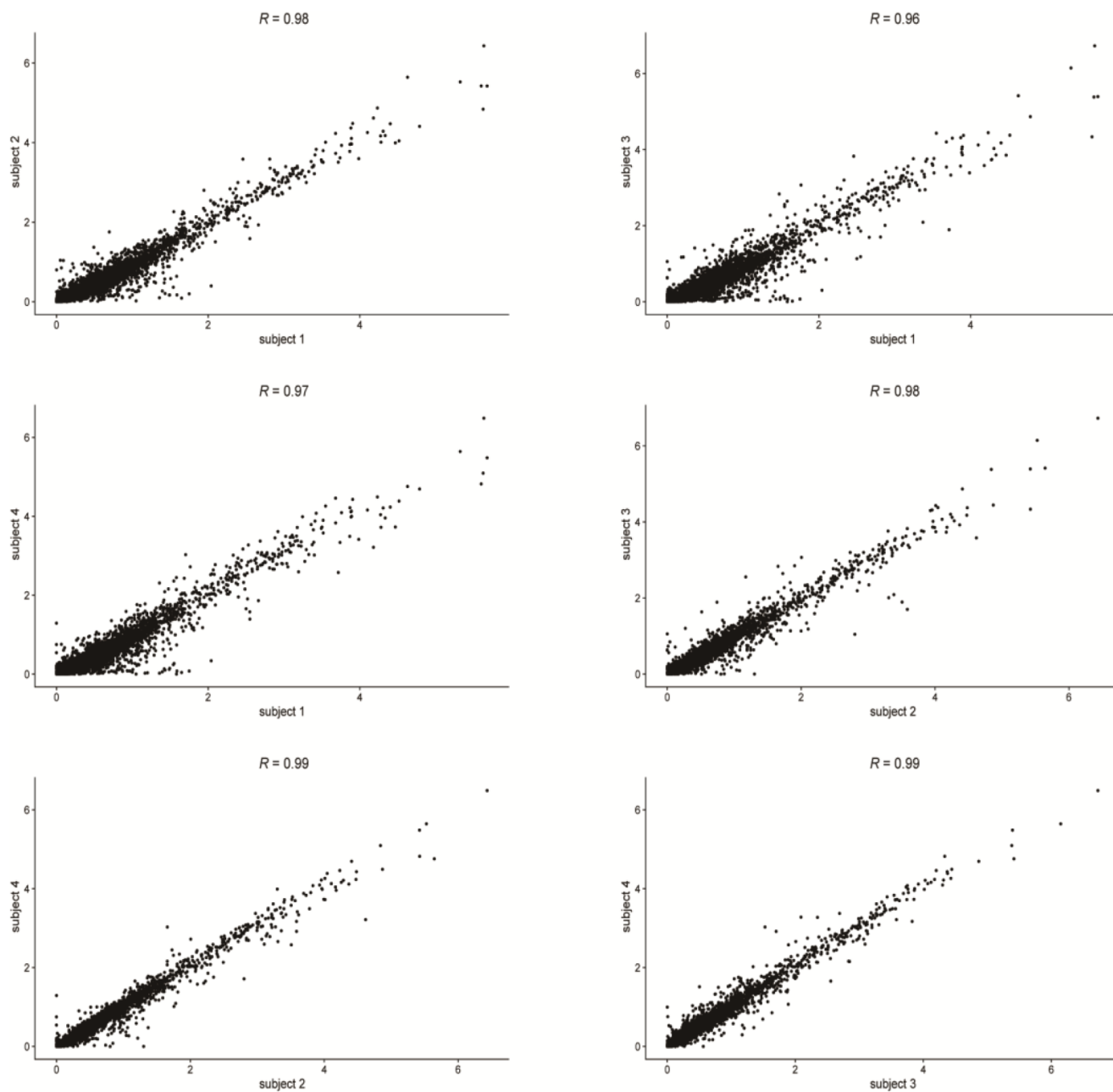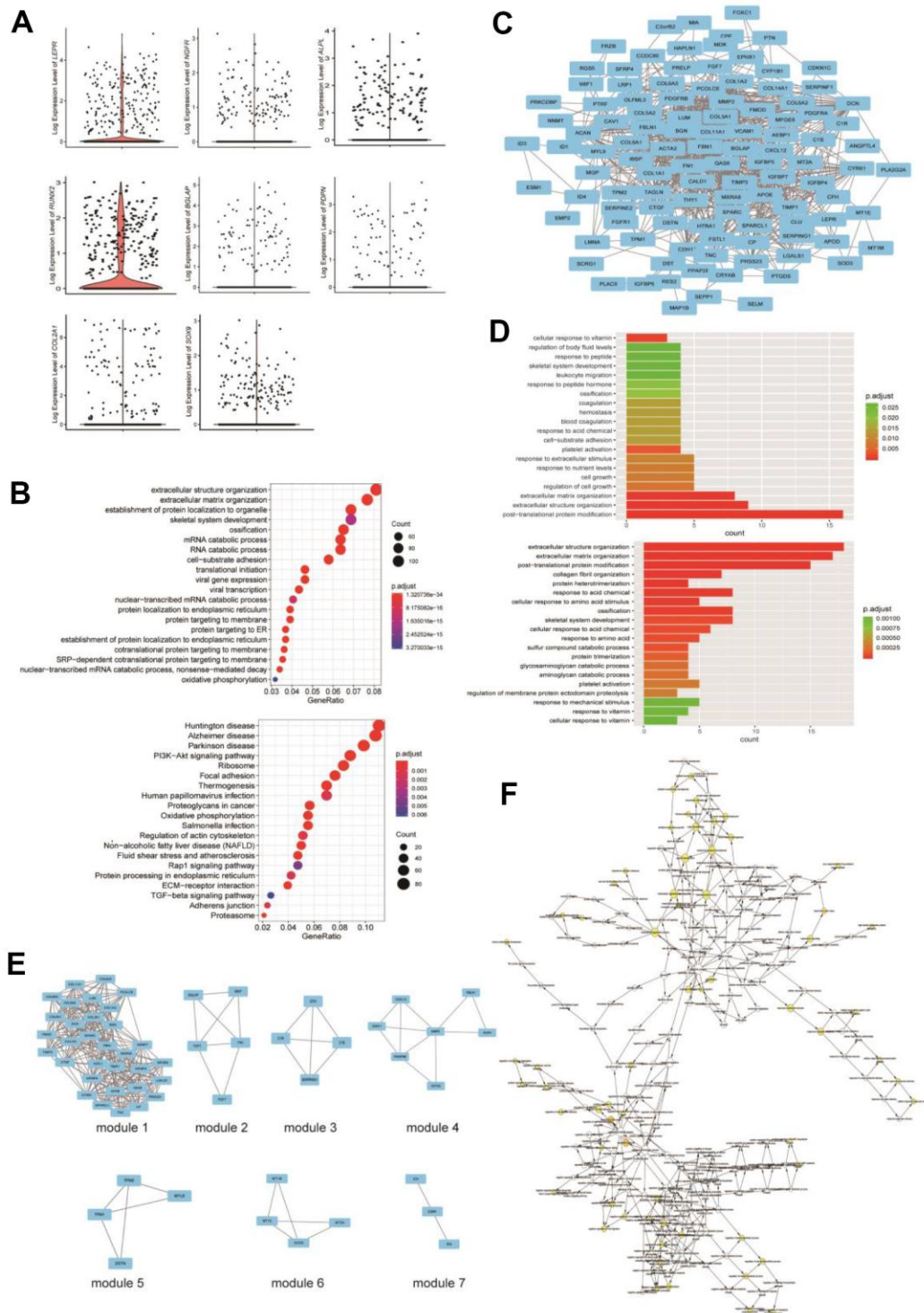# SUPPLEMENTARY FIGURES

Supplementary Figure 1. Correlation of gene expression profiles between each two subjects. Each dot represents an individual gene.

Supplementary Figure 2. PPI network and module analysis for DEGs of osteoblastic lineage cells. (**A**) Violin plots show the expression of marker genes about BM-MSCs (*LEPR*, *NGFR*), osteoblasts (*ALPL*, *RUNX2*, *BGLAP*), osteocytes (*PDPN*), and chondrocytes (*COL2A1*, *SOX9*) in the osteoblastic lineage cells. Each dot represents one cell. (**B**) GO (above) and KEGG (below) enrichment analysis for DEGs of osteoblastic lineage cells. (**C**) Visualize PPI network with Cytoscape. The PPI network consists of 111 nodes and 800 edges. (**D**) GO enrichment analysis of the 20 hub genes with a higher degree of connectivity in gene network (above). GO enrichment analysis of genes in module 1 (below). (**E**) The geometry view of seven modules. (**F**) The biological process analysis of hub genes in module 1 was constructed using BiNGO (Cytoscape). The color depth of node refers to the corrected *p* value of ontologies. The size of node refers to the number of genes that are involved in the ontologies. The corrected *p* value < 0.05 was considered statistically significant.