

Figure S1. Quality control and filtering of single cell RNA-sequencing data. (A) Number of genes detected in 34 osteoarthritis samples. (B) Sequencing depth across all samples. (C) Mitochondria gene content in each sample. High levels meant low cell activity. (D) Association between sequencing depth and mitochondrial gene content. (E) A positive correlation between sequencing depth and total intracellular sequences ($R=0.25$). (F) Volcano plot illustrating top 3,000 highly variable genes. Red indicates high variation. The names of the top 10 genes are presented.

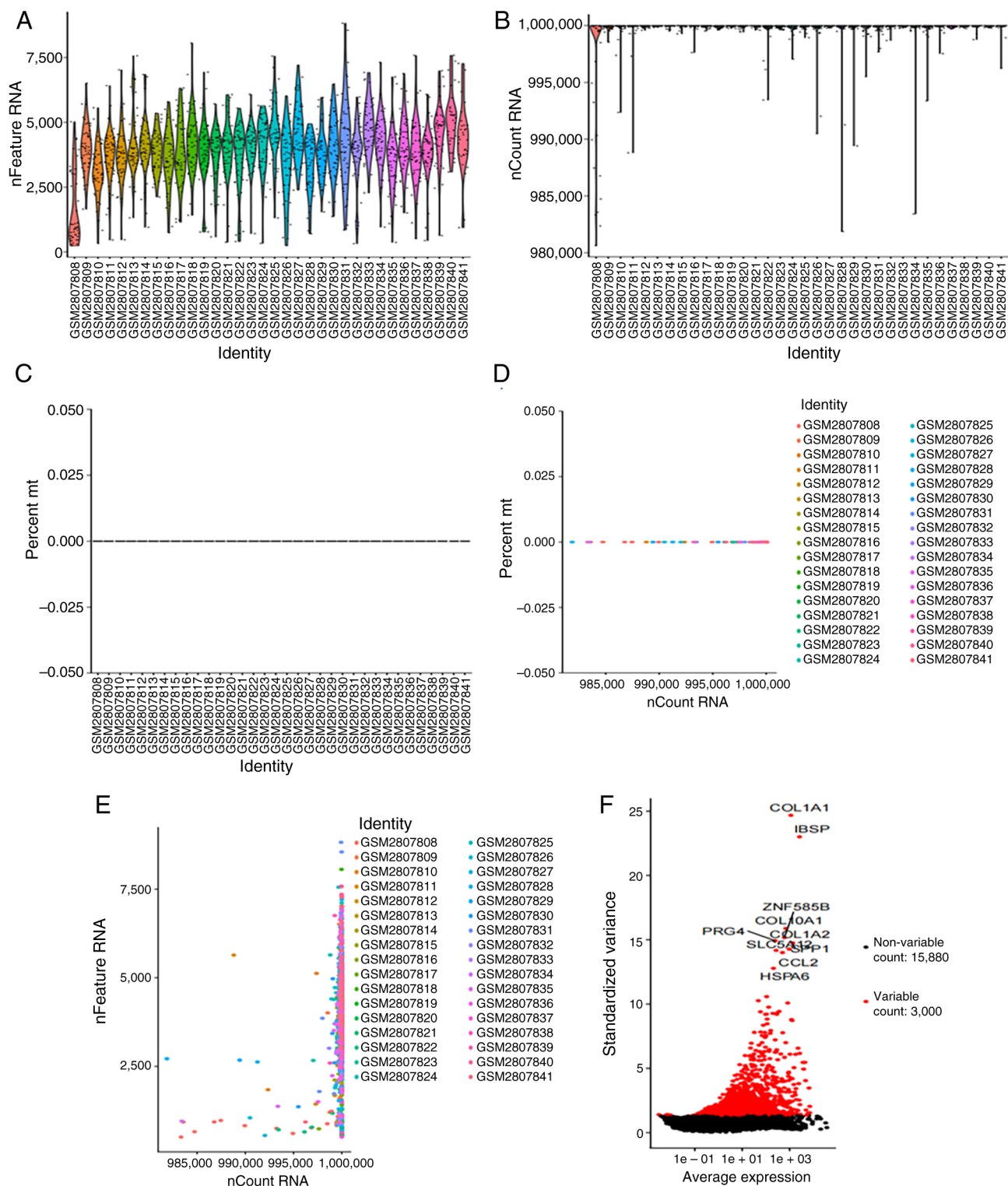


