



## Screening and functional microarray analysis of differentially expressed genes related to osteoporosis

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**ABSTRACT.** We searched for key genes that could accurately predict bone mineral density. The gene expression profile GSE7429 was downloaded from the Gene Expression Omnibus database, which includes 20 samples, 10 with high and 10 with low bone mineral density. The differentially expressed genes (DEGs) were identified with packages in R language. Further, BLASTX was used to obtain COG function classifications of all the DEGs. The GOTM software was used to find DEGs enriched modules. The functions of genes in the modules was also predicted with the software GENECODIS. Three hundred and three genes were identified as DEGs by comparing high and low bone mineral density samples; the selected genes were mapped to 14 modules collected in PPID. Genes VDR, ESR1, and NRIP1, located in the same module, were significantly enriched in intracellular receptor-mediated signaling biological processes. We conclude that the genes VDR, ESR1, NRIP1 in B cells have a close relationship with bone mineral density. The expression patterns of these genes could be used to determine osteoprotegerin function and for early diagnosis and prevention of low bone mineral density.

**Key words:** Bone mineral density; B cell; Functional analysis; Differentially expressed genes; Enrichment analysis