

Expanded View Figures

Figure EV1. Expression of IL-38 in different tissues and the expression of IL-1 family members in cSCC and DMBA/TPA-induced mouse tumors.

- A IL-38 expression in various tissues sourced from control subjects ($n = 6-860$) using the GTEx database.
- B Representative immunohistochemical staining micrographs of IL-38 and rabbit IgG in human normal skin. Scale bars represent 200 μm .
- C Relative expression of IL-1 family members in human normal tissues ($n = 9$) and cSCC ($n = 18$) were analyzed using Geo Datasets (GSE98767).
- D Relative expression of IL-1 family members in normal tissues ($n = 9$) and cSCC ($n = 38$) of mice analyzed using Geo Datasets (GSE63967).
- E Representative micrographs of human skin sections stained with anti-IL-18 antibody from normal patients ($n = 11$) and tumors of cSCC patients ($n = 13$). Scale bars represent 100 μm . The graph shows the quantification of mean IL-18 expression per high-powered field in tissues.
- F The dorsal hair of normal C57/BL6 mice was shaved and treated with DMBA/TPA twice a week for 32 weeks to induce skin tumors. Representative micrographs of mouse normal skin ($n = 6$) and tumor ($n = 6$) sections stained with anti-IL-18 antibody. Scale bars represent 100 μm . The graph shows the quantification of mean IL-38 expression in tissues.
- G Representative western blot bands indicating IL-18 in mouse normal skin ($n = 3$) and DMBA/TPA-induced tumors ($n = 3$). The graph shows the quantification of mean IL-18 expression in tissues. β -actin blots of Figs EV1G and EV3F are derived from the same experiment.

Data information: Error bars represent the mean \pm SD. All data are biological replicates. ns, not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; P values were calculated using Student's t -test.

