

Exploration and validation of the prognostic value of mitophagy and mitochondrial dynamics-related genes in cervical cancer

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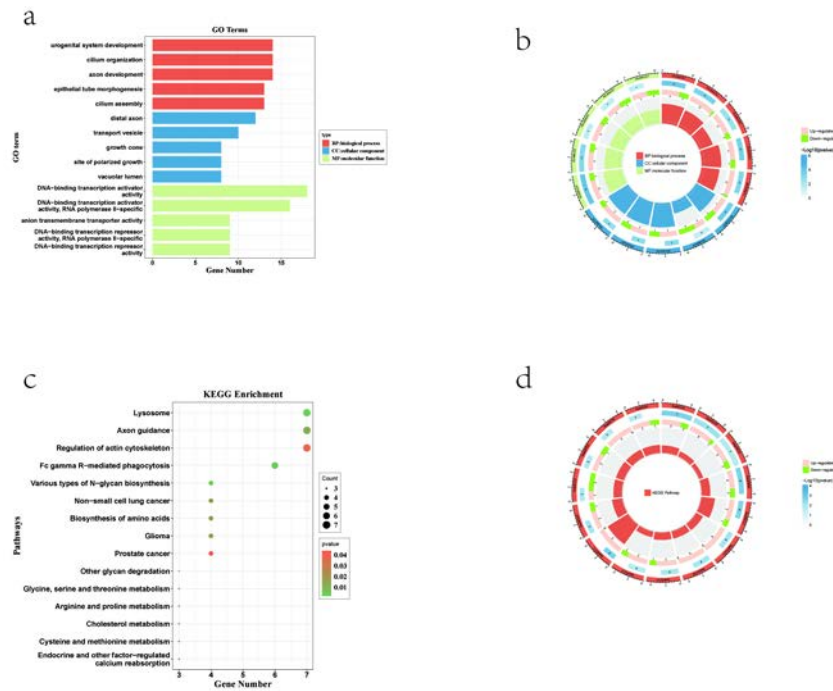


Figure S1 Functional enrichment analysis. (a-b) GO enrichment analysis of candidate genes. (c-d) KEGG enrichment results. All P -value < 0.05 .

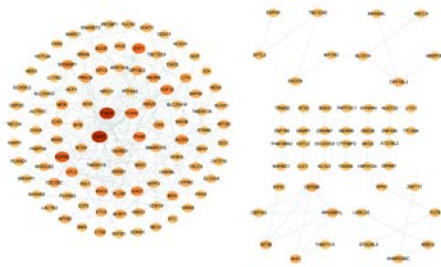


Figure S2 PPI network. P -value = 1.12×10^{-8} .

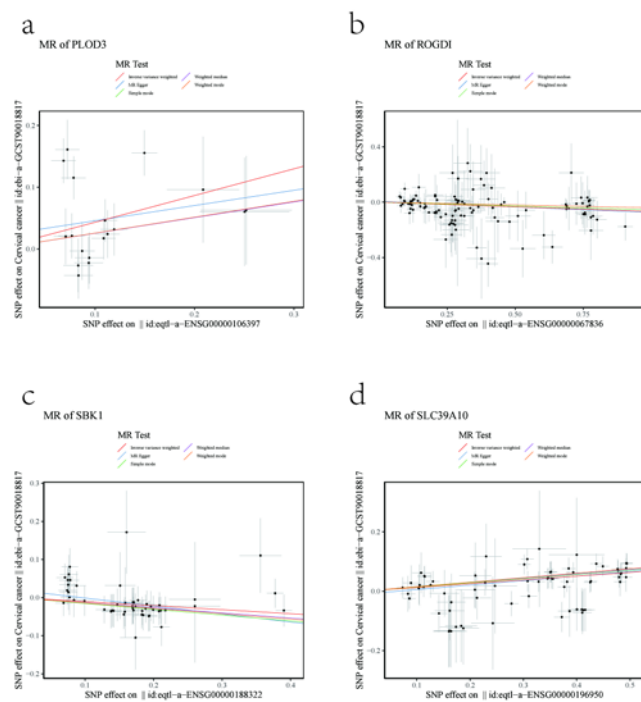


Figure S3 Correlation analysis between exposure factors and outcome. (a) Gene PLOD3 was a risk factor. **(b)** Gene ROGDI was a safety factor. **(c)** Gene SBK1 was a safety factor. **(d)** Gene SLC39A10 was a risk factor.

