

Figure S1. The effects of chronic i.c.v. infusion of RFRP-3 on the mRNA expression of feeding and energy metabolism-related genes. mRNA expression levels for (A) hypothalamus and (B) pituitary. We chose neuropeptide Y (NPY), agouti-related peptide (AgRP), and proopiomelanocortin (POMC) as neuropeptides related to feeding; thyrotropin-releasing hormone (TRH), growth hormone (GH), and thyroid-stimulating hormone β (TSH β) as neuropeptides related to energy metabolism; gonadotropin-releasing hormone (GnRH), prolactin (PRL), luteinizing hormone β (LH β), and follicle-stimulating hormone β (FSH β) as neuropeptides related to reproduction; RFRP and G protein-coupled receptor 147 (GPR147), the receptor for RFRP-3. Each value represents the mean \pm standard error of the mean. $n = 7-8$.

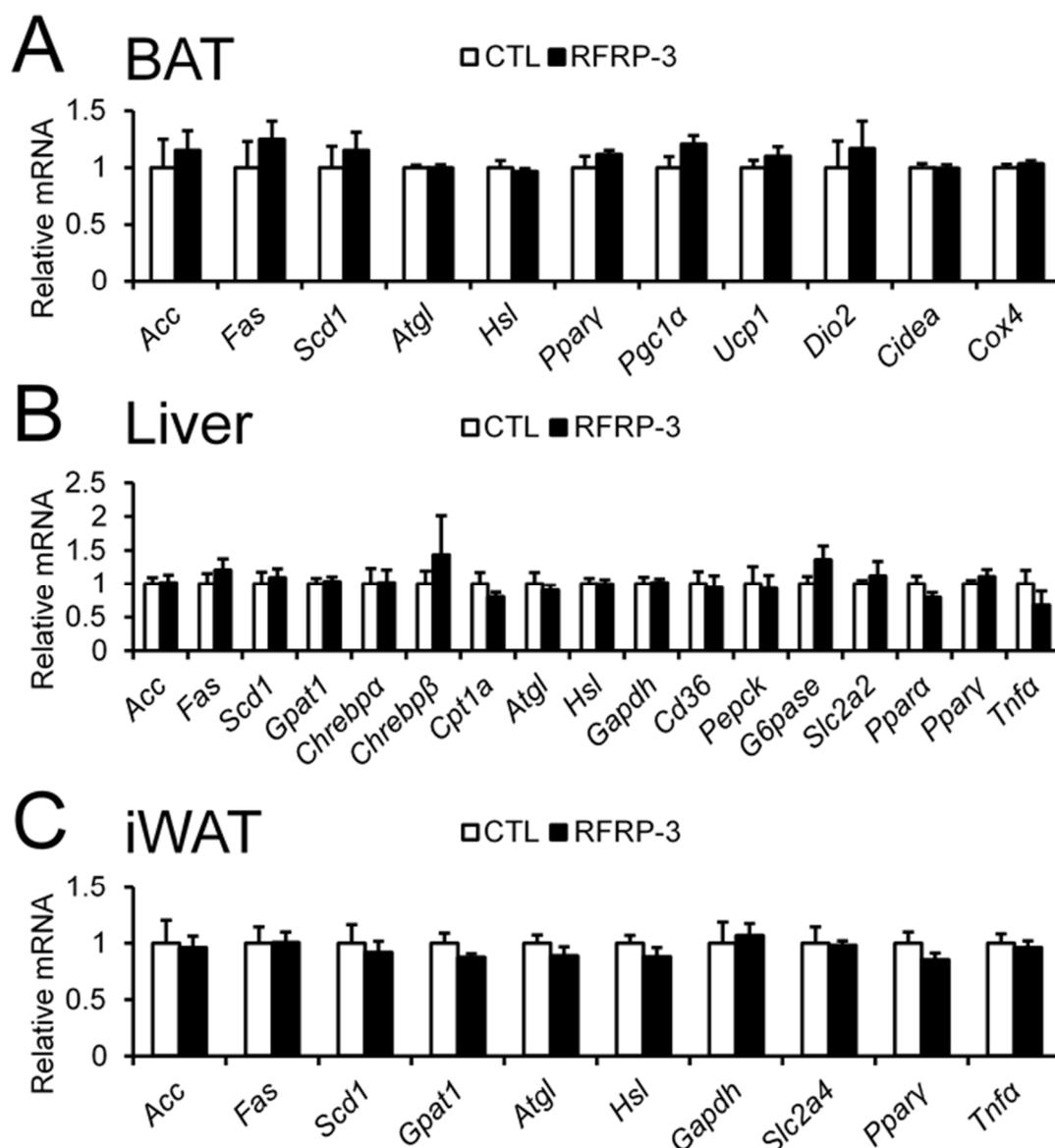


Figure S2. The effects of chronic i.c.v. infusion of RFRP-3 on the mRNA expression of lipid metabolism-related genes in the adipose tissues and liver, and thermogenesis-related genes in the BAT. mRNA expression levels for (A) BAT, (B) liver, and (C) inguinal WAT (iWAT). We chose acetyl-CoA carboxylase (ACC), fatty acid synthase (FAS), stearoyl-CoA desaturase 1 (SCD1), and glycerol-3-phosphate acyltransferase 1 (GPAT1) as lipogenic enzymes; carbohydrate-responsive element-binding protein α , β (ChREBP α , β) as lipogenic transcription factors; carnitine palmitoyltransferase 1a (CPT1a), adipose triglyceride lipase (ATGL), and hormone-sensitive lipase (HSL) as lipolytic enzymes; peroxisome proliferator-activated receptor α , γ (PPAR α , γ) as lipid-activated transcription factors; glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as a carbohydrate metabolism gene; cluster of differentiation 36 (CD36) as a fatty acid transporter; phosphoenolpyruvate carboxykinase (PEPCK) and glucose-6-phosphatase (G6Pase) as gluconeogenesis enzymes; solute carrier family 2 member 2 (SLC2A2) and solute carrier family 2 member 4 (SLC2A4) as glucose transporters; tumor necrosis factor α (TNF α) as an inflammatory cytokine; peroxisome proliferator-activated receptor γ coactivator 1 α (PGC1 α), uncoupling protein 1 (UCP1), type II iodothyronine deiodinase (DIO2), cell death-inducing DNA fragmentation factor-like effector A (CIDEA), and cytochrome c oxidase subunit 4 (COX4) as genes related to thermogenic function. Each value represents the mean \pm standard error of the mean. $n = 7-8$.