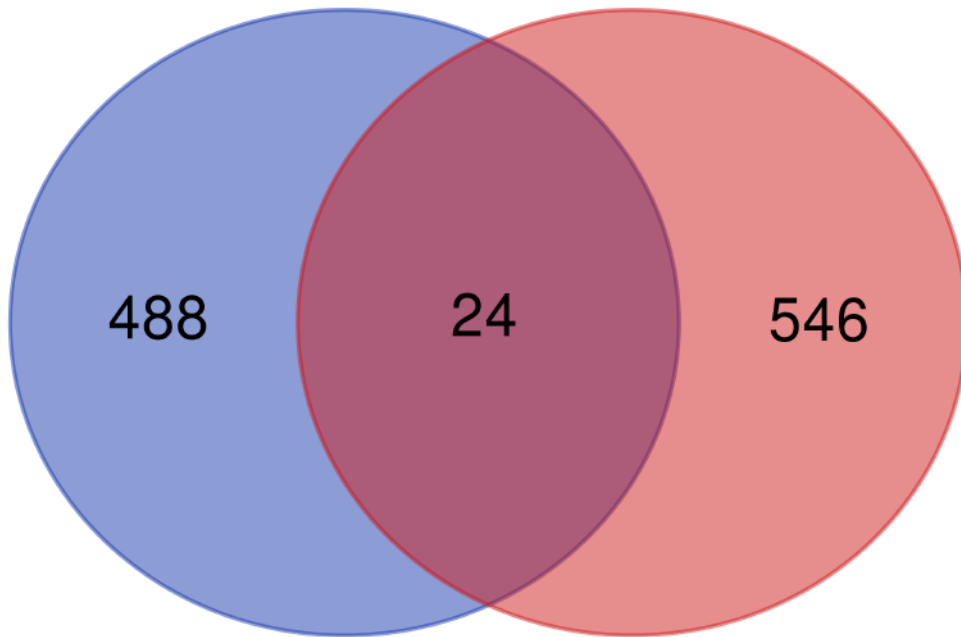


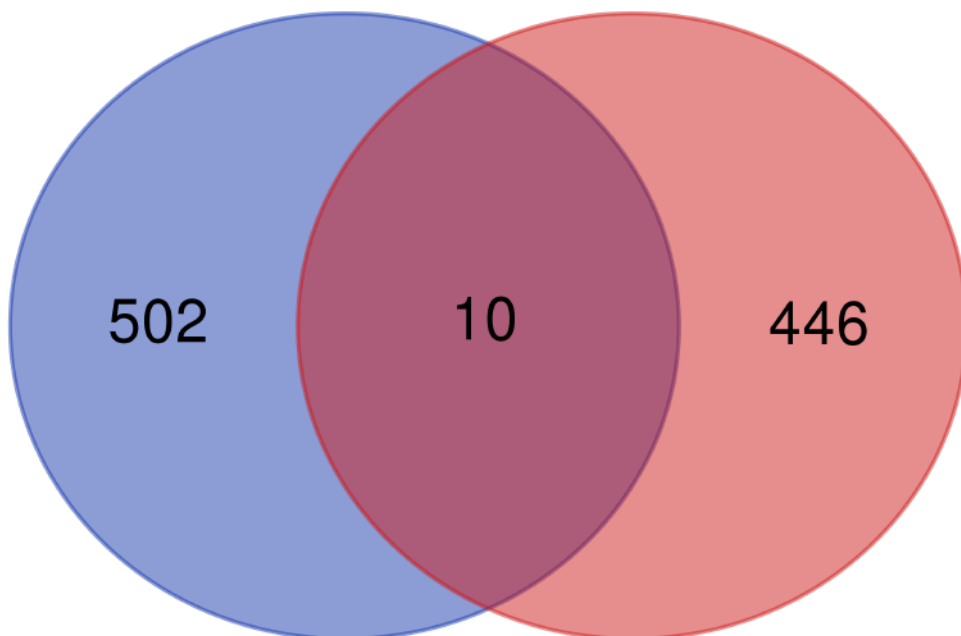
synovial tissue

peripheral blood



synovial tissue

bone marrow



RA vs OA

GSE12021

GSE100786

Supplementary Table 1 The top 10 DEGs in RA and NC were verified in GSE55235.

