Fig. S1. scRNA-seq analysis and identification of human osteoblasts. (A) Visualization of UMAP colored according to cell types for human osteoblasts single-cell transcriptomes. Definition atlas of osteoblasts (O5 and O6, erythroid cells; O8, smooth muscle cells; O9, hematopoietic cells). (B) Heatmap of the top10 specific significantly enriched genes for each cell cluster. (C) The expression of selected genes associated with the identity of each cluster in (A) were shown in a violin plot. (D) Expression of key lineage specific genes and transcription factors.
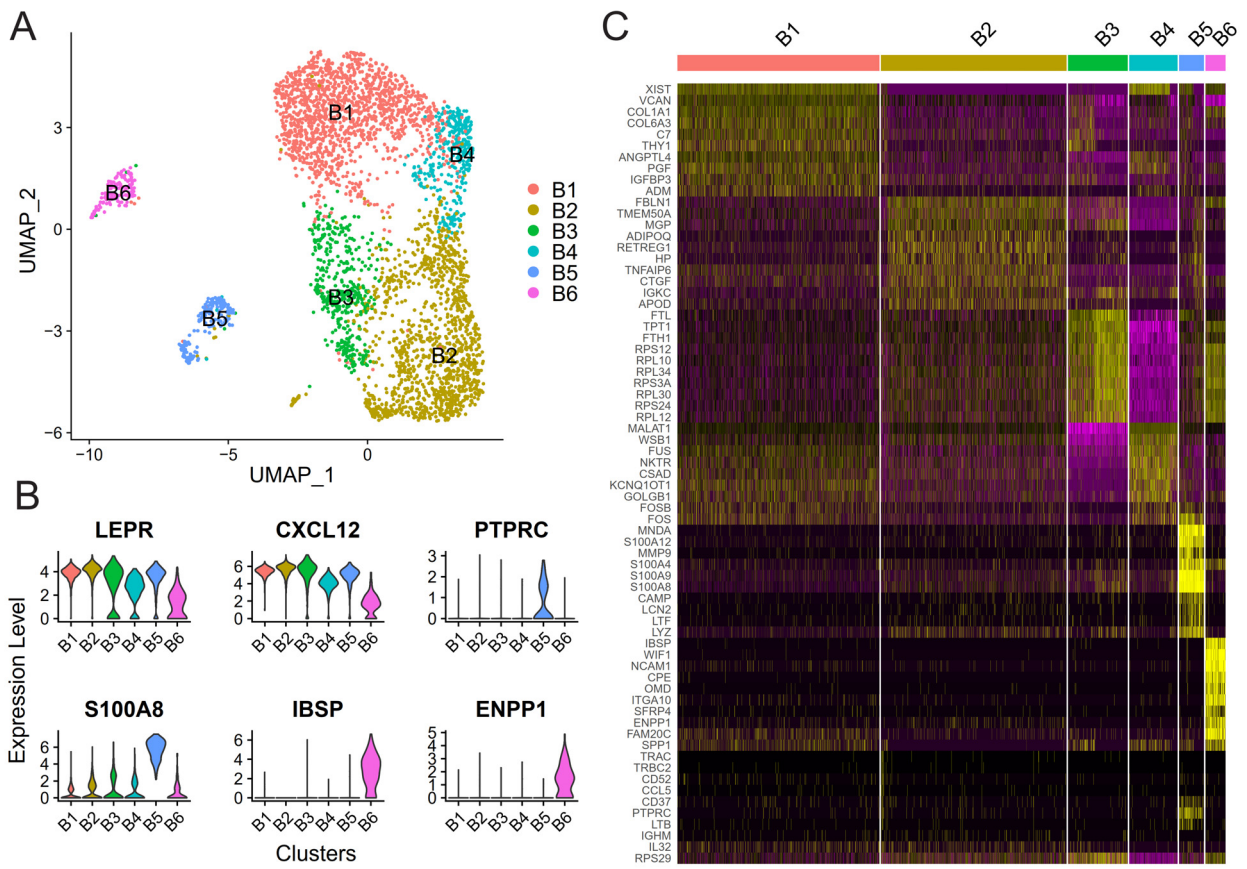
Fig. S2. scRNA-seq identification of human BMMSCs. (A) Visualization of UMAP colored according to cell types for human BMMSCs single-cell transcriptomes. Definition atlas of BMSC cells (B5, neutrophils; B6, advanced osteoblasts). (B) The expression of selected genes associated with the identity of each cluster in (A) were shown in a violin plot. (C) Heatmap of the top 10specific significantly enriched genes for each cell cluster.
