泛癌水平下内质网未折叠蛋白响应的综合评估及其与肿瘤进展的关联

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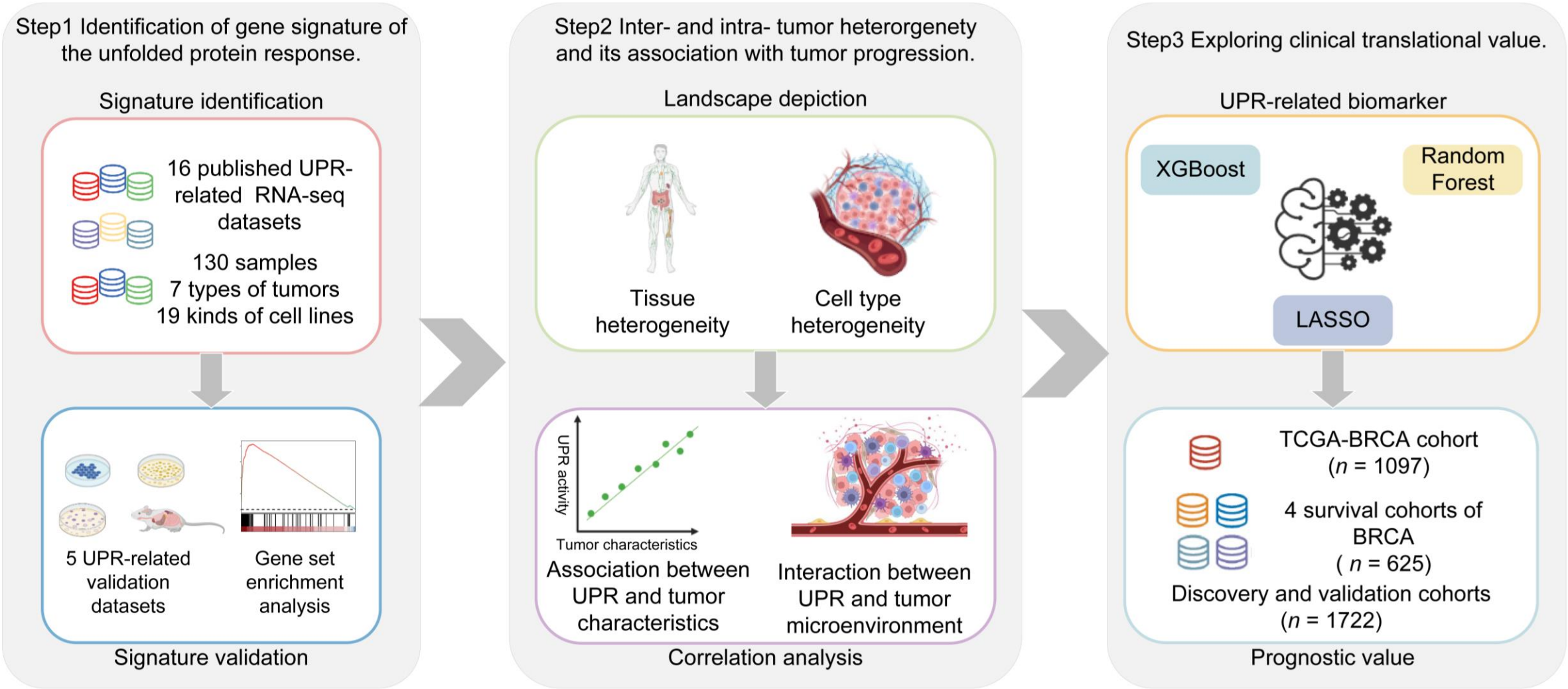
Xinyu Yang, Faming Zhao, Jing Yang, Xinran Xia, Liwei Chen, Peng Zeng, Liang Chen, et al. 2026. Comprehensive assessment of unfolded protein response and its association with tumor progression in pan-cancer. ***iMetaOmics*** 3:e70084. https://doi.org/10.1002/imo2.70084

简介

本研究提出了一种未折叠蛋白响应（UPR）基因签名，揭示了泛癌水平的UPR活性异质性，并鉴定了乳腺癌预后相关的生物标志物。

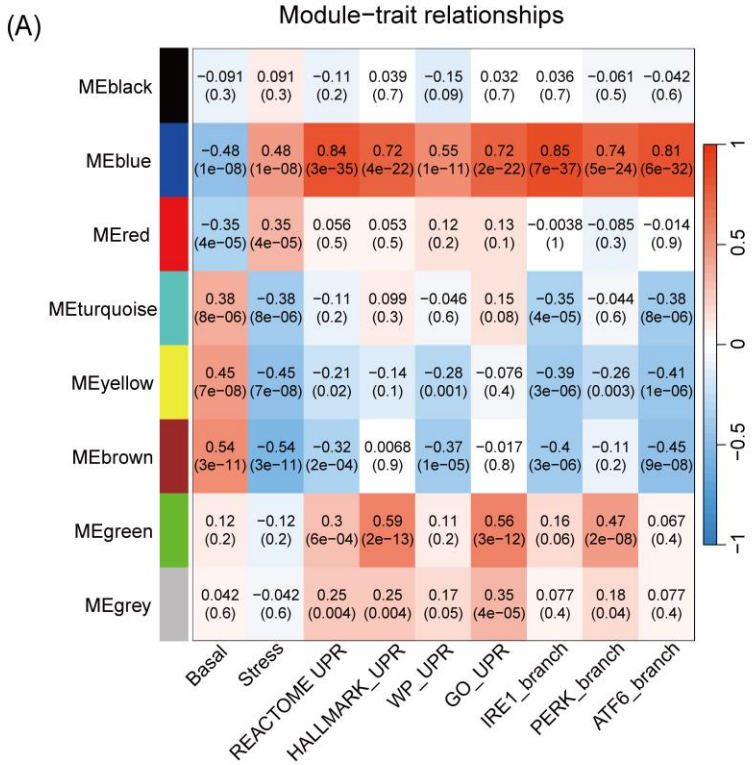


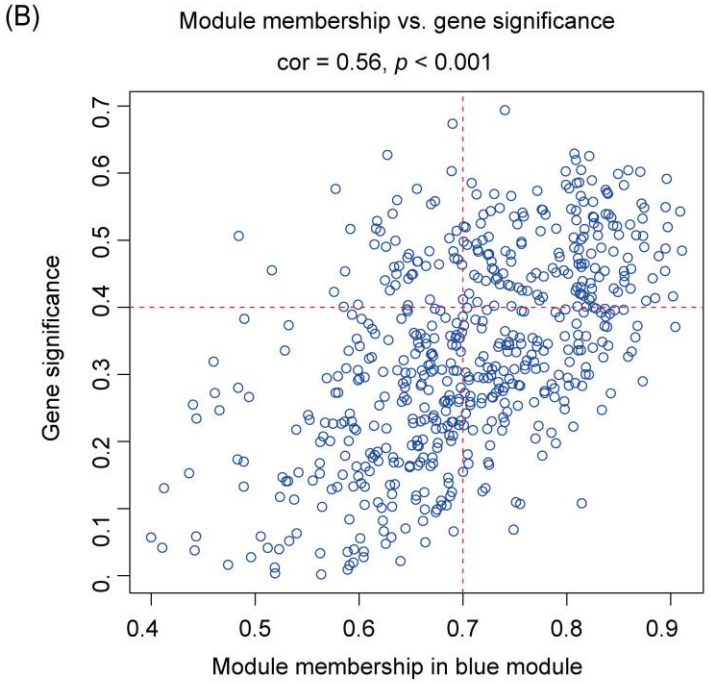
亮点

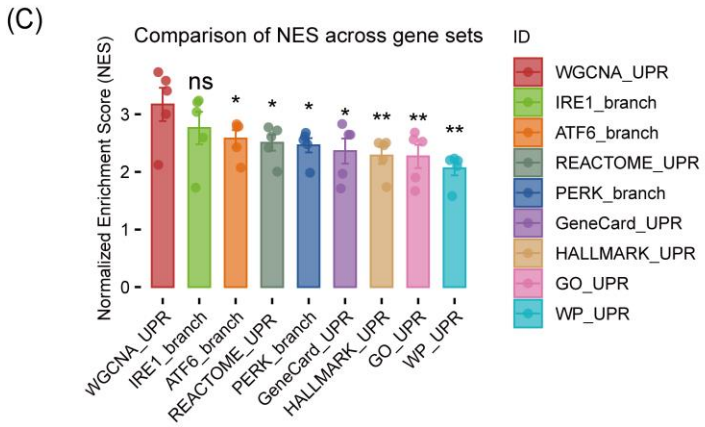
- 构建了一种基于转录组的UPR基因签名，可在泛癌水平有效评估UPR活性。
- 系统描绘了UPR异质性图谱，并揭示了其与多种关键肿瘤特征之间的关联。
- 鉴定并验证了一种具有显著预后价值的UPR相关生物标志物，适用于乳腺癌。

