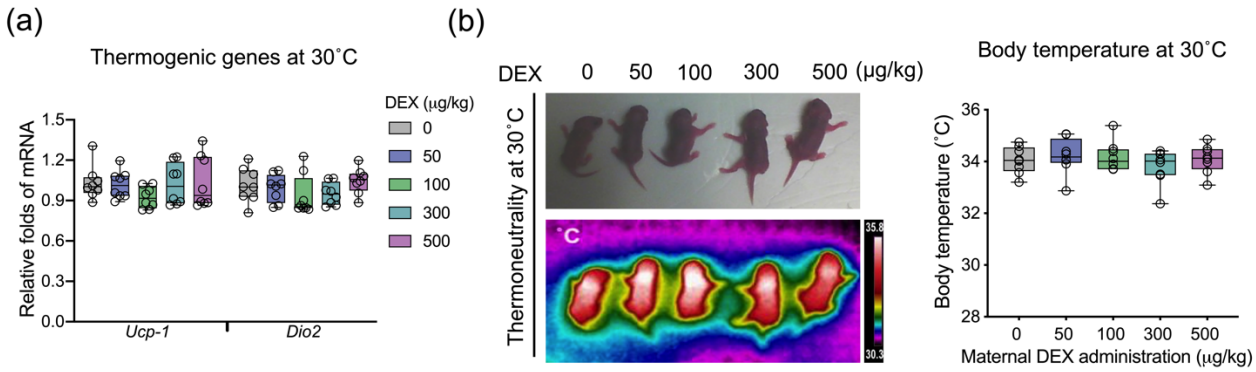

Fig. S2. (a) mRNA expression of thermogenic genes *Ucp-1* and *Dio2* in neonatal BAT at 30˚C. Gene expression was normalized to 18S rRNA (n = 8 in each group). (b) Thermal imaging of neonates on postnatal day 1 (P1) under 30˚C. After neonates were removed from nests, thermal images were recorded immediately (n = 8 in each group). Data are mean ± SEM and each dot represents one replicate (each pregnancy); *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$; unpaired one-way ANOVA multiple test was used in analyses.

