Fig. S1. MiR-145 was conservative in evolution. The sequences of all miR-145 in miRBase (18.0) were downloaded and phylogenetic analysis was conducted using software MEGA5 according to the manufacturer's instructions.

eca-miR-145 MIMAT0013064 pma-miR-145 MIMAT0019476 cfa-miR-145 MIMAT0009863 mdo-miR-145 MIMAT0004116 bta-miR-145 MIMAT0003542 rno-miR-145 MIMAT0000851 hsa-miR-145-5p MIMAT0000437 mmu-miR-145-5p MIMAT0000157 ssc-miR-145 MIMAT0002123 mml-miR-145 MIMAT0002266 ptr-miR-145 MIMAT0002267 ggo-miR-145 MIMAT0002268 ppy-miR-145 MIMAT0002269 mne-miR-145 MIMAT0002270 xtr-miR-145 MIMAT0003688 dre-miR-145 MIMAT0001842 aca-miR-145 MIMAT0021773 oan-miR-145 MIMAT0007141 ola-miR-145 MIMAT0022669 oan-miR-145* MIMAT0007142 mmu-miR-145-3p MIMAT0004534 rno-miR-145* MIMAT0017131

0.1

hsa-miR-145-3p MIMAT0004601

Fig. S2. Overexpression of miR-145. (A) Morphology of DFAT cells at 2 d after miR-145 and mock vector infection. (B) The expression levels of miR-145 in cells infected with miR-145 and mock vector control at 0 d, 4 d and 8 d after hormone stimulation were analyzed. The data were first normalized to endogenous mRNA *GAPDH* and fold changes were calculated to DFAT-MDI preadipocytes (0 d). Triplicates were made and data were shown as mean \pm SD. One-Way ANOVA analysis was conducted, *P*<0.05 was shown in one star, and *P*<0.01 was shown in two star.

