Targetscore used to Reveal Potential Targets of Mir-26a in Osteoporosis by Integrating MicroRNA Over-expression and Microarray Data

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ABSTRACT The objective of this paper was to predict the potential targets of miR-26a in osteoporosis based on the TargetScore combined miRNA over-expression information and sequence data. First, TargetScores were calculated by combining log fold-change and sequence scores obtained from TargetScan context score, probabilities of conserved targeting, and derived the distribution of targetScores. The potential target genes (PTGS) for miR-26a were predicted based on the targetScore threshold. To reveal the functions of miR-26a, the researchers implemented pathway enrichment analyses for the targets of miR-26a. Based on TargetScore>0.45, 246 PTGS for miR-26a were identified for osteoporosis, such as CEP55, CD200 and SYDE2. Besides, pathway enrichment results showed that 9 significant pathways were identified under the thresholds of P<0.05 and Counte"5, especially for Hippo, Glucagon and PI3K-Akt signaling pathway. The researchers have identified potential targets for miR-26a using TargetScore method, which might provide signatures in osteoporosis progression.