| Gene symbol | Fold-change | P-value |
|-------------|--------------|-------------|
| HLA-DRB4 | 2.745061813 | 0.020334961 |
| CXCL13 | 6.184201362 | 1.33441E-09 |
| PLA2G2D | 2.648396684 | 0.000363523 |
| CXCL9 | 2.564950266 | 5.27067E-06 |
| GABBR1 | 3.965429039 | 1.26869E-07 |
| ADAMDEC1 | 3.294369641 | 1.11079E-09 |
| IL21R | 1.837310467 | 1.96539E-06 |
| PTPRCAP | 2.100081267 | 7.72729E-06 |
| CXCL10 | 1.976383233 | 6.13273E-06 |
| SLAMF8 | 2.219171944 | 1.60026E-09 |
| SGCA | -1.627227378 | 0.000103414 |
| WIF1 | -2.626945213 | 0.000327803 |
| SCRG1 | -2.41571327 | 5.82003E-06 |
| RERGL | -2.020052254 | 6.4712E-05 |
| STMN2 | -1.692069842 | 0.000842938 |
| ZIC1 | -3.779380032 | 0.00017211 |
| TOX3 | -2.908460707 | 0.002935494 |
| NELL1 | -1.762191949 | 0.001163006 |
| C7 | -2.853407158 | 8.59428E-06 |
| SGCG | -0.305196375 | 0.595344054 |

supplementary Table 2 Functional and pathway enrichment analysis of the DEGs in RA vs NC group.

| Category | Term | Count | PValue |
|------------------|---|-------|------------|
| GOTERM_BP_DIRECT | GO:0006955~immune response | 44 | 1.80E-21 |
| GOTERM_BP_DIRECT | GO:0050853~B cell receptor signaling pathway | 18 | 1.46E-17 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 19 | 6.59E-14 |
| GOTERM_BP_DIRECT | GO:0050871~positive regulation of B cell activation | 12 | 1.85E-13 |
| GOTERM_BP_DIRECT | GO:0006910~phagocytosis, recognition | 12 | 4.98E-13 |
| GOTERM_CC_DIRECT | GO:0009897~external side of plasma membrane | 25 | 5.00E-13 |
| GOTERM_CC_DIRECT | GO:0042571~immunoglobulin complex, circulating | 9 | 5.29E-10 |
| GOTERM_CC_DIRECT | GO:0072562~blood microparticle | 18 | 1.51E-09 |
| GOTERM_CC_DIRECT | GO:0005576~extracellular region | 55 | 2.71E-06 |
| GOTERM_CC_DIRECT | GO:0005886~plasma membrane | 95 | 0.00274657 |
| GOTERM_MF_DIRECT | GO:0003823~antigen binding | 21 | 6.11E-16 |
| GOTERM_MF_DIRECT | GO:0034987~immunoglobulin receptor binding | 12 | 1.81E-13 |
| GOTERM_MF_DIRECT | GO:0008009~chemokine activity | 9 | 1.60E-06 |
| GOTERM_MF_DIRECT | GO:0004252~serine-type endopeptidase activity | 18 | 1.90E-06 |
| GOTERM_MF_DIRECT | GO:0048248~CXCR3 chemokine receptor binding | 4 | 4.79E-05 |
| KEGG_PATHWAY | hsa04060:Cytokine-cytokine receptor interaction | 18 | 1.24E-06 |
| KEGG_PATHWAY | hsa05340:Primary immunodeficiency | 7 | 2.58E-05 |
| KEGG_PATHWAY | hsa05321:Inflammatory bowel disease (IBD) | 8 | 1.31E-04 |
| KEGG_PATHWAY | hsa04662:B cell receptor signaling pathway | 8 | 2.12E-04 |
| KEGG_PATHWAY | hsa05166:HTLV-I infection | 14 | 5.71E-04 |

supplementary Table 3 Functional and pathway enrichment analysis of the DEGs in OA vs NC group.