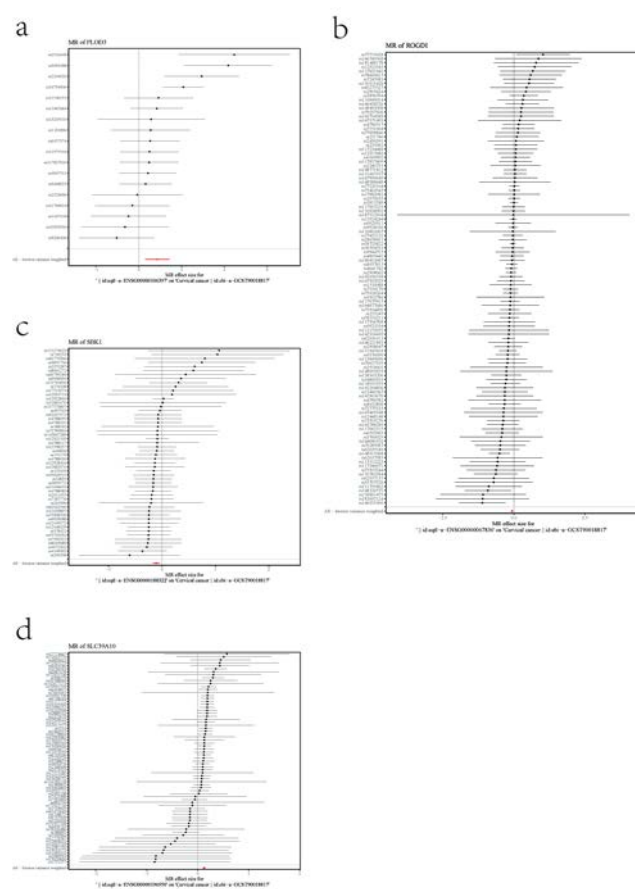


Figure S4 Prediction of outcome effects of instrumental variables. (a) PLOD3 was

a risk factor. (b) ROGDI was a safety factor. (c) SBK1 was a safety factor. (d) SLC39A10 was a risk factor.

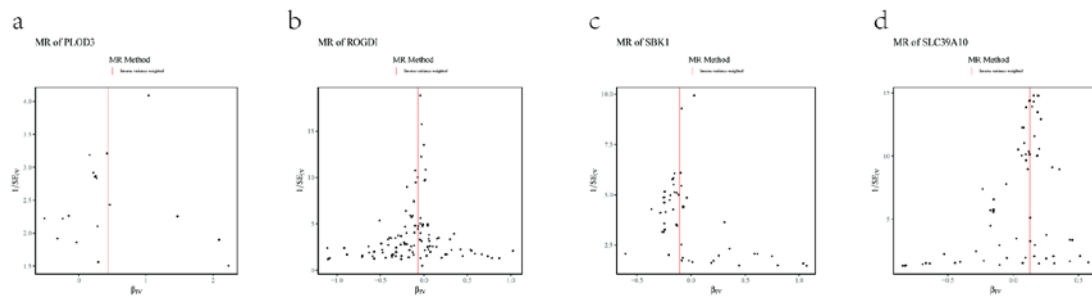


Figure S5 MR randomnes judgment is symmetrical distribution ((a) PLOD3, (b) ROGDI, (c) SBK1, (d) SLC39A10).

