

SUPPLEMENTARY FIGURES:

Figure S1

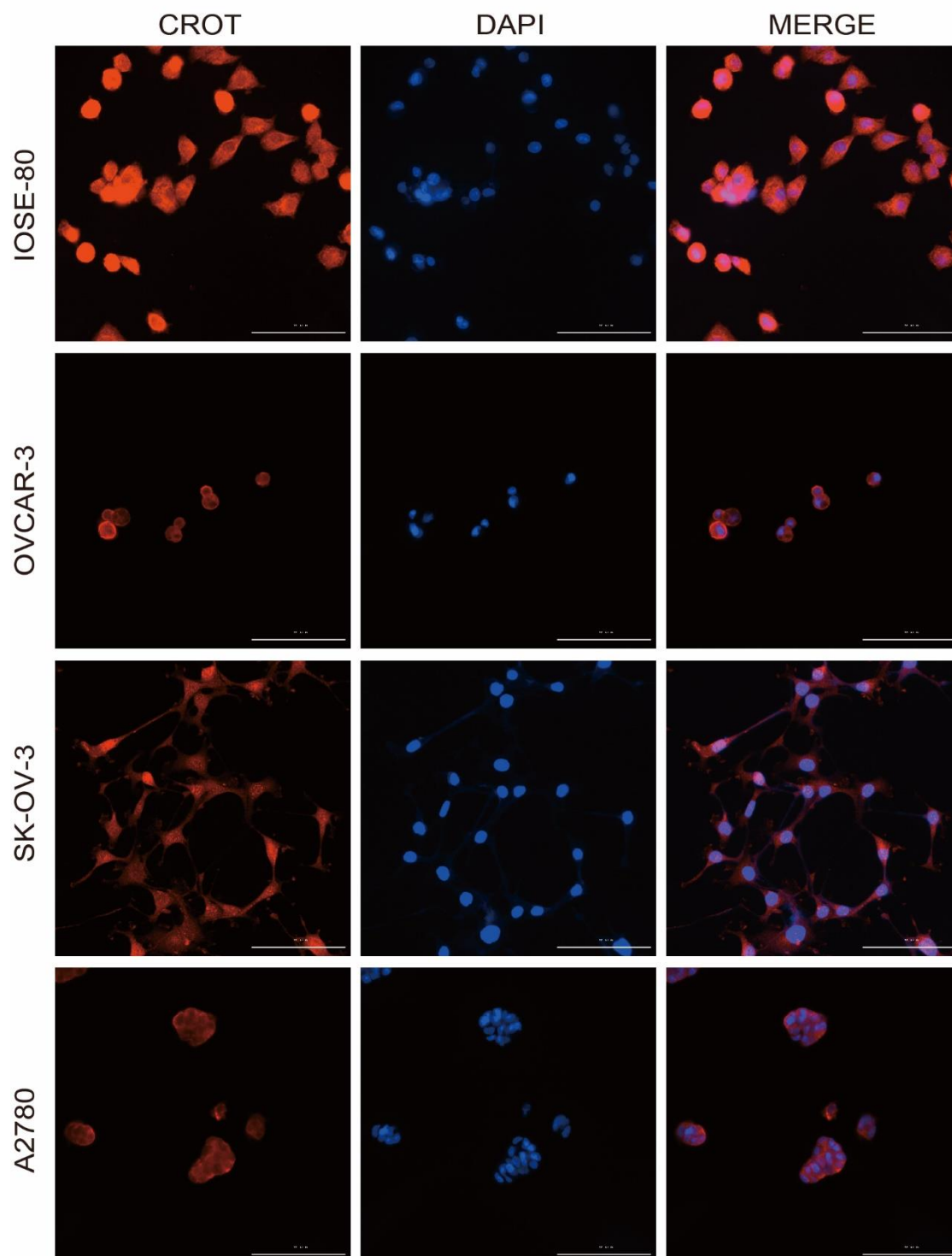


FIGURE S1 | Representative images of CROT in immortalized ovarian surface epithelium cell lines-80 (IOSE-80) and epithelial ovarian cancer cell lines (OVCAR-3, SK-OV-3, and A2780) by immunofluorescence. Original magnification, $\times 400$; Scale bar, 100 μm .

