

ORIGINAL RESEARCH ARTICLE

High expression of apoptosis-related LMNB2 predicts an unfavorable outcome: A potential prognostic biomarker for liposarcoma

Supplementary File

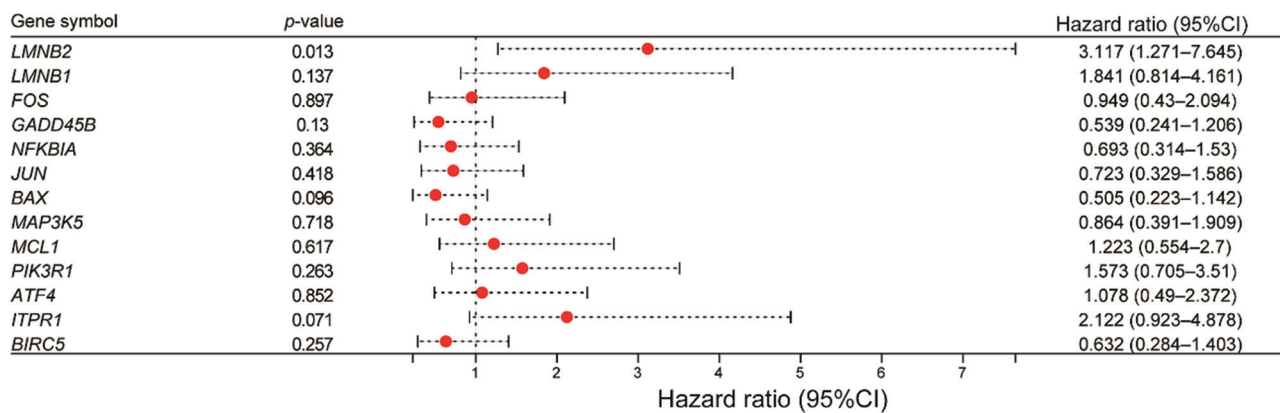


Figure S1. The forest plot shows the P-value and hazard ratio (95% CI) for the 13 selected genes. Abbreviation: CI: Confidence interval.

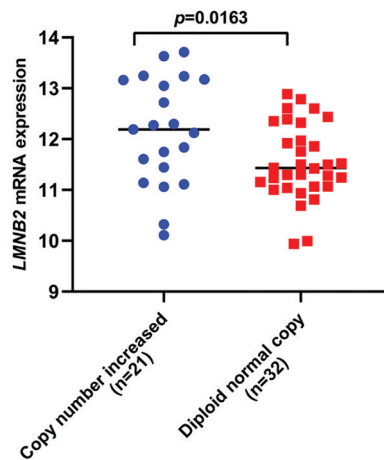


Figure S2. The expression of LMNB2 increases with the increase of its copy number.

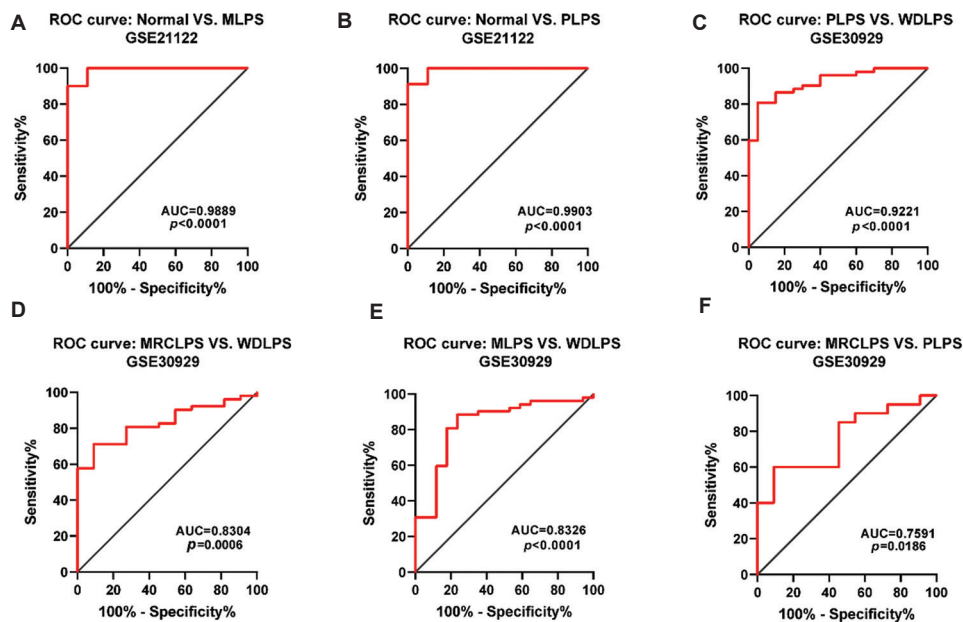


Figure S3. Expression features of LMNB2 in different types of LPS. (A and B) ROC curves of the expression of *LMNB2* in normal and two subtypes of LPS based on the GSE21122 dataset. (C-F) These figures show *LMNB2* expression among different subtypes from the GSE30929 database, respectively. Abbreviations: AUC: Area under the curve; DDLPS: Dedifferentiated liposarcoma; LPS: Liposarcoma; MLPS: Myxoid liposarcoma; MRCLPS: myxoid/round cell liposarcoma; PLPS: Pleomorphic liposarcoma; ROC: Receiver operating characteristic; WDLPS: Well-differentiated liposarcoma.

