

CORRECTION

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Correction: Construction and validation of a prognostic model of angiogenesis-related genes in multiple myeloma

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Following publication of the original article [1], it was reported that Fig. 6 is a duplicate of Fig. 5. This is a result of a typographical error. The correct Fig. 6 is given below.

Further to this, in the original article [1], only one corresponding author was erroneously listed. Xuezhong Gu and Zhixiang Lu are both corresponding authors. The original article [1] has been updated.

[†]Rui Hu and Fengyu Chen contributed equally to this work.

The online version of the original article can be found at <https://doi.org/10.1186/s12885-024-13024-9>.

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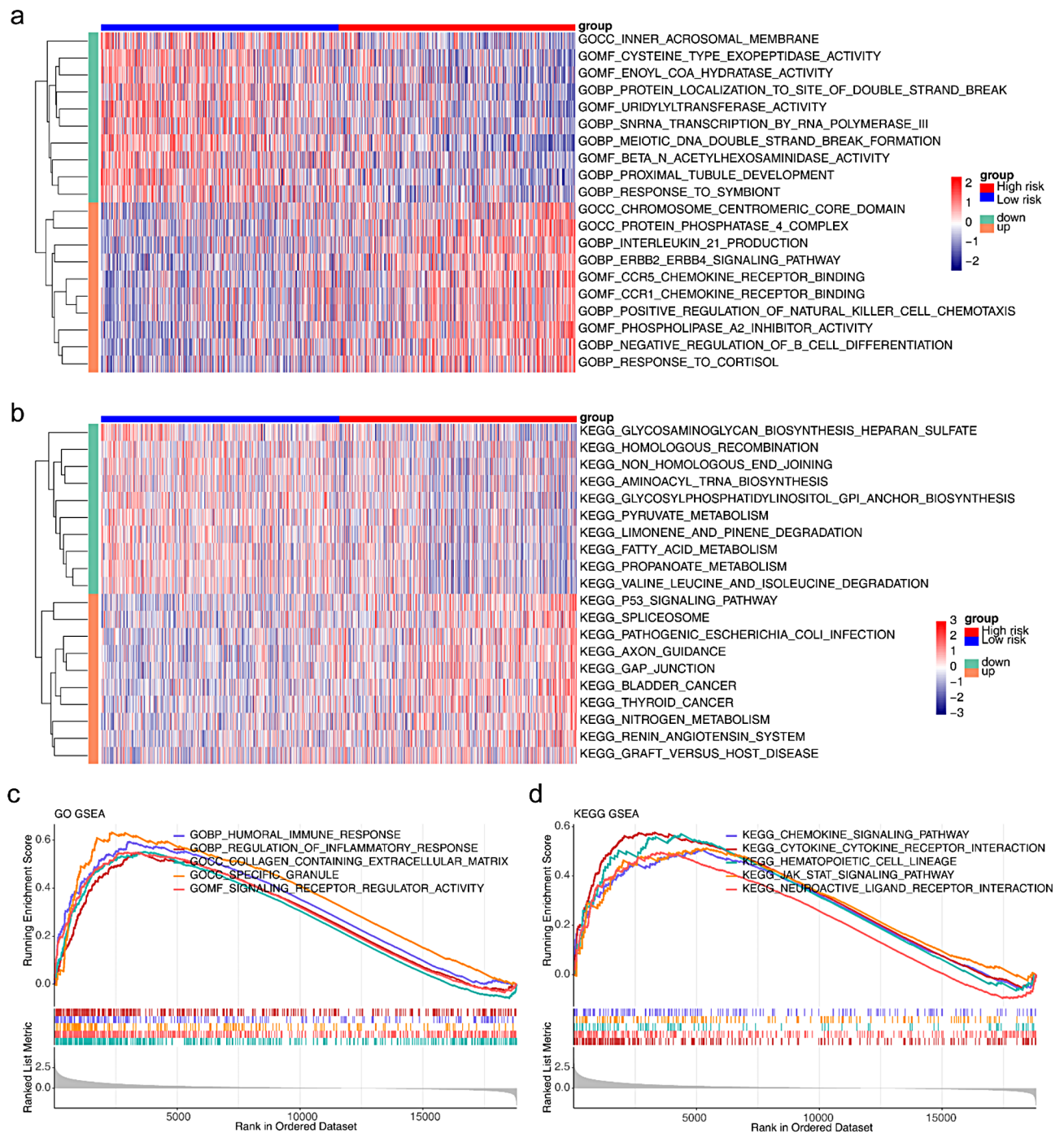


Fig. 6 Gene set variation analysis (GSVA) and gene set enrichment analysis (GSEA). **(a)** Heatmap of the results of GSVA analysis of the GO gene set. **(b)** Heatmap of the results of GSVA analysis of the KEGG gene set. **(c)** GSEA results for the GO gene set. **(d)** GSEA results for the KEGG gene set. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes

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Reference

1. Hu R, Chen F, Yu X, et al. Construction and validation of a prognostic model of angiogenesis-related genes in multiple myeloma. *BMC Cancer*. 2024;24:1269. <https://doi.org/10.1186/s12885-024-13024-9>.