FIGURE S2 | GO term and KEGG enrichment analyses of CROT in OC. **(A)** GO term annotation of biological processes (BP). **(B)** GO term annotation of cellular components (CC) based on the data from GSE63885. **(C)** GO term annotation of molecular function (MF) analysis. **(D)**. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of co-expression genes with CROT. The data were acquired from the GSE63885 dataset.

Figure S3

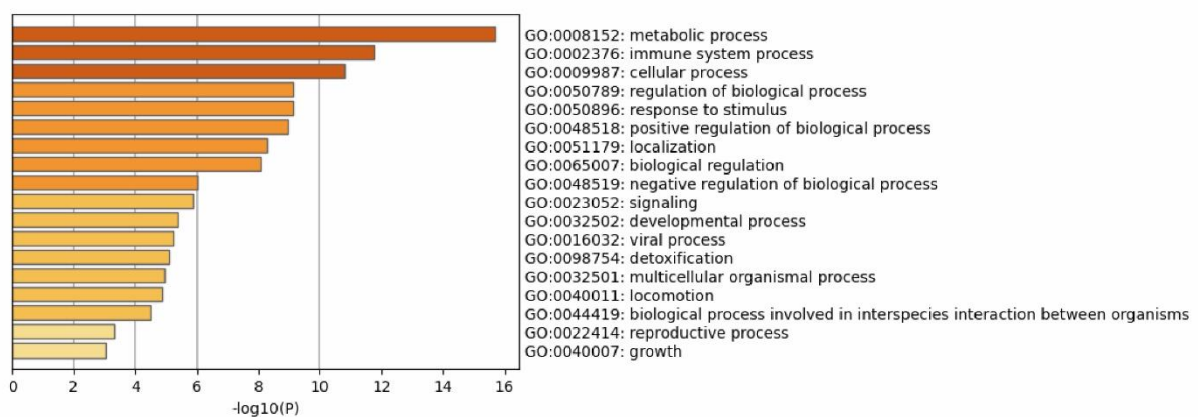


FIGURE S3 | Metascape analysis of co-expression genes with CROT. The data were acquired from the GSE26712 dataset (<https://metascape.org/gp/index.html#/main/step1>).