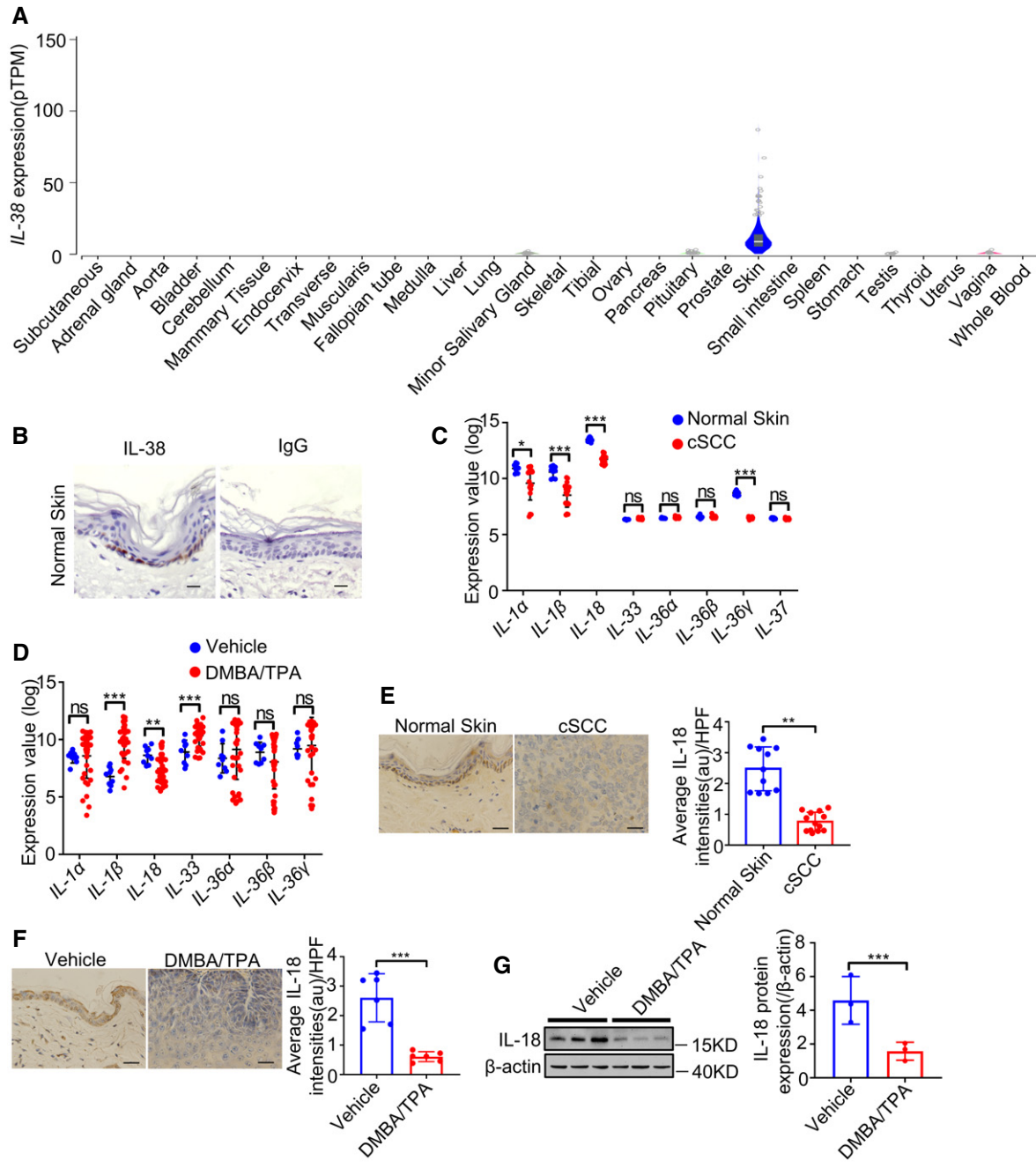


Figure EV1.

Figure EV2. Construction and identification of keratinocytes IL-38-specific knockout mice and effect of keratinocyte-specific IL-38 deficiency on epidermal barrier.

- A Construction of *Il-38-loxP* (*Il-38^{flf}*) mice.
- B Typical genetic cross scheme of keratinocyte IL-38-specific knockout (*K14^{Cre/+}-Il-38^{flf}*) mice.
- C PCR analysis of WT mice (at 317 and 245 bp) and *Il-38-loxP* mice (at 387 and 373 bp).
- D PCR analysis of keratin 14 promoter directing expression of Cre recombinase(left) and deletion of IL-38 (right).
- E Relative expression of *IL-38* in the epidermal splits of *Il-38^{flf}* ($n = 4$) and *K14^{Cre/+}-Il-38^{flf}* ($n = 4$) mice.
- F Representative western blot bands indicating IL-38 in the epidermal splits of *Il-38^{flf}* and *K14^{Cre/+}-Il-38^{flf}* mice.
- G Appearance of *Il-38^{flf}* and *K14^{Cre/+}-Il-38^{flf}* mice.
- H Cumulative body weight changes in *Il-38^{flf}* ($n = 12$) and *K14^{Cre/+}-Il-38^{flf}* ($n = 12$) mice in 60 days.
- I Representative histological photographs of skin stained with hematoxylin-eosin (H&E) from *Il-38^{flf}* ($n = 5$) and *K14^{Cre/+}-Il-38^{flf}* ($n = 5$) mice. Scale bars represent 100 μm . The graph shows the quantification of epidermal thickness.
- J Skin barrier-dependent dye exclusion assay using toluidine blue in *Il-38^{flf}* mice ($n = 5$) and *K14^{Cre/+}-Il-38^{flf}* littermate ($n = 5$) at birth.
- K TEWL assay measured on ventral surface of newborn *Il-38^{flf}* mice ($n = 6$) and *K14^{Cre/+}-Il-38^{flf}* littermate ($n = 6$).
- L Representative micrographs of cornified cell envelopes from *Il-38^{flf}* ($n = 4$) and *K14^{Cre/+}-Il-38^{flf}* ($n = 4$) mice. Scale bars represent 100 μm . The graph shows the number of cornified cell envelopes per square millimeter.
- M Representative immunohistochemical staining micrographs of CD45 in the skin of *Il-38^{flf}* ($n = 5$) and *K14^{Cre/+}-Il-38^{flf}* ($n = 5$) mice. Scale bars represent 100 μm . The graph shows average intensities of CD45 per high-powered field.

