

Comprehensive Analysis of ZFPM2-AS1 Prognostic Value, Immune Microenvironment, Drug Sensitivity, and Co-expression Network: From Gastric Adenocarcinoma to Pan-cancers

Discover Oncology

Di Chen¹, Mengmeng Wang¹, Xin Jiang¹, Zhifan Xiong¹

¹ Department of Gastroenterology, Liyuan Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China.

Corresponding author: Zhifan Xiong

Department of Gastroenterology, Liyuan Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, 430061, China.

Email: xiongzhiban@126.com

Fig. S1 Weighted Gene Co-Expression Network Analysis of GAC. (a) Analysis for various soft-thresholding powers. (b) Cluster diagram of gene cluster of GAC. (c) Heatmap of the correlation between the clinical traits and modules.

Fig. S2 The survival curve of differentially expressed immune-related lncRNAs for OS in GAC.

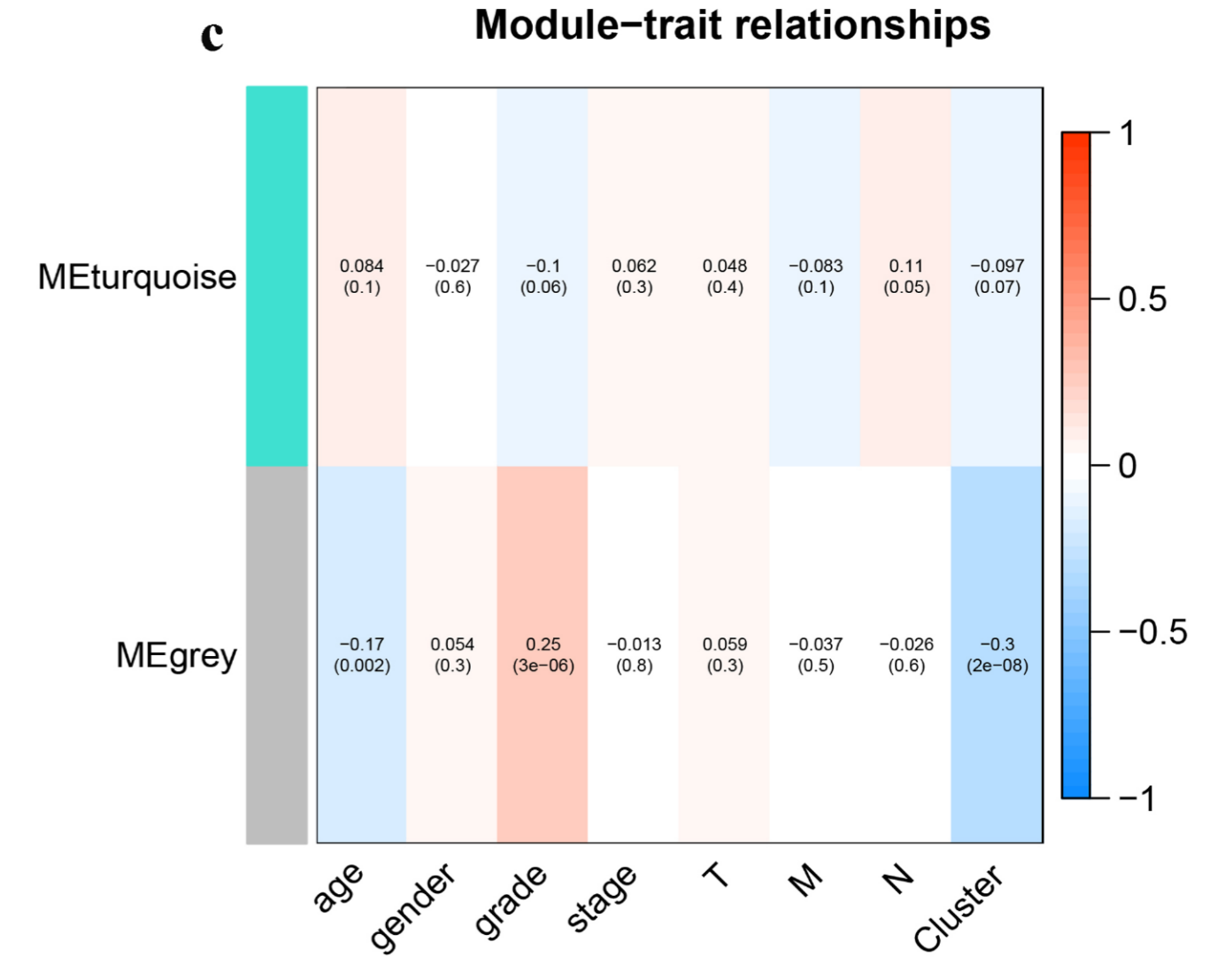
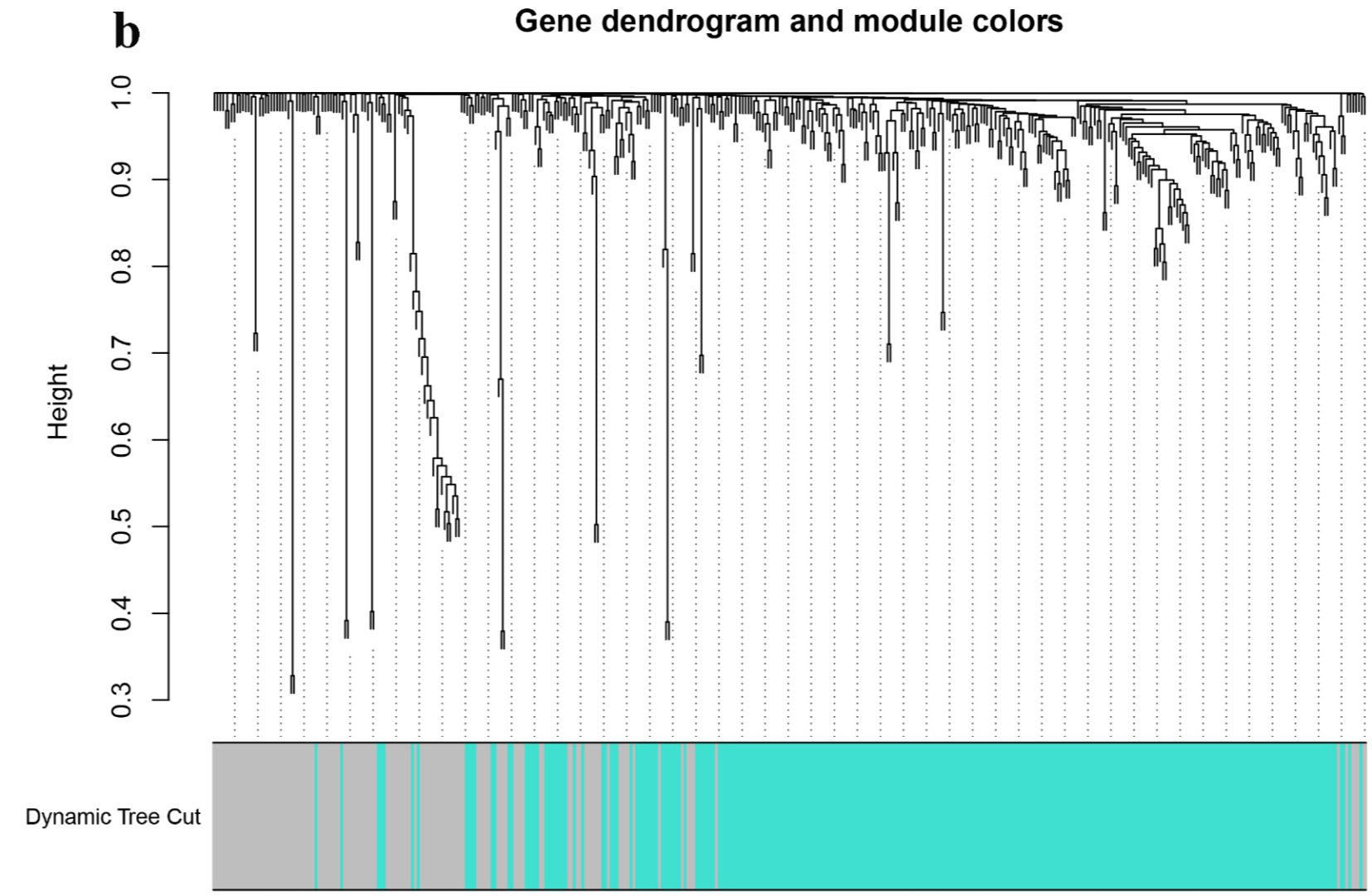
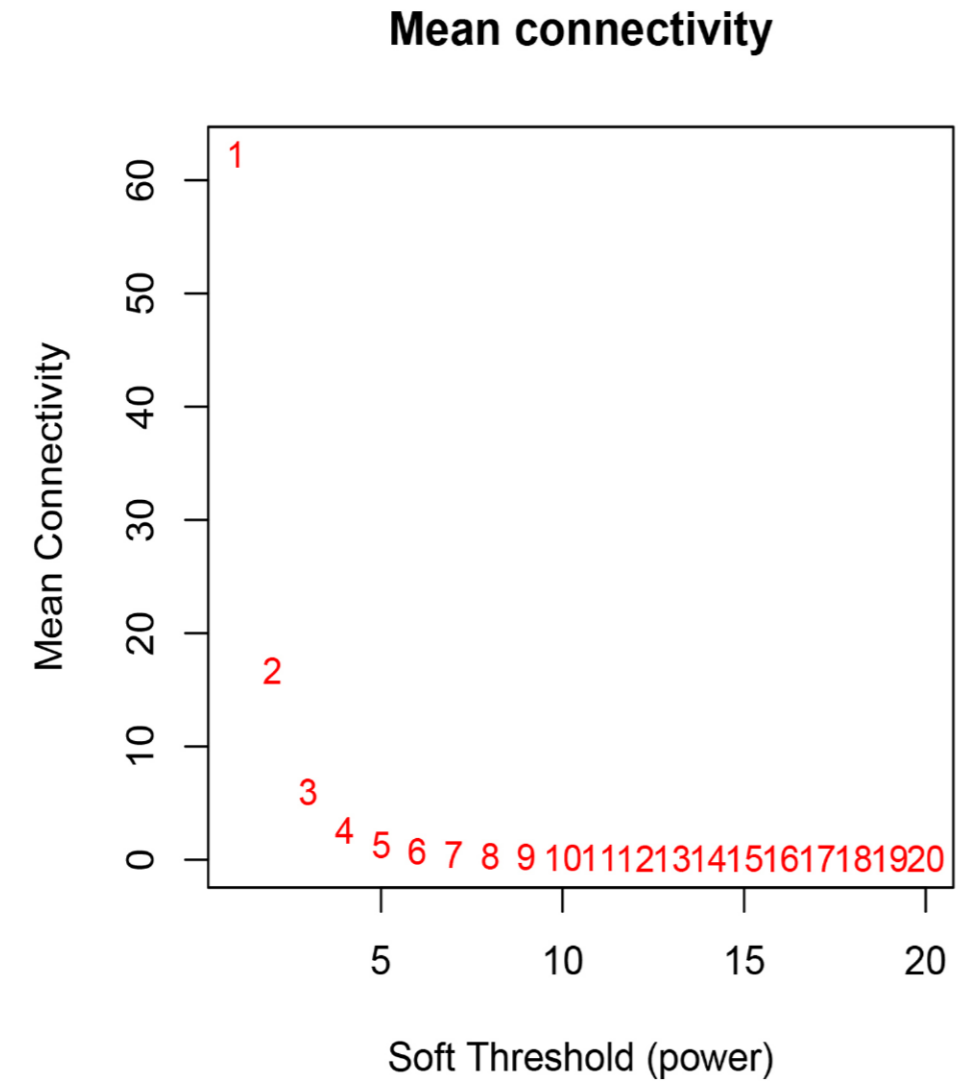
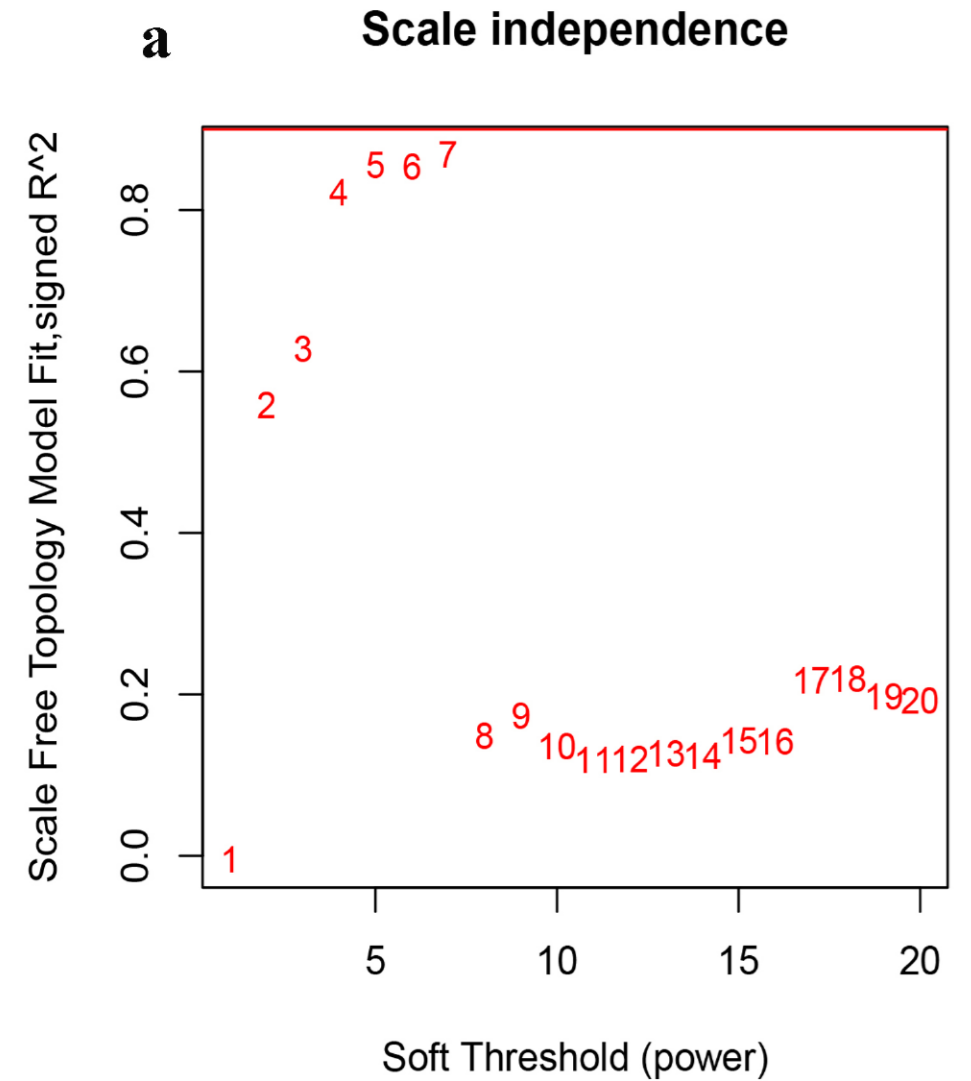
Fig. S3 The relationship between ZFPM2-AS1 expression and infiltrating immune cells in the microenvironment of pan-cancers.

