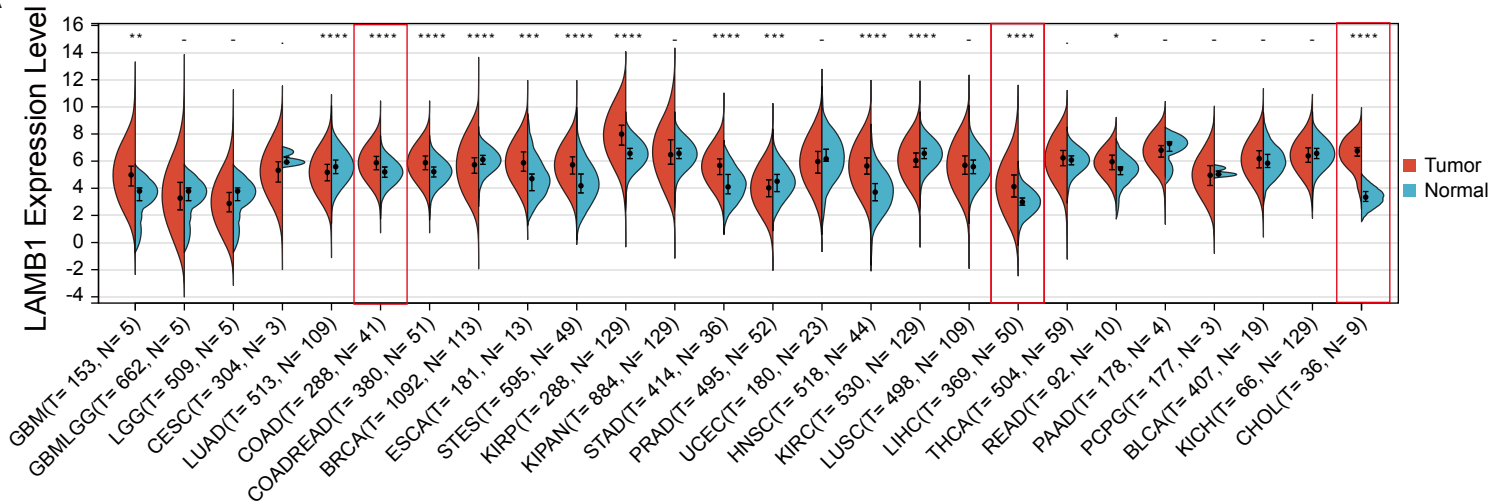
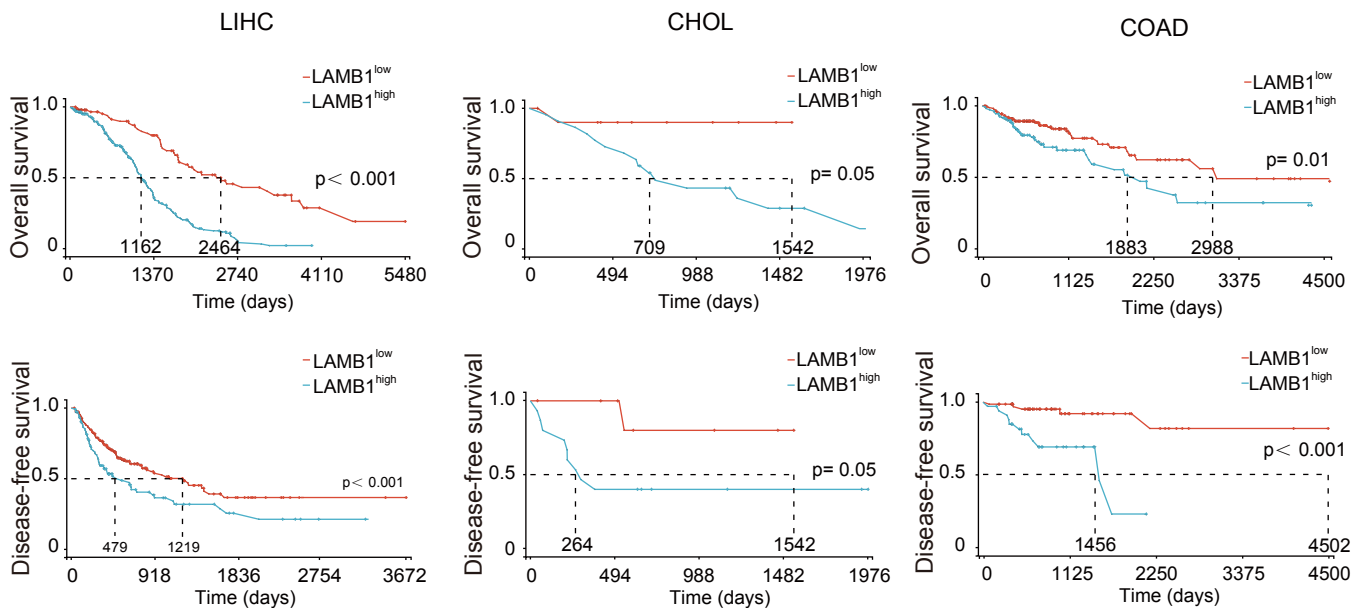


