Figure S1. Reverse transcription-quantitative PCR was used to verify (A) the successful knockdown of the target gene after the transfection of HaCaT cells with FUS/ILF2-siRNA and (B) the successful knockdown of the target gene after injection of FUS/ILF2-shRNA into the back skin tissue of C57BL/6 mice for 4 weeks. Data are presented as the mean ± SEM. FUS, fused in sarcoma; ILF2, interleukin enhancer binding factor 2; shRNA, short hairpin RNA; nc, negative control.

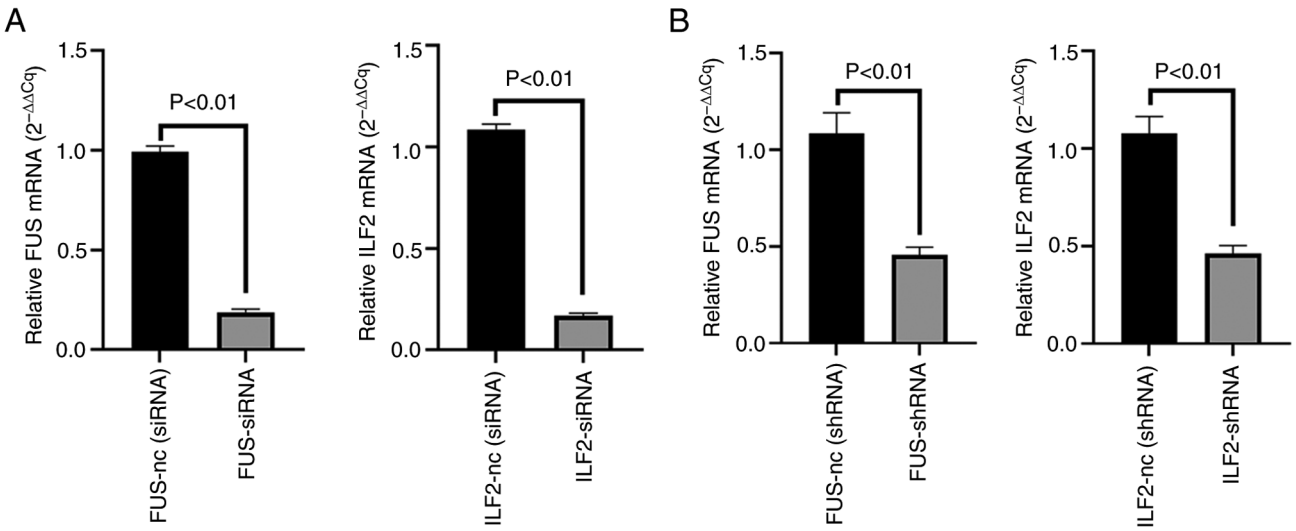

Figure S2. Expression of FUS and ILF2 in HaCaT cells under osmotic pressure and high glucose conditions. (A) mRNA expression levels of FUS and ILF2 in HaCaT cells under different conditions were determined by reverse transcription-quantitative PCR. (B) Protein expression levels of FUS and ILF2 in HaCaT cells under different conditions were determined by western blotting. Data are presented as the mean ± SEM. One-way analysis of variance were used to determine the statistical significance between groups followed by the Bonferroni post hoc test. vs. NG, $^{**}P<0.01$. FUS, fused in sarcoma; ILF2, interleukin enhancer binding factor 2; RT-qPCR, reverse transcription-quantitative PCR; NG, normal glucose; HO, high osmotic; HG, high glucose.