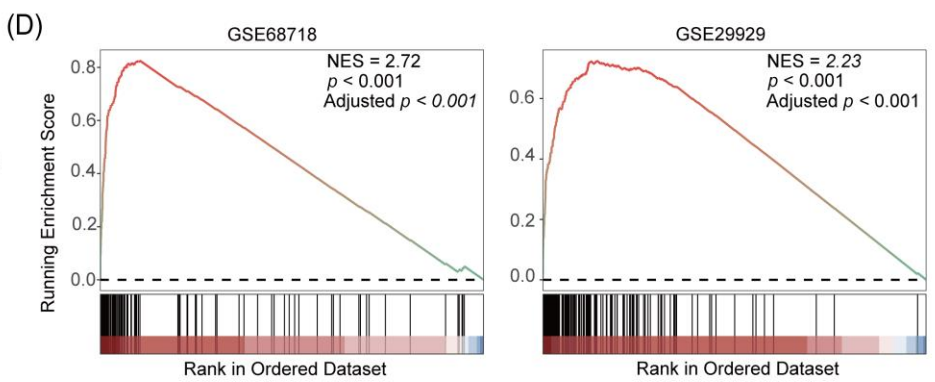
结果

鉴定并验证用于评估肿瘤中UPR状态的基因特征。





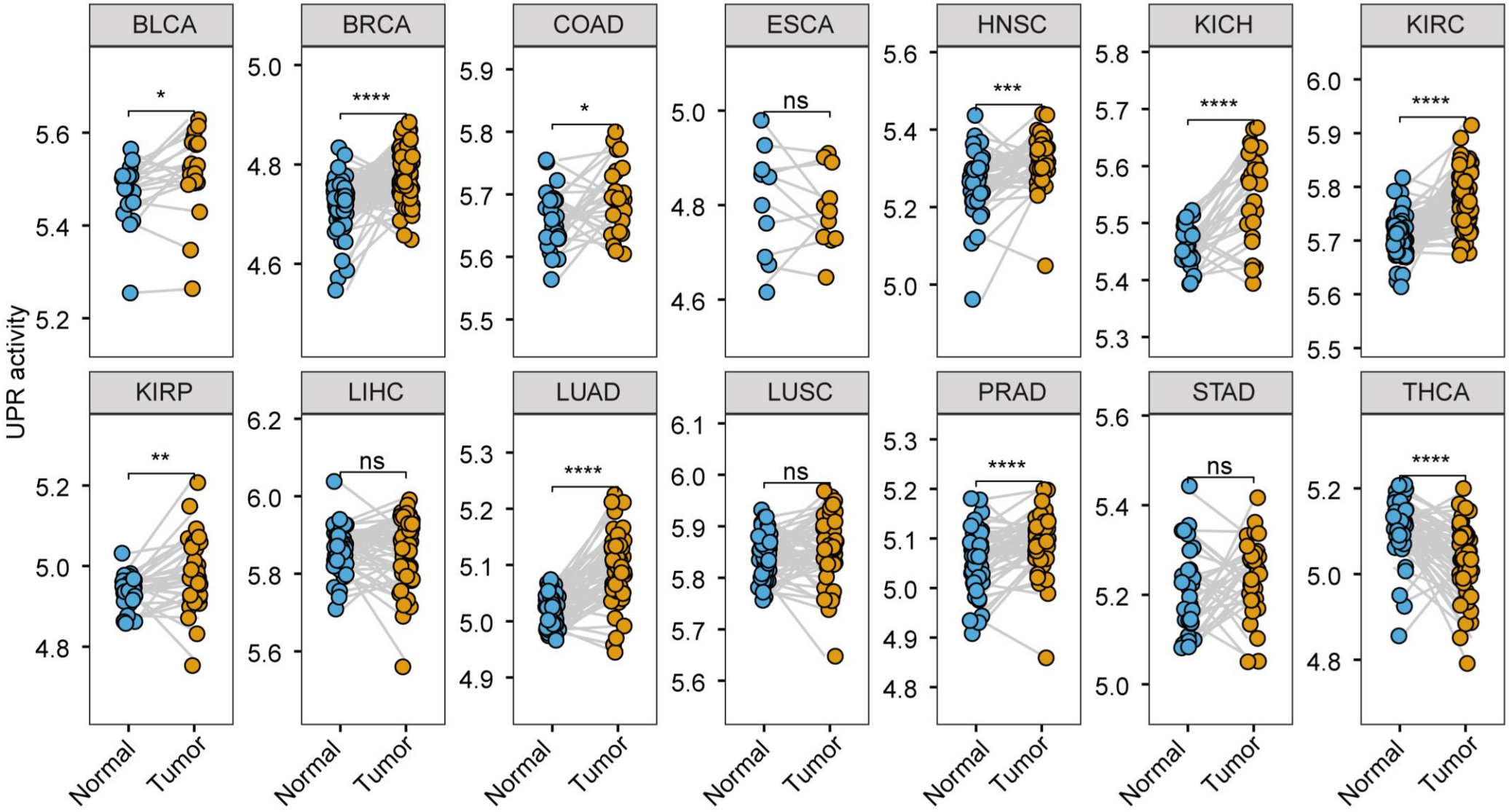




结果

UPR在肿瘤组织中普遍激活，尤其在乳腺癌、前列腺癌等癌种中尤为突出。

(E)