A

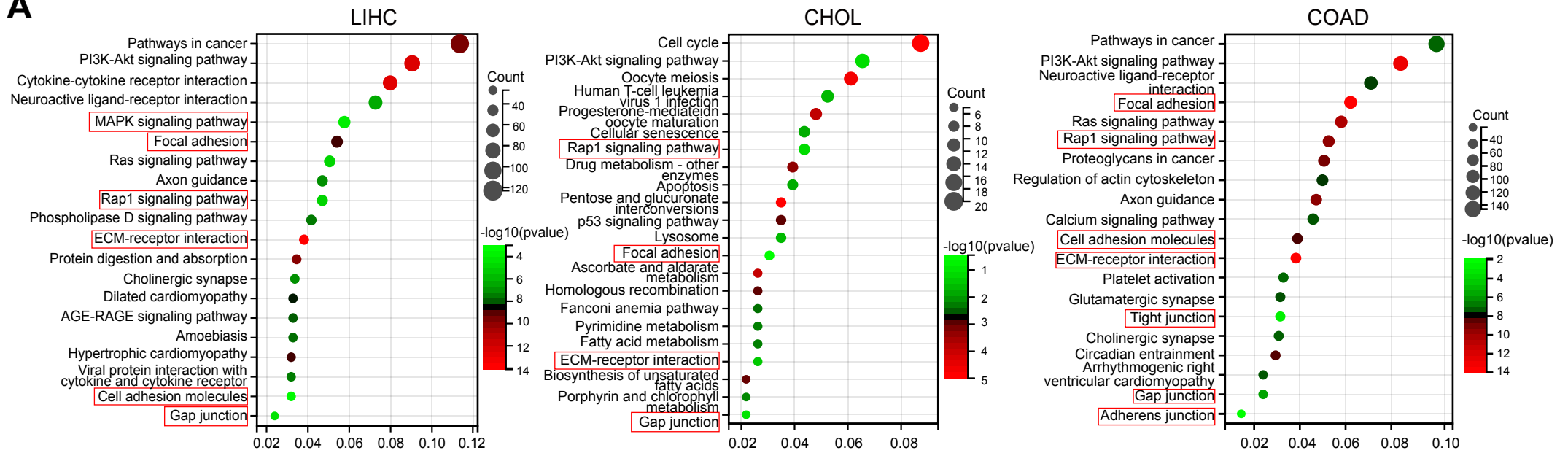


B

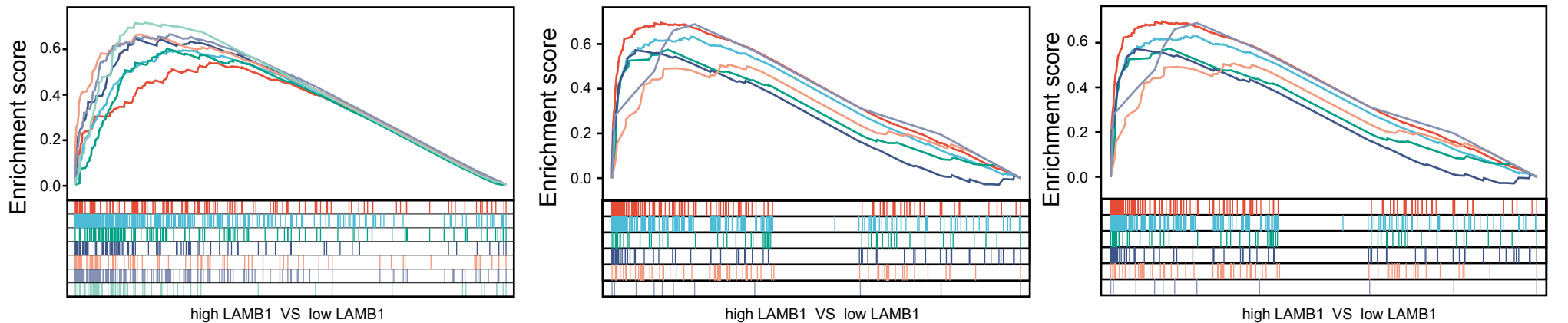


Supplementary Figure 1. **Multi-cancer analysis of the expression and prognostic role of LAMB1.** (A) LAMB1 is significantly upregulated in multiple cancer types from TCGA data. (B) Kaplan-Meier analysis of the association between LAMB1 expression and OS or DFS in LIHC, CHOL, and COAD datasets.

A



B



Pathway	NES	p-value
CELL_ADHESION_MOLECULES_CAMS	1.707	< 0.001
MAPK_SIGNALING_PATHWAY	2.014	< 0.001
TIGHT_JUNCTION	1.999	< 0.001
GAP_JUNCTION	1.996	< 0.001
ECM_RECEPTOR_INTERACTION	2.014	< 0.001
FOCAL ADHESION	2.094	< 0.001
ADHERENS JUNCTION	2.005	< 0.001

Pathway	NES	p-value
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	1.866	0.004
BIDUS_METASTASIS_UP	1.781	0.004
SUNG_METASTASIS_STROMA_DN	1.679	0.008
RAMASWAMY_METASTASIS_UP	1.673	0.016
RIZKI_TUMOR_INVASIVENESS_2D_UP	1.564	0.027
GOUYER_TUMOR_INVASIVENESS	1.555	0.032

Pathway	NES	p-value
ADHERENS_JUNCTION	1.939	< 0.001
FOCAL_ADHESION	1.916	< 0.001
GAP_JUNCTION	1.907	< 0.001
TIGHT_JUNCTION	1.954	< 0.001
MAPK_SIGNALING_PATHWAY	1.969	< 0.001
ECM_RECEPTOR_INTERACTION	1.718	0.045

Supplementary Figure 2 **Multi-cancer analysis of biological functions and significant pathway of LAMB1.** (A) Top 20 pathways enriched in the KEGG analysis in LIHC, CHOL, and COAD datasets. The red box represents pro-metastatic processes, including focal adhesion, ECM-receptor interaction, and cellular junction. (B) GESA analysis of gene signatures of indicated pathways in LIHC, CHOL, and COAD datasets.