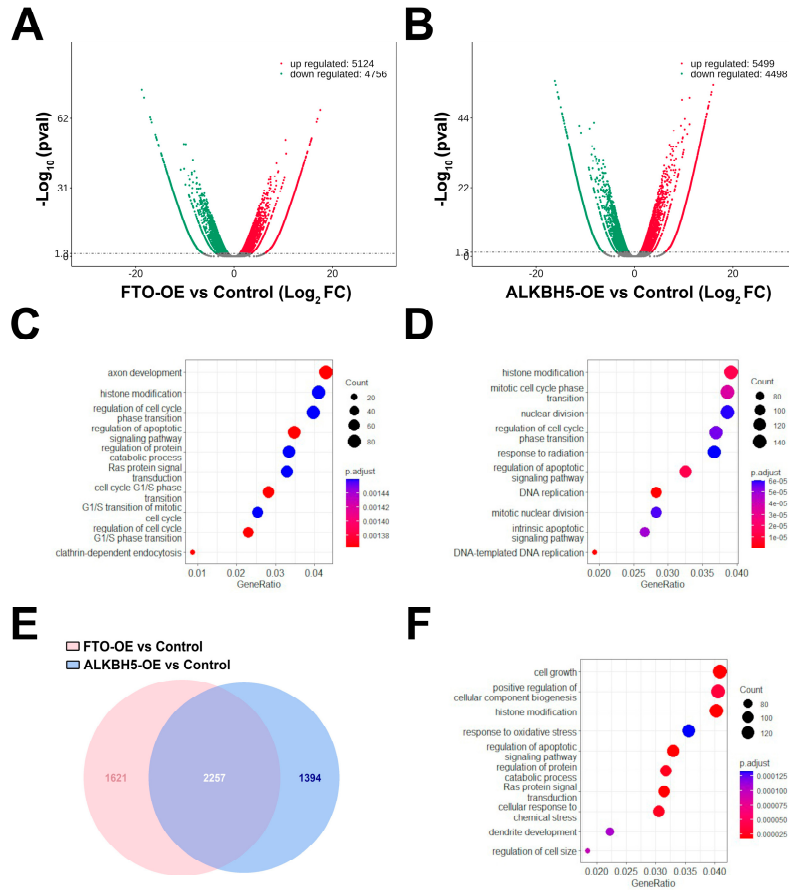


**Figure S1.** Expression patterns of RUNX2 and Osterix in FTO-OE and ALKBH5-OE DFSCs. Expression pattern of RUNX2 (**A**) or Osterix (**B**) was not obviously influenced during the 12 days' osteogenesis induction in either FTO-OE or ALKBH5-OE DFSCs. n = 3.



**Figure S2.** RNA sequencing of FTO-OE and ALKBH5-OE DFSCs versus vehicle control. (**A**) Volcano plot of the  $\log_2$  (fold change) between FTO-OE and vehicle control and the negative  $\log_{10}$  (p-value). (**B**) Volcano plot of the  $\log_2$  (fold change) between ALKBH5-OE and vehicle control and the negative  $\log_{10}$  (p-value). (**C**) Gene ontology classification and enrichment analysis of differentially expressed genes in FTO-OE DFSCs. (**D**) Gene ontology classification and enrichment analysis of differentially expressed genes in ALKBH5-OE DFSCs. (**E**) A total of 2257 genes were identified in the intersection of differentially expressed genes between FTO-OE cells and ALKBH5-OE DFSCs. (**F**) Gene ontology classification and enrichment analysis of commonly altered genes in FTO-OE and ALKBH5-OE DFSCs.