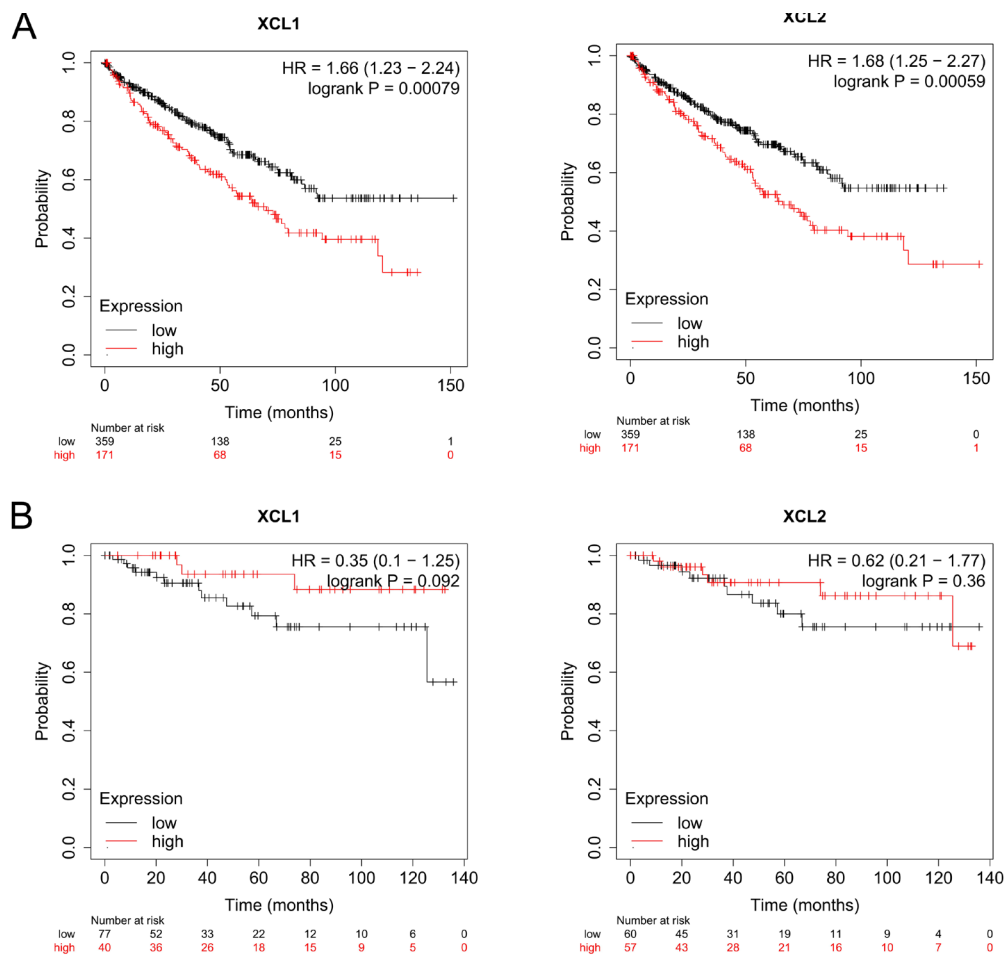
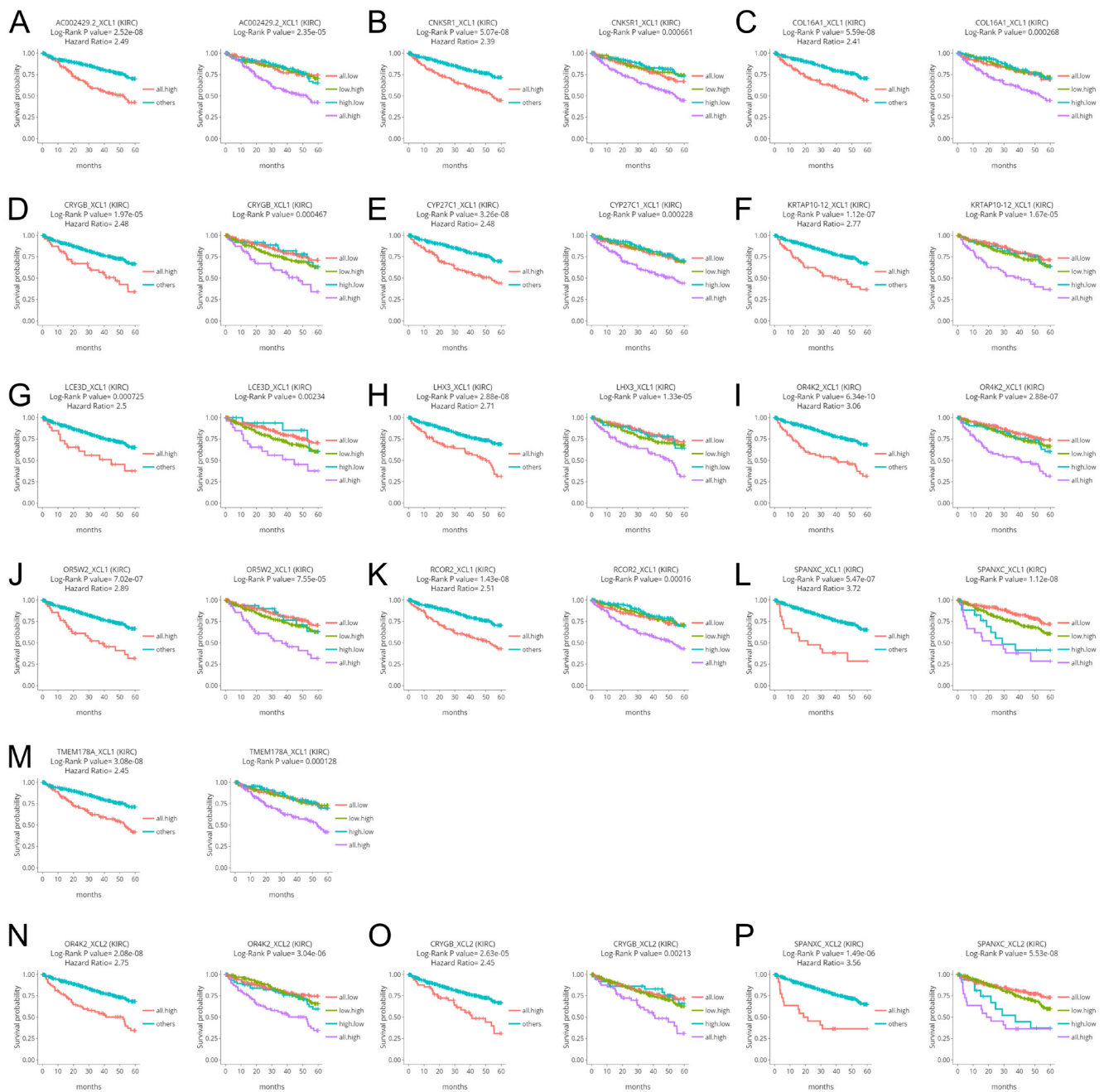


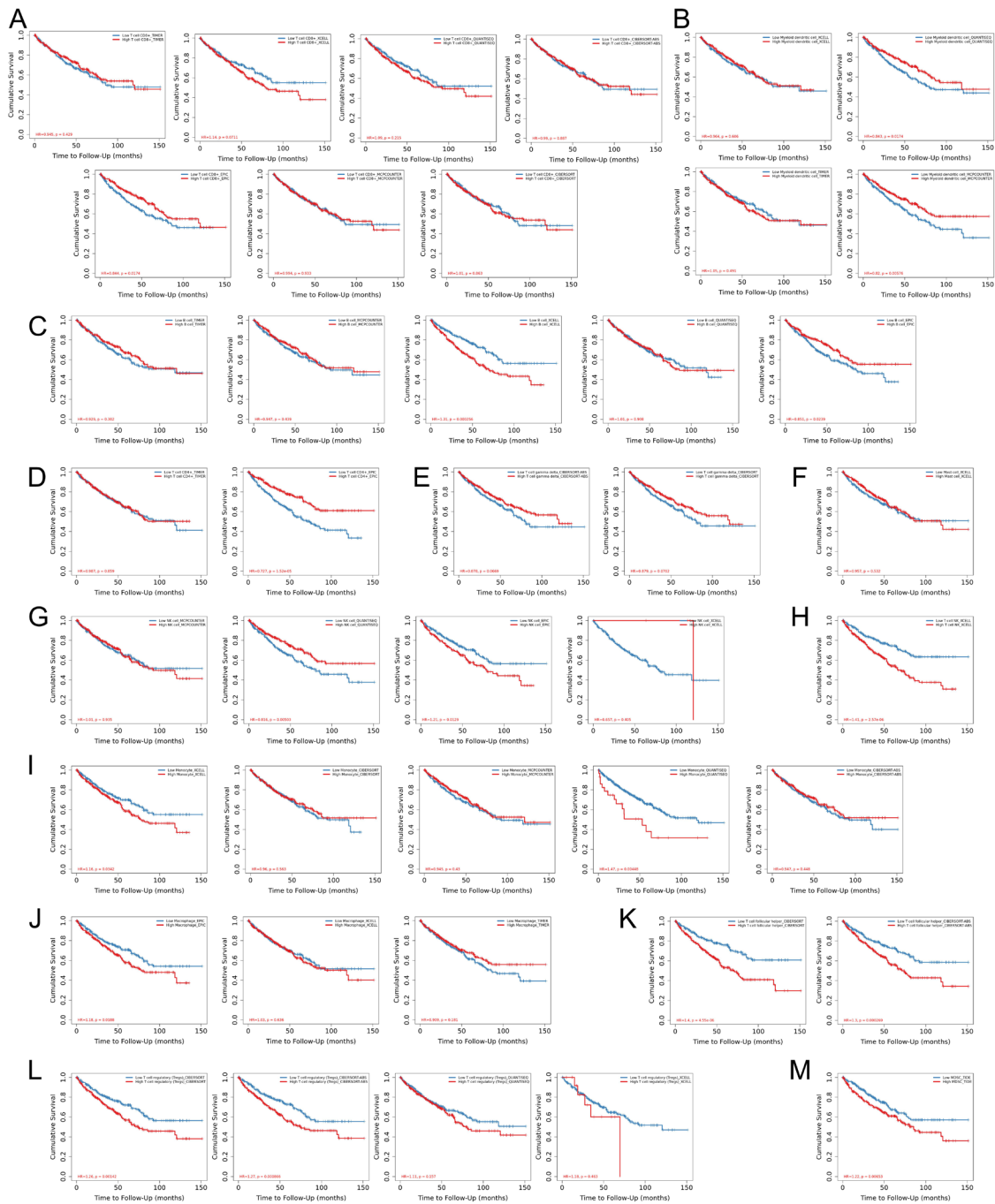
**Figure S1** The expression of XCL1 in RCC analyzed by GEO database. The expression of XCL1 in GSE15641 dataset (A), GSE46699 dataset (B) and GSE53757 dataset (C). \*\*\*\*,  $P < 0.0001$ . RCC, renal cell carcinoma; GEO, Gene Expression Omnibus.



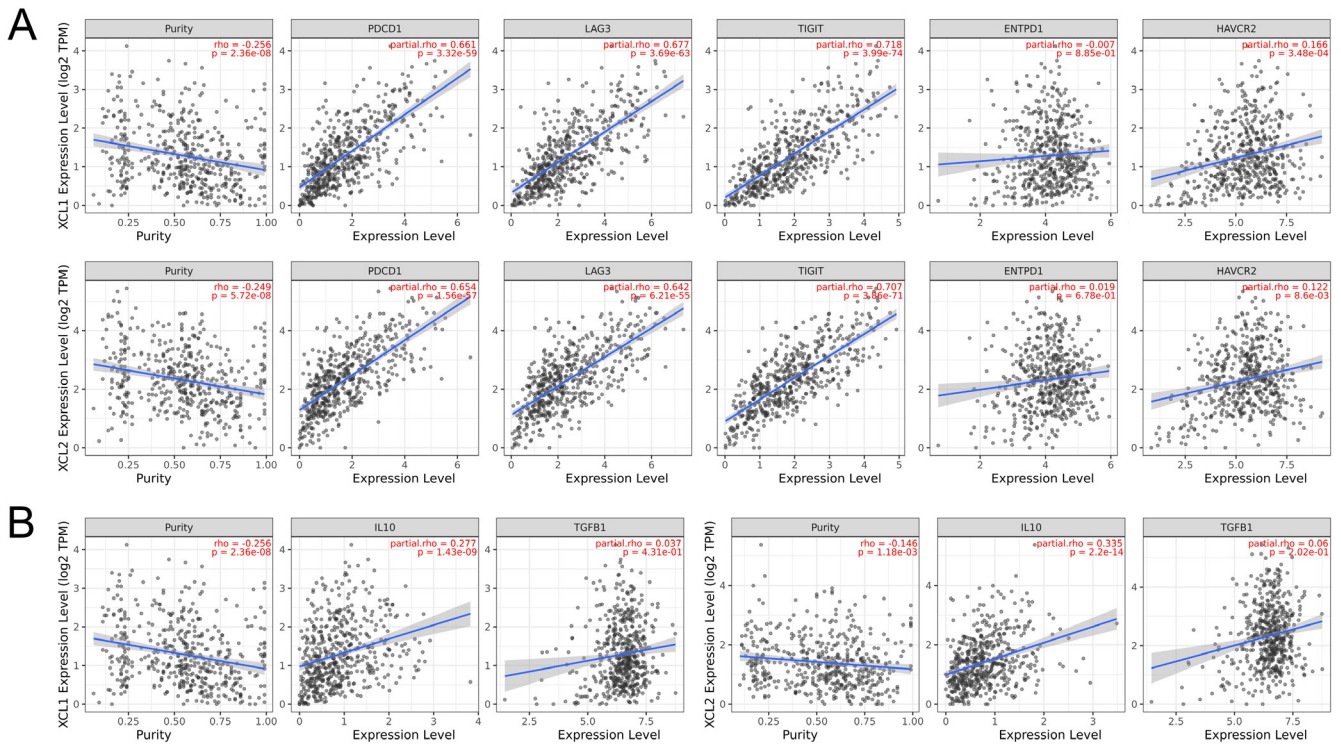
**Figure S2** The prognostic value of C chemokines in KIRC analyzed by Kaplan-Meier plotter. The effects of C chemokines on the OS (A) and DFS (B) of KIRC patients. KIRC, kidney renal clear-cell carcinoma; OS, overall survival; DFS, disease-free survival.