Fig. S4 Gene set enrichment analysis of ZFPM2-AS1 in pan-cancers.

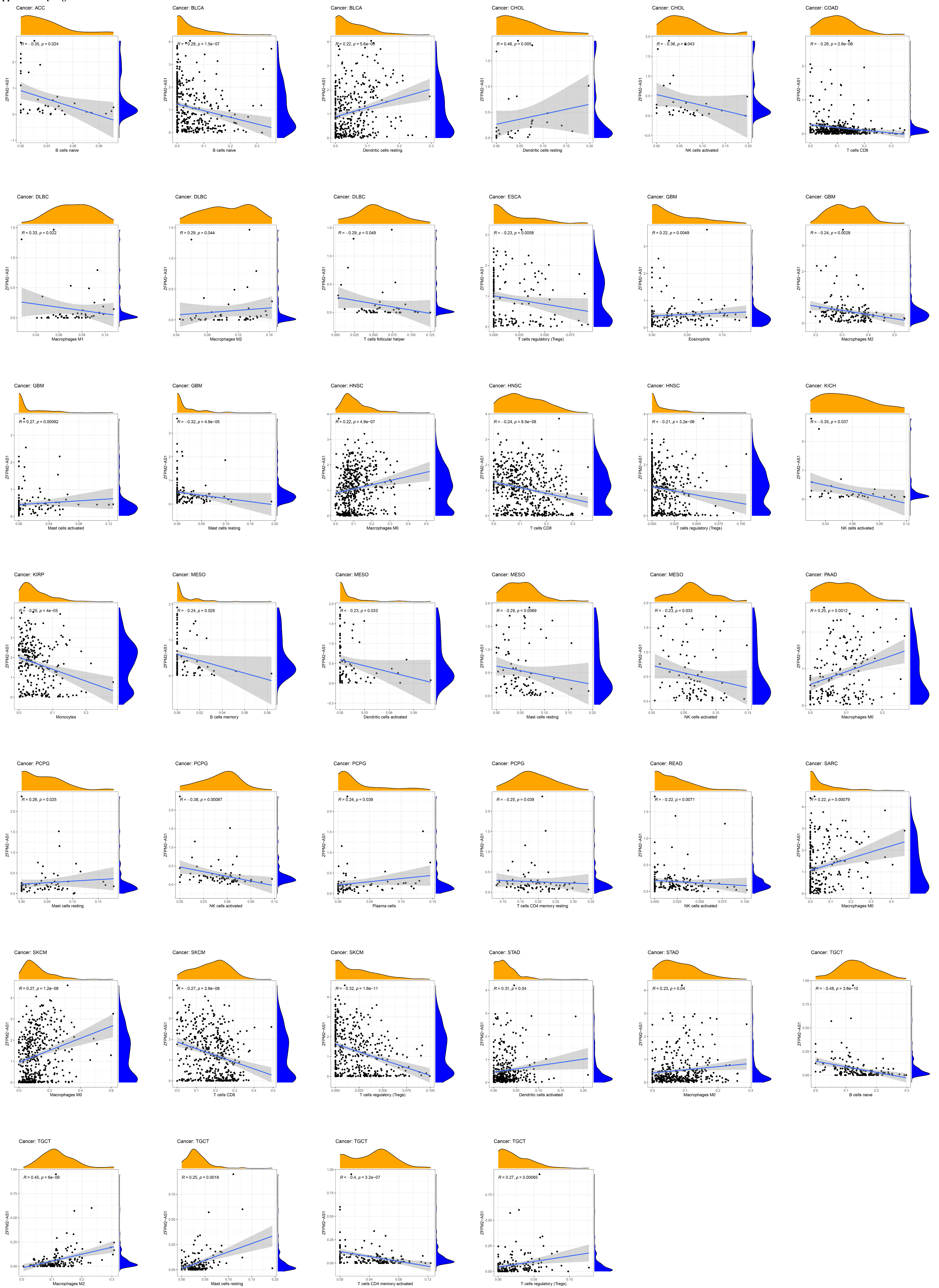
Fig. S5 Differential expression of target mRNAs in paired GAC samples and normal samples from TCGA.

Fig. S6 The survival curve of target mRNAs for OS in GAC.