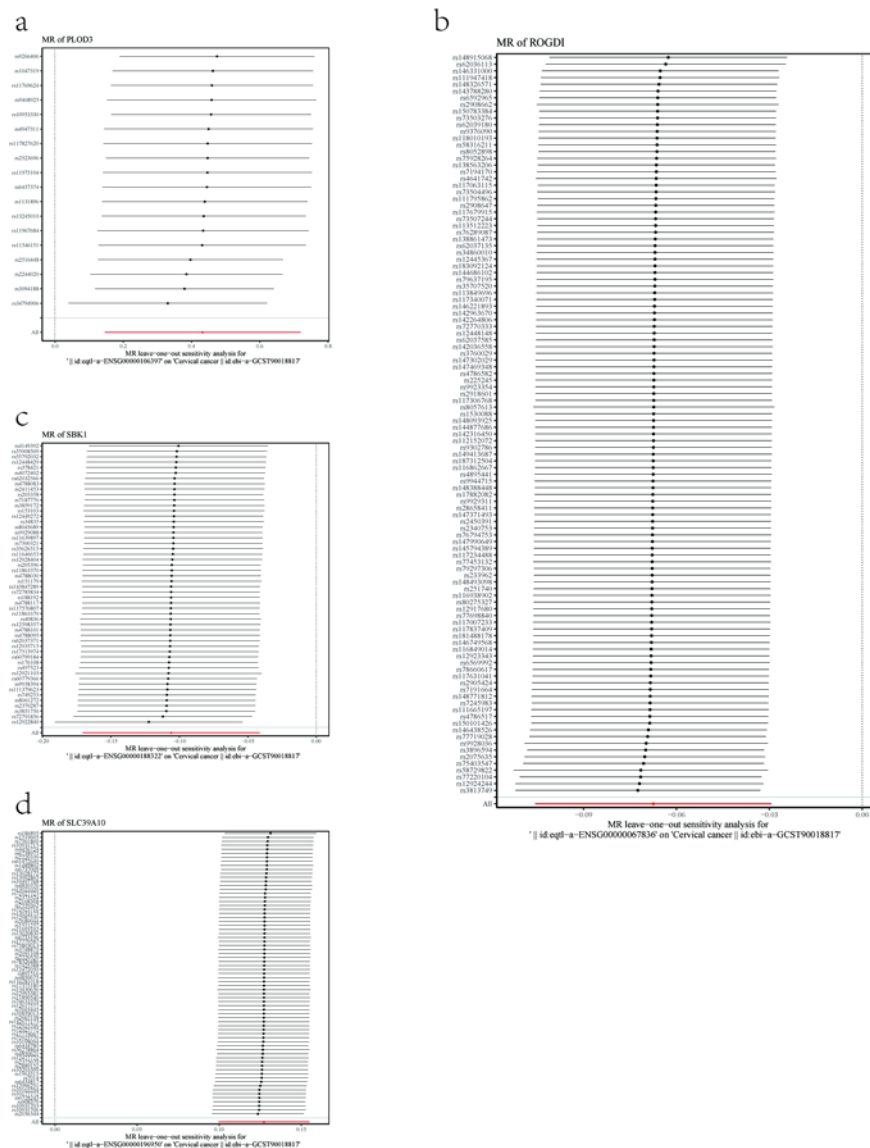


Figure S6 MR leave-one-out sensitivity analysis (PLOD3 (a), ROGDI (b), SBK1 (c), SLC39A10 (d)).

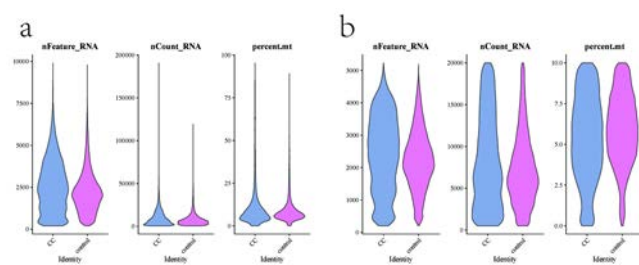


Figure S7 Single cell quality control. (a) Before quality control, nFeature_RNA, nCount_RNA, percent.mt distribution. (b) after quality control, nFeature_RNA, nCount_RNA, percent.mt distribution.



Figure S8 Go enrichment results (endothelial cells (a), epithelial cells (b), T cells (c)).

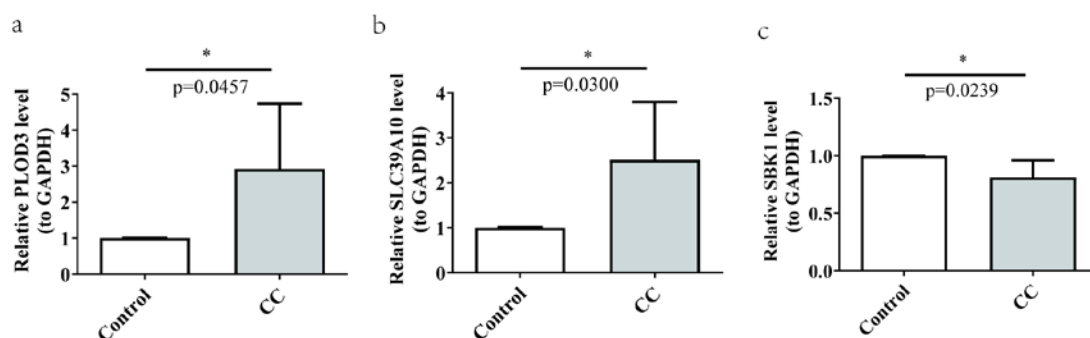


Figure S9 Reverse transcription quantitative polymerase chain reaction. (a) PLOD3 was highly expressed in CC. (b) SLC39A10 was highly expressed in CC. (c) SBK1 was low expression in CC. All P -value < 0.05.

