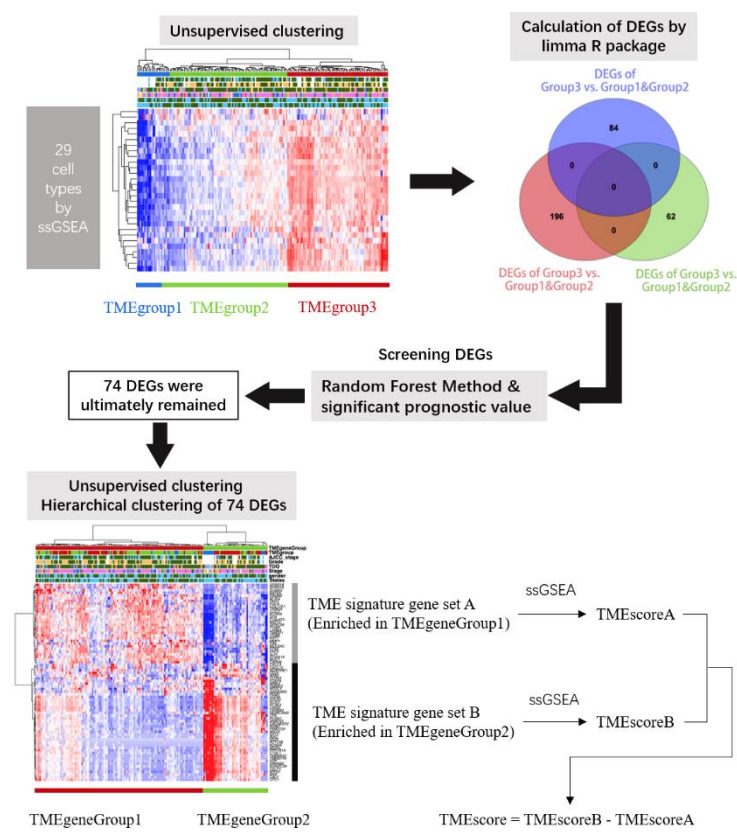
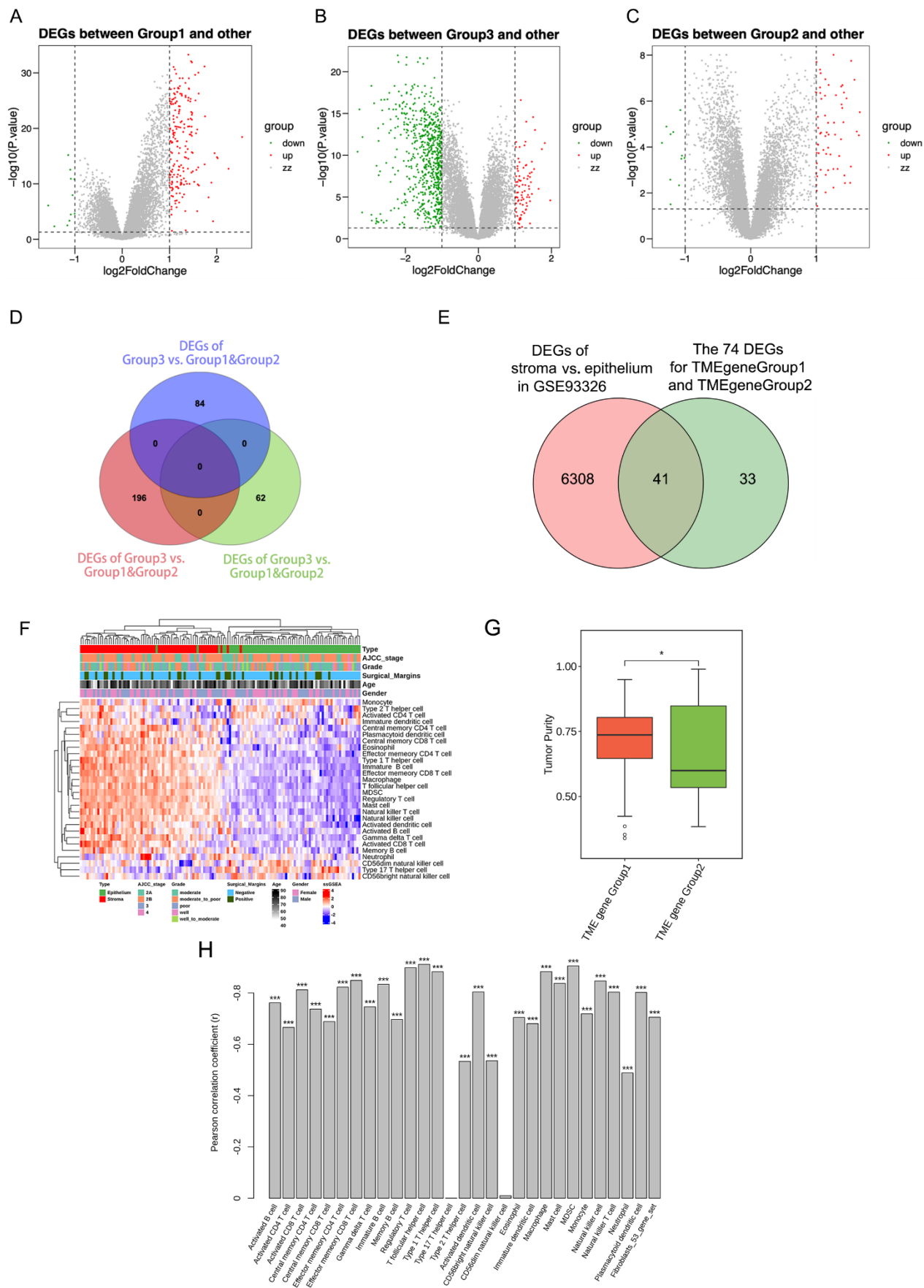


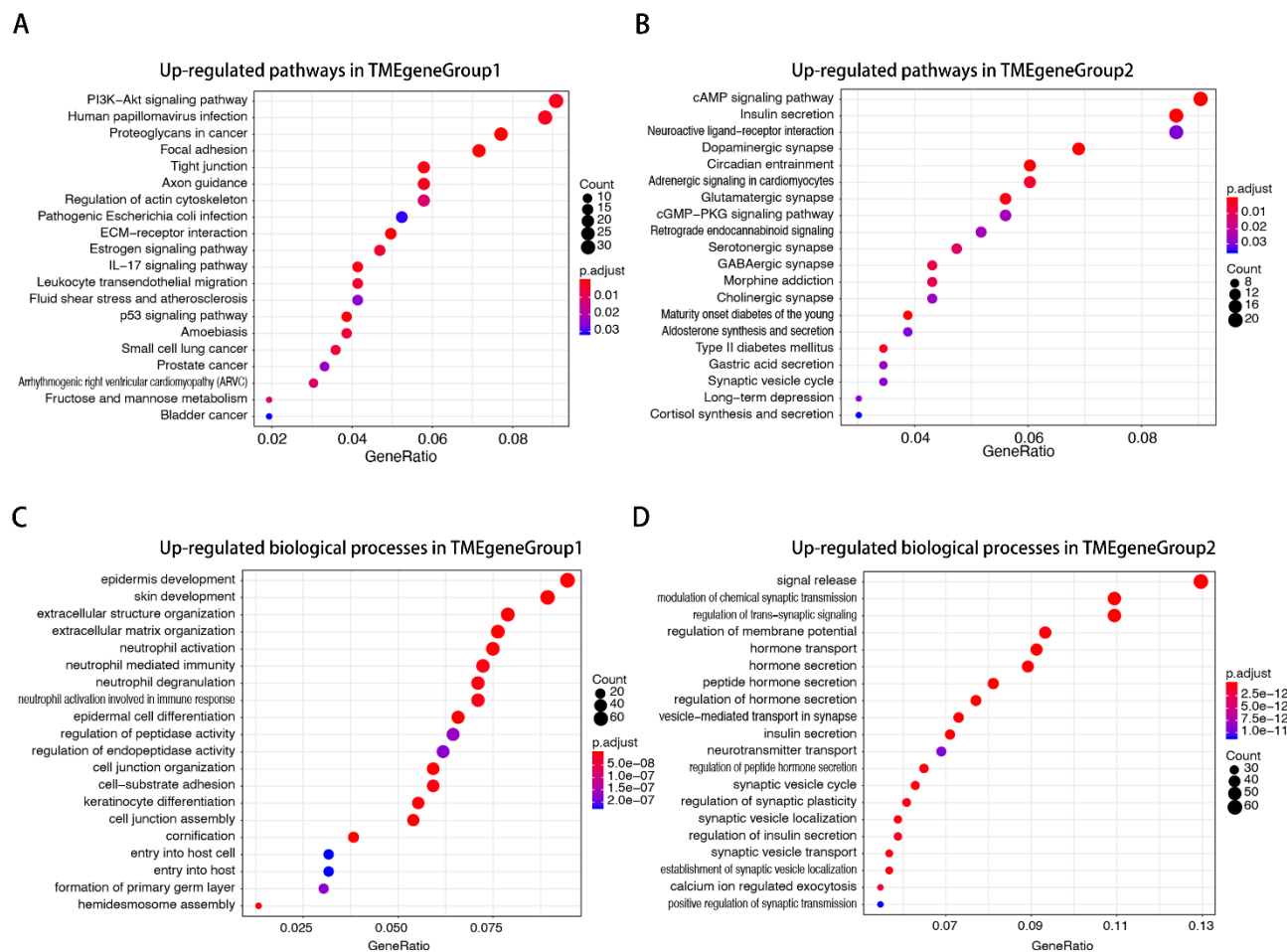
*Supplementary Figures*



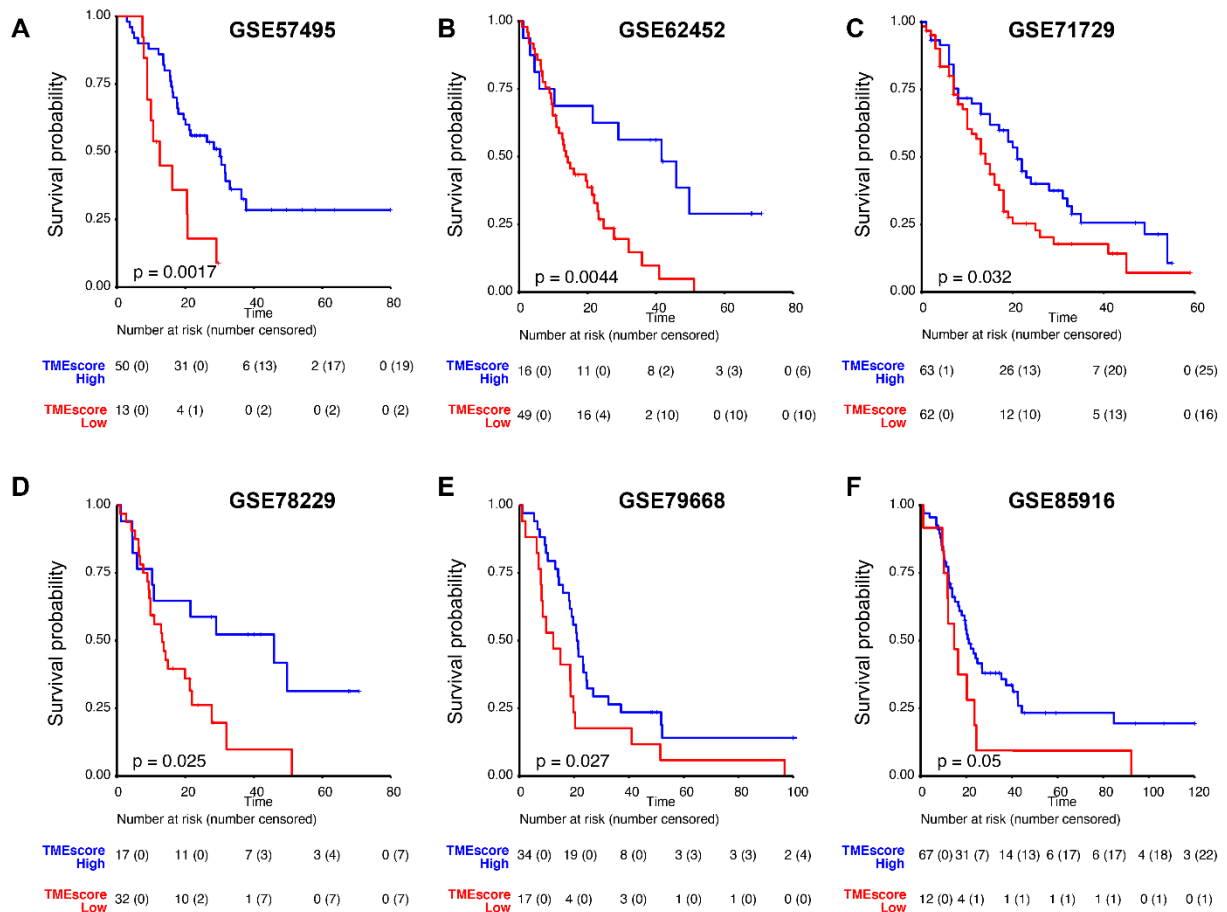
**Supplementary Figure S1.** A schematic diagram of the process of generation of the TMEscore.



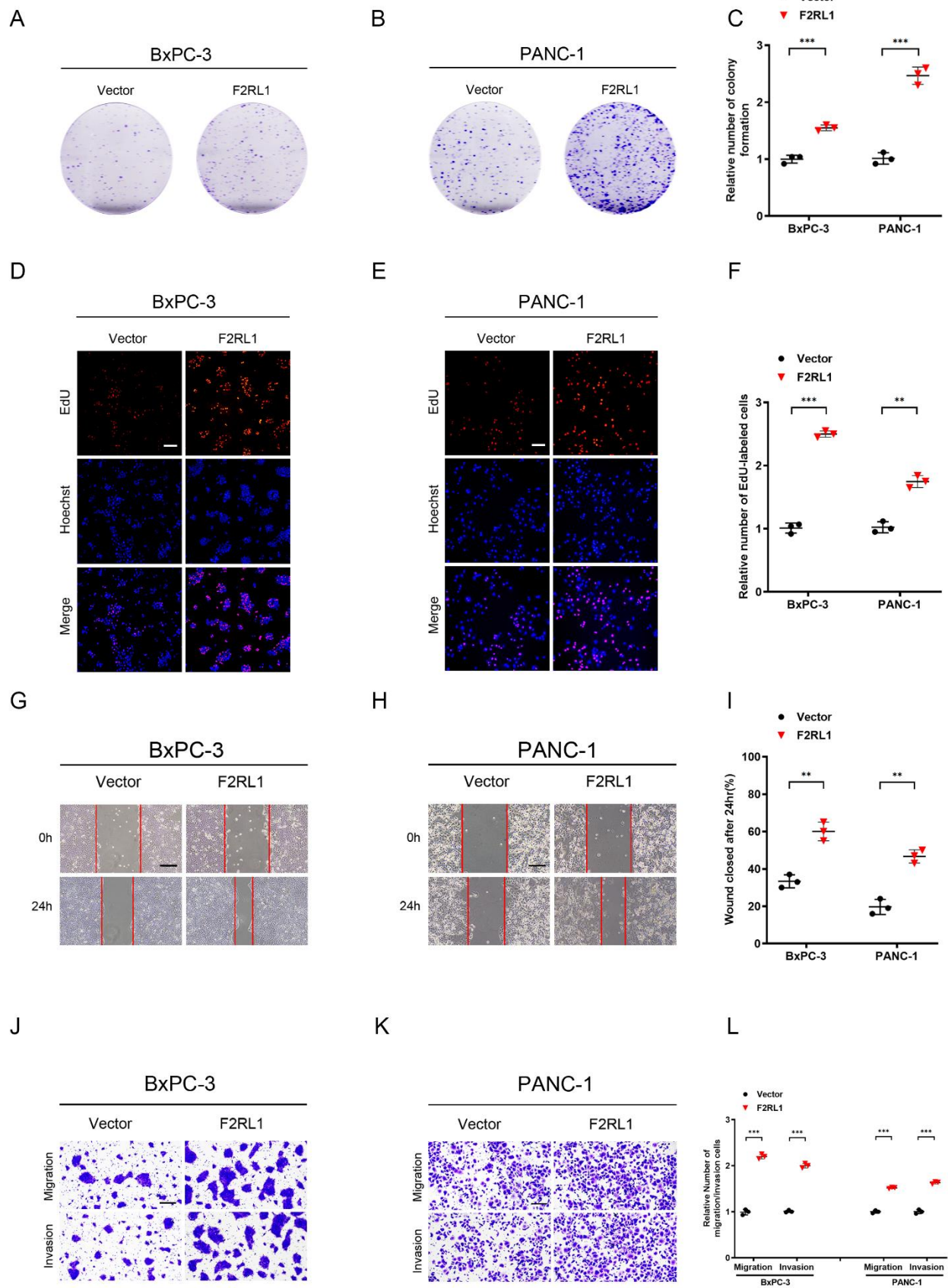
**Supplementary Figure S2.