Supplementary Figure 1

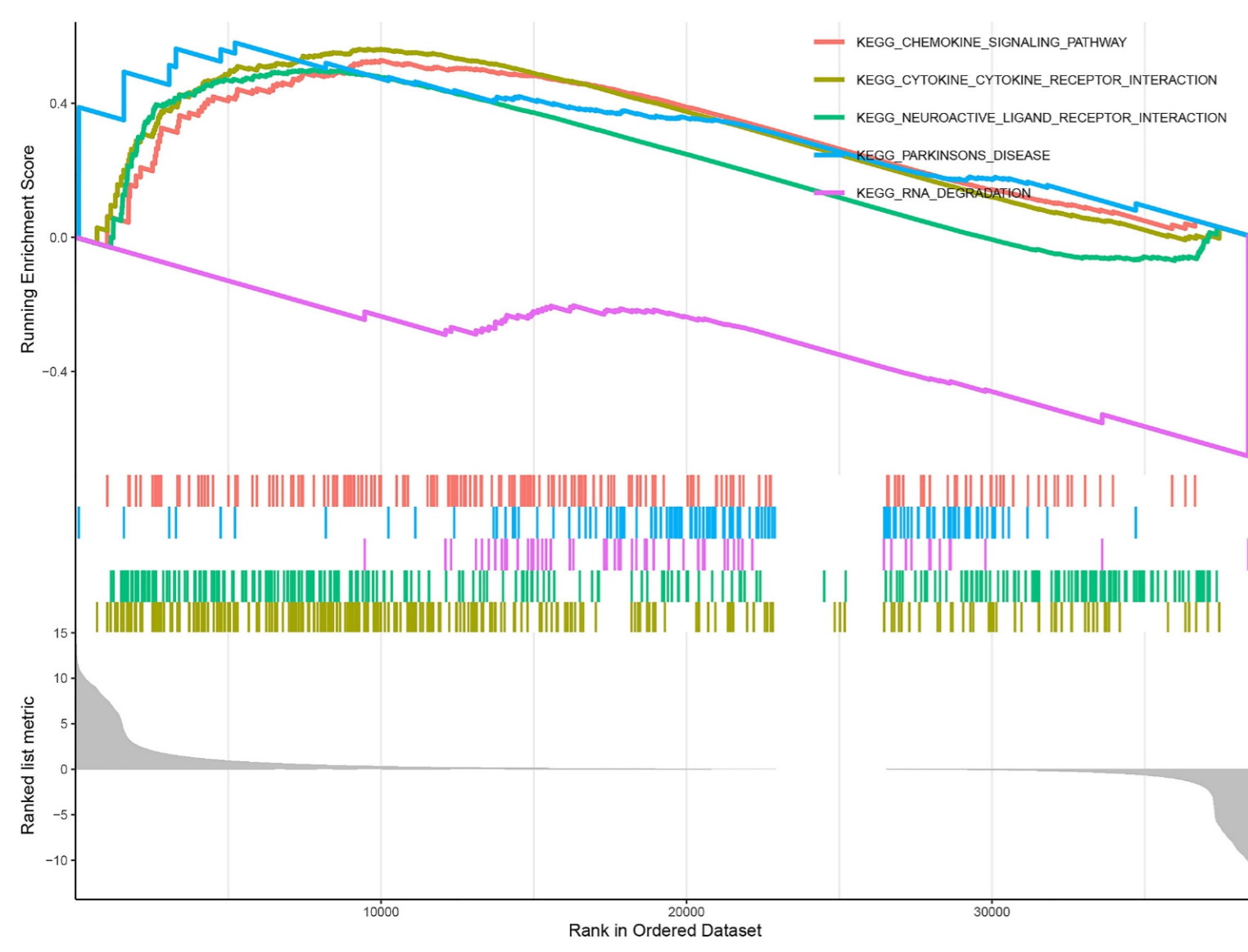


Supplementary Figure 3

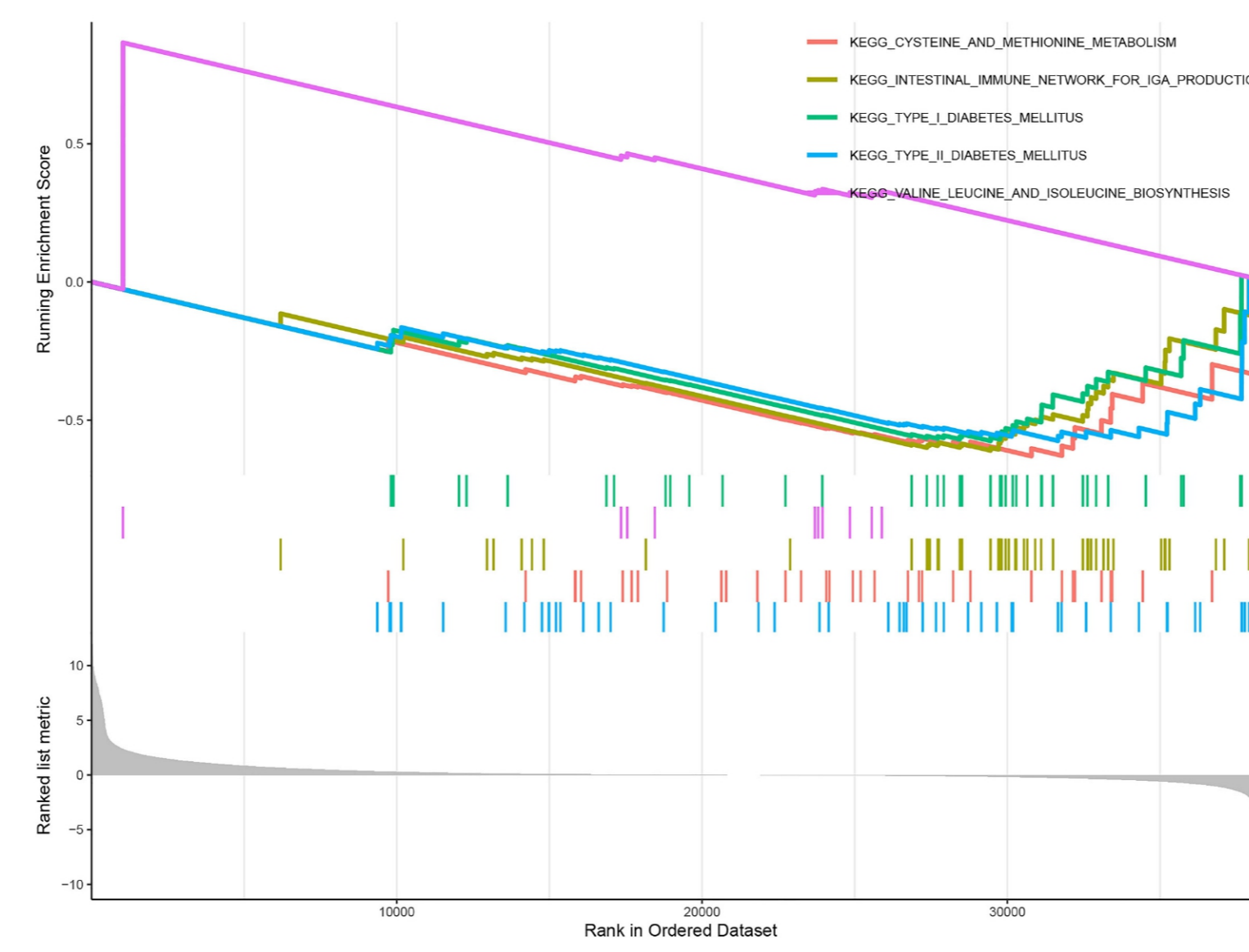


Supplementary Figure 4

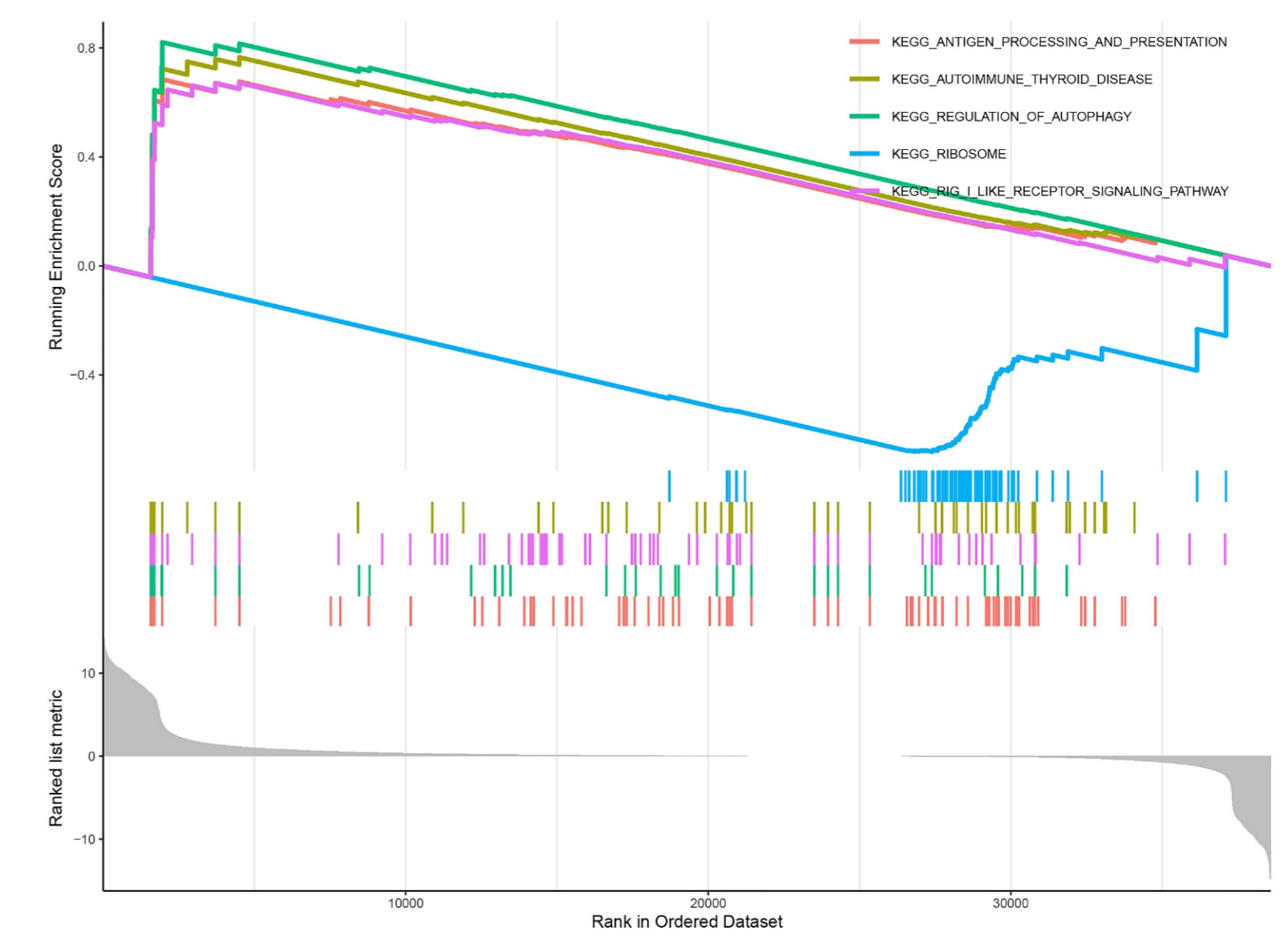