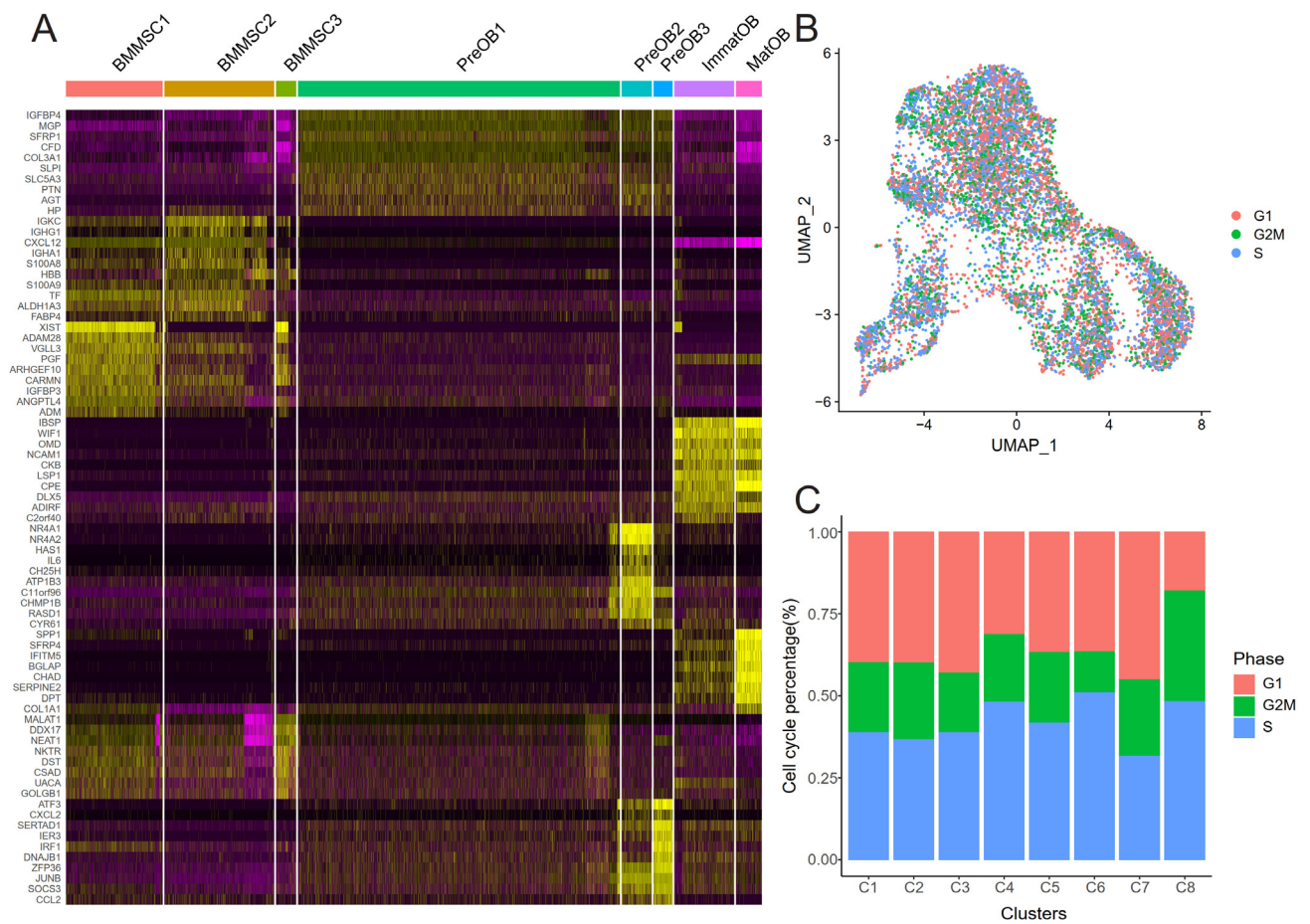
Fig. S3. Integrate result correlation analysis, cell cycle analysis, and heat map. (A) Heatmap of the top 10 specific significantly enriched genes for each cell cluster. (B) Cell cycling phases identified by Seurat. Phases of cell cycle are depicted in different colors, G0/G1 in orange, S in azure, and G2/M in green. (C) The percentage of G0/G1, S and G2/M in each cell cluster during the cell cycle.
