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Selecting key genes associated with osteosarcoma based on a differential expression network

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ABSTRACT. Despite recent advances in osteosarcoma diagnosis and therapy, much remains unclear about the molecular mechanisms involved in the disorder, and the discovery of novel drug-targeted genes is essential. We explored the potential molecular mechanisms and target genes involved in the development and progression of osteosarcoma. First, we identified the differentially expressed genes in osteosarcoma patients and matching normal controls. We then constructed a differential expression network based on differential and non-differential interactions. Pathway-enrichment analysis was performed based on the nodes contained in the main differential expression network. Centrality analysis was used to select hub genes that may play vital roles in the progression of human osteosarcoma. Our research revealed a total of 176 differentially expressed genes including 82 upregulated and 94 downregulated genes. A differential expression network was constructed that included 992 gene pairs (1043 nodes). Pathway-enrichment analysis indicated that the nodes in the

differential expression network were mainly enriched in several pathways such as those involved in cancer, cell cycle, ubiquitin-mediated proteolysis, DNA replication, ribosomes, T-cell receptor signaling, spliceosomes, neurotrophin signaling, oxidative phosphorylation, and tight junctions. Six hub genes (*APP*, *UBC*, *CAND1*, *RPA*, *YWHAG*, and *NEDD8*) were discovered; of these, two genes (*UBC* and *RPA*) were also found to be disease genes. Our study predicted that *UBC* and *RPA* had potential as target genes for the diagnosis and treatment of osteosarcoma.

Key words: Osteosarcoma; Differential expression network; Centrality analysis; Pathway-enrichment analysis

