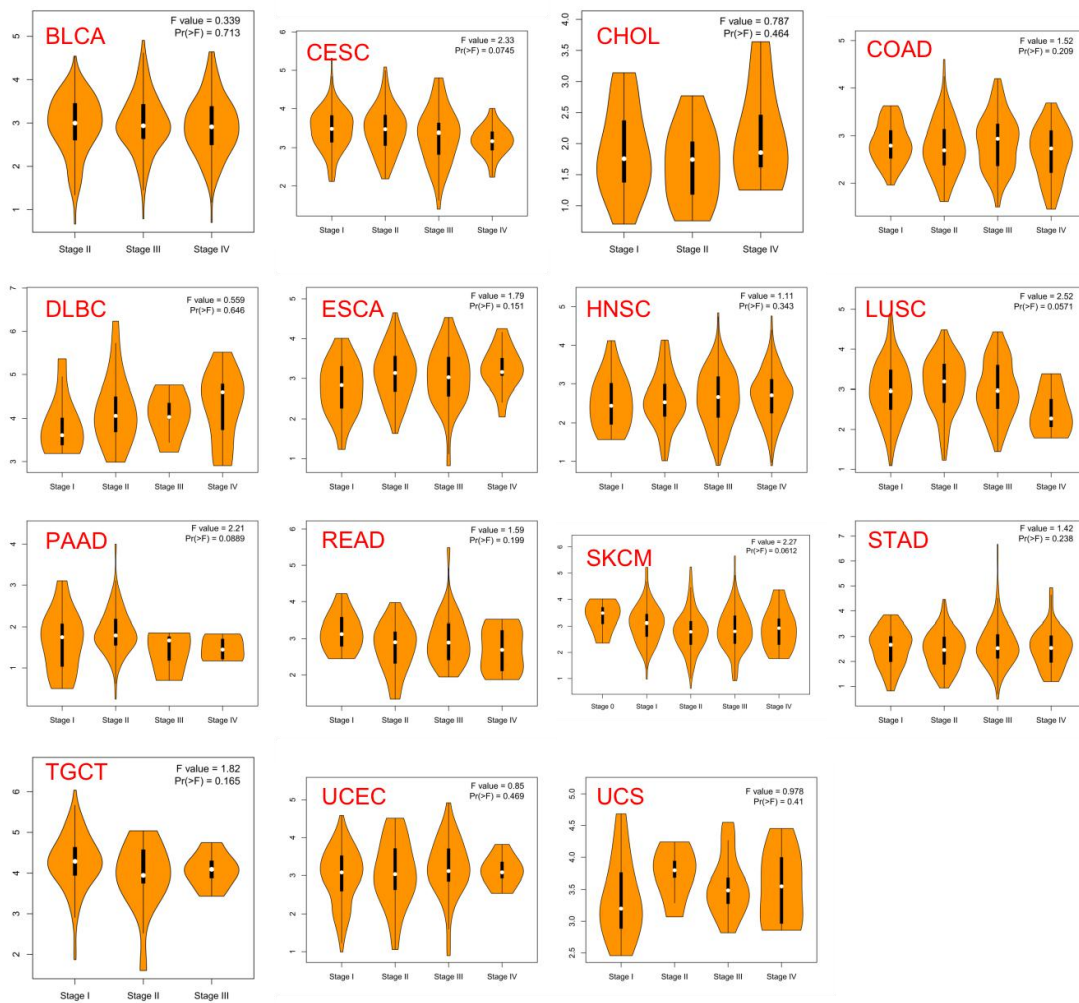