Data information: Error bars represent the mean \pm SD. All data are biological replicates. ns, not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; P values were calculated using Student's t -test.

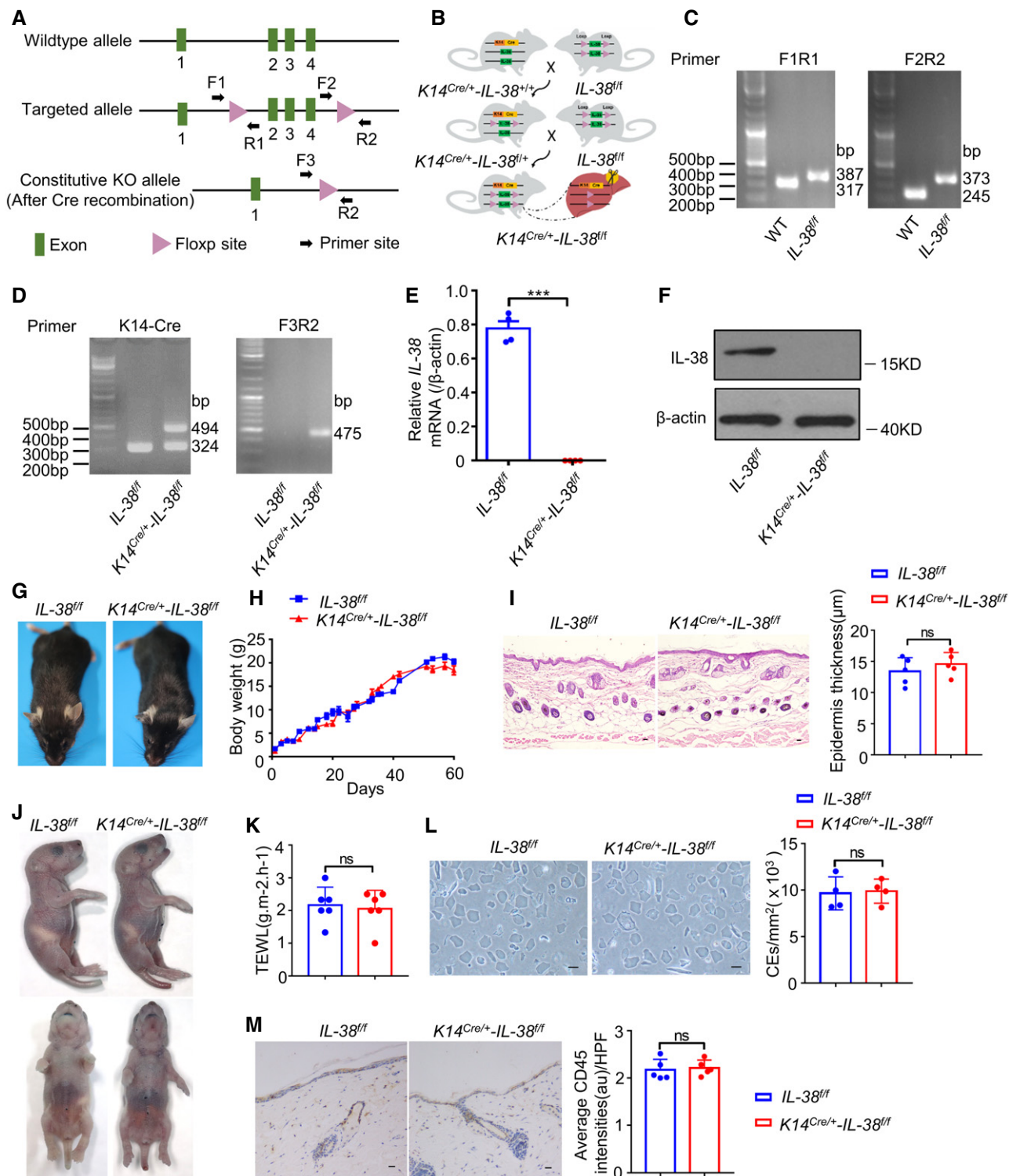


Figure EV2.

