Figure S1. *In silico* prediction of endometriosis-related pathways that may represent preliminary targets of myrrh. (A) Potential target genes of myrrh were obtained from the Traditional Chinese Medicine Integrative Database and analyzed with the JEPPETO plugin in Cytoscape. KEGG, (B) Biocarta, and (C) GO_MF enrichment analyses indicate that these genes are enriched in pathways related to apoptosis, mitochondrial dysfunction, proteolytic regulation and stress responses, which are dysregulated in endometriosis and may represent putative targets for myrrh.

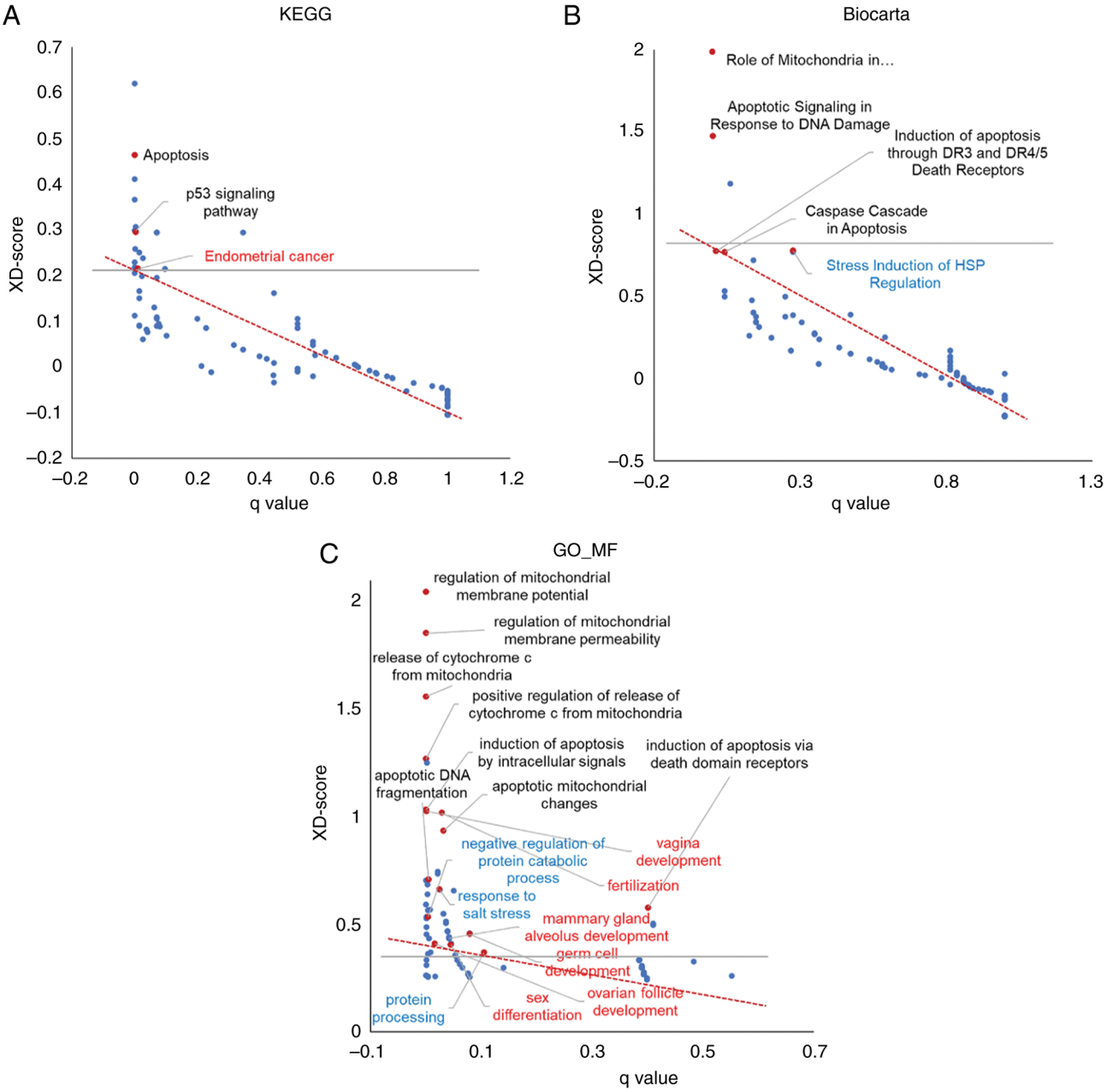

Figure S2. Histological analysis of kidney and liver tissues after myrrh treatment in endometriosis-induced mice. H&E staining results of (A) kidney and (B) liver tissue. The mice were treated indicated dose of myrrh (0.7 or 3.5 mg/kg/day) after induction of endometriosis. The microphotographic images of H&E-stained kidney and liver sections were presented (magnification, x100). Con, control.

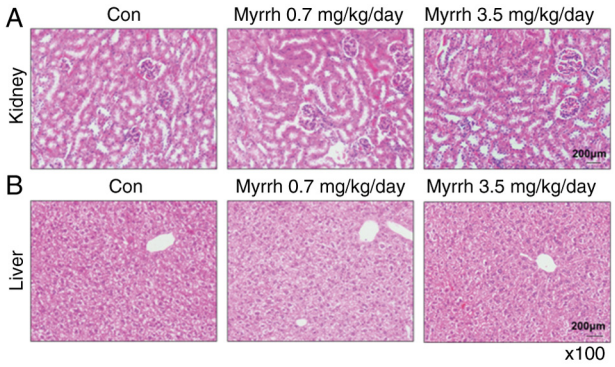

Figure S3. Effects of myrrh on TP53 expression and p53 protein levels (A) TP53 expression levels were visualized using RNA sequencing data. (B) Analysis of alterations in p53 protein by myrrh. Immunoblot analysis revealed that p53 was detected after 24 h of treatment with each concentration of myrrh. GAPDH was used as a internal control. CON, control.