Figure S4

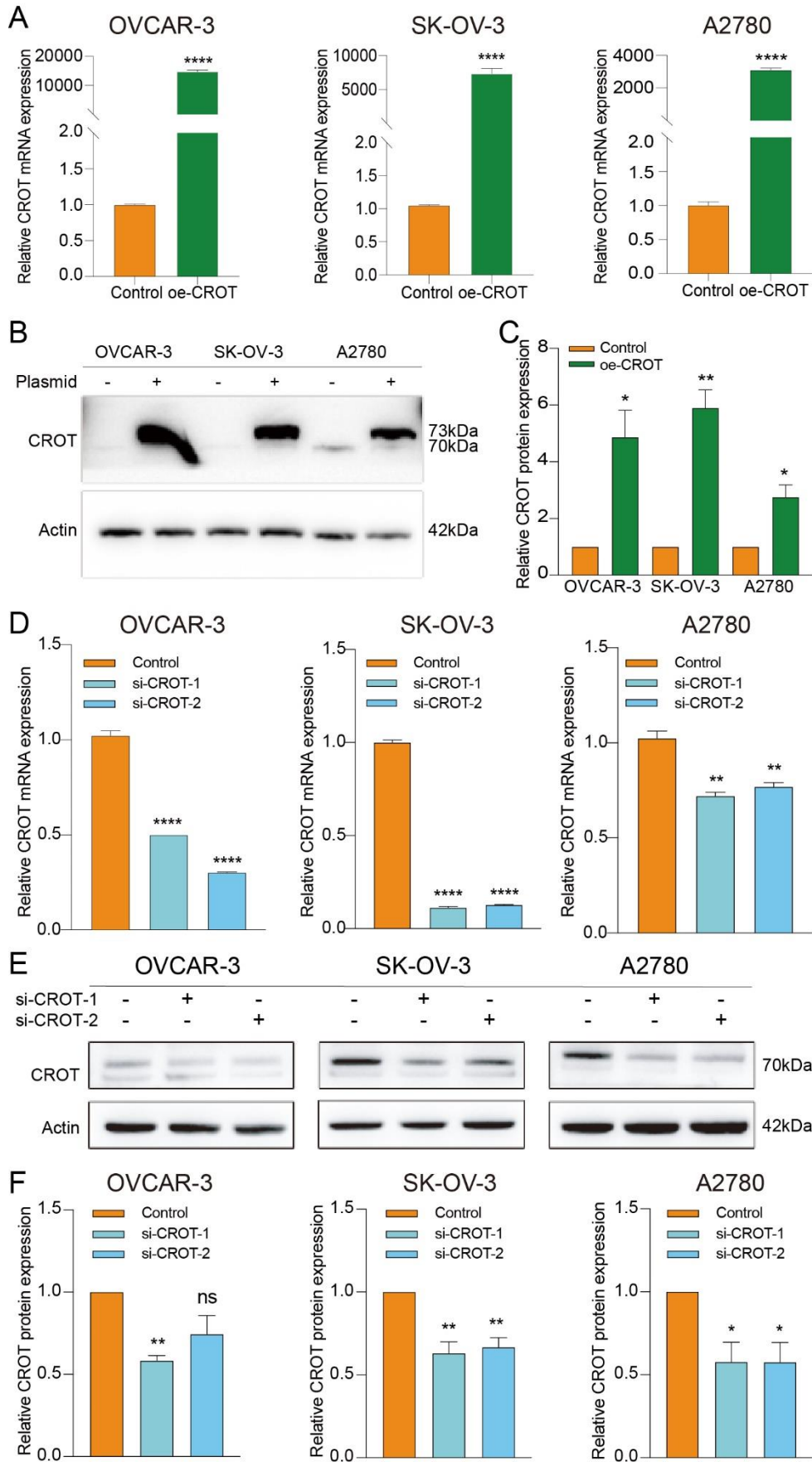


FIGURE S4 | Detection of CROT mRNA and protein expression by qRT-PCR and Western blot. **(A-C)** Expression of CROT mRNA and protein in OVACR-3, SK-OV-3, and A2780 cells after CROT-overexpressing plasmid (oe-CROT) transfection for 48 h. **(D-F)** Expression of CROT mRNA and protein detected in OVACR-3, SK-OV-3, and A2780 cells after CROT-siRNAs (si-CROT) transfection for 48 h. Assays were repeated at least three times. Data were presented as mean \pm SEM. *, $P < 0.05$; **, $P < 0.01$; ****, $P < 0.0001$; ns, not significant.