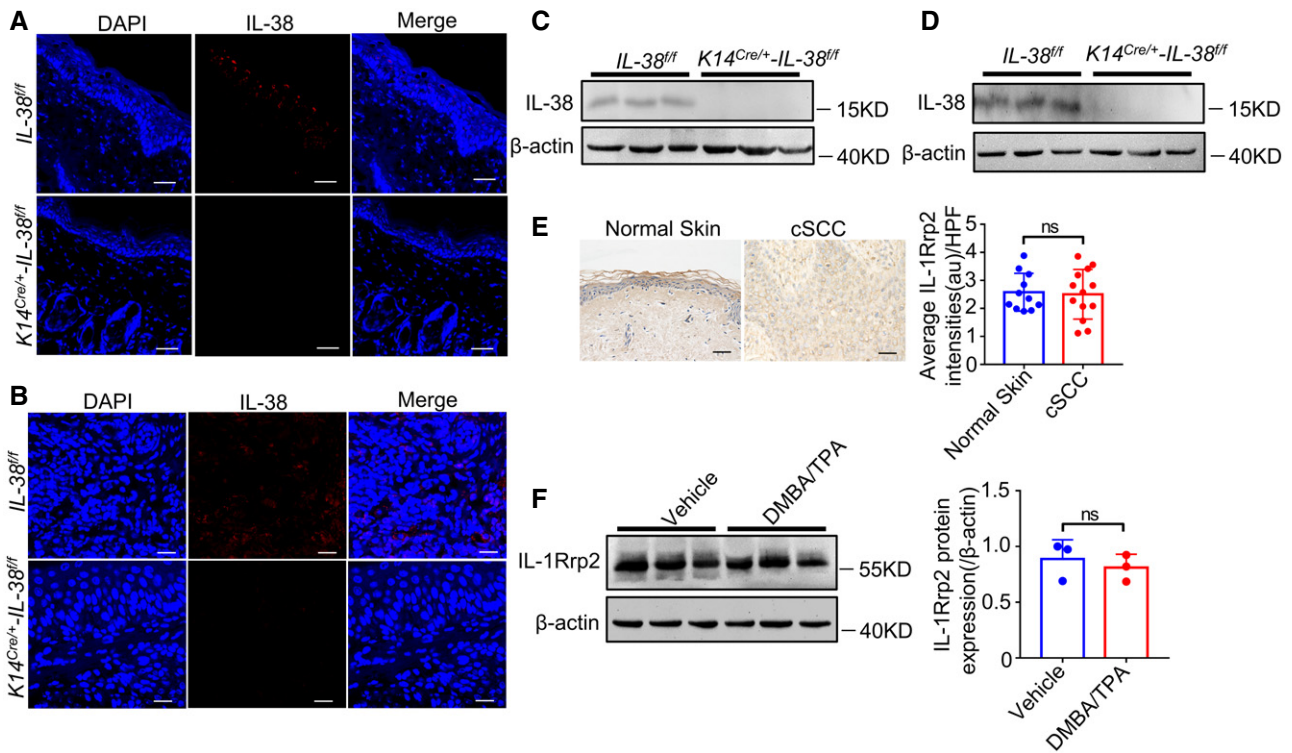


Figure EV3. Expression of IL-38 and IL-1Rrp2 in tissues.

