

Figure S1. Heatmap of BCR-related genes in primary PCa and BCR PCa tissues. The heatmap was applied to visualize the differential expression of 44 BCR-related genes between 312 primary PCa tissues and 97 BCR PCa tissues in the GEO-merged cohort (GSE46602, GSE70768 and GSE116918). BCR, biochemical recurrence; PCa, prostate cancer; GEO, Gene expression Omnibus; Pri-, primary.

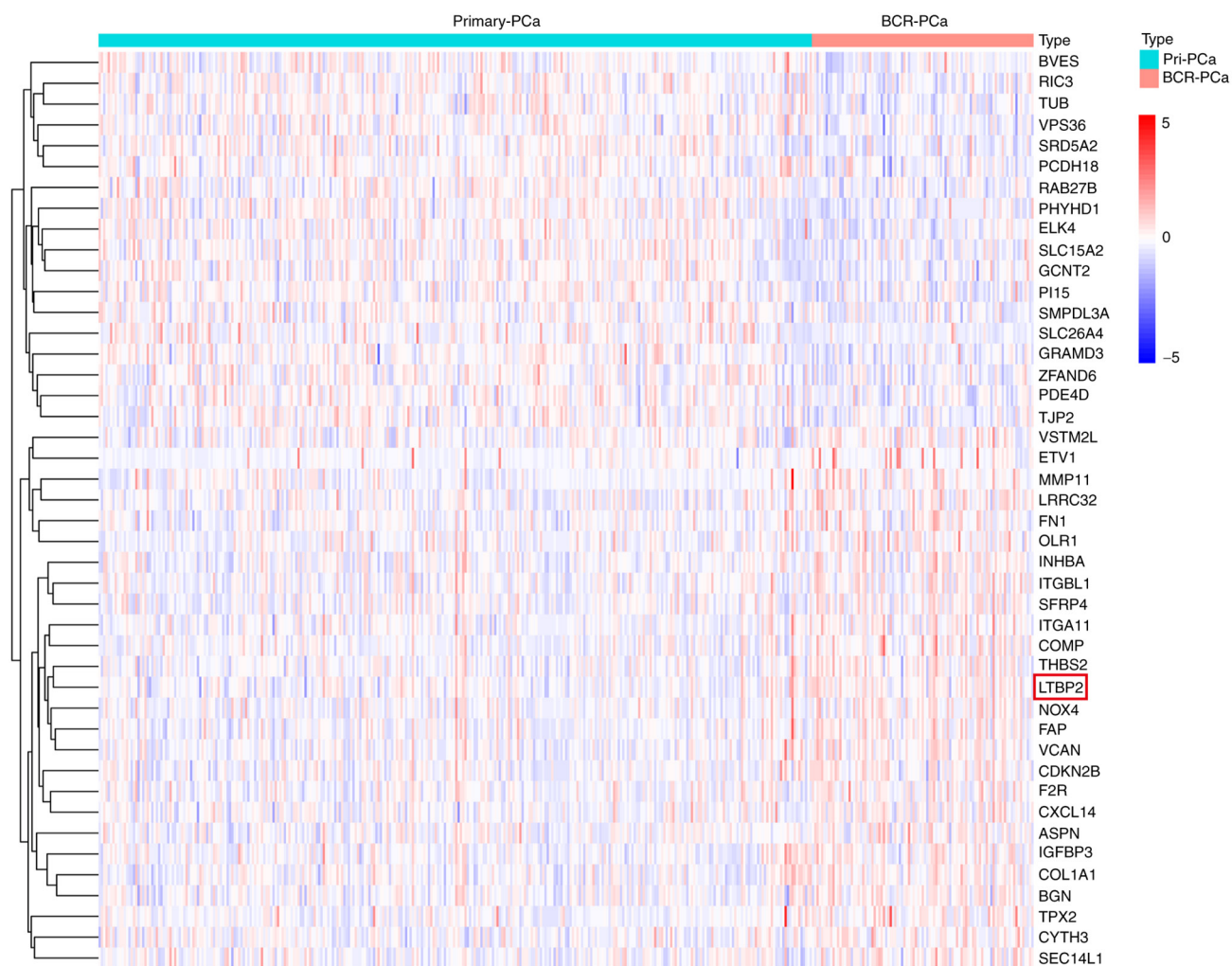


Figure S2. Expression of LTBP2 in pan-cancer. Differential expression of LTBP2 between 33 solid human cancers and normal control tissues in TCGA database. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. LTBP2, latent transforming growth factor β -binding protein 2; TCGA, The Cancer Genome Atlas; GTex, Genotype-Tissue Expression; PRAD, prostate adenocarcinoma.

