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.

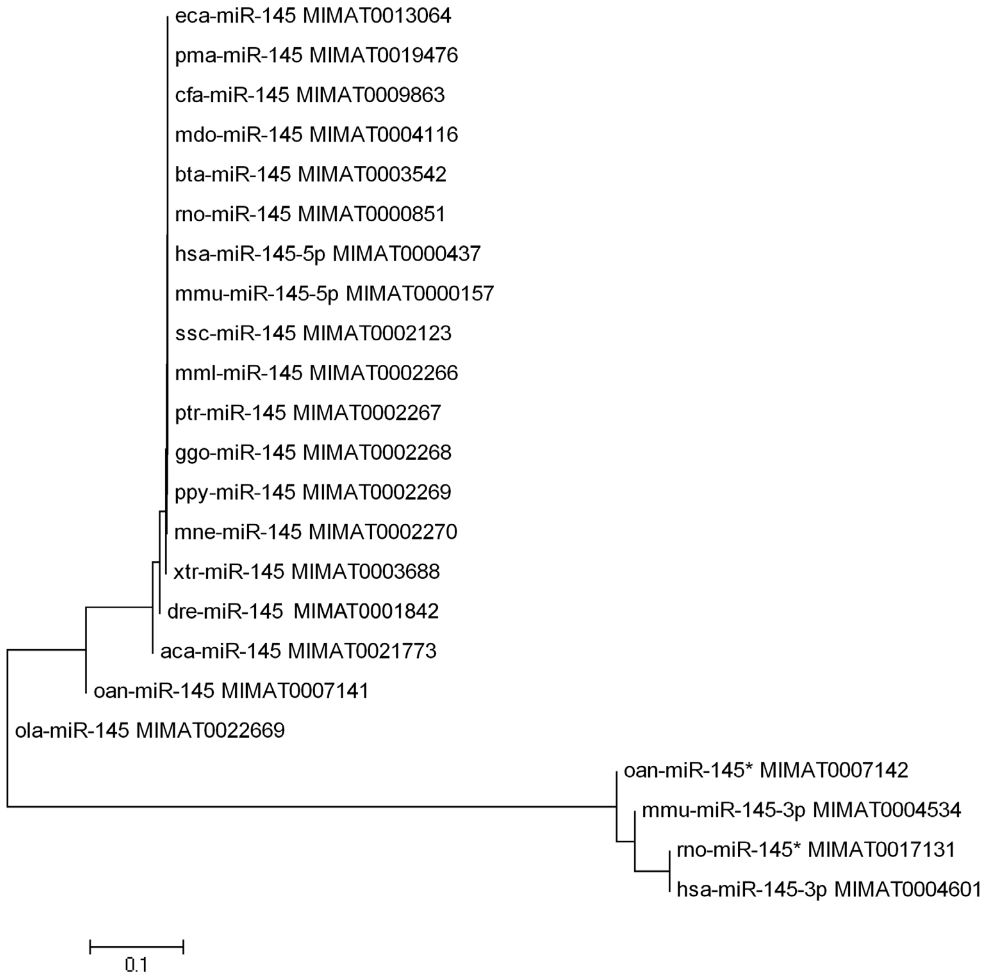

Fig. S2. Overexpression of miR-145. (A) Morphology of DFAT cells at 2 d after miR-145 and mock vector infection. (B) The expression levels of miR-145 in cells infected with miR-145 and mock vector control at 0 d, 4 d and 8 d after hormone stimulation were analyzed. The data were first normalized to endogenous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