

Table S1. Gene-specific primer sequences

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
GAPDH	GGAGCGAGATCCCTCCAAAAT	GGCTGTTGTCATACTTCTCATGG
IL1B	CTAAAAGCTTGGTGATGTCTGG	AAGACGGGCATGTTTTCTGC
JUND	GTTGTCGCCCATCGACATG	TTGTTTGCTGTTGACGTGGCTG
FOS	AACAATTACGCGCTACCTGG	TTGTTTAGGGCTCGGTCTTC
IL6	ACAACAATTACGCGCTAGCAG	ACTCTCAAATCTGTTCTGGAGG
JUNB	CCGTGAAGAAATGGCAGTTC	CTGAGTCCTCCCATATACCAT

Note: GAPDH = glyceraldehyde-3-phosphate dehydrogenase; IL1B = interleukin 1 beta; JUND = JUN proto-oncogene, AP-1 transcription factor subunit; FOS = FBJ murine osteosarcoma viral oncogene homolog; IL6 = interleukin 6; JUNB = JUNB proto-oncogene, AP-1 transcription factor subunit.

Table S2. Multivariate Analysis of Bone Turnover Markers in Osteoarthritis

Bone Marker	Unadjusted β (95% CI)	P-value	Adjusted β^* (95% CI)	P-value
β -CTX [†]	0.35 (0.27-0.44)	<0.001	0.34 (0.25-0.43)	<0.001
N-MID	0.58 (0.46-0.70)	<0.001	0.57 (0.45-0.70)	<0.001
PINP	0.64 (0.50-0.79)	<0.001	0.64 (0.48-0.81)	<0.001

*Adjusted for age, sex, BMI, hypertension, diabetes mellitus, dyslipidemia, and NSAIDs use.

[†]Log-transformed for analysis due to non-normal distribution (Shapiro-Wilk test, p=0.031).

β represents the difference in bone turnover marker levels between osteoarthritis and control groups. Positive values indicate higher levels in the osteoarthritis group.

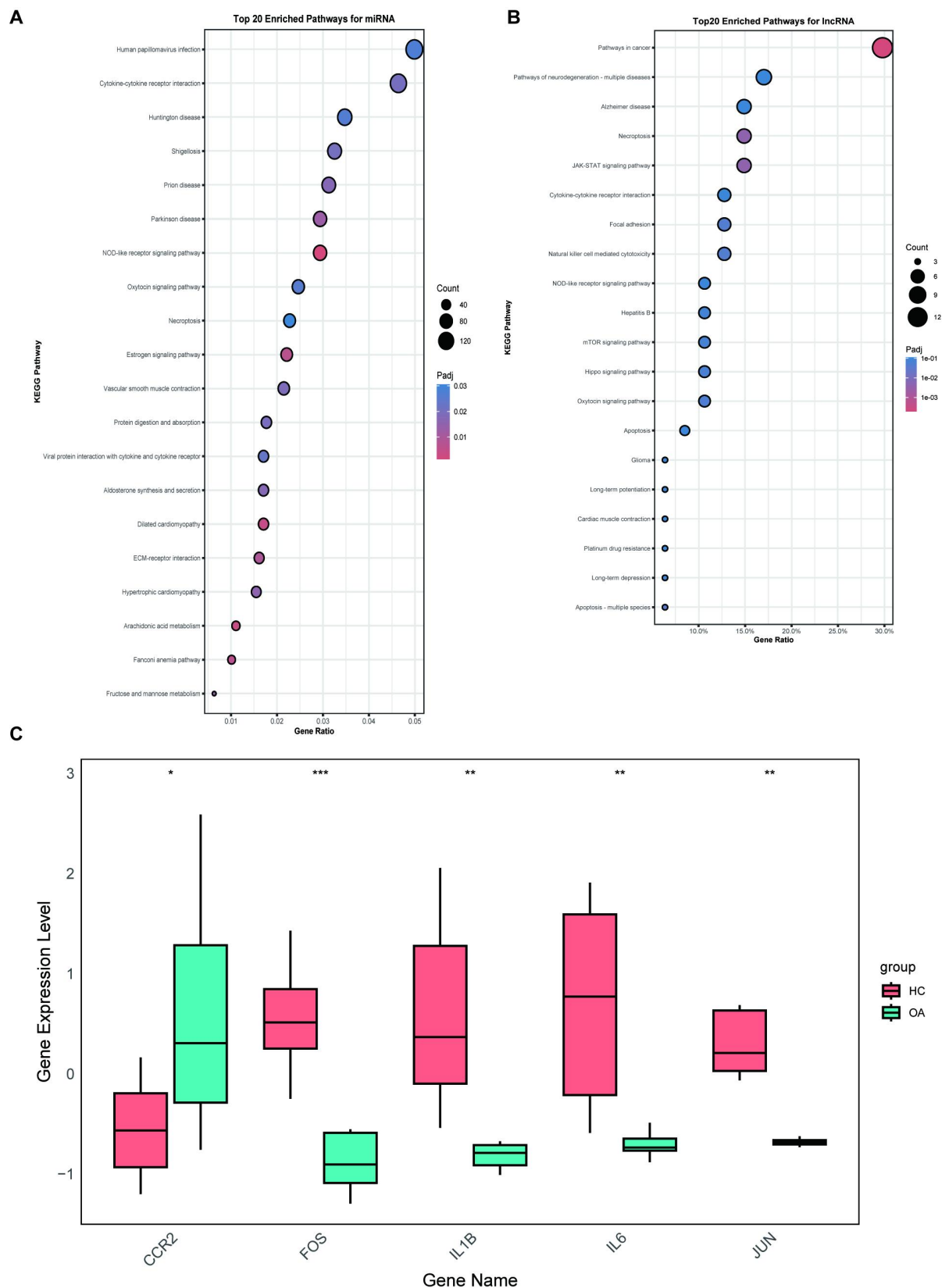


Figure.S1 Pathway enrichment and gene expression analysis.

A Top 20 significantly enriched pathways from miRNA analysis. Bubbles represent pathway terms. Bubble size corresponds to gene count, and color gradient indicates adjusted Padj. **B** Top 20 significantly enriched pathways

from lncRNA analysis. Bubble size reflects gene count, and color represents Padj. C Differential expression of CCR2, FOS, IL1B, IL6, and JUN between healthy controls (HC, pink) and osteoarthritis patients (OA, green). Statistical significance: * $P < 0.05$, * $P < 0.01$, * $P < 0.001$.