| Category | Term | Count | PValue |
|------------------|--|-------|------------|
| GOTERM_BP_DIRECT | GO:0045444~fat cell differentiation | 8 | 3.70E-04 |
| GOTERM_BP_DIRECT | GO:0001701~in utero embryonic development | 12 | 6.71E-04 |
| GOTERM_BP_DIRECT | GO:0001525~angiogenesis | 13 | 8.53E-04 |
| GOTERM_BP_DIRECT | GO:0030728~ovulation | 4 | 0.00117787 |
| GOTERM_BP_DIRECT | GO:0002053~positive regulation of mesenchymal cell proliferation | 5 | 0.00119207 |
| GOTERM_CC_DIRECT | GO:0097381~photoreceptor disc membrane | 4 | 0.00475457 |
| GOTERM_CC_DIRECT | GO:0000439~core TFIID complex | 3 | 0.01107251 |
| GOTERM_CC_DIRECT | GO:0042995~cell projection | 6 | 0.01217713 |
| GOTERM_CC_DIRECT | GO:0005813~centrosome | 16 | 0.01248841 |
| GOTERM_CC_DIRECT | GO:0005923~bicellular tight junction | 7 | 0.01784125 |
| GOTERM_MF_DIRECT | GO:0044822~poly(A) RNA binding | 34 | 0.00738839 |
| GOTERM_MF_DIRECT | GO:0019901~protein kinase binding | 15 | 0.01165975 |
| GOTERM_MF_DIRECT | GO:0005515~protein binding | 183 | 0.02608831 |
| GOTERM_MF_DIRECT | GO:0005509~calcium ion binding | 22 | 0.02908331 |
| GOTERM_MF_DIRECT | GO:0005251~delayed rectifier potassium channel activity | 4 | 0.02942848 |
| KEGG_PATHWAY | hsa04668:TNF signaling pathway | 9 | 7.64E-04 |
| KEGG_PATHWAY | hsa04744:Phototransduction | 5 | 0.00139913 |
| KEGG_PATHWAY | hsa05164:Influenza A | 10 | 0.00473497 |
| KEGG_PATHWAY | hsa03420:Nucleotide excision repair | 5 | 0.01071053 |
| KEGG_PATHWAY | hsa05200:Pathways in cancer | 15 | 0.01321574 |

supplementary Table 4 Functional and pathway enrichment analysis of the DEGs in RA vs OA group.

| Category | Term | Count | PValue |
|------------------|--|-------|------------|
| GOTERM_BP_DIRECT | GO:0006955~immune response | 23 | 1.50E-09 |
| GOTERM_BP_DIRECT | GO:0006954~inflammatory response | 19 | 2.12E-07 |
| GOTERM_BP_DIRECT | GO:0070098~chemokine-mediated signaling pathway | 8 | 1.29E-05 |
| GOTERM_BP_DIRECT | GO:0030816~positive regulation of cAMP metabolic process | 4 | 2.57E-05 |
| GOTERM_BP_DIRECT | GO:0016525~negative regulation of angiogenesis | 7 | 6.07E-05 |
| GOTERM_CC_DIRECT | GO:0005576~extracellular region | 49 | 5.28E-12 |
| GOTERM_CC_DIRECT | GO:0009897~external side of plasma membrane | 17 | 5.58E-10 |
| GOTERM_CC_DIRECT | GO:0005615~extracellular space | 39 | 6.60E-09 |
| GOTERM_CC_DIRECT | GO:0005886~plasma membrane | 67 | 3.46E-05 |
| GOTERM_CC_DIRECT | GO:0005887~integral component of plasma membrane | 32 | 3.73E-05 |
| GOTERM_MF_DIRECT | GO:0008201~heparin binding | 13 | 1.29E-07 |
| GOTERM_MF_DIRECT | GO:0048248~CXCR3 chemokine receptor binding | 4 | 1.14E-05 |
| GOTERM_MF_DIRECT | GO:0008009~chemokine activity | 6 | 1.61E-04 |
| GOTERM_MF_DIRECT | GO:0004896~cytokine receptor activity | 5 | 5.41E-04 |
| GOTERM_MF_DIRECT | GO:0004872~receptor activity | 9 | 0.00216207 |
| KEGG_PATHWAY | hsa04060:Cytokine-cytokine receptor interaction | 15 | 2.33E-06 |
| KEGG_PATHWAY | hsa05340:Primary immunodeficiency | 5 | 9.03E-04 |
| KEGG_PATHWAY | hsa04062:Chemokine signaling pathway | 9 | 0.00267603 |
| KEGG_PATHWAY | hsa04514:Cell adhesion molecules (CAMs) | 7 | 0.00994524 |
| KEGG_PATHWAY | hsa04630:Jak-STAT signaling pathway | 7 | 0.01095865 |