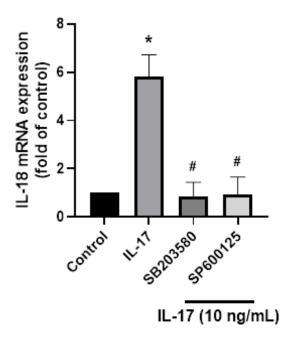


Supplementary Figure 1. IL-1 family members and its receptor are up-regulated in specimens of OA patients. The GEO dataset (GSE890408) contained mRNA expression pattern from the synovial tissues of OA patients and normal donors were used to analyze IL- 1α , IL- 1β , IL-33 and IL-RA expressions. Results are expressed as the means \pm S.D. * p<0.05 compared with controls.



Supplementary Figure 2. IL-17-induced promotion of IL-18 production in OASFs requires p38 and JNK signaling. OASFs were pretreated with p38 and JNK inhibitors SB203580 (5 μ M) or SP600125 (5 μ M) for 1 h, then incubated with IL-17 (10 ng/mL) for 24 h. IL-18 expression was determined by qPCR. Results are expressed as the means \pm S.D. * p<0.05 compared with controls; # p<0.05 compared with the IL-17-treated group.

Ensembl Gene Id 1 ENSG00000100030 (MAPK1)		miRNA name hsa-miR-4492 0	miTG score A 0.885935706270861	Also Predicted	^
JCSC graphi	ls [©] s: <u>miRNA</u> <u>gene</u> c [©]	7975 200mm 8300	2	22 W	
Region	Binding Type			Conservation	-
UTR3	7mer	9659-9675	0.01597682444655	2 5	Y
UTR3	6mer	9542-9548	0.002960857398356	13 2	
UTR3	7mer	9282-9306	0.01235522316297	3 4	
UTR3	6mer	7818-7835	0.0016317672136308	82 2	
UTR3	8mer	7690-7711	0.0014733289403428	86 2	
UTR3	6mer	695-714	0.0027109094812094	46 2	~
UTR3	6mer	309-337	0.003252221390144	4 2	v
UTR3	SWADOWS	92-110	0.0038478160863324	U/U 1	

Supplementary Figure 3. Prediction result of mir-4492 binding to ERK (MAPK1) 3'UTR using the DIANA-microT-CDS tool. The online database for miRNA target prediction (DIANA-microT-CDS) was utilized to predict miR-4492, which is a potential target for ERK mRNA.