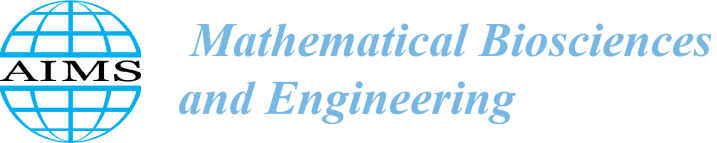
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***Research article***

**Development and validation of two redox-related genes associated with prognosis and immune microenvironment in endometrial carcinoma**

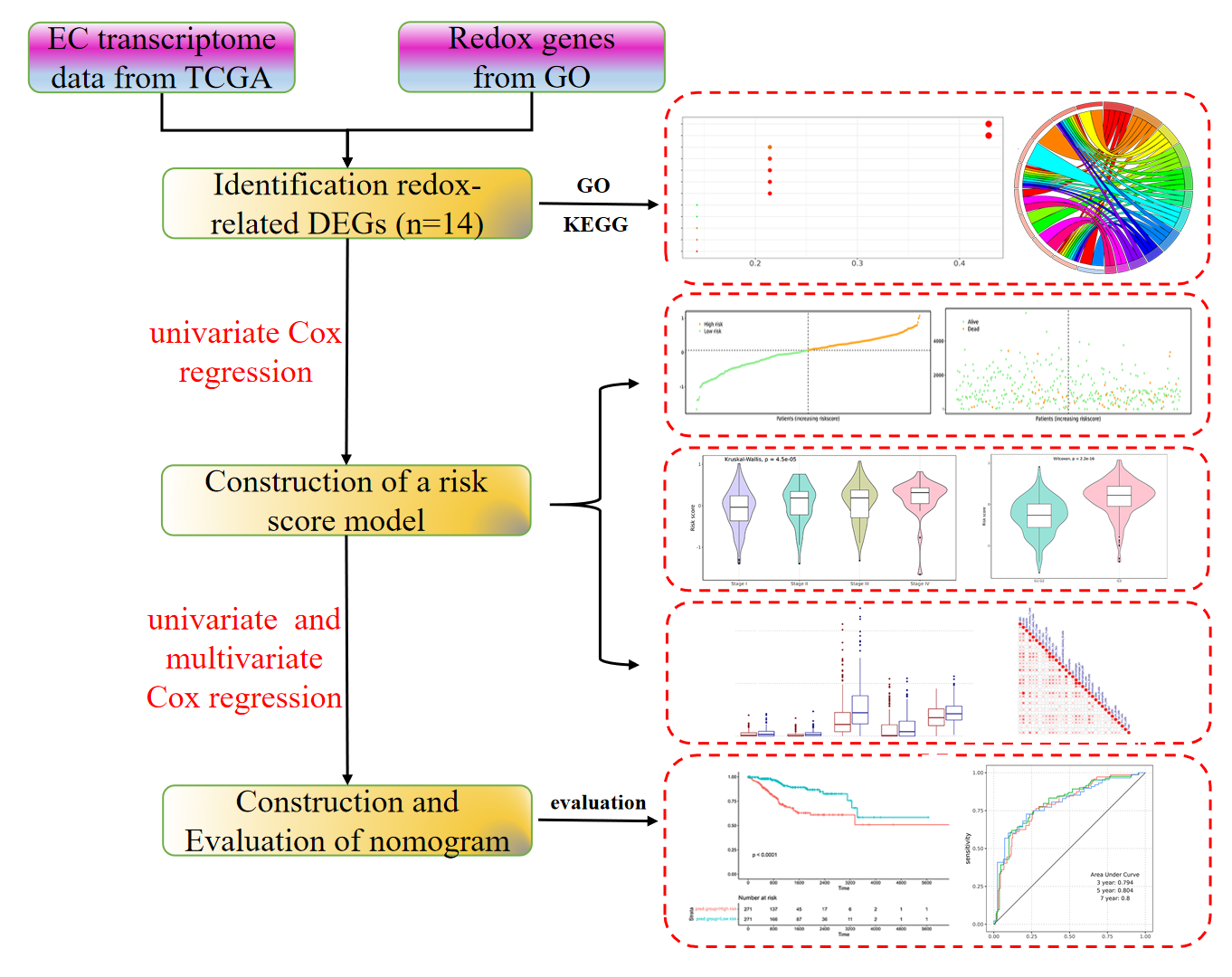
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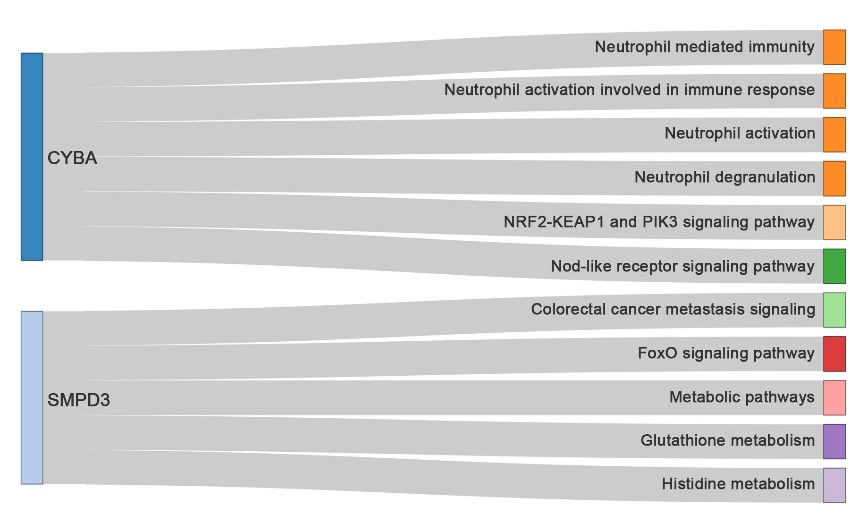
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**Supplementary**

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**Figure S1.** The flowchart of this study.



**Figure S2.** Signal pathways and GO terms involved in two key genes in certain tumors.



**Figure S3.** Difference of the risk scores in EC patients with different clinical characteristics. (a) The relationship between the risk scores and clinical stage in TCGA-UCEC datasets. (b) The relationship between the risk scores and tumor grade in TCGA-UCEC datasets.



**Figure S4.** GSVA analysis of low- and high-risk groups. (a) KEGG analysis of low- and high-risk groups. (b–d) BP, CC and MF of low- and high-risk groups. Red dots indicate high risk group samples, blue dots indicate low risk group samples. *P* value < 0.05.



**Figure S5.** The immune cell infiltration in the TCGA-UCEC cohort. (a) Heatmap of immune cells infiltration in low- and high-risk groups. (b) The correlation analysis between immune cells.



**Figure S6.** The gene mutation profile in low-risk and high-risk groups. (a, b) the top 20 mutated genes in low-risk and high-risk groups. (c) The mutation profile among low-risk and high-risk groups. (d) Word cloud of mutated genes.



**Figure S7.** Analysis of gene variant classifications and types in the TCGA-UCEC cohort.



**Figure S8.** The mutation profile and co-occurence of *CYBA* and *SMPD3*. (a) The mutation frequency of *CYBA* and *SMPD3* in the TCGA-UCEC cohort. (b) Co-occurence among somatic mutation genes.

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