A–D The dorsal hair of normal C57/BL6 mice was shaved and treated with DMBA/TPA twice a week for 3 weeks to induce the skin inflammation (A and C). (A) Representative immunofluorescent staining micrographs of IL-38 in the skin of *Il-38^{fl/fl}* and *K14^{Cre/+}-Il-38^{fl/fl}* mice. Scale bars represent 100 μ m. (C) Relative expression of IL-38 in the skin of *Il-38^{fl/fl}* ($n = 3$) and *K14^{Cre/+}-Il-38^{fl/fl}* ($n = 3$) mice was detected by western blot. The dorsal hair of normal C57/BL6 mice was shaved and treated with DMBA/TPA twice a week for 32 weeks to induce the skin tumors (B and D). (B) Representative immunofluorescent staining micrographs of IL-38 in the tumors of *Il-38^{fl/fl}* and *K14^{Cre/+}-Il-38^{fl/fl}* mice. Scale bars represent 100 μ m. (D) Relative expression of IL-38 in the tumors of *Il-38^{fl/fl}* ($n = 3$) and *K14^{Cre/+}-Il-38^{fl/fl}* ($n = 3$) mice was detected by western blot.

E Representative immunohistochemical staining micrographs of IL-1Rrp2 from normal patients ($n = 11$) and tumors of cSCC patients ($n = 13$). Scale bars represent 100 μ m. The graph shows average intensities of IL-1Rrp2 per high-powered field in tissues.

F Relative expression of IL-1Rrp2 in mouse normal skin ($n = 3$) and DMBA/TPA-induced tumors ($n = 3$). The graph shows the quantification of mean IL-1Rrp2 expression in tissues.

Data information: Error bars represent the mean \pm SD. All data are biological replicates. ns, not significant; P values were calculated using Student's t -test.

