

An Immune-Related Gene Prognostic Index for Triple-Negative Breast Cancer Integrates Multiple Aspects of Tumor-Immune Microenvironment

Xiaowei Wang ¹, Wenjia Su ², Dabei Tang ¹, Jing Jing ¹, Jing Xiong ³, Yuwei Deng ¹, Huili Liu ¹, Wenjie Ma ¹, Zhaoliang Liu ^{4,5,*} and Qingyuan Zhang ^{1,*}

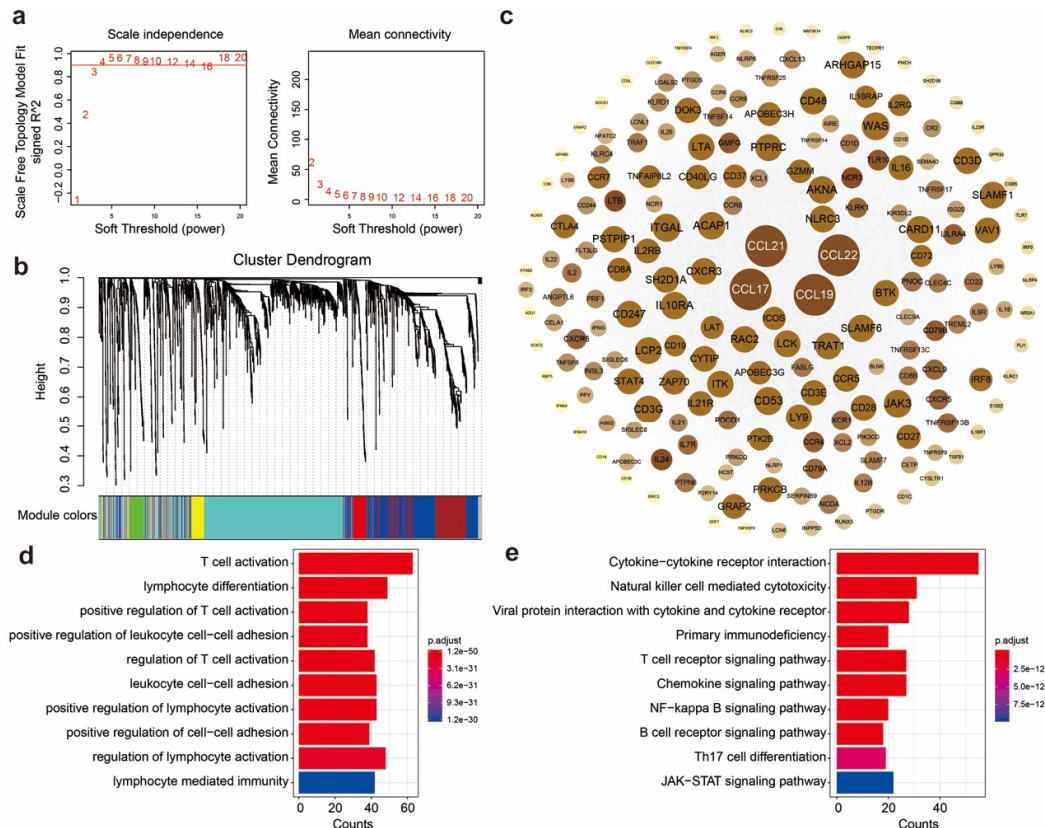


Figure S1. Identify co-expressed immune genes related to CC chemokine genes by WGCNA. (a) Selection of Soft Threshold in WGCNA analysis; (b) Gene distribution in WGCNA network analysis; (c) Co-expression network of genes in the brown module; (d) GO enrichment of genes in the brown module of co-expression network; (e) KEGG enrichment of genes in the brown module of co-expression network.