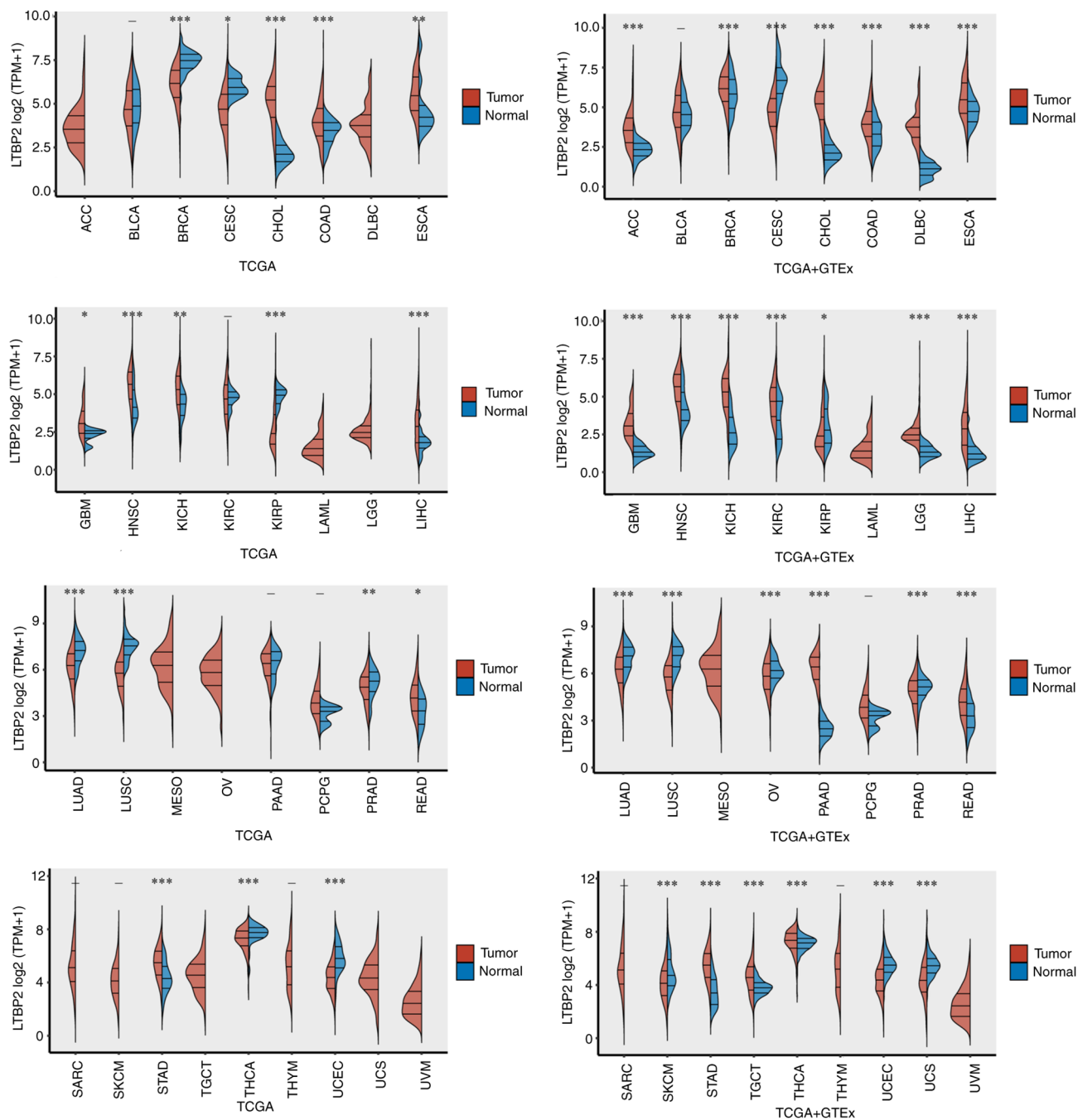


Figure S3. Prognostic value of LTBP2 in pan-cancer. (A-C) Univariate Cox regression analysis was performed to assess the (A) OS, (B) DSS, and (C) PFI of LTBP2 in different cancer types in TCGA database. LTBP2, latent transforming growth factor β -binding protein 2; OS, overall survival; DSS, disease-specific survival; PFI, progression-free interval; TCGA, The Cancer Genome Atlas.