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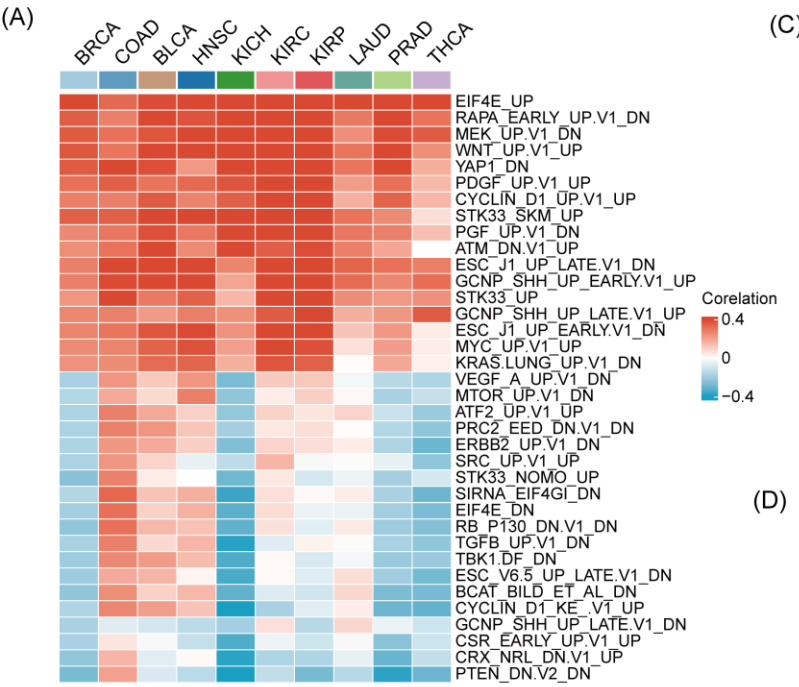
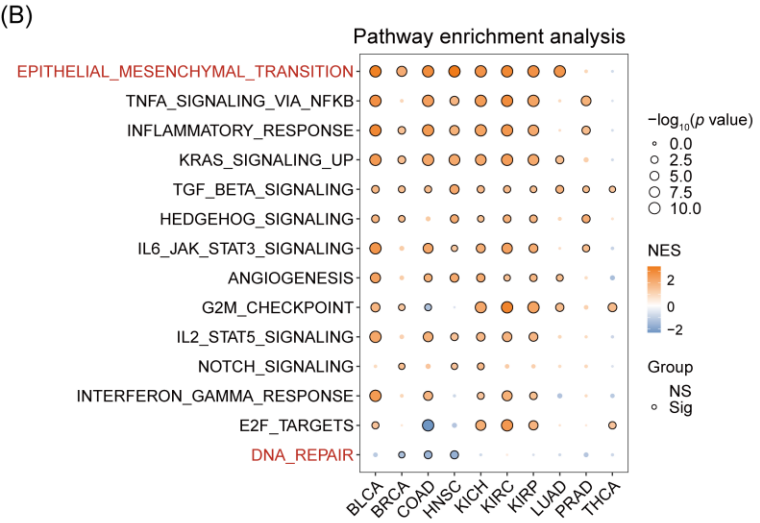
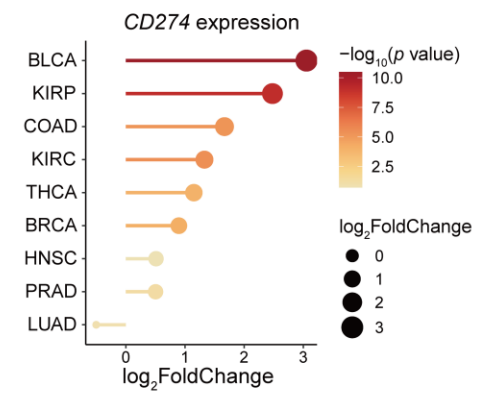
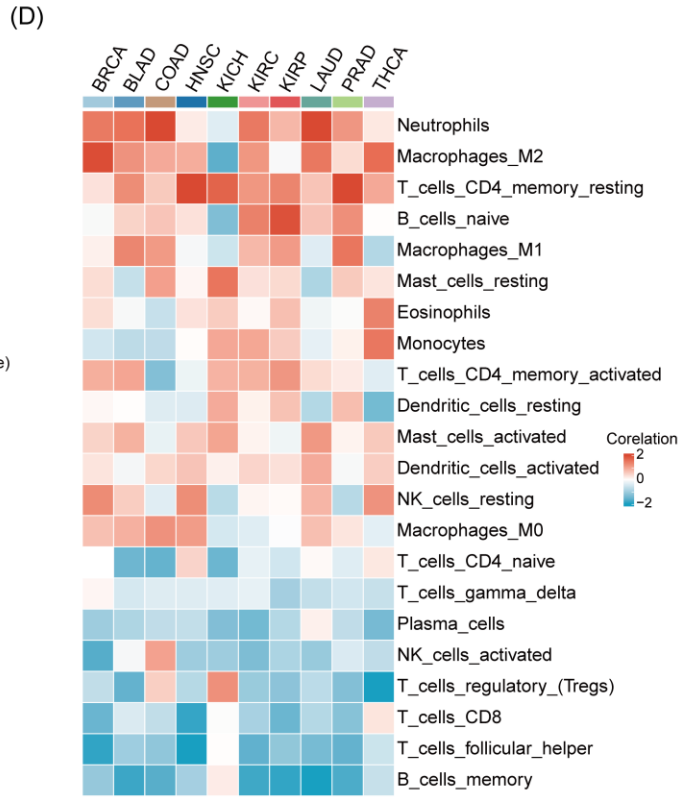
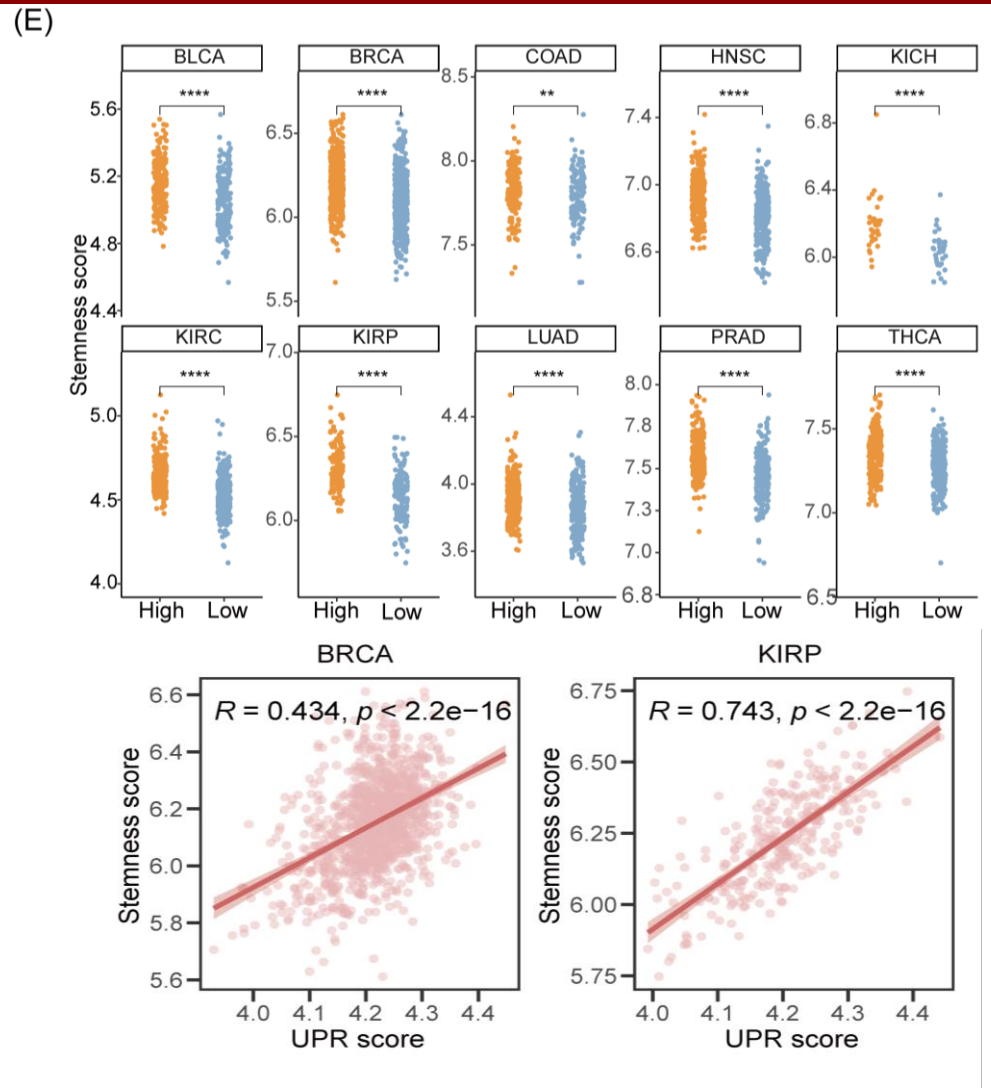