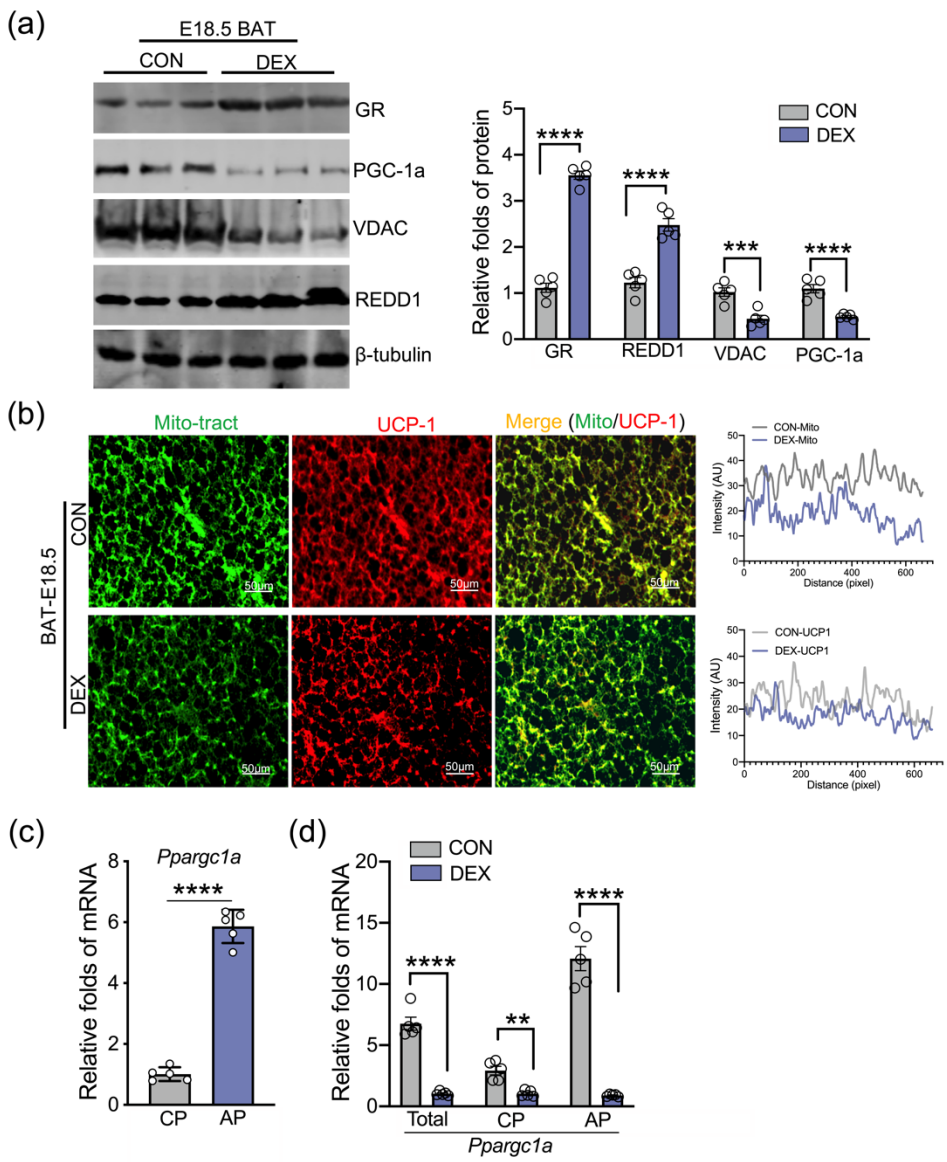

Fig. S3. (a–d) Pregnant mice were administrated with 100 μg/kg dexamethasone (DEX) in the last trimester. Brown fat was collected in fetuses on embryonic day E18.5. (a) Immunoblotting measured the protein expression of glucocorticoid receptor (GR), PGC-1a, VDAC and REDD1 in fetal BAT. β-tubulin was used as a loading control (n = 5). (b) Immunostaining measurements of mitochondria (mito-tracker; green) and UCP-1 (red) in fetal BAT. Intensity of UCP-1 and mito-tracker was quantified by Image-J (n = 3 in each group). Scale bar: 50 μm. (c) Relative *Ppargc1a* expression transcribed from canonical promoter (CP) and alternative promoter (AP) in

fetal BAT (n = 4). (d) Relative *Ppargc1a* total, CP and AP transcriptions in fetal BAT affected by DEX exposure (n = 5). mRNA was normalized to 18S rRNA. Data are mean ± SEM and each dot represents one replicate; *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, **** $P < 0.0001$; unpaired Student's t-test with two-tailed distribution was used in two treatment data analyses.