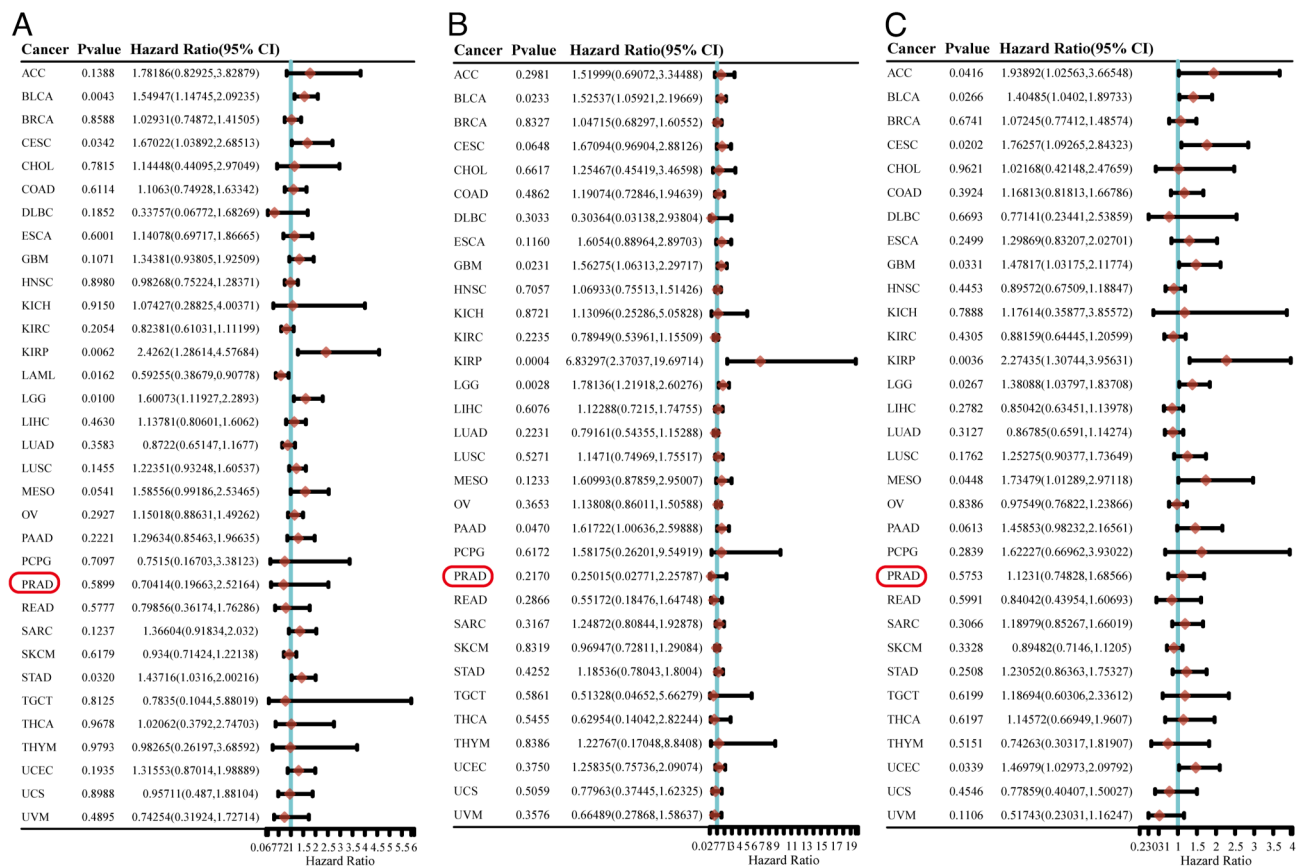


Figure S4. Prognostic value of LTBP2 in pan-cancer. (A-C) The Kaplan-Meier survival plot revealed the difference in the (A) OS, (B) DSS, (C) PFI between high and low expression of LTBP2 in TCGA-PRAD dataset. LTBP2, latent transforming growth factor β -binding protein 2; OS, overall survival; DSS, disease-specific survival; PFI, progression-free interval; TCGA, The Cancer Genome Atlas; PRAD, prostate adenocarcinoma.

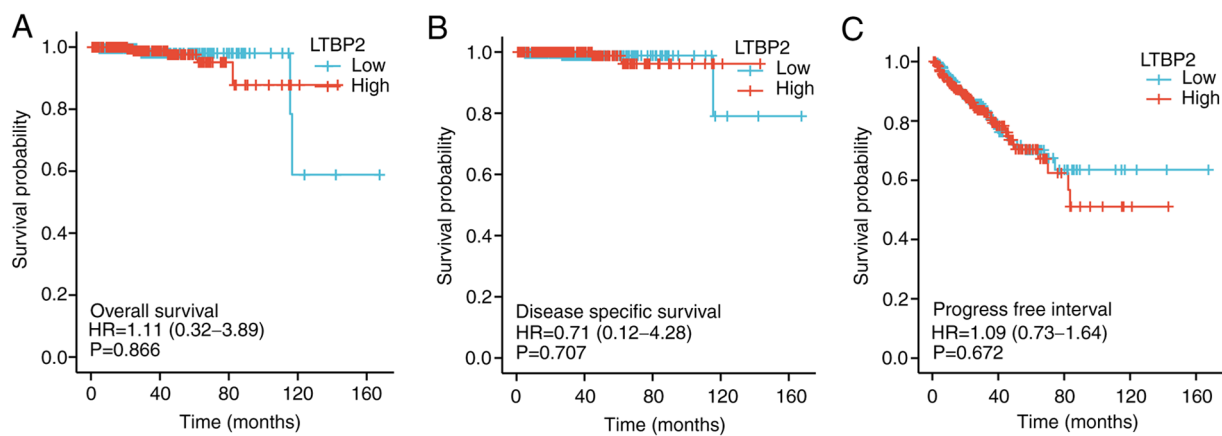


Figure S5. Spearman correlation analysis indicated the correlation between LTBP2 expression and tumor-infiltrating immune cells in TCGA database for 33 pan-cancers. $P < 0.05$ suggested a correlation between LTBP2 and tumor-infiltrating immune cells. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. TCGA, The Cancer Genome Atlas; PRAD, prostate adenocarcinoma.