** The filter screening of DEGs. (A-C) Volcano plots showing the DEGs between a TMEgroup with two other TMEgroups. The detailed information of DEGs was summarized in the Supplementary Table S4. (D)Venn diagram analysis revealed that unique DEGs appeared in all three comparisons. (E) Venn diagram shows the difference between 74 DEGs of TMEgeneGroup and DEGs in GSE93326. (F) Immune cells differences between epithelium and stroma in GSE93326. (G) Tumor purity analysis between TMEgeneGroup1 and TMEgeneGroup2. (H) The bar chart shows the Pearson’s correlation coefficient between 29 cell types and tumor purity.



**Supplementary Figure S3.** GO function and KEGG pathway enrichment analysis of the DEGs between TMEgeneGroup1 and TMEgeneGroup2.



**Supplementary Figure S4.** Prognostic value of TMEscore in six pancreatic cancer cohorts.



**Supplementary Figure S5.** Overexpression of F2RL1 promotes proliferation, migration and invasion of PDAC cells in vitro. (A-C) The colony formation assay showing representative images (A, B) and quantitative analysis (C) of BxPC-3 and PANC-1 after overexpression of F2RL1. (D-F) EdU assay showing representative images (D, E) and quantitative analysis (F) of BxPC-3 and PANC-1 after overexpression of F2RL1. Scale bars: 100  $\mu$ m. (G-I) Wound healing assay showing representative images (G, H) and quantitative analysis (I) of BxPC-3 and PANC-1 after overexpression of F2RL1. Scale bars: 100  $\mu$ m. (J-L) Transwell assay showing representative images (J, K) and quantitative analysis (L) of BxPC-3 and PANC-1 after overexpression of F2RL1. Scale bars: 100  $\mu$ m. Error bars represent the standard deviations from three independent experiments. (\*\*:  $p < 0.01$ , \*\*\*:  $p < 0.001$ )