Combined differential gene expression profile and pathway enrichment analyses to elucidate the molecular mechanisms of uterine leiomyoma after gonadotropin-releasing hormone treatment

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摘要

Abstract

Composite regulatory signature database (CRSD), a self-developed comprehensive Web server for composite regulatory signature discovery, used to compare the published microarray data with our data on patients with uterine leiomyoma treated with or without GnRH analogue (GnRH-a), revealed that the focal adhesion, mitogen-activated protein kinase (MAPK), CXC chemokine receptor 4/stromal-derived factor-1 (CXCR4/SDF-1), T-cell receptor, integrin, vascular endothelial growth factor (VEGF), GnRH, and transforming growth factor-beta (TGF-beta) signaling pathways are highly expressed in uterine leiomyoma and significantly down-regulated after GnRH-a treatment. According to the results these signaling pathways could be involved in inflammation, proliferation, and remodeling processes of leiomyoma development and possibly in the regression of leiomyoma after GnRH-a treatment, which might improve our understanding of the mechanisms of leiomyoma formation and help us to find novel drug targets or specific markers for diagnosis and prognosis in uterine leiomyoma.