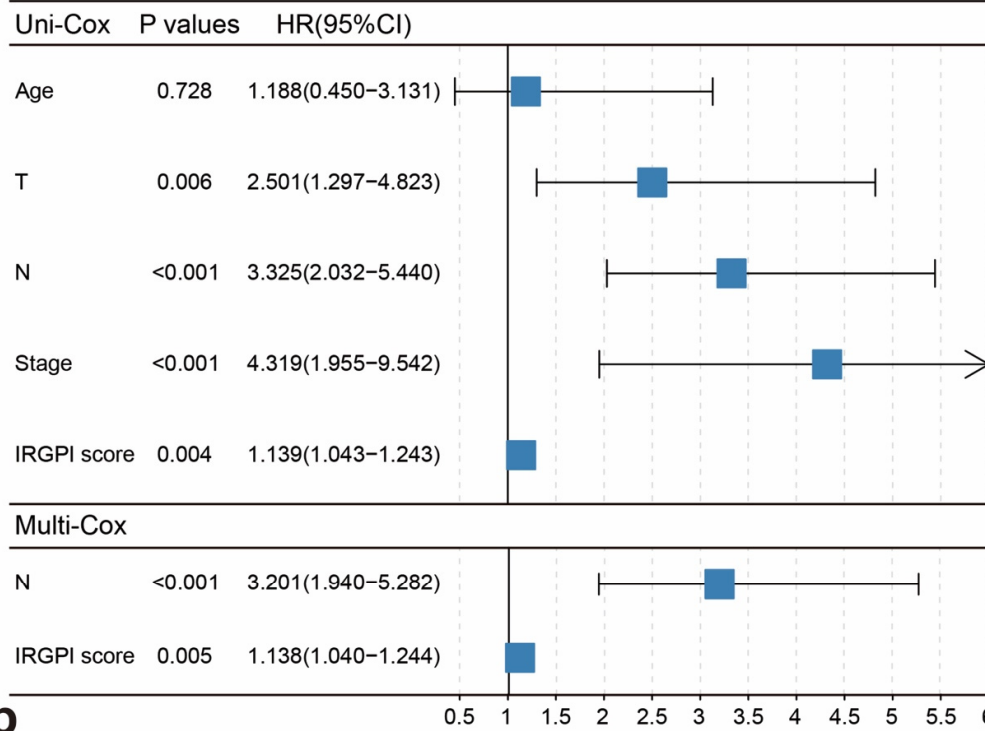
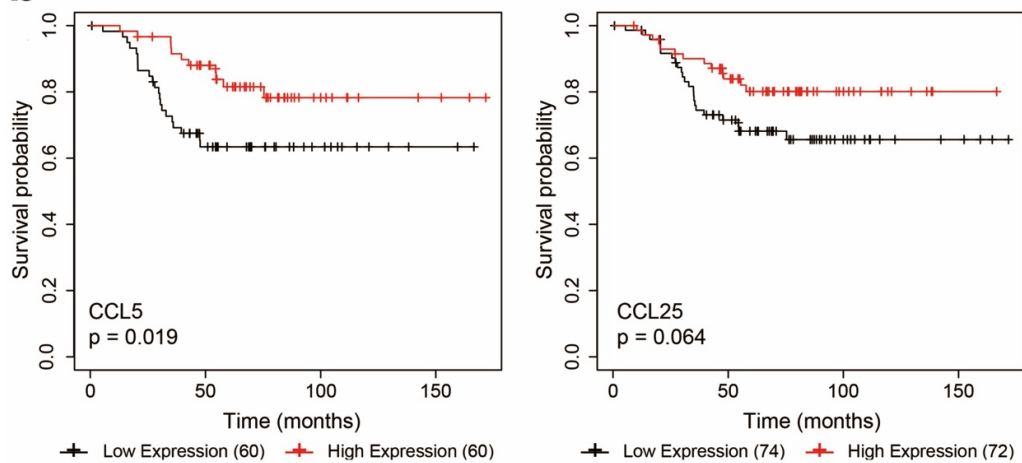
a**b**

Figure S2. Validation of the prognostic value of IRGPI. **(a)** Univariate and multivariate Cox analysis of clinicopathological factors and the IRGPI scores ($p < 0.05$); **(b)** Effect of CCL5 and CCL25 expression on the survival in TNBC cohort of Kaplan-Meier plotter database.