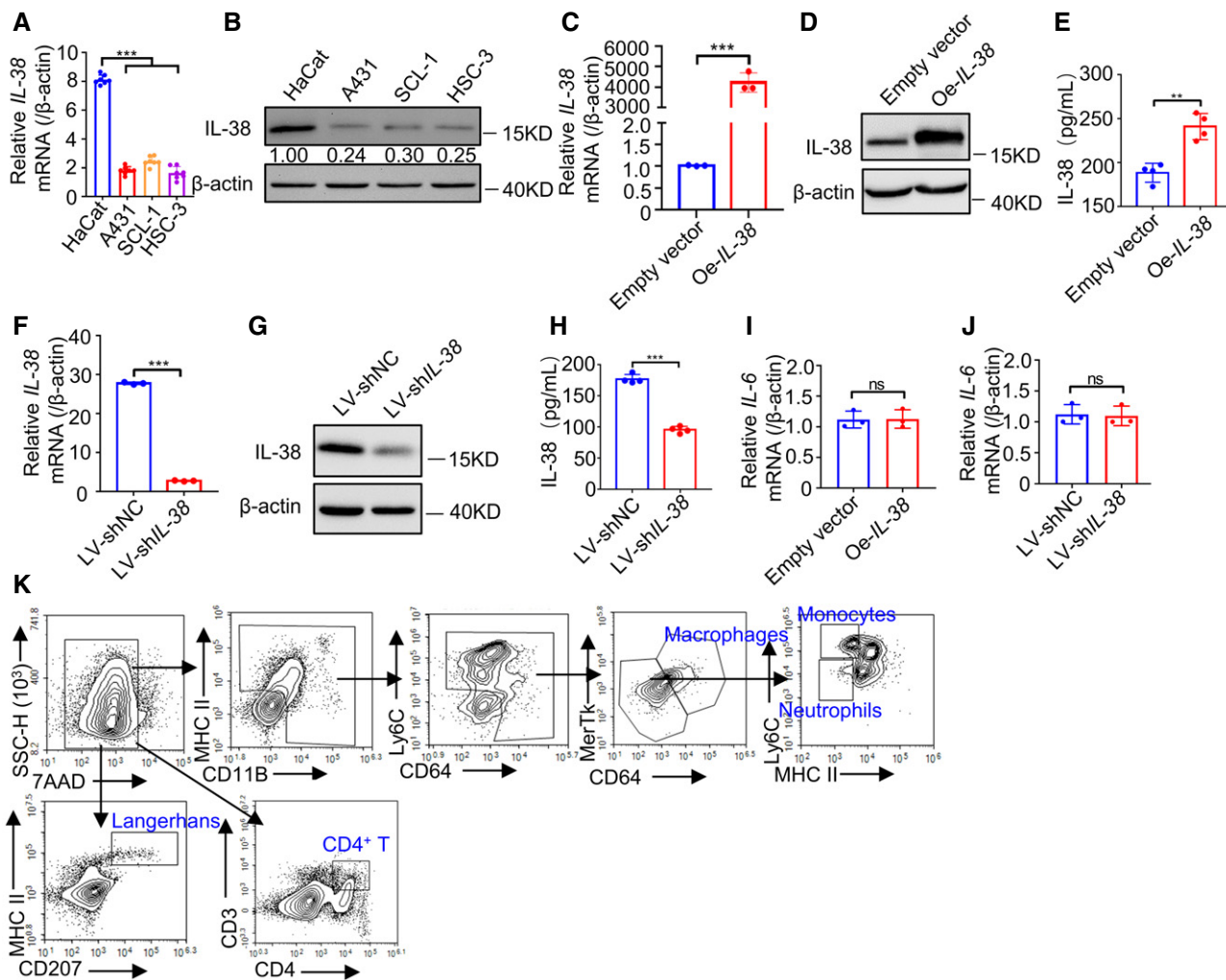


Figure EV4. Expression of IL-38 and IL-6 in SCC cell lines and the gating strategy for flow cytometry.

- A Relative expression of *IL-38* in normal skin cells ($n = 7$) and SCC cells ($n = 7$) determined using qPCR.
- B Relative expression levels of IL-38 in normal skin and SCC cells were detected using western blot.
- C–E The *IL-38* overexpression cell line was constructed by transfecting A431 cells with the pcDNA3.1-*IL-38* vector expressing IL-38 and pcDNA3.1 empty vector. (C) Relative expression of *IL-38* was determined using qPCR. (D) Relative expression of IL-38 was detected using western blotting. (E) The secretion of IL-38 was measured using ELISA.
- F–H Lentiviruses containing IL-38 shRNA or Negative Control shRNA were used to infect A431 cells. (F) Relative expression of *IL-38* was determined using qPCR. (G) Relative expression of IL-38 was detected using western blot. (H) IL-38 secretion was measured using ELISA.
- I Relative expression of *IL-6* in *IL-38*-overexpressed A431 cells ($n = 3$) was determined using qPCR.
- J Relative expression of *IL-6* in *IL-38*-knockdown A431 cells ($n = 3$) was determined using qPCR.
- K The flow cytometry gating strategy for immune cell detection in DMBA/TPA-treated skin.

Data information: Error bars represent the mean \pm SD. All data are biological replicates. ns, not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; P values were calculated using one-way ANOVA (A) or Student's t -test (C, E, F, and H–J).