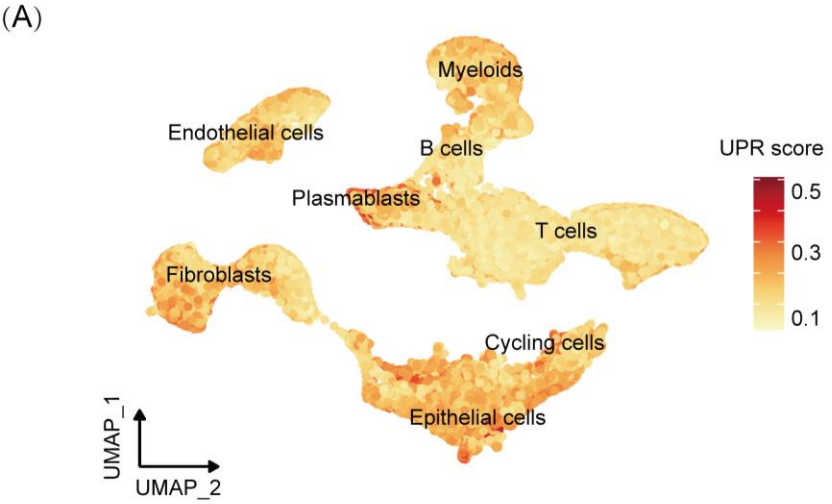


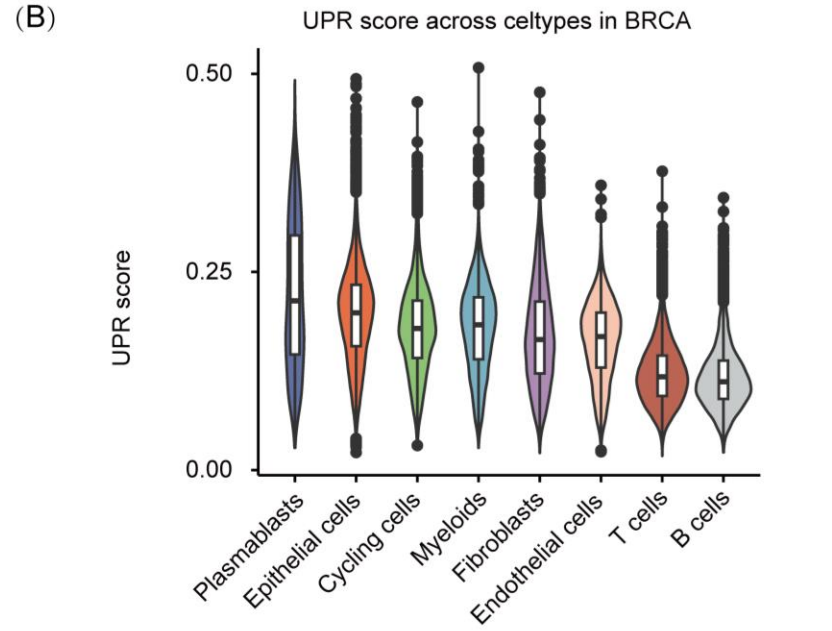


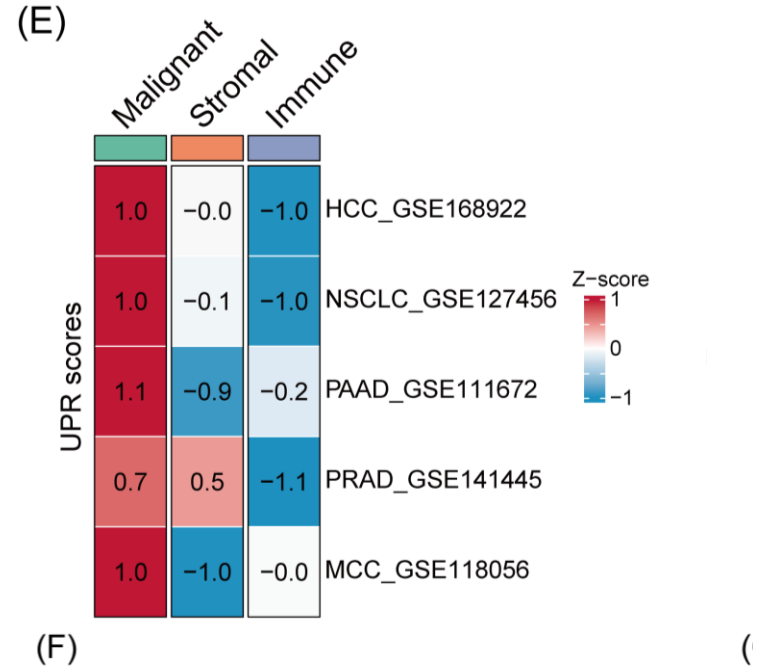
UPR激活与免疫抑制、肿瘤干性及其他关键肿瘤特征呈现癌种特异性关联。

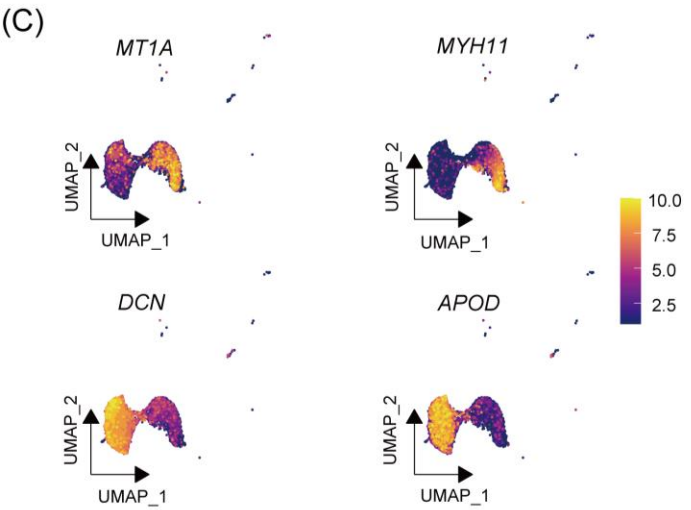
结果

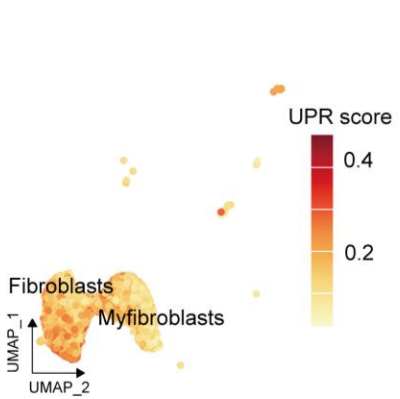
肿瘤内部存在明显的UPR异质性，其中肿瘤细胞的UPR评分最高，而基质细胞和免疫细胞的UPR评分相对较低。

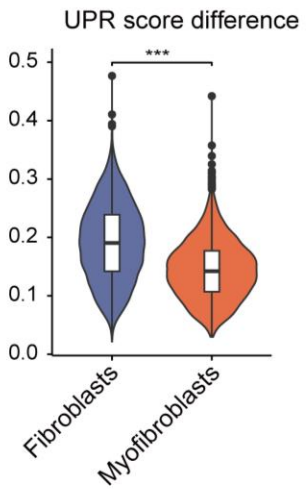


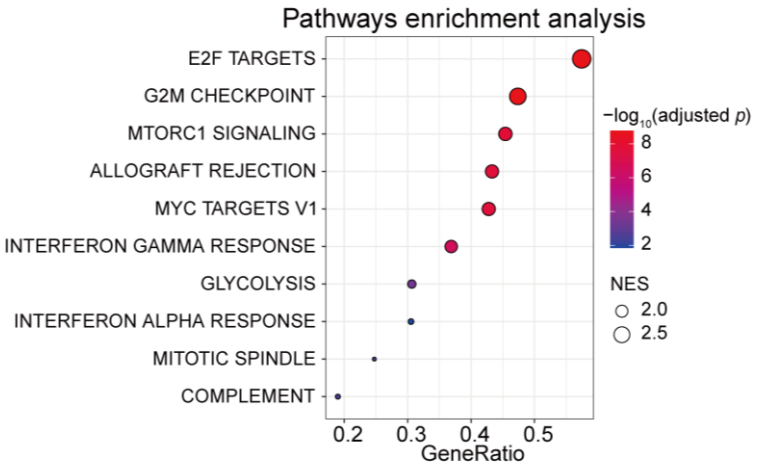








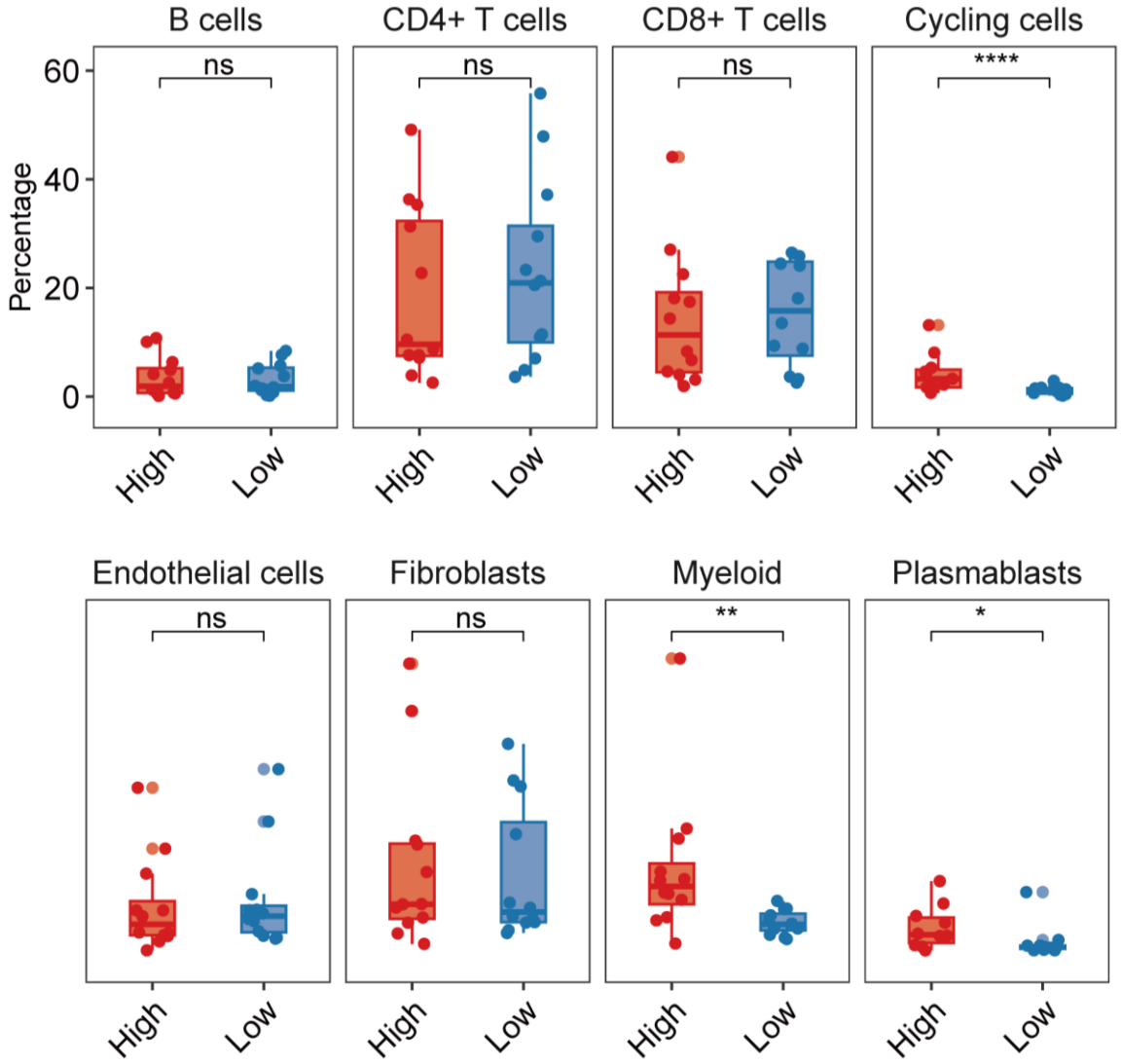




结果

UPR评分较高的乳腺癌患者通常伴随髓系细胞浸润增加。

(H)



