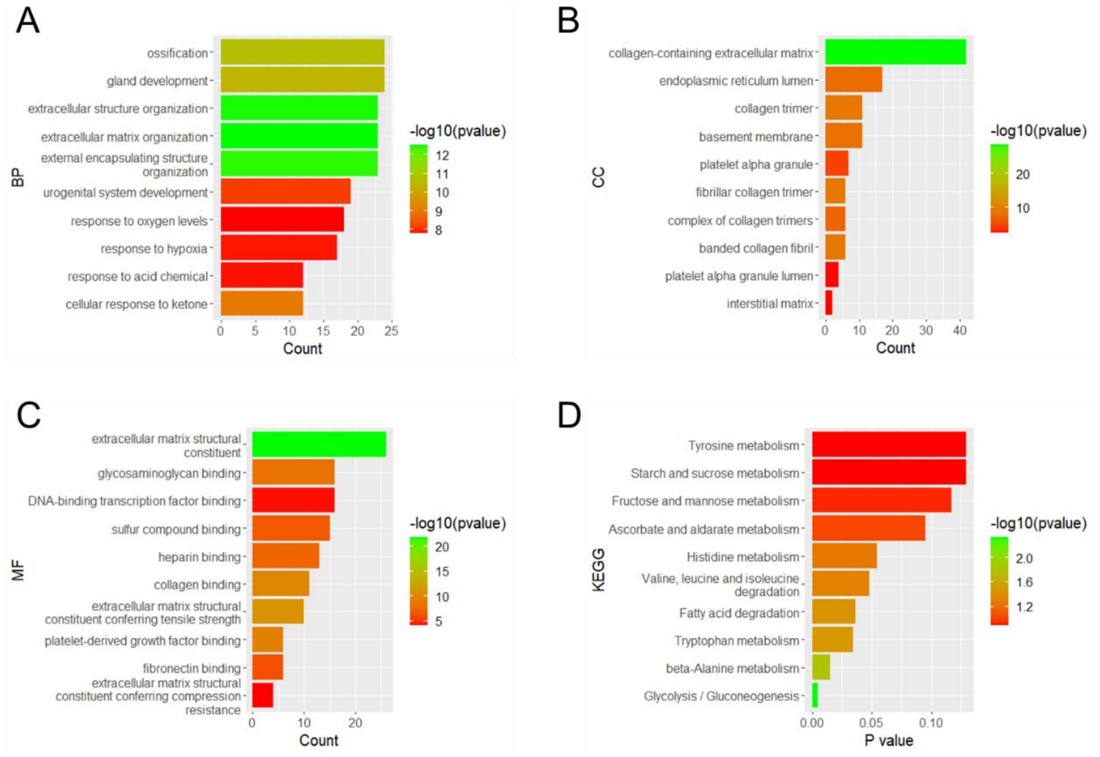
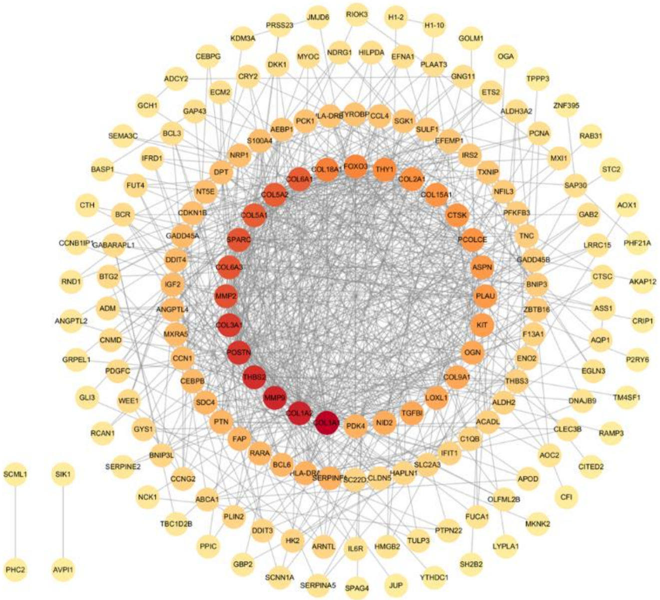
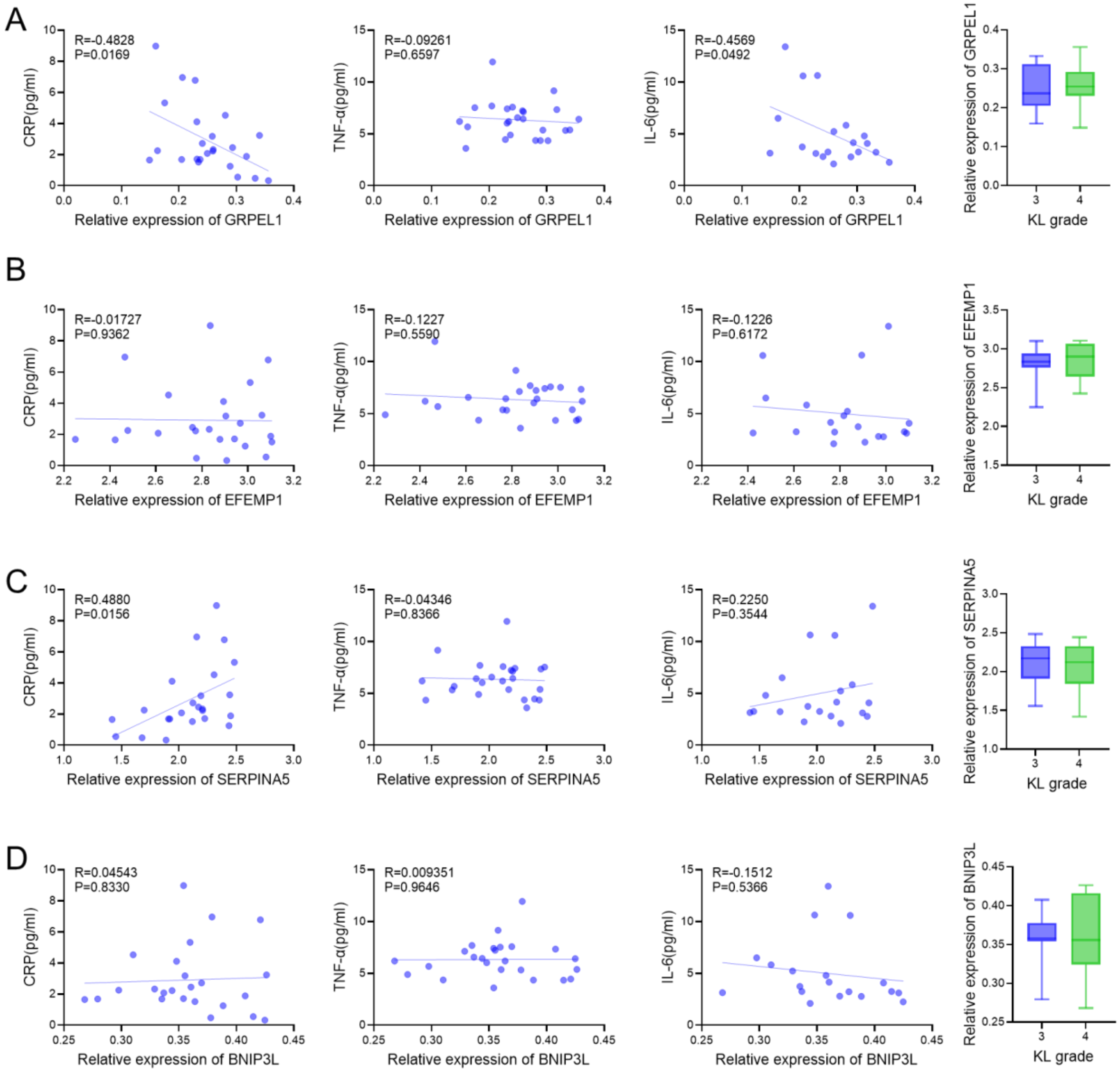


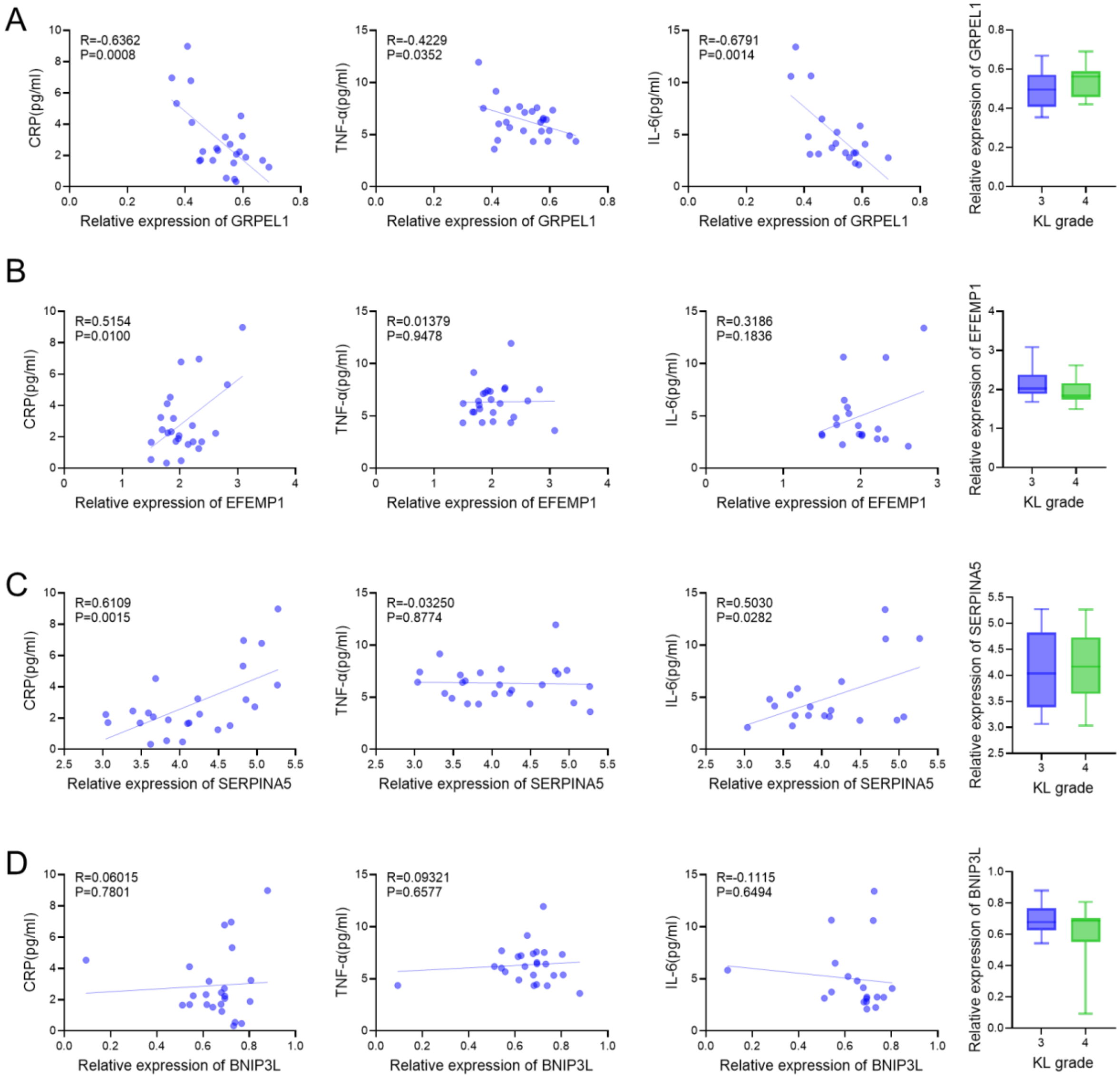
**Supplementary Figure 1 Enrichment analysis of differentially expressed genes.** A-C: Gene Ontology enrichment analysis of overlapping differentially expressed genes