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Integrated Analyses of Gene Profile Digs out Suitable Biomarkers for Ankylosing Spondylitis using Three Different Methods

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ABSTRACT In the current study, the researchers aimed to extract suitable genes which contributed to ankylosing spondylitis (AS) using three popular meta-analysis approaches (combining p-values, convergent evidence, and rank product). Candidate genes across multiple methods were respectively identified. The common genes between any two methods were extracted as the optimal genes, following by functional enrichment analysis for the optimal genes. Context likelihood of relatedness algorithm was utilized to establish mutual information network (MIN) using the optimal genes. Simultaneously, classification ability analysis for hub genes was implemented. A MIN (93 genes and 2212 interactions) was constructed, and 3 hub genes (TALDO1, LCP1, and RPS27A) were identified. The classification analysis showed that hub genes separated AS from controls with the high accuracy, sensitivity, and specificity of 0.962, 0.937, and 0.953, respectively. Hub genes LCP1 and RPS27A might be used as genetic biomarkers for AS diagnosis and treatment.