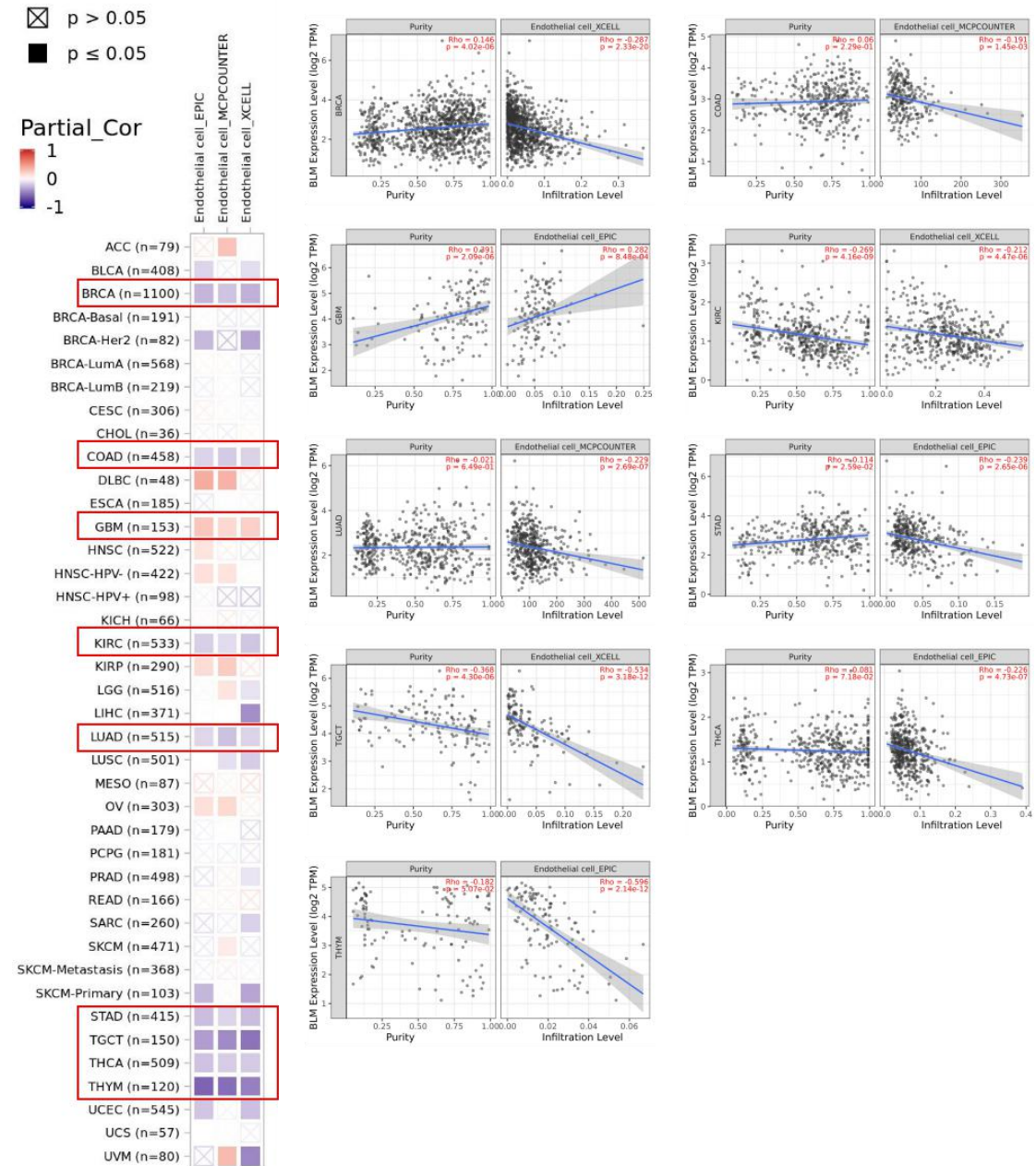