Figure S3. Silencing MYC, ADM or NFKBIA reduces cell viability in ATDC5 chondrocytes. (A) Western blotting was carried out to detect the protein levels of MYC, ADM and NFKBIA in ATDC5 cells after shRNA transfection. (B) A Cell Counting Kit-8 assay was carried out to evaluate cell viability in ATDC5 cells after shRNA transfection. *** $P < 0.001$. ADM, adrenomedullin; NFKBIA, NF- κ B inhibitor- α ; OD, optical density; sh, short hairpin.

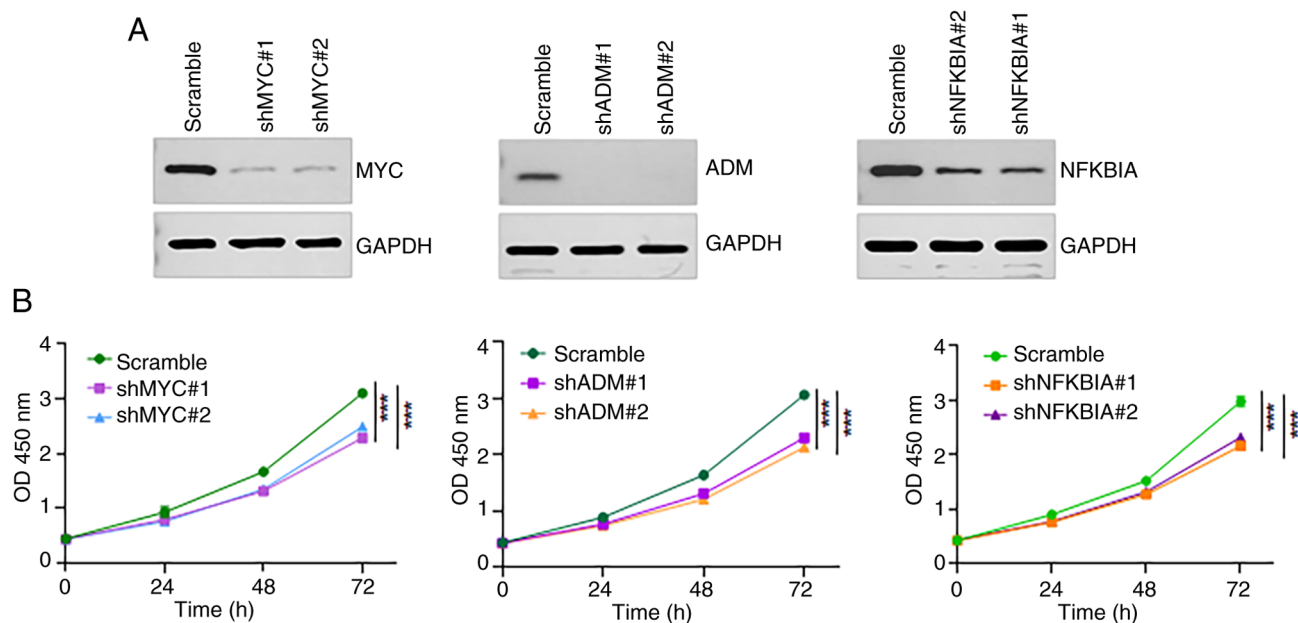


Figure S4. Silencing MYC, ADM and NFKBIA induces apoptosis in ATDC5 chondrocytes. (A) Annexin V/PI flow cytometry was used to measure the apoptosis of ATDC5 cells after shRNA transfection. (B) Quantitative results for apoptosis. *** $P < 0.001$. ADM, adrenomedullin; NFKBIA, NF- κ B inhibitor- α ; sh, short hairpin.