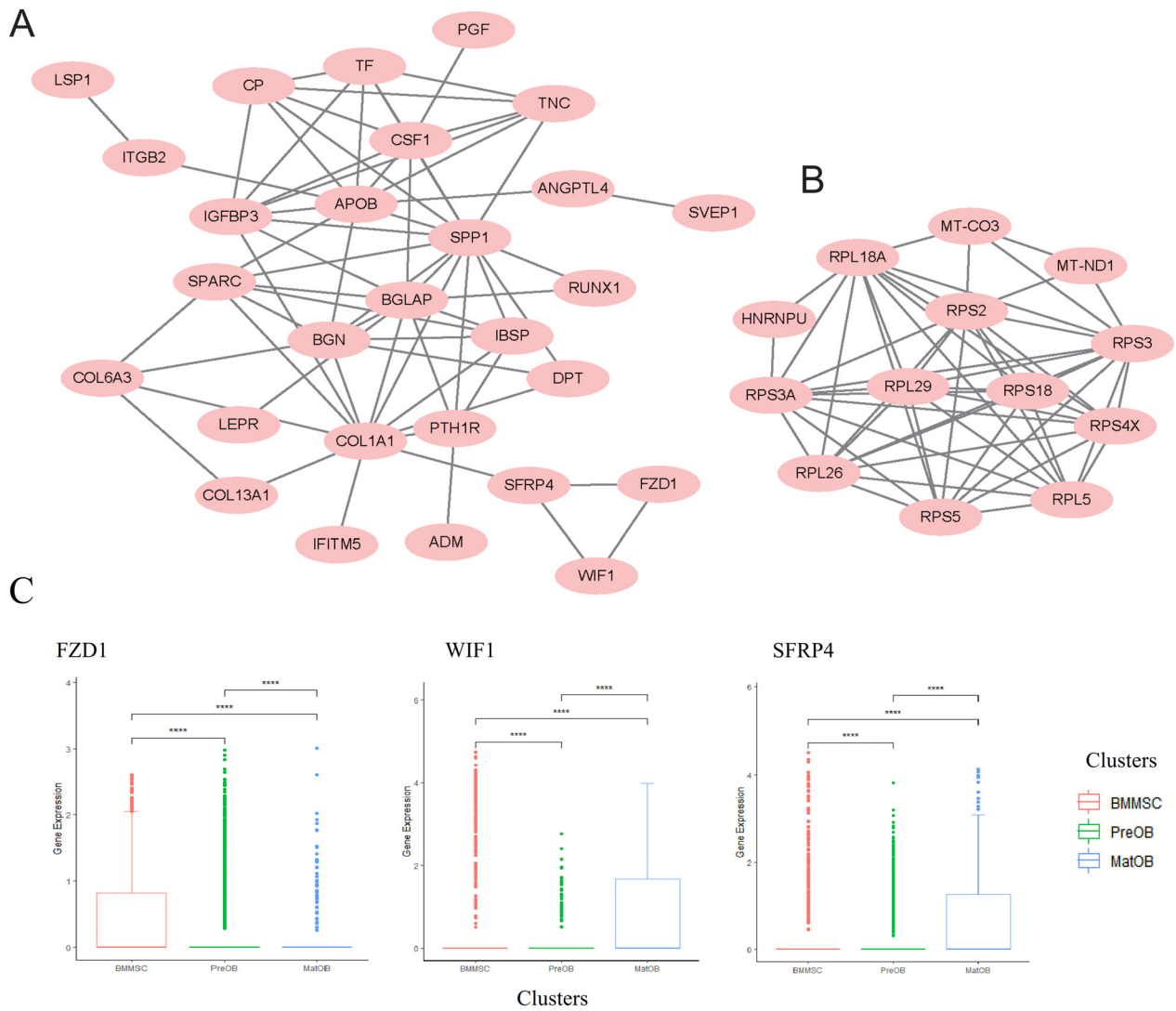
Fig. S4. PPI network. (A, B) PPI network of BMMSC1 and MatOB clusters. (C) Violin plots demonstrated the expression of FZD1, WIF1, and sFRP4 in each cluster. ns:not significant, ****p-adjusted ≤0.001.