in three categories: Biological processes, cellular components, and molecular functions; D: Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis of overlapping differentially expressed genes. BP: Biological processes; CC: Cellular components; MF: Molecular functions; KEGG: Kyoto Encyclopedia of Genes and Genomes.



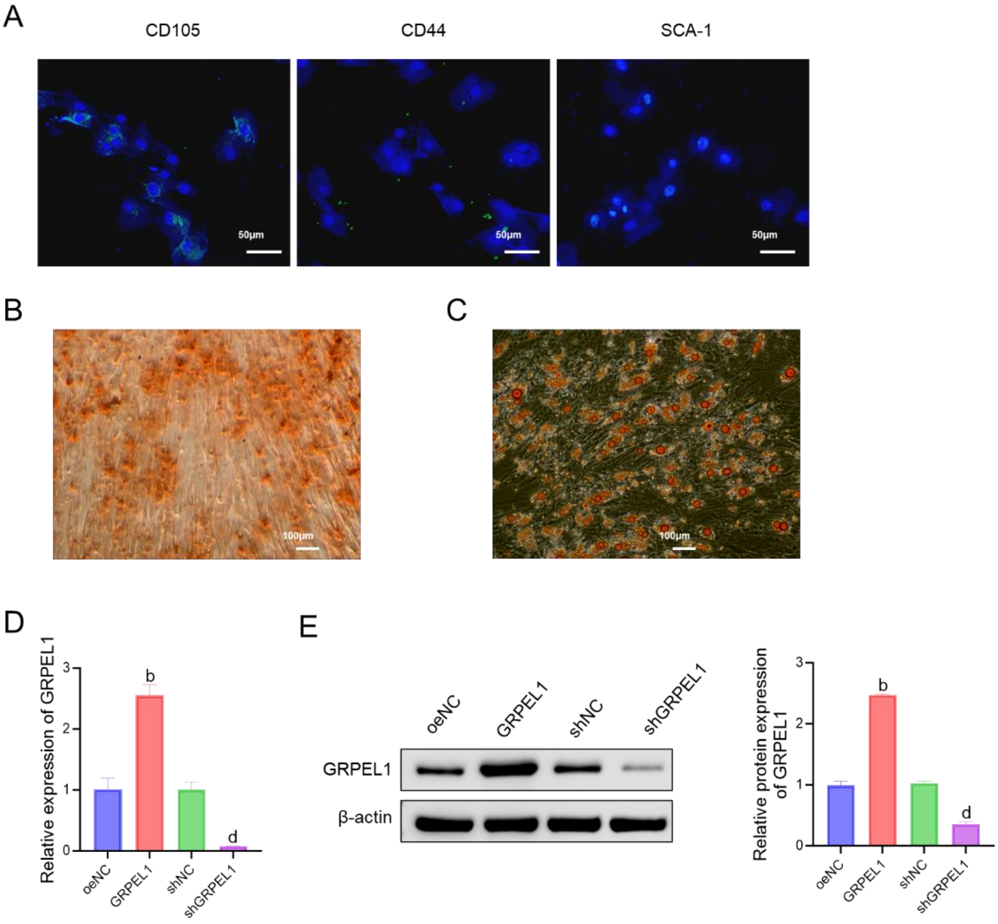
**Supplementary Figure 2 Protein-protein interaction network of overlapping differentially expressed genes.** The protein-protein interaction network illustrates the interactions among overlapping differentially expressed genes, highlighting key genes and potential hubs involved in the studied pathways.