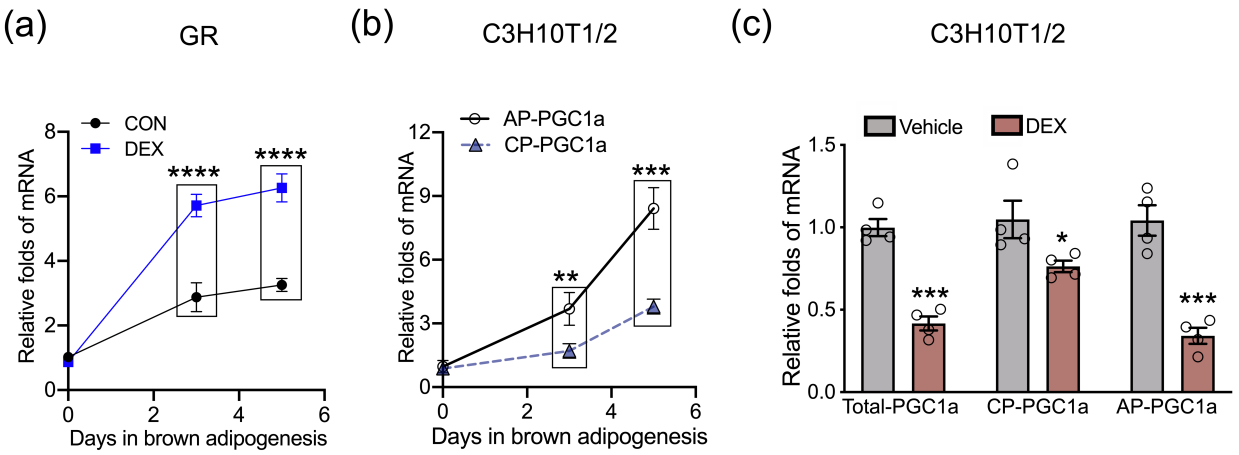

Fig. S4. (a) Glucocorticoid receptor (GR) expression in brown adipocyte differentiation of mouse embryonic fibroblasts treated with 10 μmol/L dexamethasone (n = 4). Gene expression was normalized to 18S rRNA. (b and c) C3H10T1/2 cell lines were induced for brown adipocyte differentiation. During brown adipogenesis, cells were also treated with vehicle or 10 μmol/L dexamethasone (DEX) (n = 4). *Ppargc1a* transcription from the alternative (AP) and canonical promoters (CP) during brown adipocyte differentiation (b). (c) *Ppargc1a* transcription from AP and CP in differentiated brown adipocytes on day 5. Gene expression was normalized to 18S rRNA. Data are representative of three separate experiments. Data are mean ± SEM and each dot represents one replicate; *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, **** $P < 0.0001$; unpaired Student's t-test with two-tailed distribution was used in two treatment data analyses.

Table S1. qPCR primer sequences for gene expression analyses

Name	Forward primers	Reverse primers
18s	GTAACCCGTTGAACCCCATT	CCATCCAATCGGTAGTAGCG
UCP-1	ACTGCCACACCTCCAGTCATT	CTTTGCCTCACTCAGGATTGG
PRDM16	CAGCACGGTGAAGCCATTC	GCGTGCATCCGCTTGTG
Total Ppargc1a	TAGATGAAGAGAATGAGGCAAACTTGCTA	ACTGGCCTCGTTGTCAGTGGTC
Alternative Ppargc1a	GCACTCCAGCAGAATGAG	TTTCAAAATTGAATCCATGG
Canonical Ppargc1a	GTGTGCTGTGTGTCAGAGTGGAT	CTCTATGTCACTCCATACAGAGTCTT
Cidea	ATCACAACTGGCCTGGTTACG	TACTACCCGGTGTCCATTTCT
Elvol3	TCCGCGTTCTCATGTAGGTCT	GGACCTGATCCAACCCTATGA
PPARg	AAACTCTGGGAGATTCTCCTGTT	GCATCTCTGTGTCAACCATGGT
C/EBPa	TGCGCAAGAGCCGAGATAAA	CCTTCTGTTGCGTCTCCACG
Fasn	GGAGGTGGTGATAGCCGGTAT	TGGGTAATCCATAGAGCCCAG
Dio2	ATTATGCCTCGGAGAAGA	ACCAAAGTTGACCACCAG
Slc27a2	CCAAAAGCGGCAACCATCAA	GGTACCGAAGCAGTTCACCA
Ppara	TGGTGTTCGCAGCTGTTTTG	GTCAGTTCACAGGGAAGGCA
Gaphdh	CCCTTAAGAGGGATGCTGCC	ACTGTGCCGTTGAATTTGCC
Cytochrome c	GTTCAGAAGTGTGCCCAGTG	GGTTAACCCAAGCAACCTGTG
LPL	CATGGATGGACGGTAACGGG	GTCAGACTTCCTGCTACGCC
Zfp423	GTCACCAGTGCCCAGGAAGAAGAC	AACATCTGGTTGCACAGTTTACACTCAT
Slc7a10	GGAGTCACTATCCTGGGCCT	AGCGTGTCATGGACTCTGTG
Agt	AGGTTGGCGCTGAAGGATAC	AGGCTCGAACGTTGACTCTG
Cirbp	CTTTTTCCGTGGGGGACGAA	TCGTTGTGTGTAGCATAACTGTCA
Dazap2	CACCATGAACAGCAAAGGTCAA	TGGGGATTGTGGAGCCTAGA
Hsbp1	ATCACTGGCAAGCACGAAGA	GGCCTCGAAAGTAACCGGAA

Hsp70	CCGACAAGGAGGAGTTCGTG	GACAGTCCTCAAGGCCACAT
Nrf1	ACGTTACAGGGCGGTGAAAT	ATCTGGACCAGGCCATTAGC
Nrf2	GCCCTCAGCATGATGGACTT	TGGTGTCTGTCTGGATGTGC
Tfam	CCTGAGGAAAAGCAGGCATA	ATGTCTCCGGATCGTTTCAC
Tfb1m	CACCGAGGGCTTGGAATGTT	TAGAACCCGCAGCTTTCTGG
Tfb2m	TAAAGCTGGTGCCAGAGTGG	AGGAACACCTGCTGACCAAG
VDAC	CTCCGCCGAGAGGACGAA	CTCCCTATGGGGTCTCGCTC