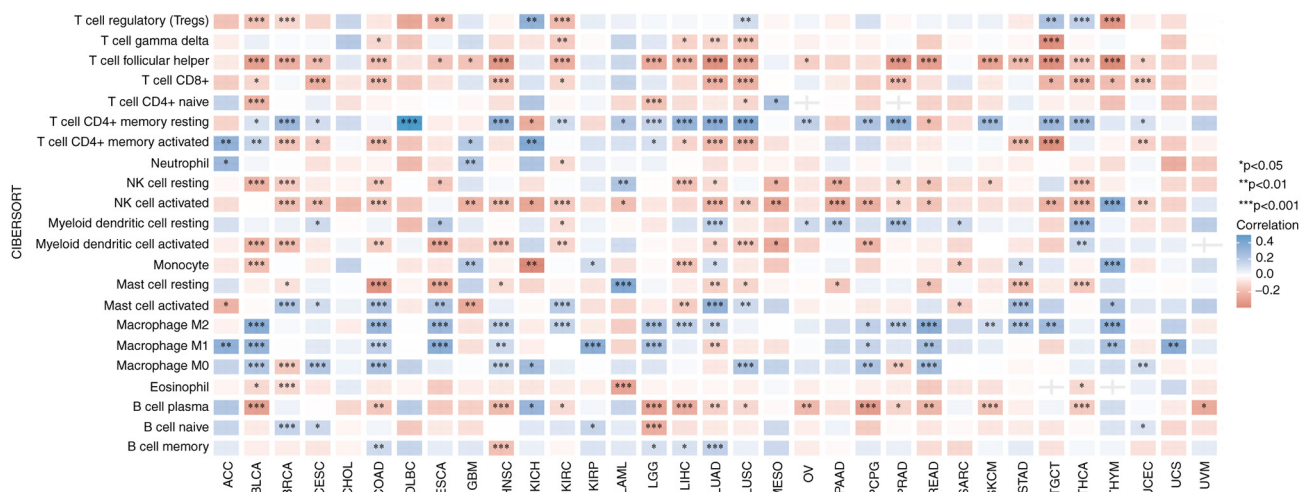


Figure S6. Landscape and correlation of tumor-infiltrating immune cells in PCa in the GEO-merged dataset. (A) The proportions of immune infiltrating cells in primary PCa subgroup and biochemical recurrence PCa subgroup. (B) Spearman analysis indicated the correlation between different tumor-infiltrating immune cells. Red represents a positive correlation and blue represents a negative correlation. PCa, prostate cancer; GEO, Gene expression Omnibus; Pri-, primary; BCR, biochemical recurrence.