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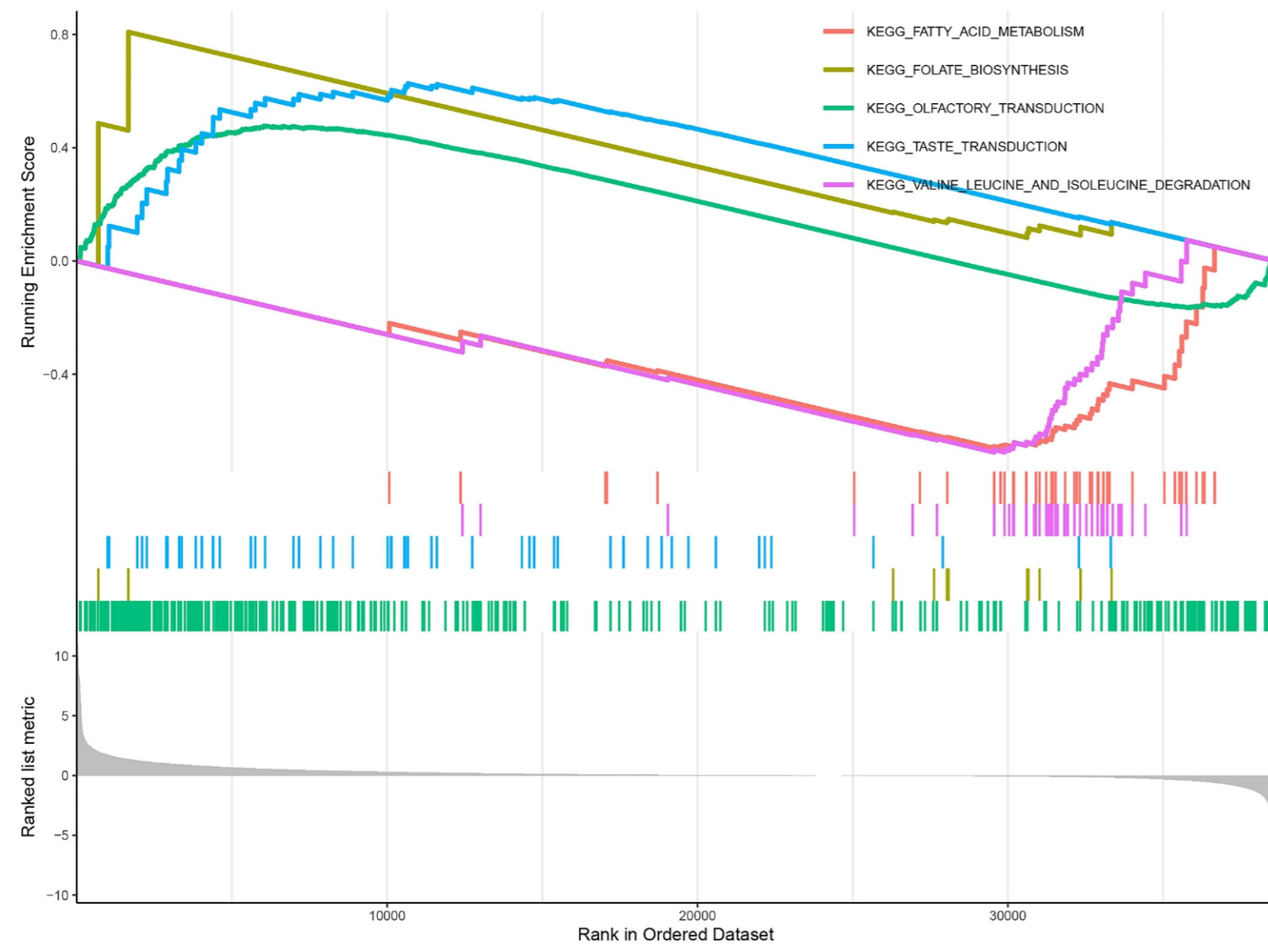
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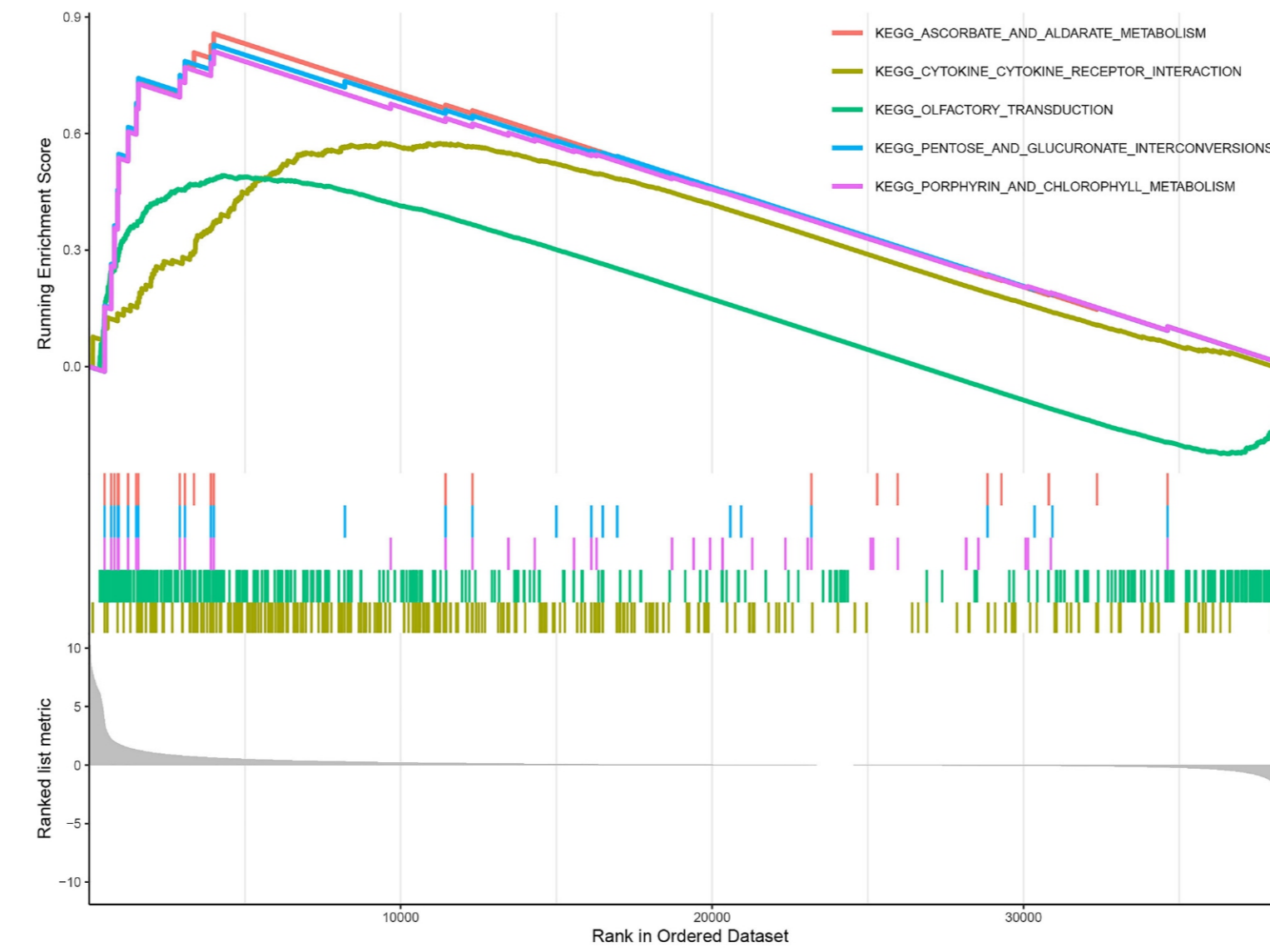
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