**Supplementary Figure 3 Correlation of GrpE-like 1, extracellular matrix protein 1, serine protease inhibitor, and Bcl2 interacting protein 3 expression levels in synovial fluid with C-reactive protein, tumor necrosis factor-alpha, interleukin-6, and Kellgren-Lawrence grading in osteoarthritis patients.** A-D: Scatter plots and box plots showing the correlations between the relative expression levels of GrpE-like 1 (A), extracellular matrix protein 1 (B), serine protease inhibitor (C), and Bcl2 interacting protein 3 expression levels (D) in synovial fluid of osteoarthritis patients and C-reactive protein (pg/mL), tumor necrosis factor-alpha (pg/mL), interleukin-6 (pg/mL), and Kellgren-Lawrence grading. Pearson’s correlation coefficients (*R*) and *P*-values are indicated on the scatter plots. GRPEL1: GrpE-like 1; CRP: C-reactive protein; TNF-α: Tumor necrosis factor-alpha; IL-6: Interleukin-6; KL: Kellgren-Lawrence; EFEMP: Extracellular matrix protein 1; SERPINA5: Serine protease inhibitor; BNIP3 L: Bcl2 interacting protein 3 expression levels.



**Supplementary Figure 4 Correlation of GrpE-like 1, extracellular matrix protein 1, serine protease inhibitor, and Bcl2 interacting protein 3 expression levels expression levels in cartilage tissue with C-reactive protein, tumor necrosis factor-alpha, interleukin-6, and Kellgren-Lawrence grading in osteoarthritis patients.** A-D: Scatter plots and box plots showing the correlations between the relative expression levels of GrpE-like 1 (A), extracellular matrix protein 1 (B), serine protease inhibitor (C), and Bcl2 interacting protein 3 expression levels (D) in cartilage tissue of osteoarthritis patients and C-reactive protein (pg/mL), tumor necrosis factor-alpha (pg/mL), interleukin-6 (pg/mL), and Kellgren-Lawrence grading. Pearson's correlation coefficients (*R*) and *P*-values are indicated on the scatter plots. GRPEL1: GrpE-like 1; CRP: C-reactive protein; TNF-α: Tumor necrosis factor-alpha; IL-6: Interleukin-6; KL: Kellgren-Lawrence; EFEMP: Extracellular matrix protein 1; SERPINA5: Serine protease inhibitor; BNIP3 L: Bcl2 interacting protein 3 expression levels.



**Supplementary Figure 5 Characterization of human synovial mesenchymal stem cells.** A: Immunofluorescence analysis showing the expression of CD105, CD44, and SCA-1 in human synovial mesenchymal stem cells (hSMSCs); B: Alizarin Red S staining of hSMSCs after osteogenic induction, confirming osteogenic differentiation; C: Oil Red O staining of hSMSCs after adipogenic induction, confirming adipogenic differentiation; D: Quantitative real-time polymerase chain reaction analysis of *GRPEL1* mRNA expression in oeNC, GRPEL1, shNC, and shGRPEL1 groups of hSMSCs; E: Western blot analysis of GrpE-like 1 protein expression in oeNC, GRPEL1, shNC, and shGRPEL1 groups of hSMSCs. Scale bar: 50 μm;100 μm. $^{b}P < 0.01$ *vs* OeNC; $^{d}P < 0.01$ *vs* shNC. oeNC: The empty vector control group; GRPEL1: The GRPEL1 overexpression group; shNC: The corresponding negative control group; shGRPEL1: The GRPEL1 knockdown group; GRPEL1: GrpE-like 1.