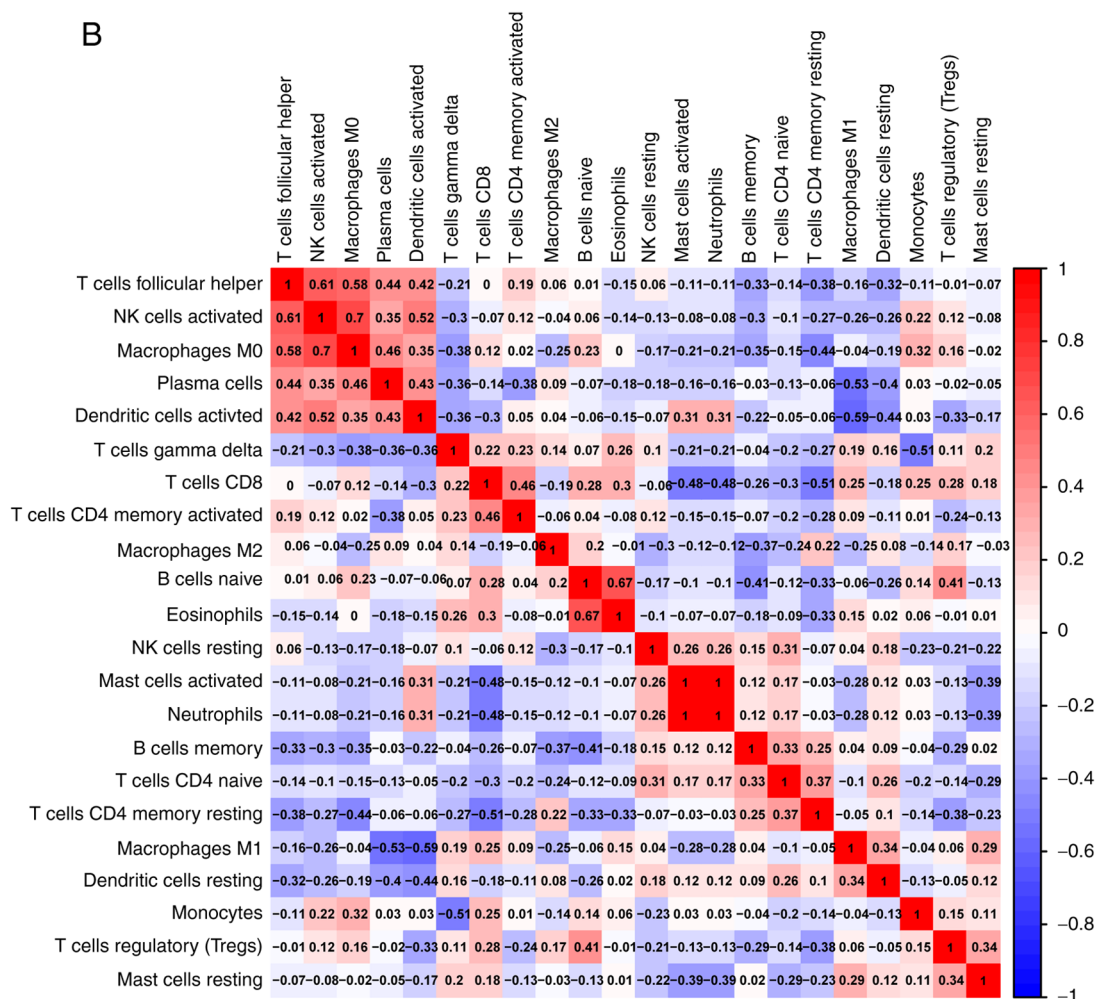
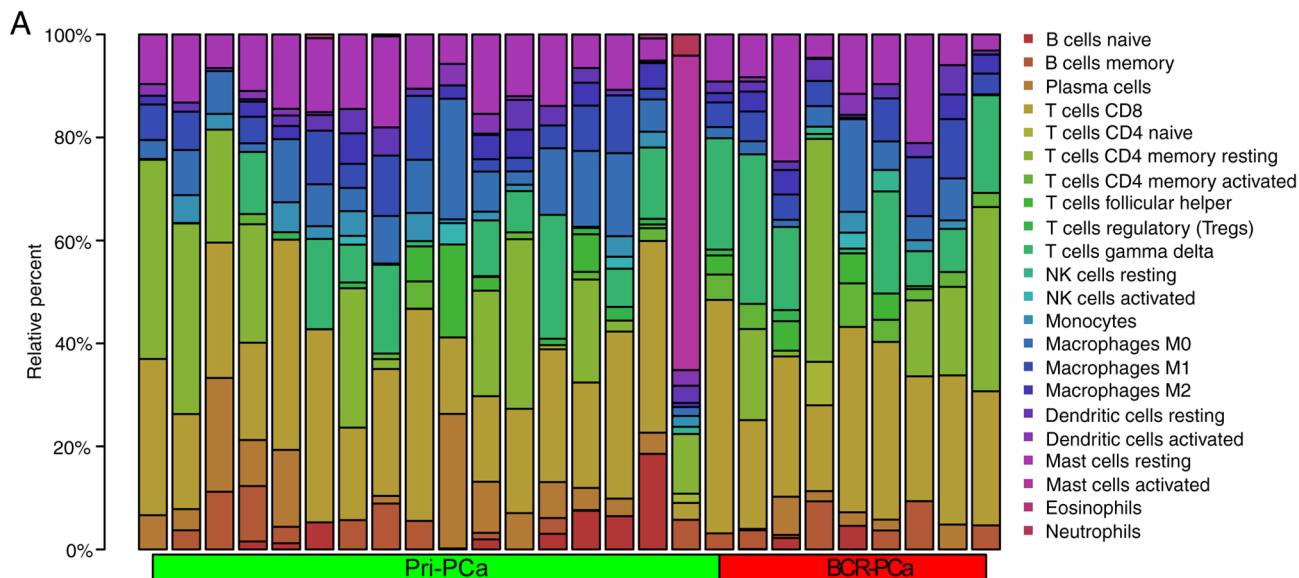


Figure S7. Correlation between LTBP2 expression with immune-cell marker genes. The correlation scatter plot confirmed that LTBP2 expression was significantly positively correlated with immune-cell marker genes, except for CEACAM8. LTBP2, latent transforming growth factor β -binding protein 2.

