Supplementary Figure 1. The differential expression and diagnostic analysis of IL18RAP in pan-cancer. (A) The expression of IL18RAP in pan-cancer obtained from TIMER2.0 database. *p < 0.05; **p < 0.01 and ***p < 0.001. (B) Receiver Operator Characteristic (ROC) curve of IL18RAP in ACC, BRCA, COADREAD, DLBC, KICH, KIRC, LAML, LUADLUSC, OV, TGCT, THYM, and UCS. The AUC value (0.5 - 0.7, 0.7 - 0.9, 0.9 - 1) represents low, good and high accuracy respectively.
Supplementary Figure 2. Genetic alterations of IL1R1, IL1R2, IL18, IL18R1, IL18BP, and IL18RAP in pan-cancer. (A) The mutation frequency and types of IL1R1, IL1R2, IL18, IL18R1, IL18BP, and IL18RAP in 31 cancers. (B) The heterozygous amplification (left) and deletion (right) of IL18RAP and other 5 genes in pan-cancer. The analyses were based on GSCALite platform.
Supplementary Figure 3. Correlation of IL18RAP with immunostimulators, MHC molecules, chemokines and chemokine receptors genes in 33 cancers. (A–D) The correlation analysis between IL18RAP expression and Immunostimulators (A), Chemokines (B), MHC molecules (C), Chemokine receptors (D) genes using Spearman correlation analysis.

Supplementary Figure 4. The HALLMARK gene sets analysis on each cell clusters based on 4 datasets. (A–D) The HALLMARK gene sets analysis on each cell clusters based on LAML (GSE154109) (A), Glioma (GSE131928_10X) (B), OV (GSE130000) (C), and PRAD (GSE150692) (D) datasets. The analyses were based on TISCH2 platform.
Supplementary Figure 5. The drug sensitivity of IL18RAP in cancers. (A, B) The correlation analysis between IL18RAP expression and IC50 level of various drugs in cancer cell lines based on the CTRP (A) and GDSC (B) databases. The analyses were based on GSCALite platform.