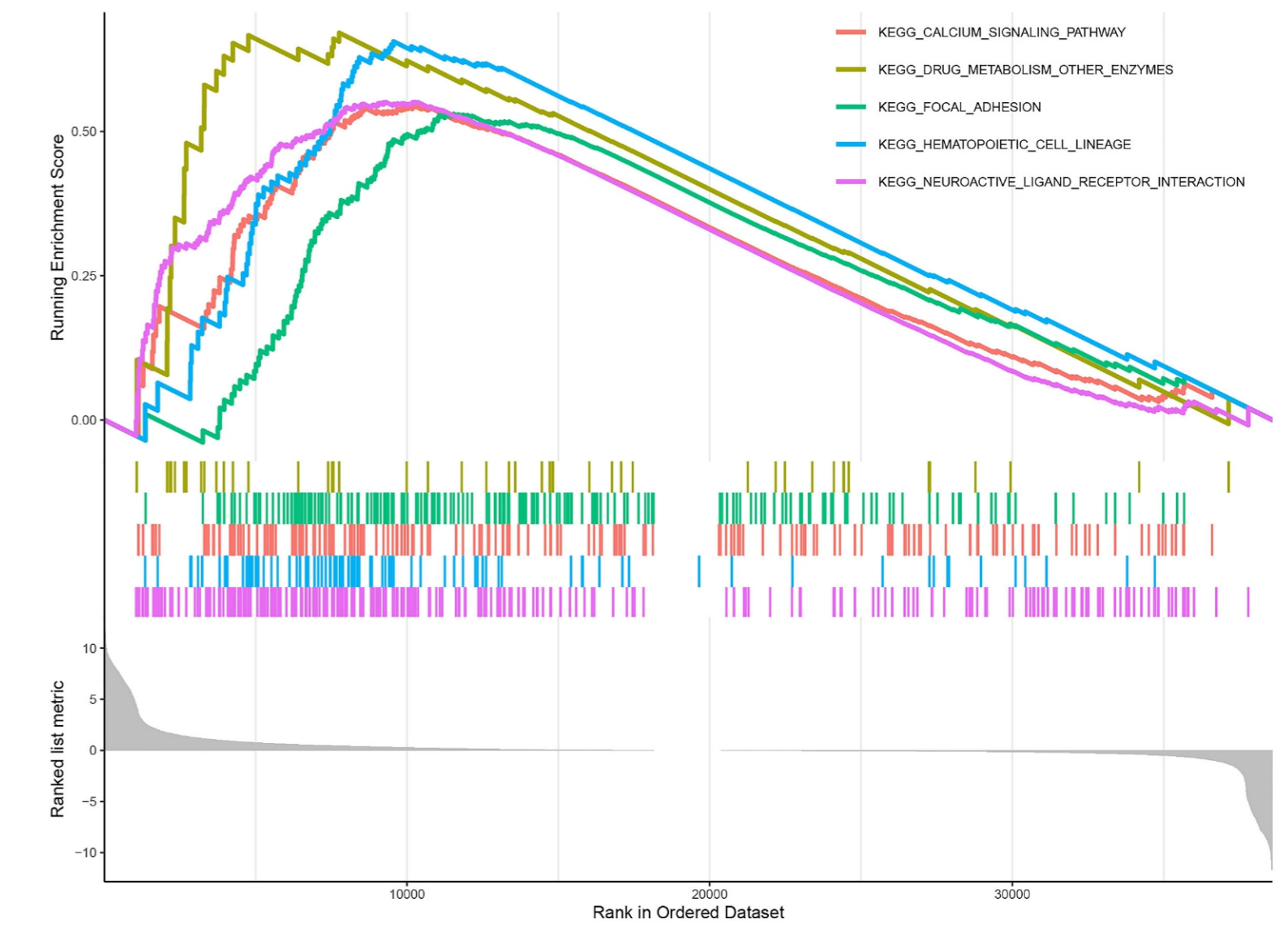
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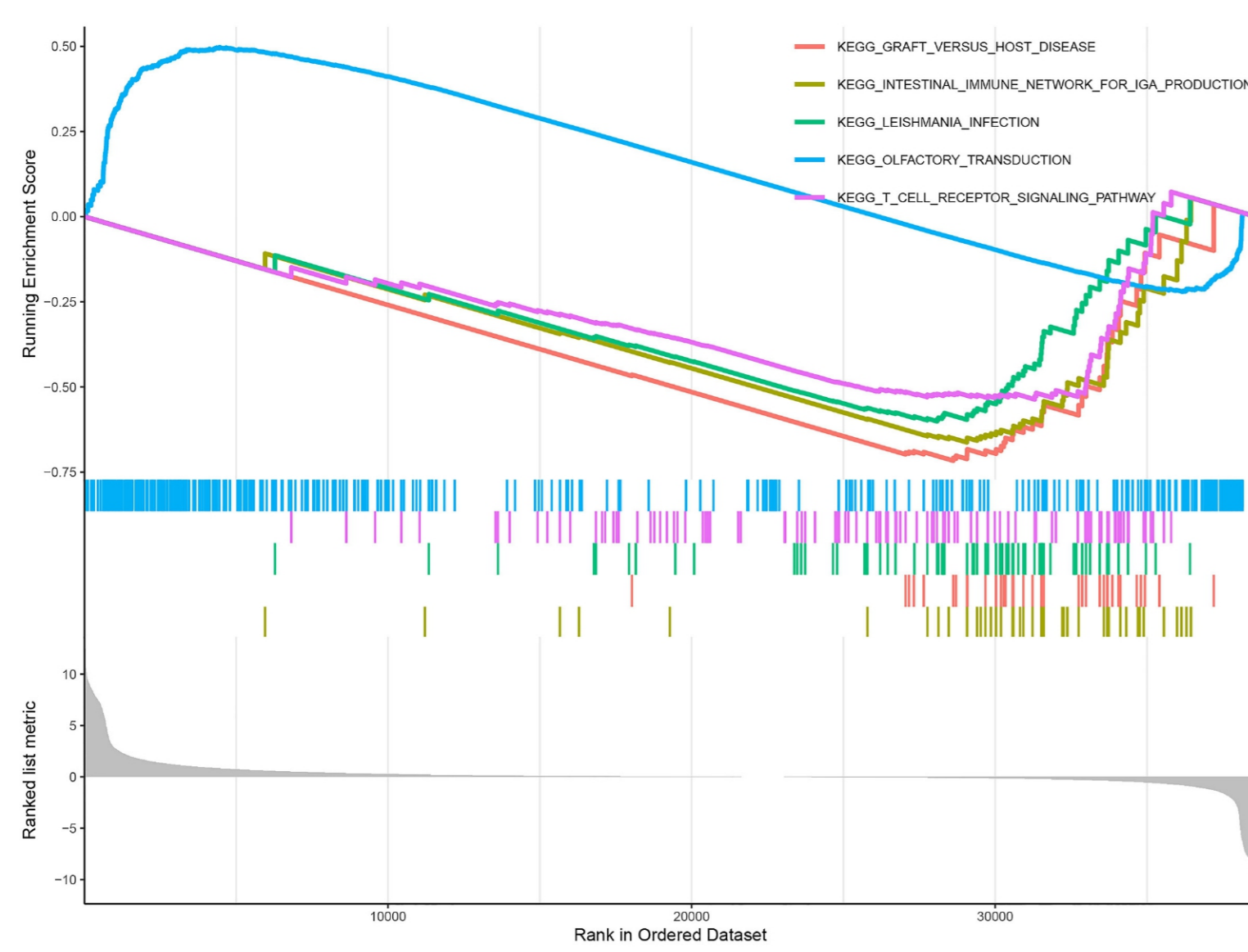
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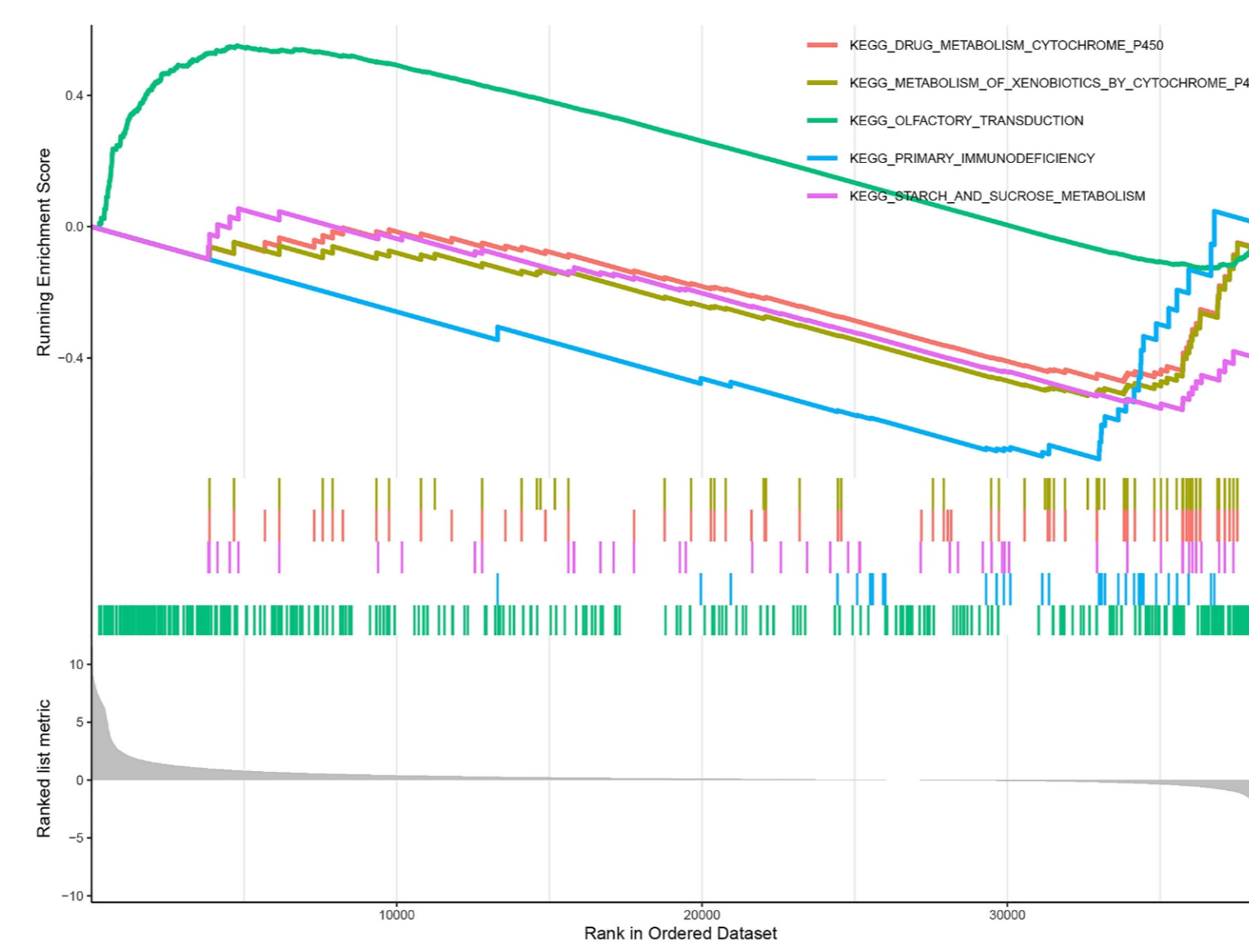