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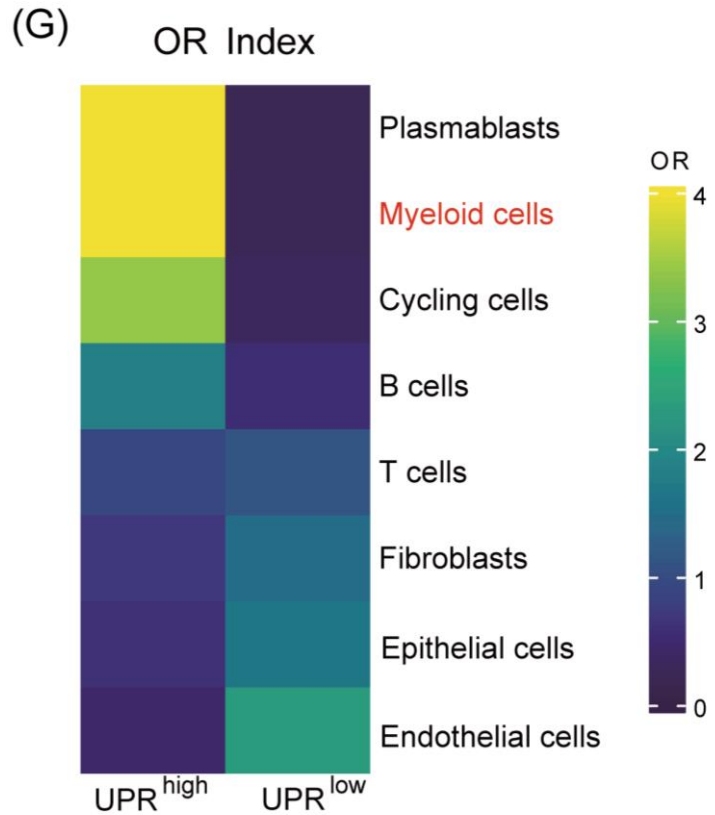

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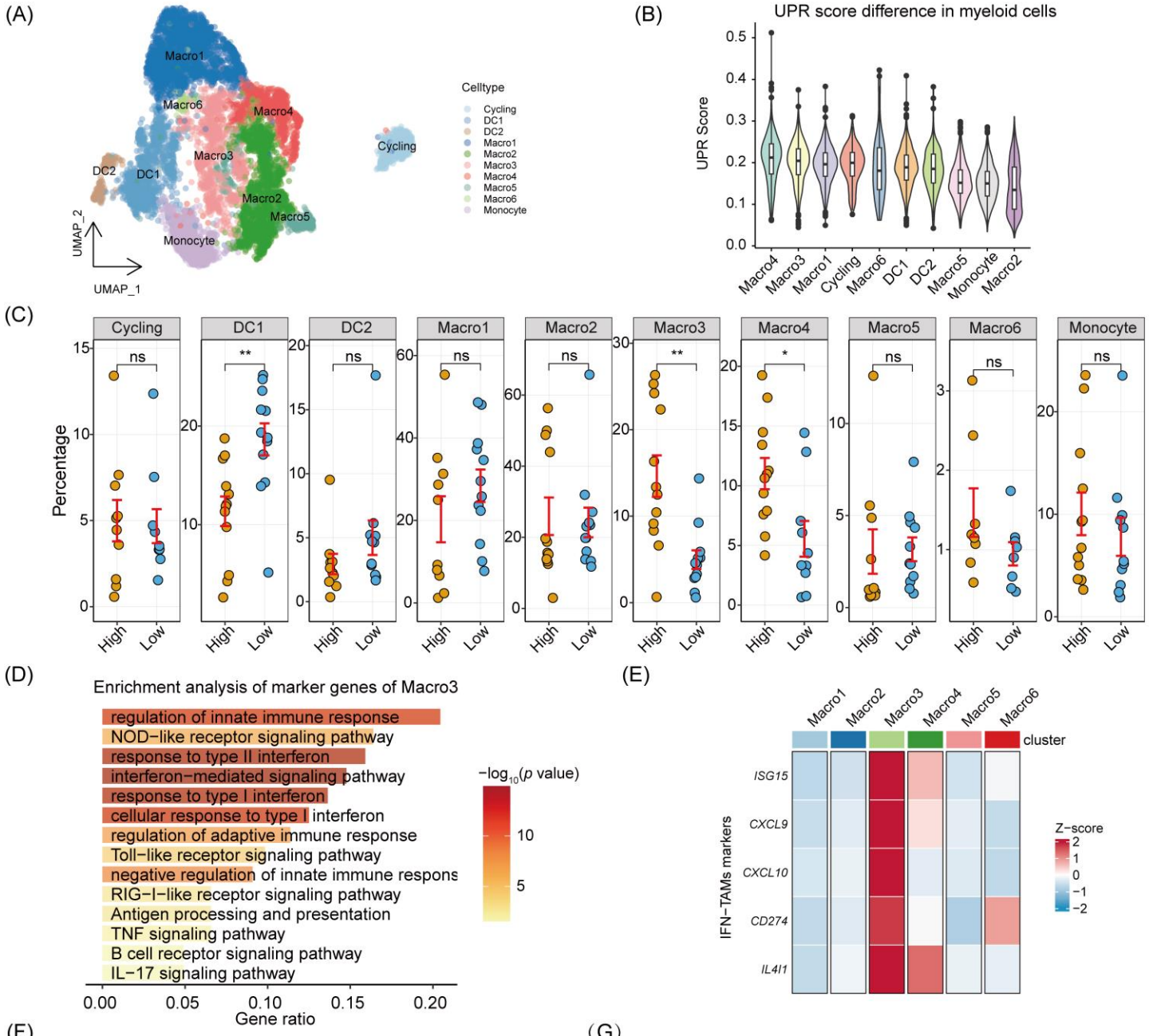
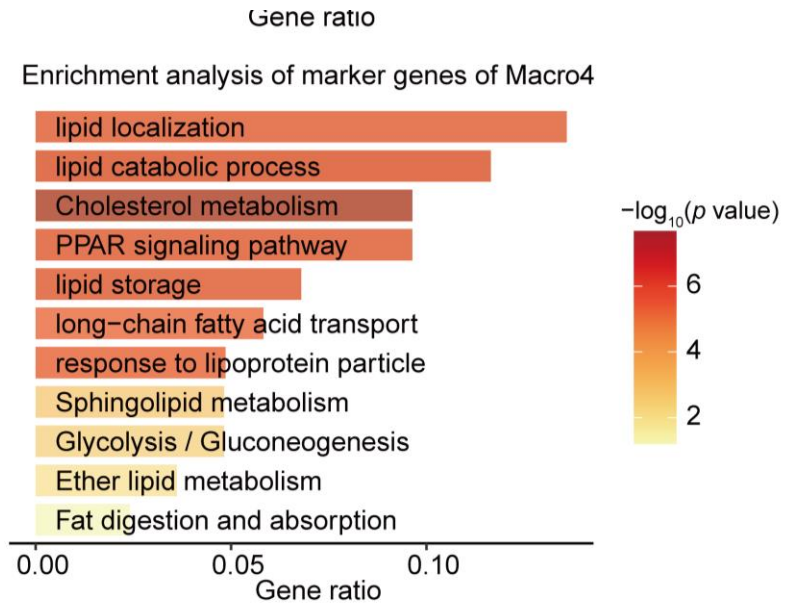


高UPR组肿瘤微环境中特定髓系细胞亚群的浸润增加，且可能通过MIF信号通路促进肿瘤细胞与其互作。

结果

(F)



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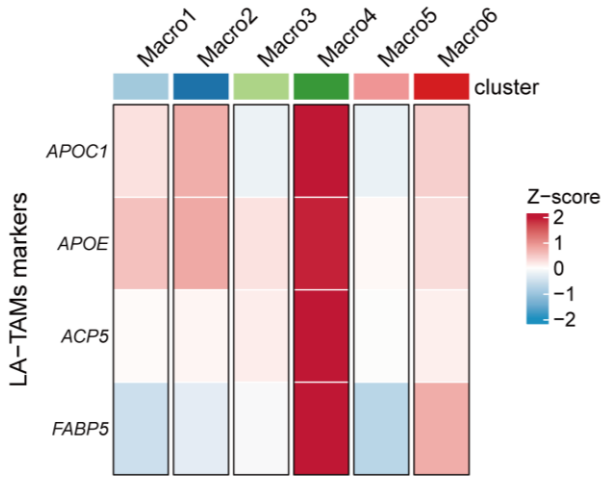

