

Int J Hum Genet, 18(2): 129-136 (2018) DOI: 10.31901/24566330.2018/18.2.696

## Revealing Dysregulated Modules and Genes for Postmenopausal Osteoporosis Based on Module Inference and Attract Method

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KEYWORDS Protein-Protein Interaction Network. Dysregulated Genes. Attract. Biomarkers. Treatment

ABSTRACT Postmenopausal osteoporosis (PO) imposes a significant burden on the individual and society. This work aimed to investigate dysregulated modules and genes for PO. Firstly, protein-protein interaction (PPI) data were prepared for the Retrieval of Interacting Genes/Proteins (STRING) database and gene expression data. Subsequently, attracted modules were explored from PPI networks by clique-merging algorithm and module correlation density (MCD) analyses. Ultimately, dysregulated modules between PO and normal were determined, and genes in the dysregulated modules were defined. A total of 7,953 genes and 48,778 interactions were collected for PPI data. Module 1 and Module 2 were identified for PO, and the two modules also detected as dysregulated modules. Module 1 included 6 dysregulated genes, while Module 2 with 7 dysregulated genes. The dysregulated modules and genes might be potential biomarkers for prevention and treatment of PO, which give new insights for revealing molecular mechanism of PO.