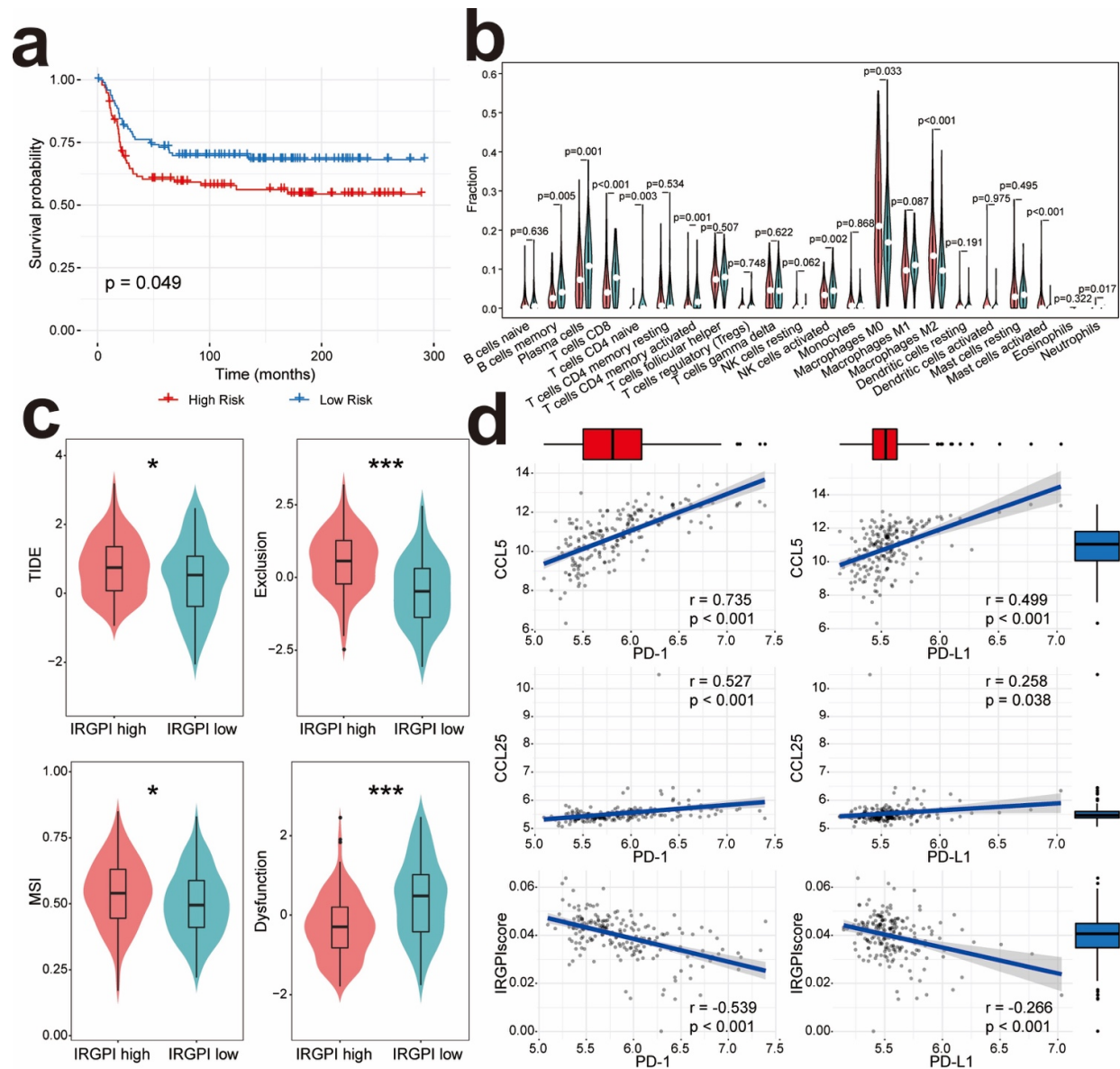


Figure S3. Validation of the prognostic value of IRGPI and its associations with immune characteristics in METABRIC database. (a) Kaplan-Meier survival analysis of IRGPI scores using METABRIC data ($p < 0.05$); (b) The difference of immune cell infiltration in different IRGPI groups (pink: IRGPI-high group; and blue: IRGPI-low group). (c) Scores of TIDE, MSI, and T cell exclusion and dysfunction in different IRGPI groups (ns: not significant, $*p < 0.05$; $**p < 0.01$; $***p < 0.001$); (d) Correlations between CCL5/CCL25/IRGPI scores and PD-L1/PD1 expression.

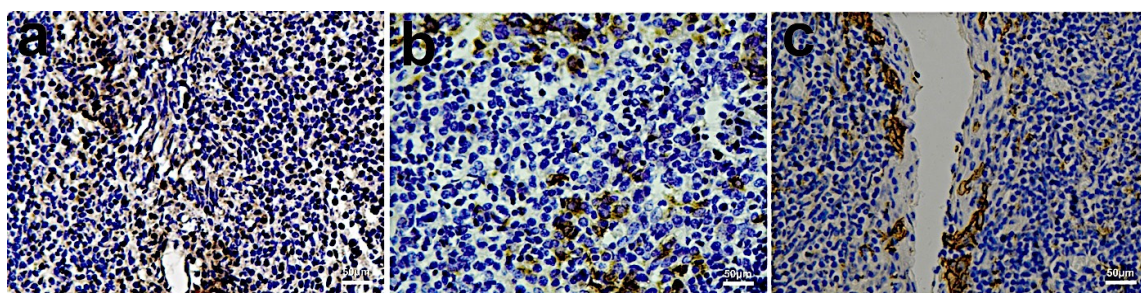


Figure S4. Pictures of CCL5, CCL25 and PD-L1 immunohistochemistry using the known tissue positive for CCL5, CCL25, and PD-L1. (a) CCL5 IHC in Tonsil; (b) CCL25 IHC in Thymus; (c) PD-L1 IHC in Tonsil. Scale bar: 50µm.