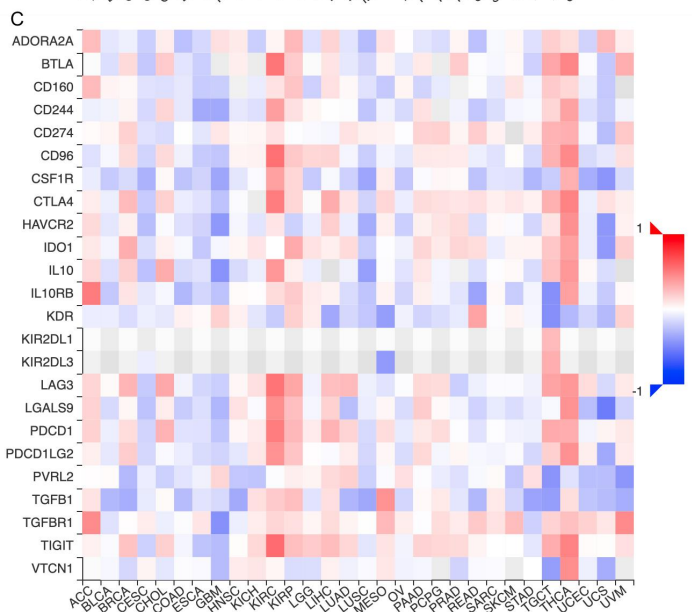
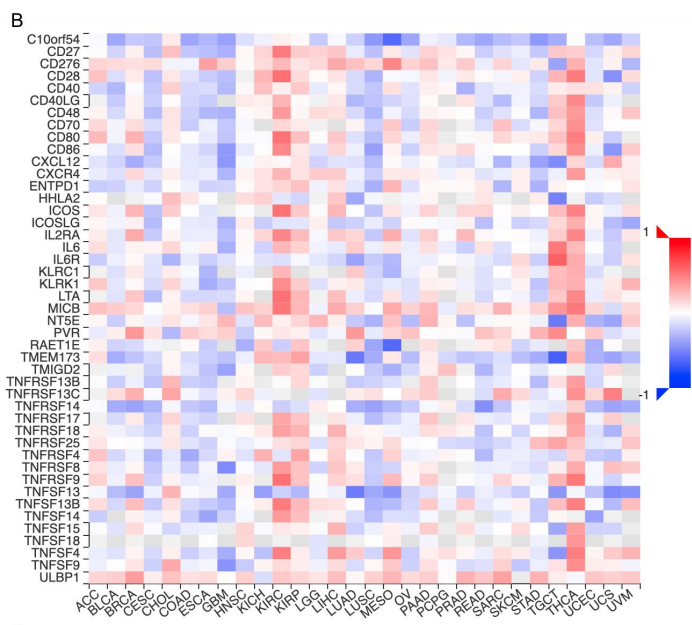
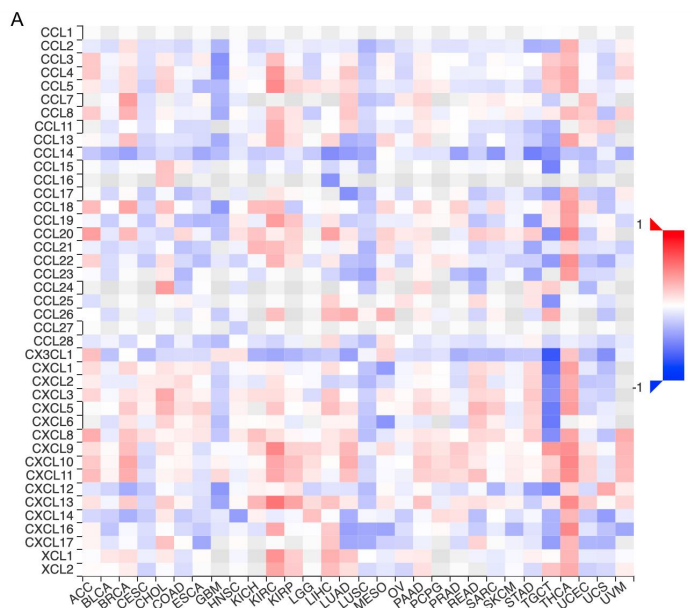
1.Expression level of BLM gene in pathological stages of different tumors

By using GEPIA2 (Gene Expression Profiling Interactive Analysis, version 2, <http://gepia2.cancer-pku.cn/#analysis>) tool, the expression levels of the BLM gene in varied main pathological stages (stage I, stage II, stage III, and stage IV) of BLCA, CESC, CHOL, COAD, DLBC, ESCA, HNSC, LUSC, PAAD, READ, SKCM, STAD, TGCT, UCEC, and UCS were analyzed based on the TCGA data. Log2 (TPM+1) was applied for log-scale.



2. Correlation of BLM and immune infiltration of endothelial cells

By using TIMER2 (tumor immune estimation resource, version 2, <http://timer.cistrome.org/>) tool, the correlation of BLM gene expression and immune infiltration of endothelial cells across all types of cancer in TCGA was analyzed.



3. Correlations of BLM with immune-related chemokines, immunostimulator, and immunoinhibitor

By using TISIDB (<http://cis.hku.hk/TISIDB/index.php>) approach, the correlations of BLM gene expression with immune-related chemokines, immunostimulator, and immunoinhibitor across different cancers in TCGA were shown.