**Figure S3** Kaplan-Meier plots of C chemokines and their synergistic genes. Synergistic genes of XCL1 (A-M). Synergistic genes of XCL2 (N-P). KIRC, kidney renal clear-cell carcinoma.

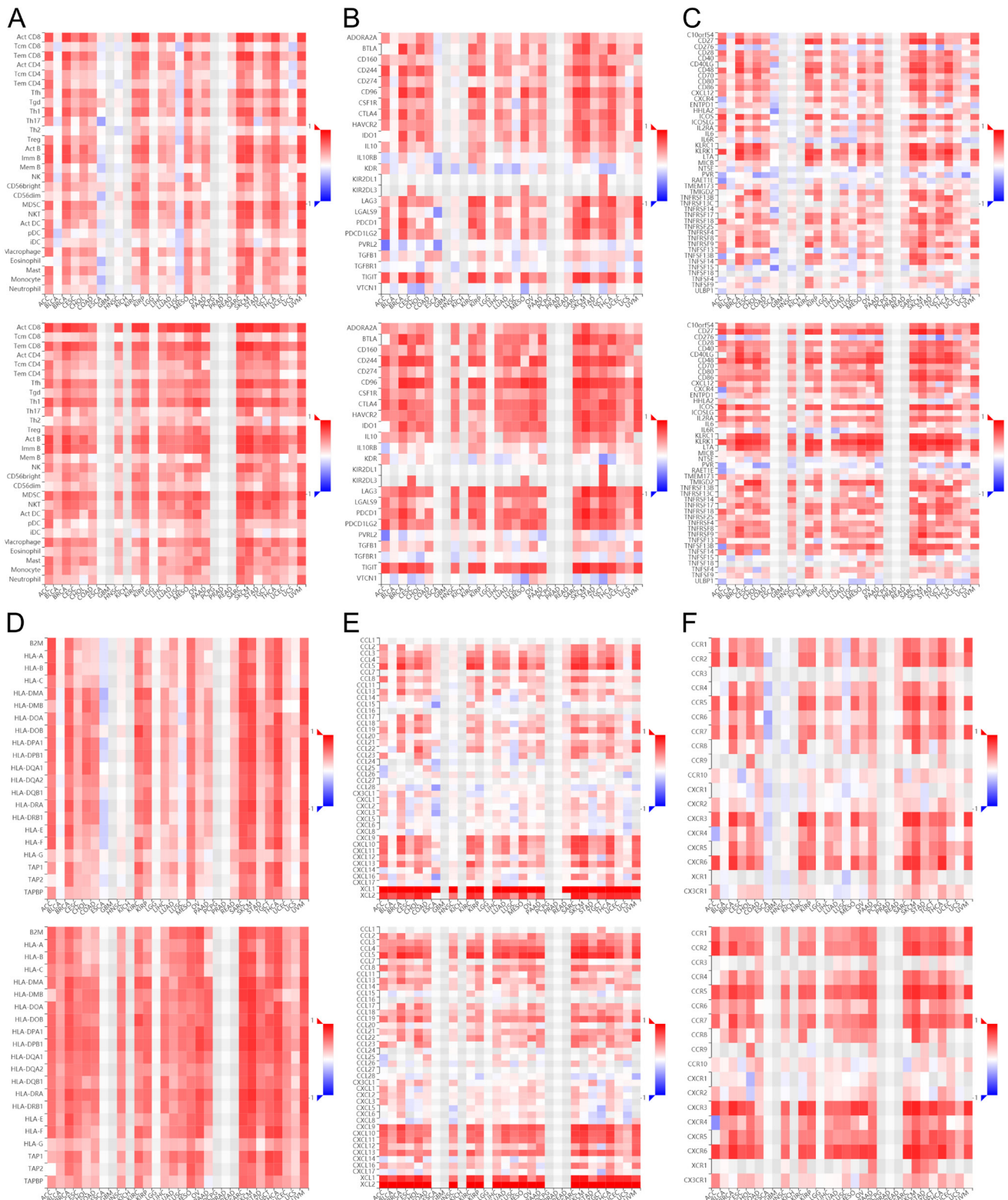


**Figure S4** Associations between immune cell infiltrations and the prognosis of KIRC. Kaplan-Meier plots for the infiltrates of CD8<sup>+</sup> T cell (A), DC (B), B cell (C), CD4<sup>+</sup> T cell (D), Tgd (E), mast cell (F), NK (G), NKT (H), monocyte (I), macrophage (J), Tfh (K), Treg (L), MDSC (M) in KIRC. KIRC, kidney renal clear-cell carcinoma; DC, dendritic cell; Tgd, Gamma delta T cell; NK, natural killer cell; NKT, Natural killer T cell; Tfh, T follicular helper cell; Treg, Regulatory T cell; MDSC, Myeloid derived suppressor cell; XCELL, xCell is a webtool that performs cell type enrichment analysis from gene expression data for 64 immune and stroma cell types; QUANTISEQ, quanTlseq is a computational pipeline for the quantification of the Tumor Immune contexture from human RNA-seq data; CIBERSORT, Cell-type Identification By Estimating Relative Subsets Of RNA Transcripts; CIBERSORT-ABS, CIBERSORT absolute mode; EPIC, Estimating the Proportion of Immune and Cancer cells; MCPOUNTER, Microenvironment Cell Populations-counter; TIDE, Tumor Immune Dysfunction and Exclusion.



**Figure S5** Associations between the expression of C chemokines and different genes validated by TIMER. Correlation analysis of C chemokines expression and the markers of T cell exhaustion (A), IL10 and TGF- $\beta$  (B). TIMER, Tumor Immune Estimation Resource; PD1/PDCD1, programmed cell death 1; LAG3, lymphocyte activating 3; TIGIT, T cell immunoreceptor with Ig and ITIM domains; ENTPD1, ectonucleoside triphosphate diphosphohydrolase 1; HAVCR2, hepatitis A virus cellular receptor 2.





**Figure S6** Associations between C chemokines and several categories analyzed by TISIDB. Heatmaps of Spearman correlations between the expression of C chemokines and lymphocytes (A), immunoinhibitors (B), immunostimulators (C), MHC molecules (D), chemokines (E), and receptors (F) in KIRC. Upper: XCL1. Down: XCL2. TISIDB, Tumor-Immune System Interactions Database; KIRC, kidney renal clear-cell carcinoma; MHC, major histocompatibility complex.