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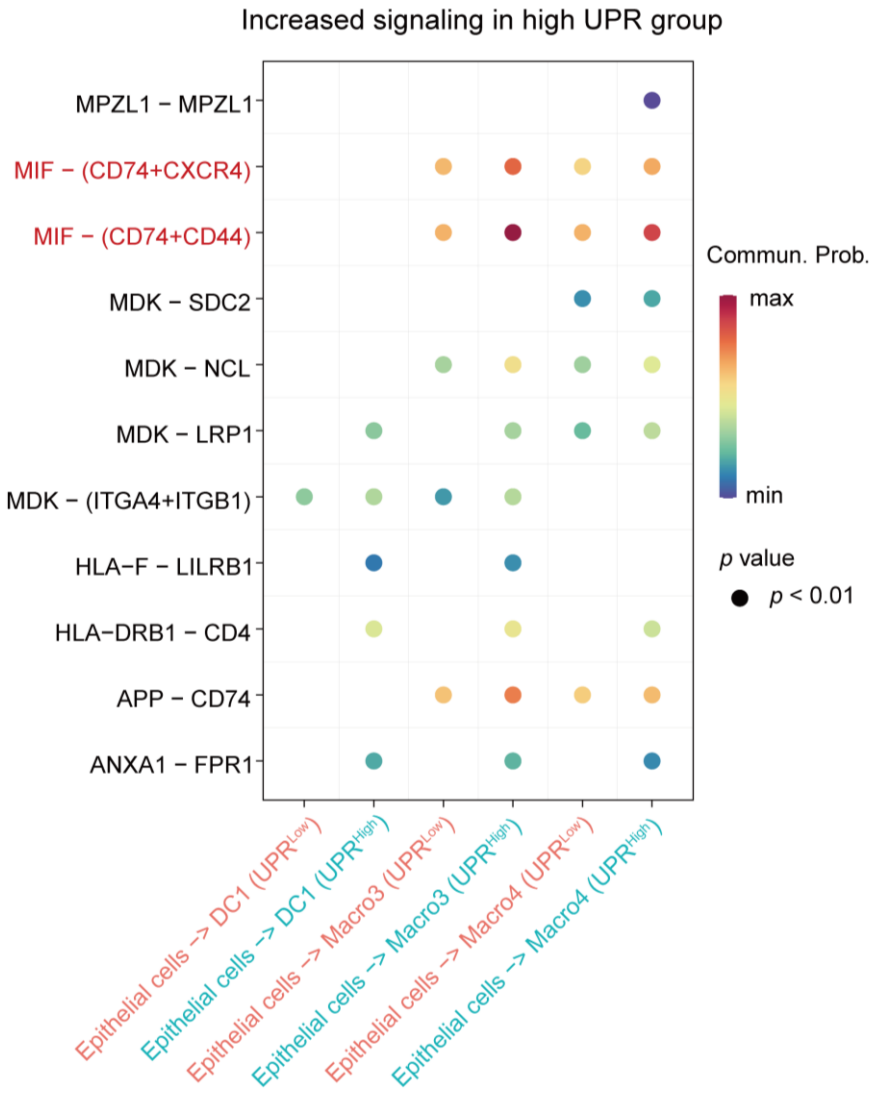

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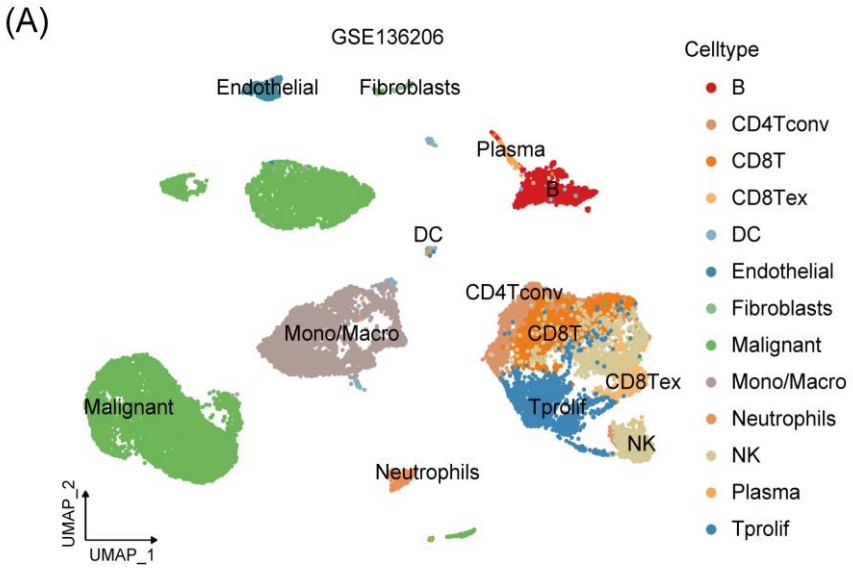
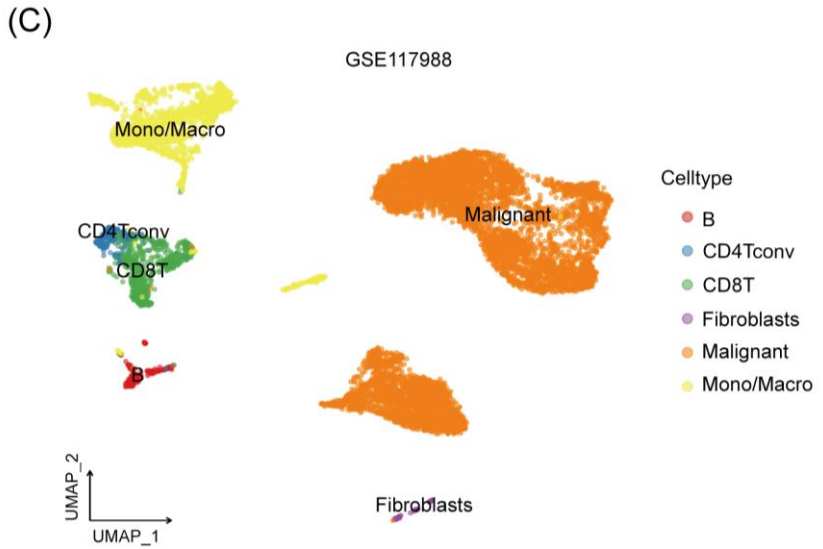
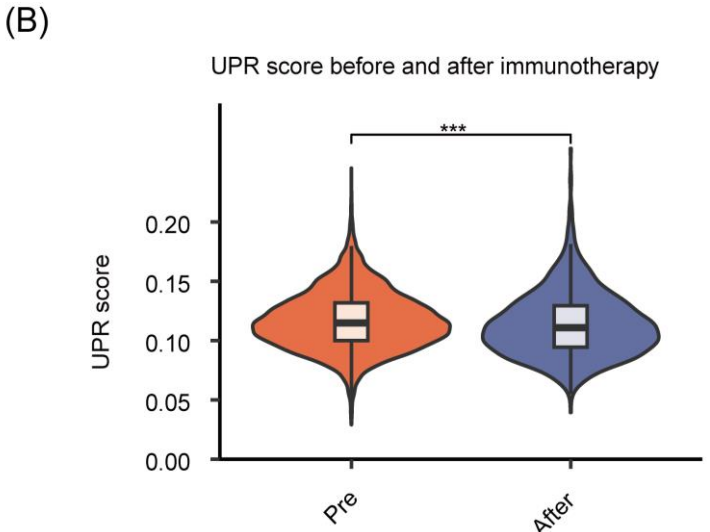
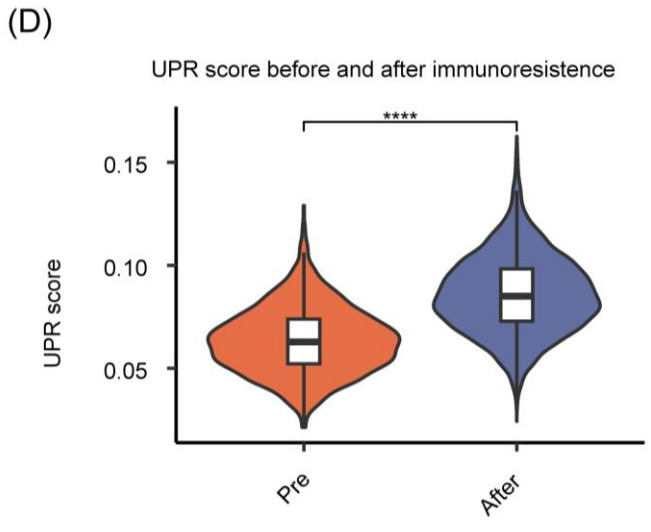
结果

