**Figure S1.** The obesity-induced differentially expressed genes (DEGs) in adipose tissues were screened. **A**, Adipose tissues in dataset GSE112740 (containing 3 high-fat diet (HFD) and 3 low-fat diet (LFD) mice) were analyzed, and 295 increased genes (log2FC>1, P<0.05) and 344 decreased genes (log2FC<–1, P<0.05) were obtained. **B**, The dataset GSE112999 (containing 9 HFD and 9 LFD mouse cases) was analyzed using the limma tool. The DEGs in the adipose tissues of HFD and LFD mice were screened, and 262 increased genes (log2FC>1, P<0.05) and 203 decreased genes (log2FC<–1, P<0.05) were finally obtained. **C**, DEGs in datasets GSE112999 and GSE112740 were intersected, and 41 common upregulated genes (log2FC>1, P<0.05) and 17 common decreased genes (log2FC<–1, P<0.05) were identified. **D**, The subcutaneous adipose tissues of 3 morbidly obese patients and 3 lean individuals in GSE48964 were analyzed, and 100 increased genes (log2FC>1, P<0.05) and 53 decreased genes (log2FC<–1, P<0.05) were obtained.

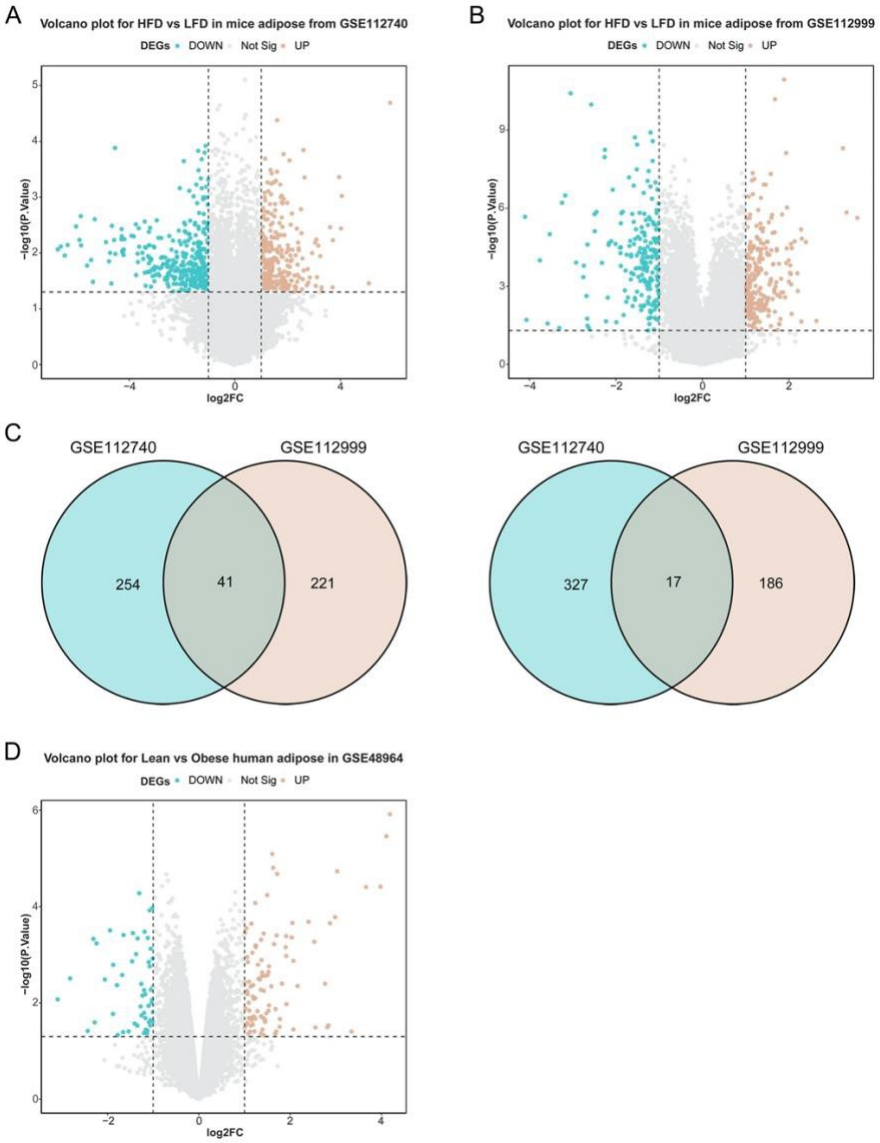

**Figure S2.** Validation of the adipogenic differentiation cell model. 3T3-L1 cells were cultured for a total of six days to induce adipogenic differentiation. **A**, After induction of lipid formation, Oil red O staining was used to detect the formation of lipid droplets in cells; magnification 400×, scale bar 40 μm. **B**, Western blot was used to detect the protein level of adipocyte markers (Fabp4 and PPARγ). Data are reported as means and SD; n=3 (biological replicates). **P<0.01 *vs* the normal group; Student's *t*-test.