

Identification and Characterization of Long Non-coding RNAs in Osteogenic Differentiation of Human Adipose-derived Stem Cells

Supplementary files

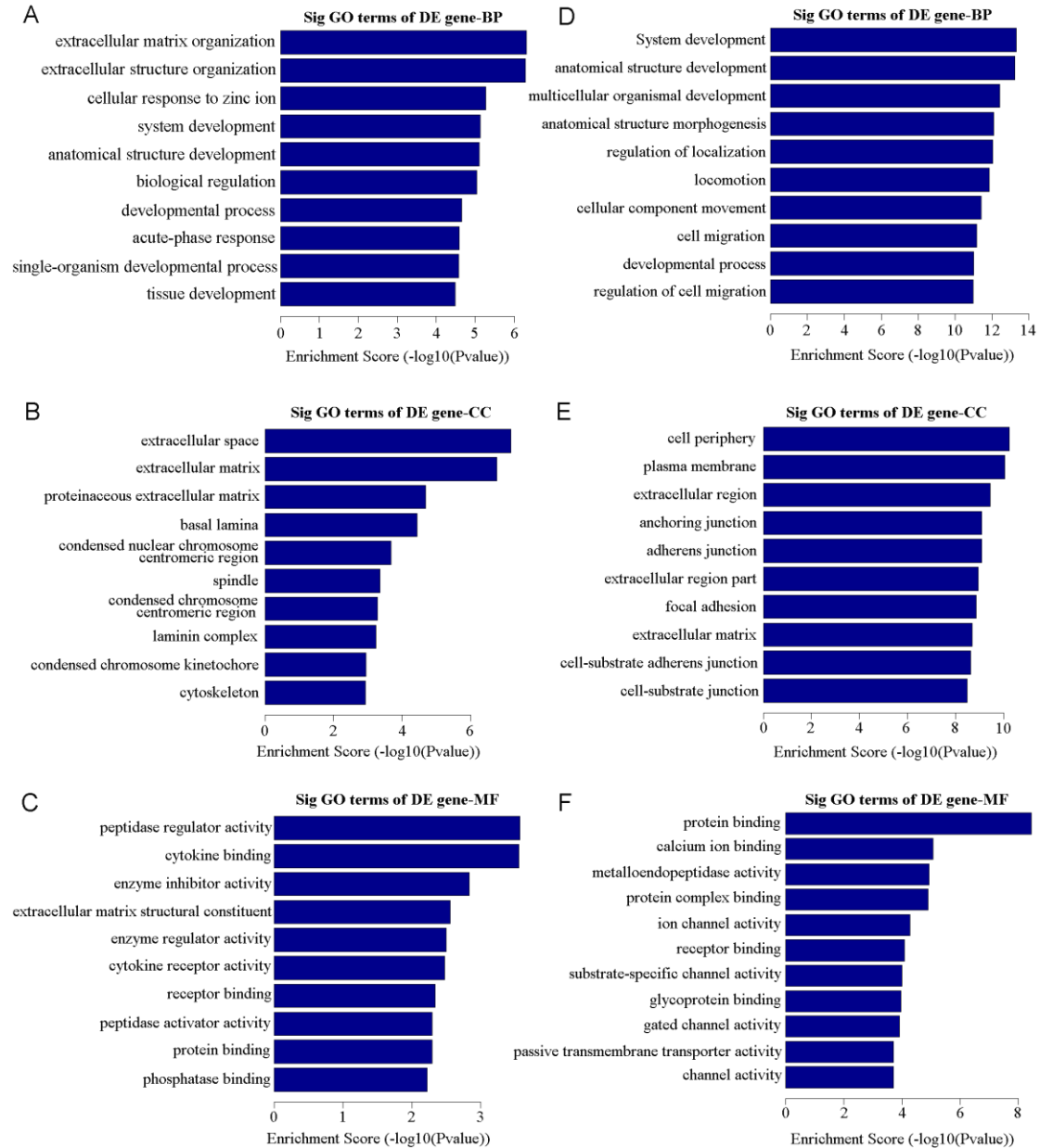


Figure S1. GO analysis of dysregulated mRNAs. A-C. The top 10 highest enriched GO terms in three domains targeted by upregulated mRNAs were ranked by enrichment score. D-E. The top 10 highest enriched GO terms in three domains targeted by downregulated mRNAs were ranked by enrichment score. BP, biological process; CC, cellular component; MF, molecular function.