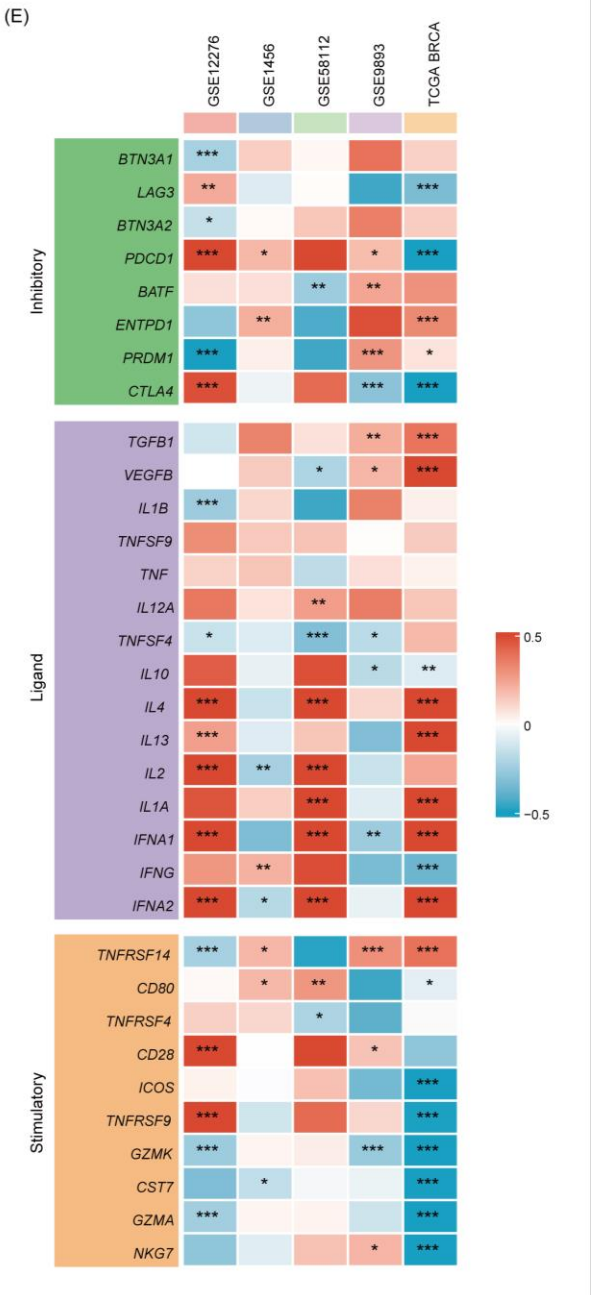
较高的UPR激活与抗肿瘤免疫功能受损相关，同时UPR评分升高的肿瘤可能对免疫治疗具有耐受性。











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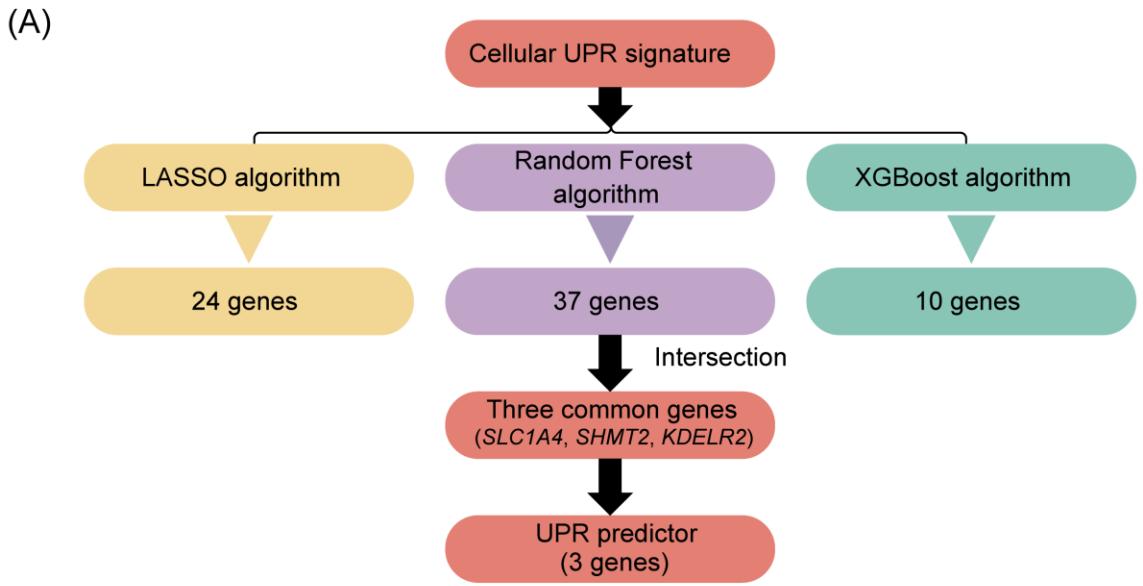
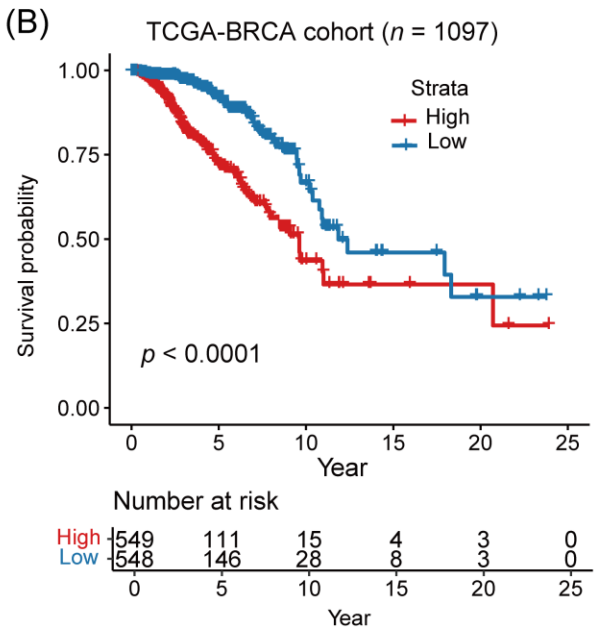
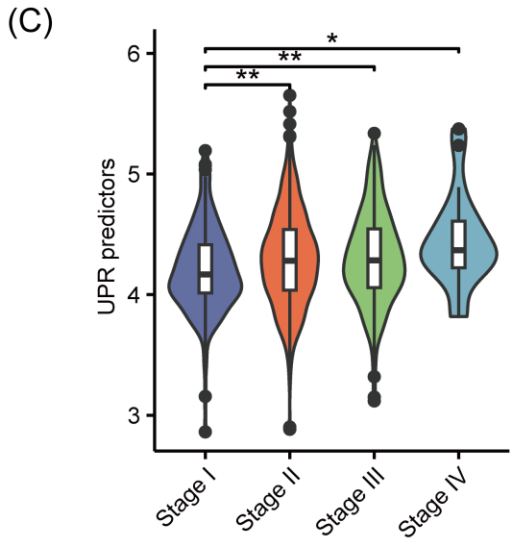
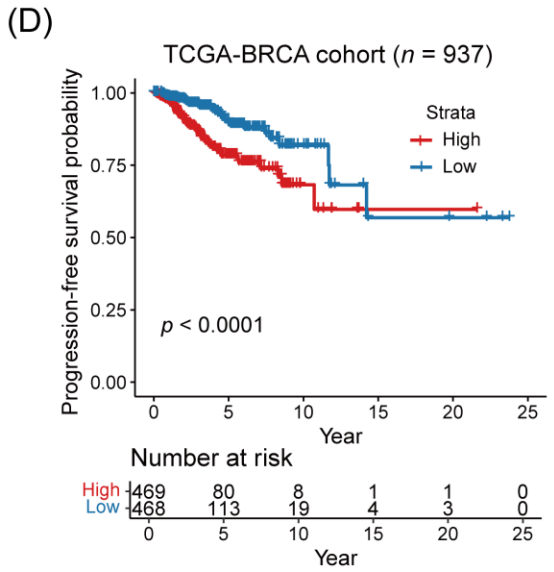
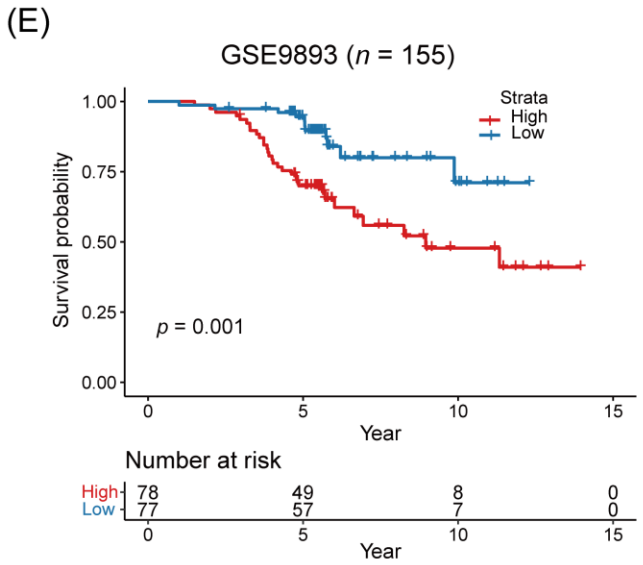