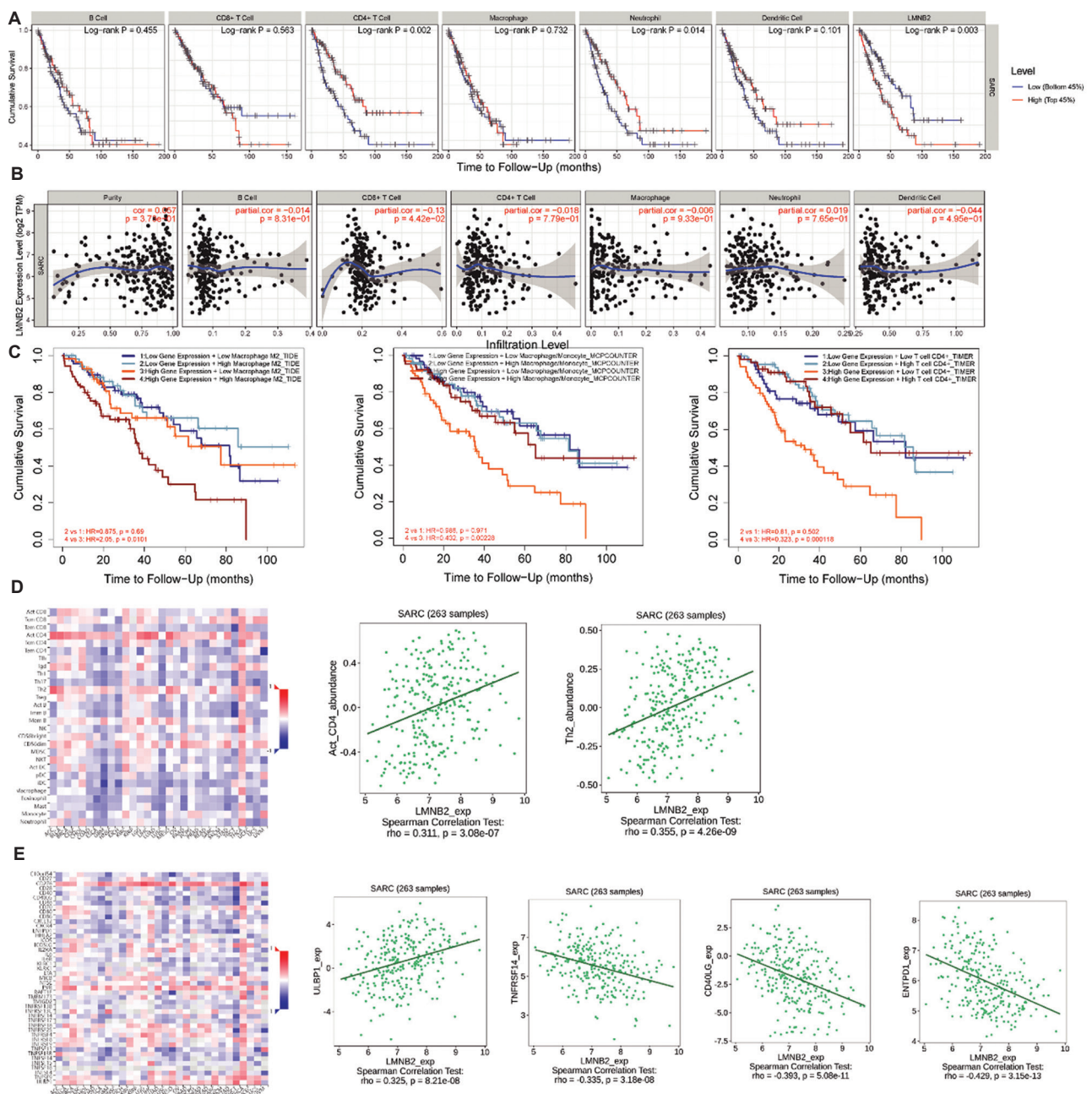


Figure S4. Correlation between *LMNB2* expression and immune infiltration level in sarcoma. (A) The expression of *LMNB2* was positively correlated with the infiltration of “CD8+ T cells” in sarcoma. (B) The survival of patients with sarcoma is significantly correlated with the level of *LMNB2* expression and the level of “T cell CD4+” and neutrophil infiltration. (C) When *LMNB2* is highly expressed, the survival of sarcoma patients is significantly related to “Macrophage M2,” “Macrophage/Monocell,” and “T cell CD4+.” (D) Relationship between the abundance of tumor-infiltrating lymphocytes (TILs) and *LMNB2* expression. Top four TILs displaying the greatest Spearman’s correlation with *LMNB2* expression. (E) The top two immunostimulators displaying the greatest Spearman’s correlation with *LMNB2* expression.