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Investigation of lncRNA Biomarkers in Postmenopausal Osteoporosis Using an lncRNA-Mediated, Competitive Endogenous RNA Network

Hong-Zhuan Li, Ji-Rong Zhao, Fei Li, Jiu-Xia Wang and Hong Zhou

Department of Orthopedics, Gansu Provincial Hospital of TCM, Lanzhou, 730050, Gansu Province, China

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ABSTRACT In the present study, the researchers aimed to investigate long non-coding RNA (lncRNA) biomarkers for postmenopausal osteoporosis (PO) based on an lncRNA-mediated competitive endogenous RNAs (ceRNAs) network (LMCN). The LMCN was constructed by integration of lncRNA and mRNA expression profiles, miRNA-target interactions and Pearson correlation coefficient (PCC) algorithm. Topological degree centrality analysis was conducted on the LMCN to investigate optimal lncRNAs. Subsequently, a synergistic, competing module which correlated to optimal lmcRNAs closely was extracted from the LMCN utilizing the Biclique algorithm. As a result, the LMCN was comprised of 50 lncRNAs, 1,205 mRNAs and 1,393 ceRNA interactions, from which a module with 13 lncRNAs, 54 mRNAs and 117 interactions was extracted. The top 5 lncRNAs in descending order of degree were defined as optimal lncRNA biomarkers. In summary, the findings provide lncRNA biomarkers for target treatment and detection of PO patients, and give great insights to revealing the molecular mechanism underlying this disease.