基于UPR特征，筛选关键基因构建的预测模型能够有效评估乳腺癌患者的预后。







结果

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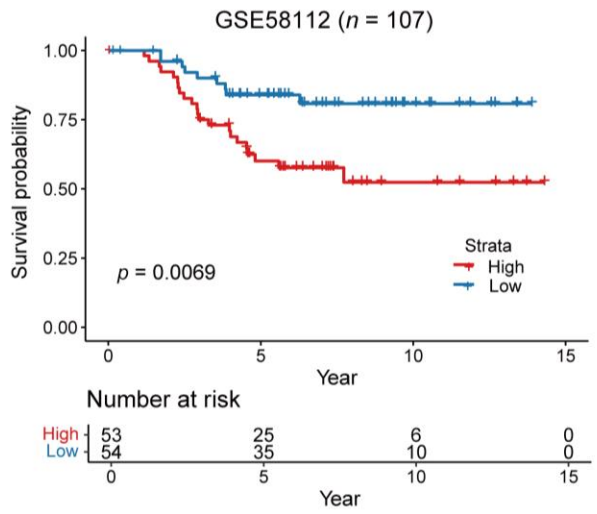

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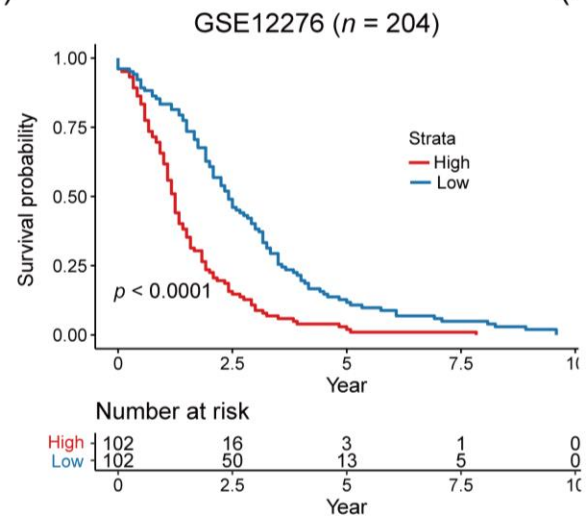

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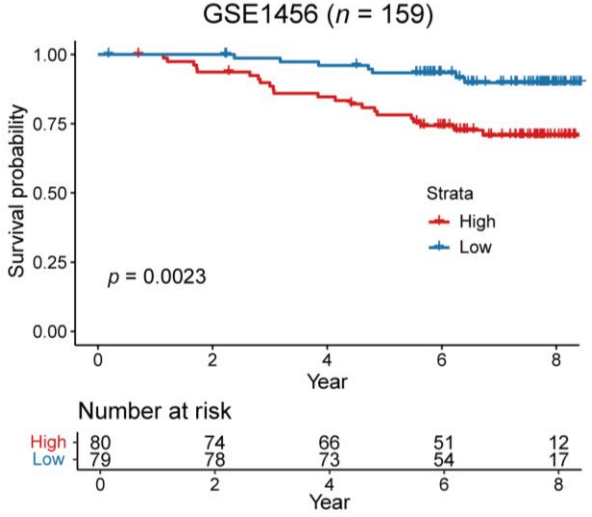

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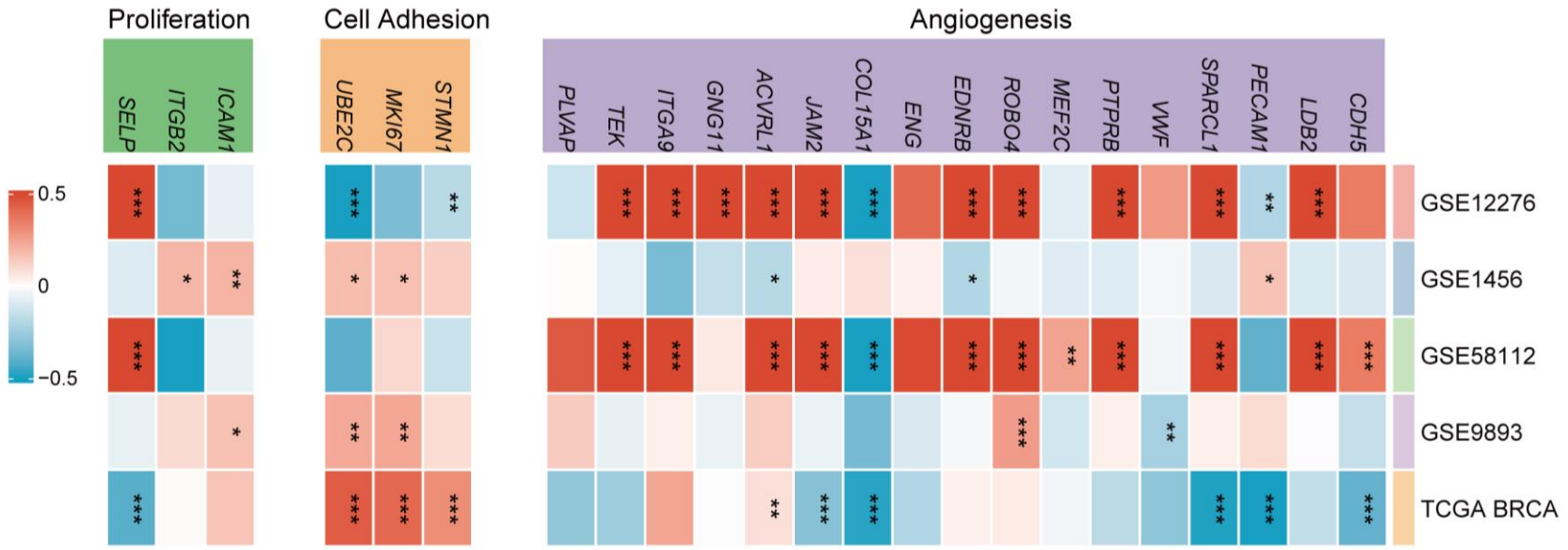

总结

- 本研究系统评估了人类癌症中的UPR活性，揭示其在不同肿瘤类型和细胞环境中的异质性，并发现与关键基因组特征及免疫特征相关。
- 我们还鉴定了一个与UPR相关的乳腺癌预后生物标志物，具有潜在的临床应用价值。这些发现为进一步研究UPR在癌症中的作用及治疗潜力提供了重要参考。

Xinyu Yang, Faming Zhao, Jing Yang, Xinran Xia, Liwei Chen, Peng Zeng, Liang Chen, et al. 2026. Comprehensive assessment of unfolded protein response and its association with tumor progression in pan-cancer. ***iMetaOmics*** 3:e70084. https://doi.org/10.1002/imo2.70084

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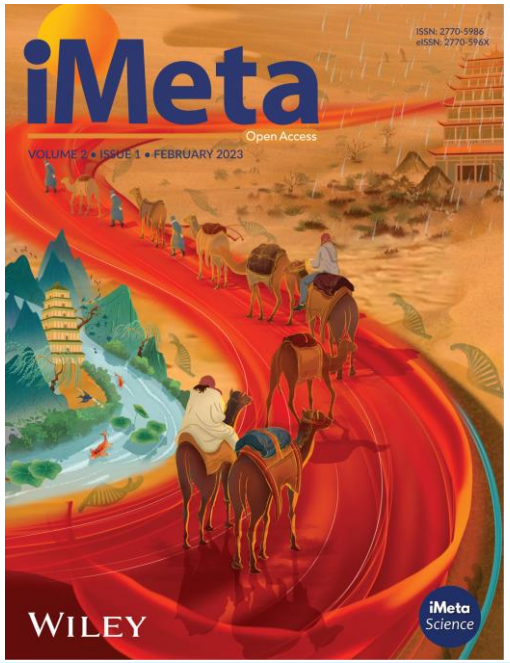

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