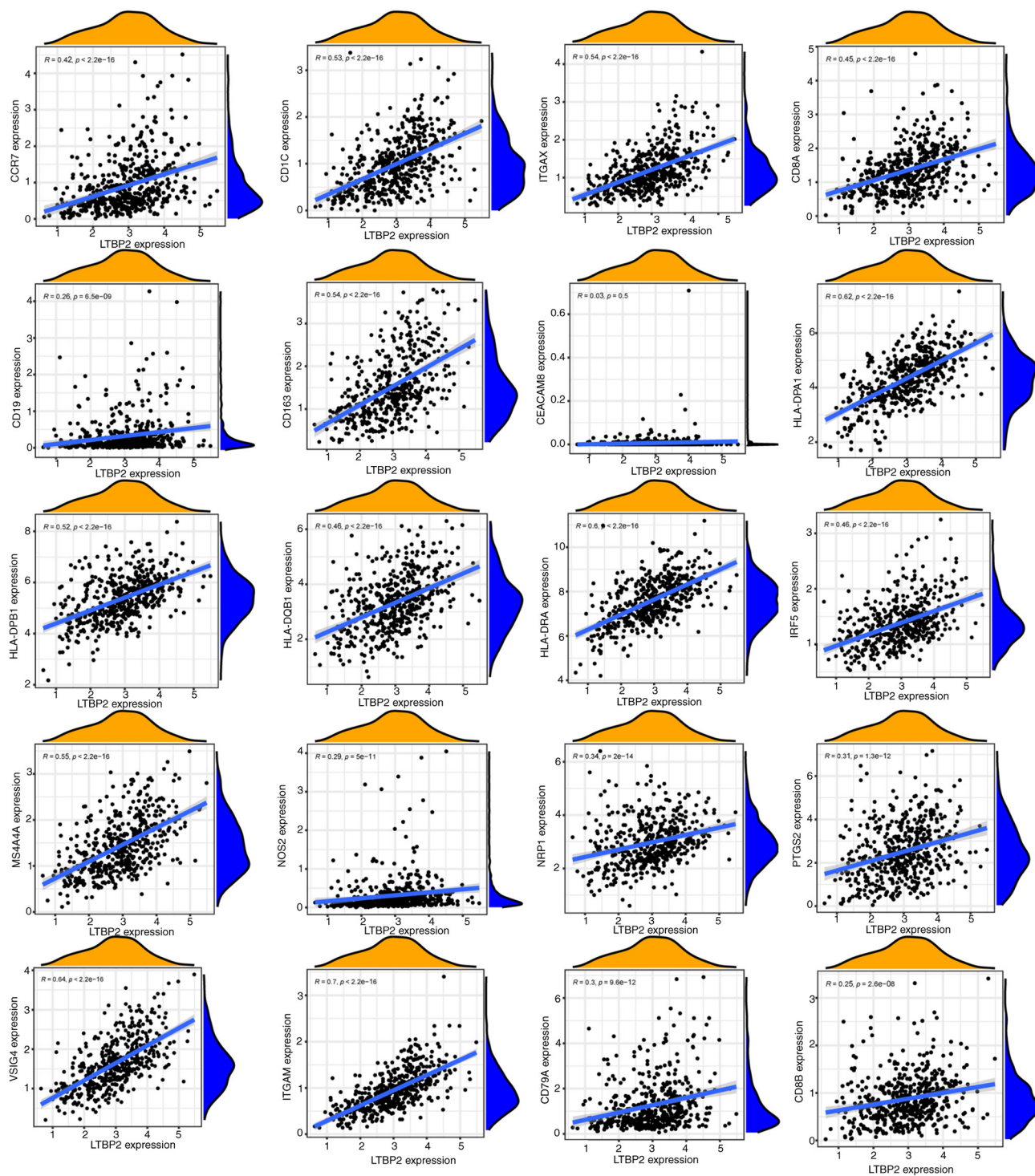


Figure S8. Construction of lncRNA-miRNA-LTBP2 ceRNA regulatory network. LTBP2-associated ceRNA regulatory network was mapped based on co-expression analysis and starBase database, where green ovals represent lncRNAs and purple triangles represent miRNAs (cor >0.3; P-value <0.01). LTBP2, latent transforming growth factor β -binding protein 2; ceRNA, competitive endogenous RNA.