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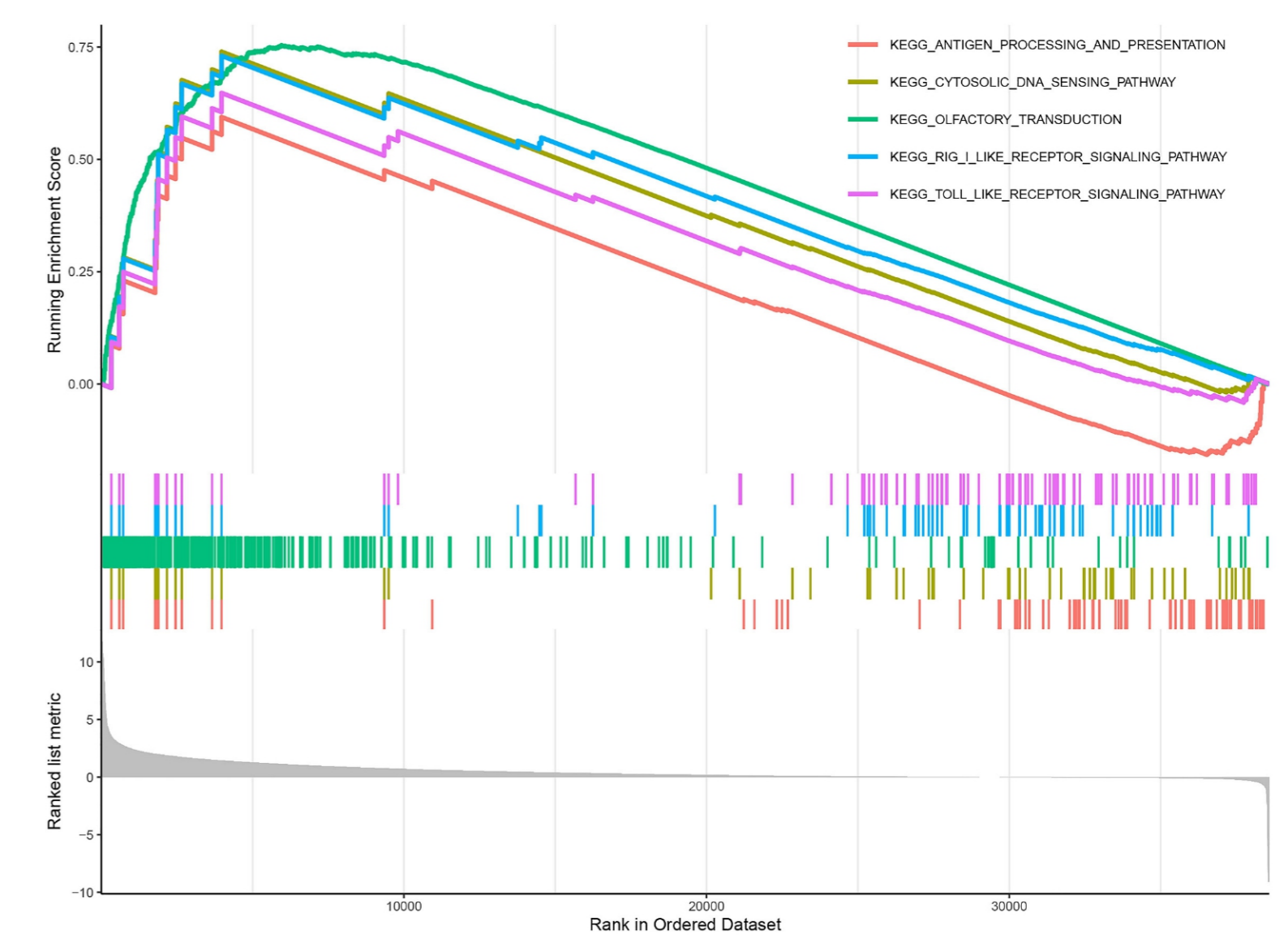
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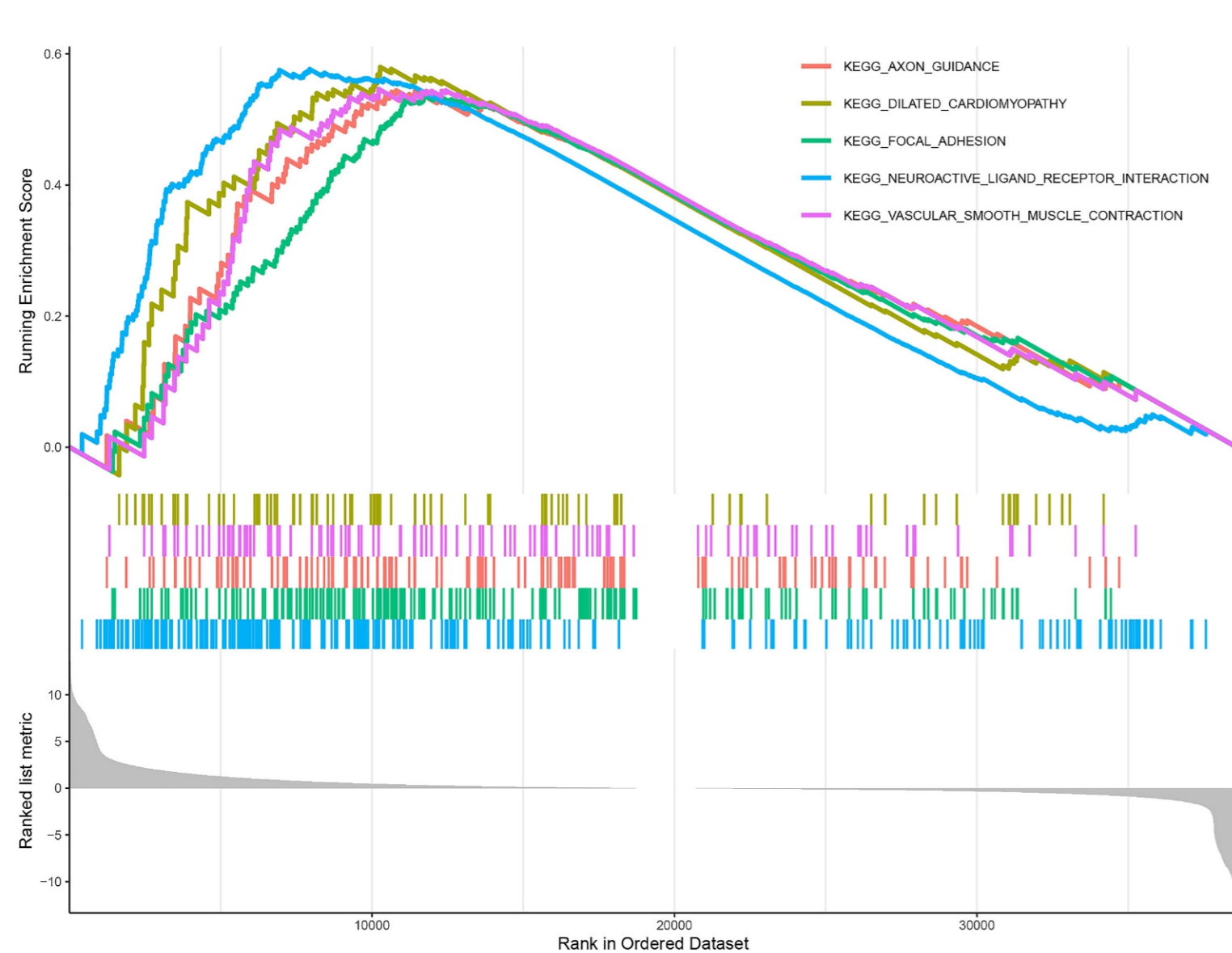