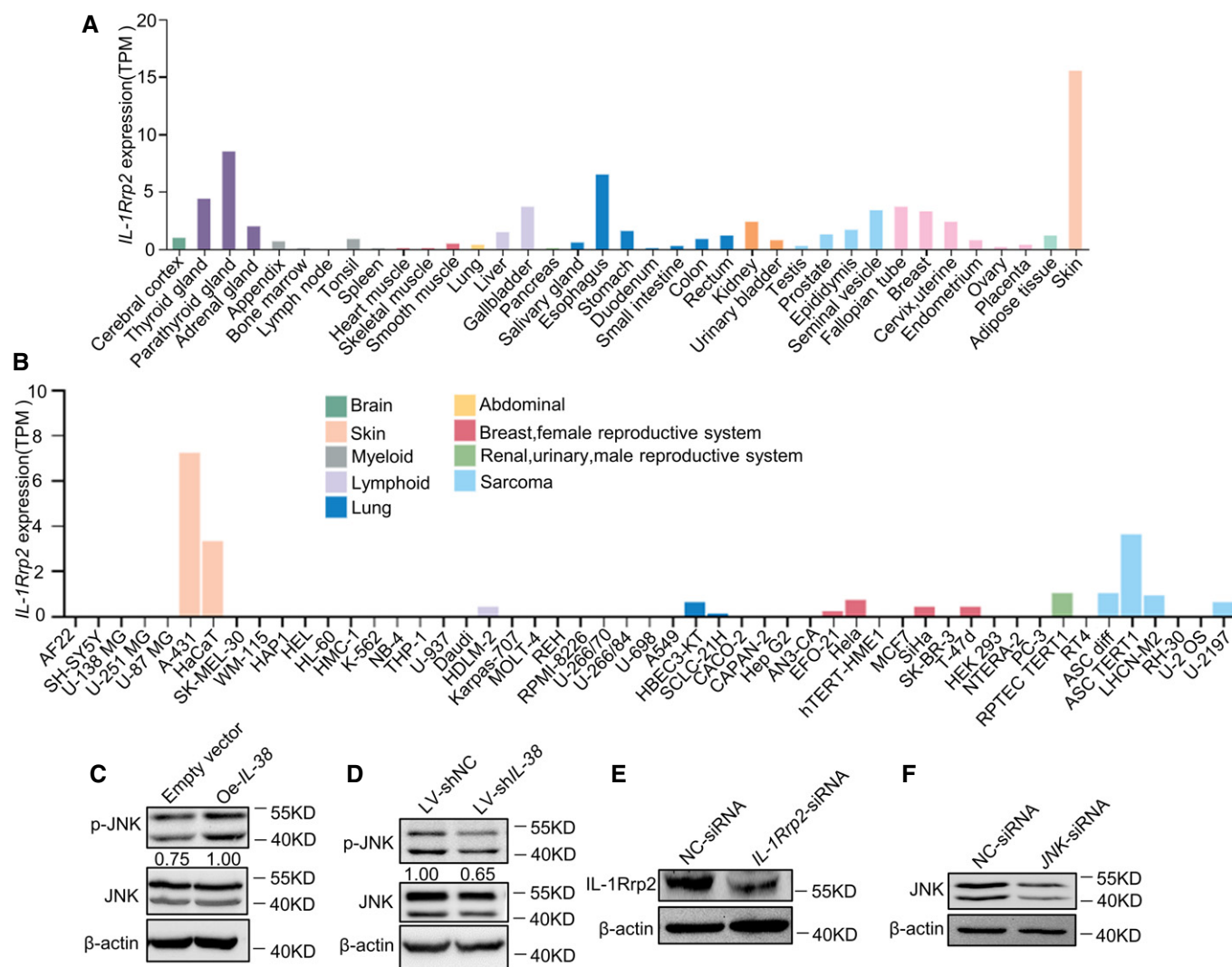


Figure EV5. Expression of IL-1Rrp2 in tissues and cell lines and the effect of IL-38 on JNK activation in A431 cell line.

A, B Relative expression of *IL-1Rrp2* in human normal tissues (A) or cell lines (B) based on TPM values. Data were obtained from the Human Protein Atlas Dataset available from [proteinatlas.org](https://www.proteinatlas.org).

C Cell extracts prepared from A431 cells transfected with a mock mammalian expression vector (left) or an expression vector encoding IL-38 (right), were blotted with anti-phospho-JNK, anti-JNK, or anti- β -actin antibodies.

D Cell extracts prepared from A431 cells infected with lentiviruses containing Negative Control shRNA (left) or *IL-38* shRNA (right) were probed using anti-phospho-JNK, anti-JNK, or anti- β -actin antibodies.

E The expression of IL-1Rrp2 in A431 cells transfected with *IL-1Rrp2*-siRNA was detected using western blot.

F The expression of JNK in A431 cells transfected with *JNK*-siRNA was detected using western blot.