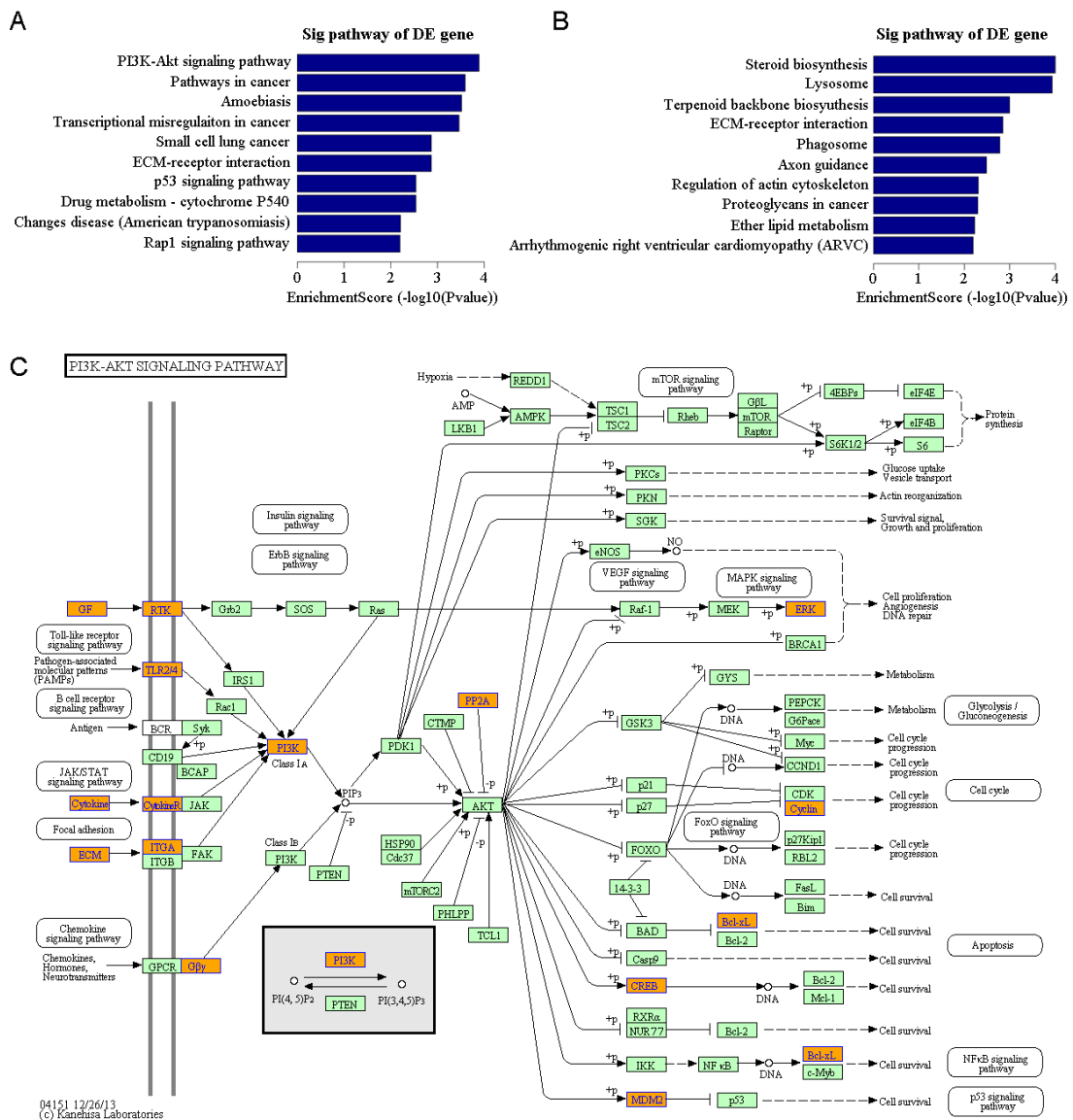


Figure S2. Pathway analysis of differentially expressed mRNAs. The top 10 highest enriched pathways associated with upregulated mRNAs (A) and downregulated mRNAs (B) were ranked by enrichment score. (C). The schematic diagram of PI3K/Akt signaling pathway associated with osteogenesis. The orange nodes are associated with upregulated mRNAs, and the green nodes represent the mRNAs that did not exhibit significant changes.

Table S1 Primers used for qRT-PCR

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')	Efficiency
SAA3P	CATCATTTTCTGCTCCCTGGTC	CCAGCTGCCTTGAGGAATGTT	97.16%
LOC284080	AAGGCGGCTTCTGTTTATTAG	CAGGTAGAGGAAGACTTGTGGG	94.46%
HHIP-AS1	CAAGAGCACATAAAGTGGGAGC	TGGATAGGACCAGGGTATGAGG	95.42%
XLOC_00261	ATCTTCTTACAAATGAAGTGAC	ACAGAGGCTGCTCAGATAGGG	97.80%
9	GC		
XLOC_01039	GACTGACCACTCACCACCAGAT	CCCTTAGGTTTCATGCAAGATACA	94.53%
7			
XLOC_01198	GCCTGTGACTTTATTATGGGT	CAAGGTTTCTAACTGAATACACT	94.21%
0		C	
CTC-564N23	AAGATAAATACCTGGAGTGGGA	TGTCAGTAAGGATGTGGAGCA	98.85%
.3			
XLOC_00145	GCCGGTATGGAGTGAGTGGAG	GCAGGTCACAGGAAATGGGTAG	98.97%
3			
XLOC_00748	ATGTGCCACTCTGCCTTCTGT	TTTCCTACCCTCTTCAGTGCC	90.48%
9			
LINC00638	CACCTCCAGTTCGGCATTCT	GGGAGACTGCACCCCTTAAC	90.65%
COL1A1	CCTAGTCTGTCCTGCGTCCTC	GAGTCTTTTGCTTCCTCCAC	100.7%
ALPL	CCCCGTGGCAACTCTATCTTT	CCTGGTAGTTGTTGTGAGCATAG	98.04%
		TC	
Runx2	AGTGGACGAGGCAAGAGTTTC	GCGGGACACCTACTCTCATACT	95.83%
H19	GCACCTTGGACATCTGGAGT	TTCTTTCCAGCCCTAGCTCA	93.53%
GAPDH	GGGAAACTGTGGCGTGAT	GAGTGGGTGTCGCTGTTGA	96.89%