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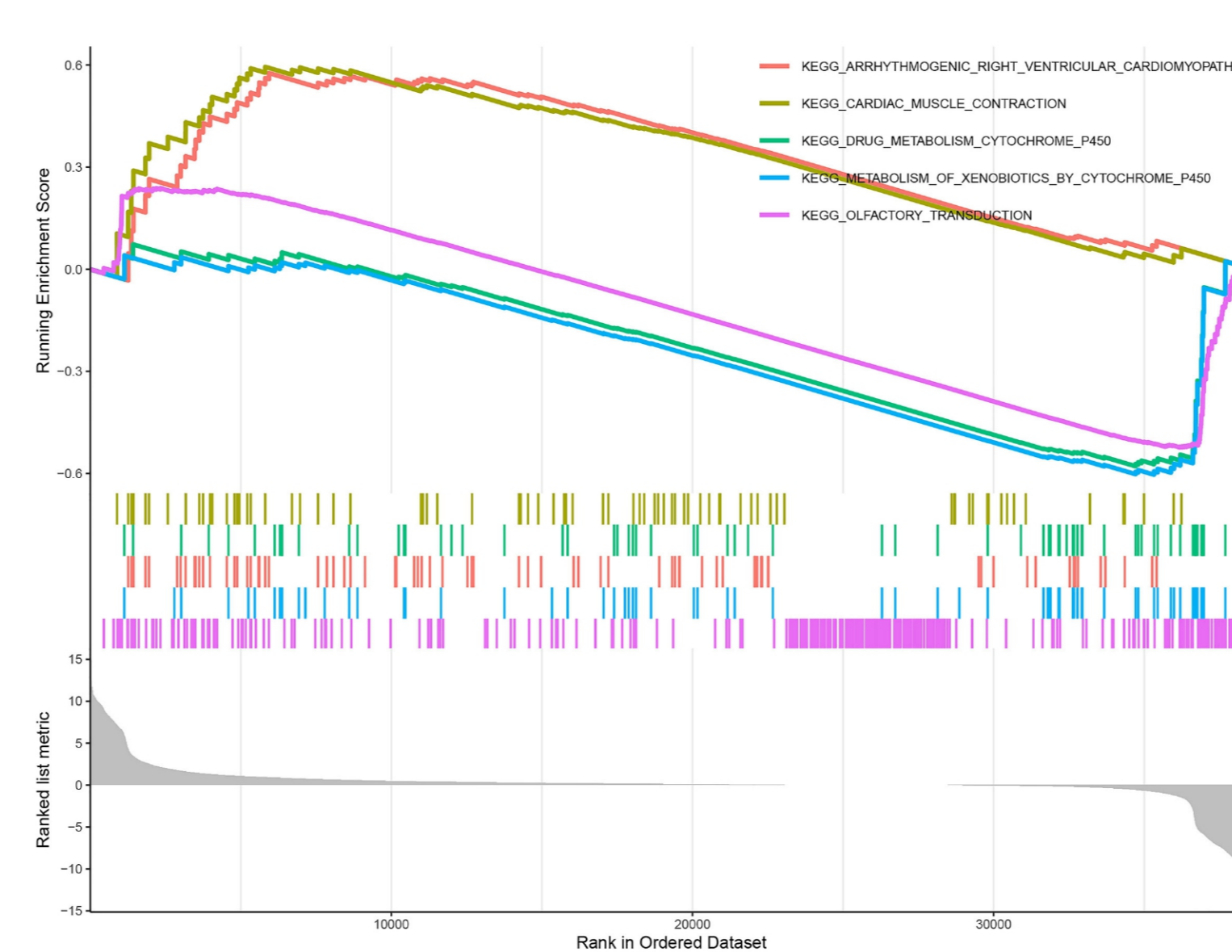
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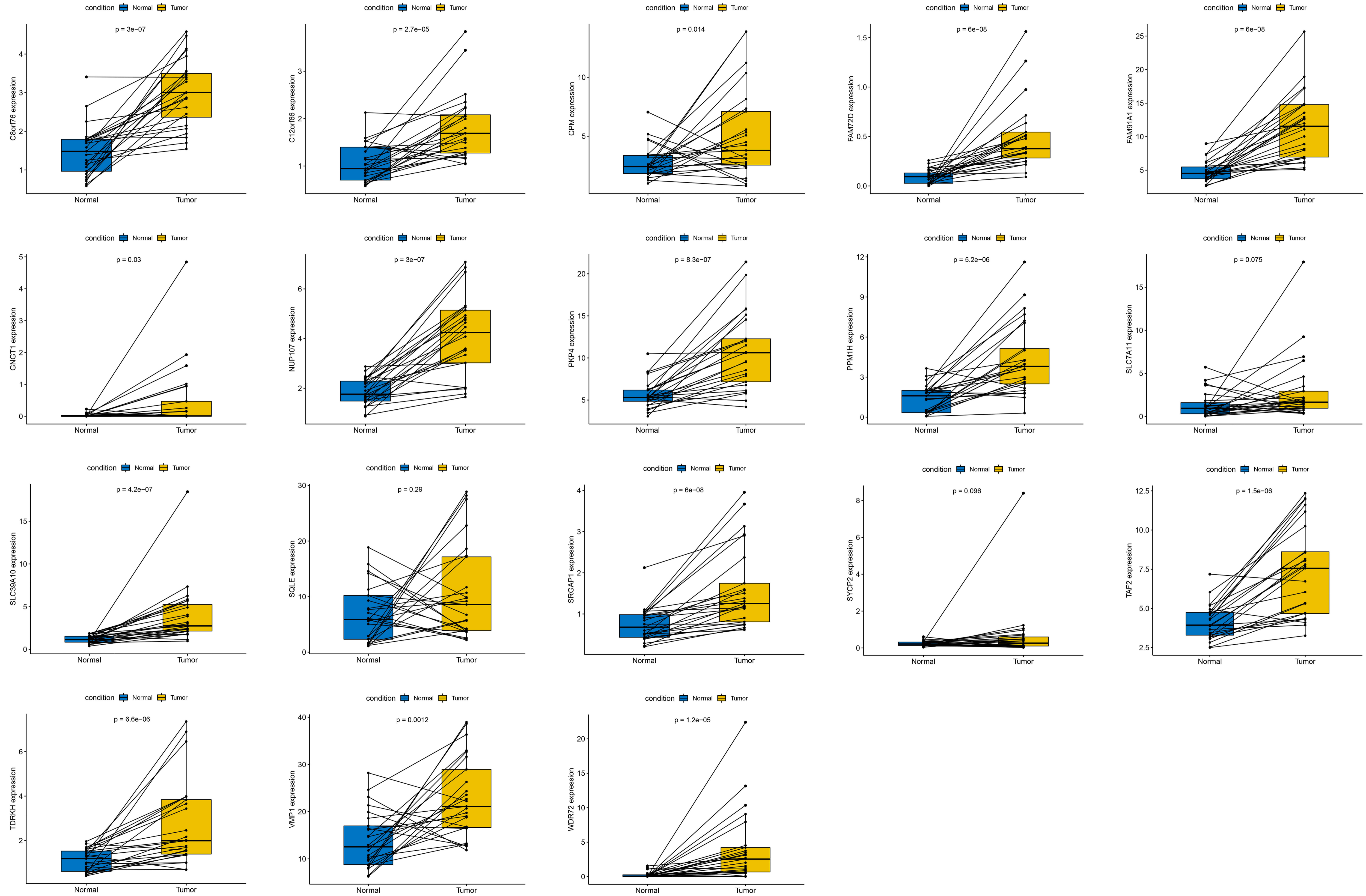
TGCT



UVM



Supplementary Figure 5



Supplementary Figure 6