Figure S5

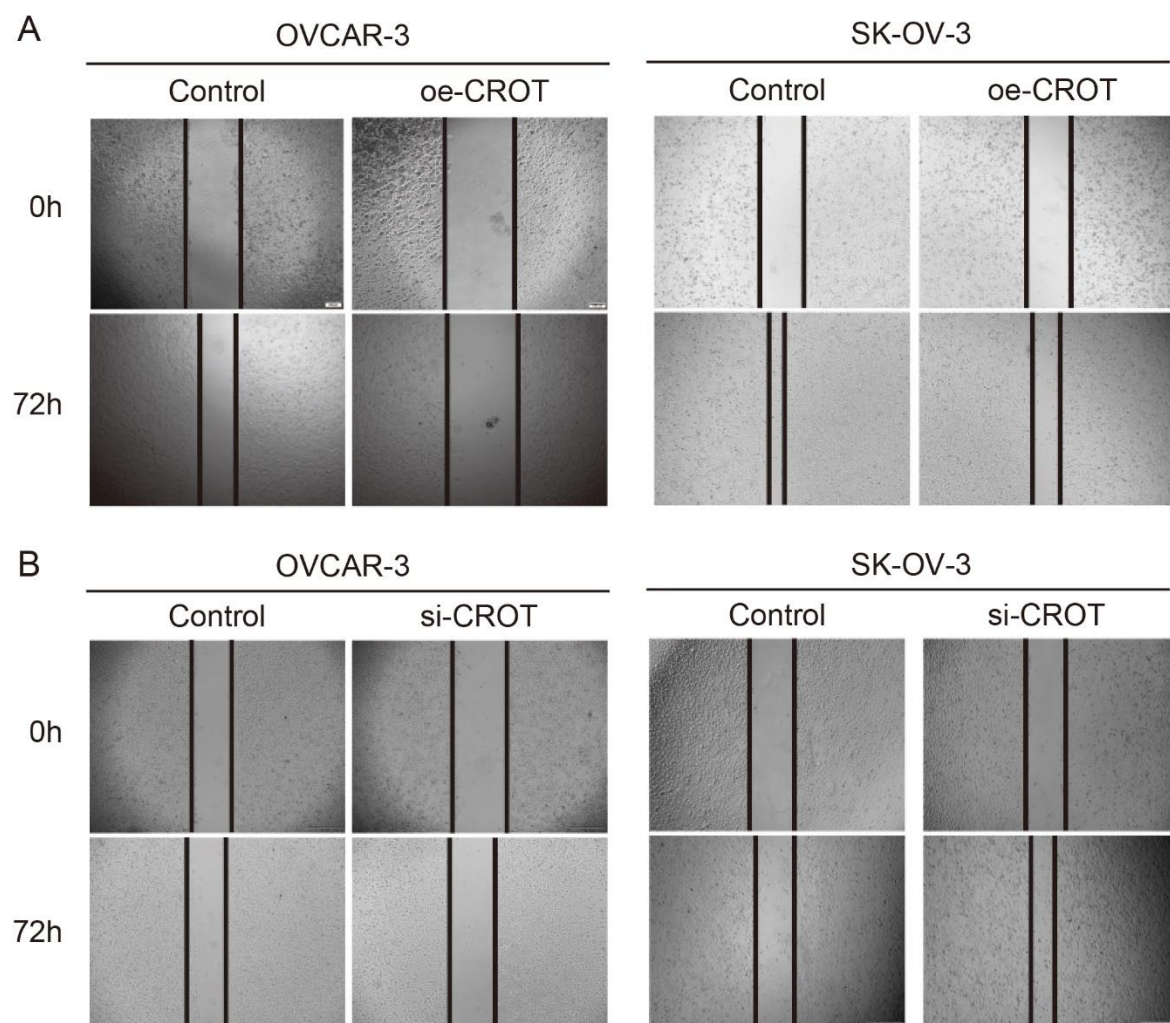


FIGURE S5 | Detection of cell migration by the wound healing assay. **(A)** Measurement of wound healing in OVCAR-3 and SK-OV-3 cells after CROT-overexpressing plasmid (oe-CROT) transfection for 0 and 72 h. **(B)** Measurement of wound healing in OVCAR-3 and SK-OV-3 cells after CROT-siRNAs (si-CROT) transfection for 0 and 72 h. Negative controls were compared. Scale bar, 100 μ m.

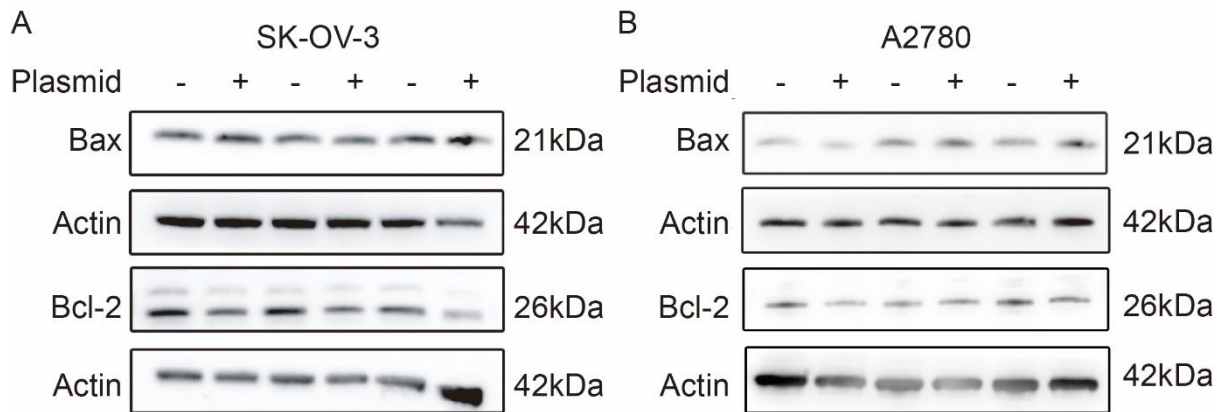


FIGURE S6 | Detection of Bax and Bcl-2 proteins by Western blot. (A-B) SK-OV-3 cells and A2780 cells were transfected with CROT-overexpressing plasmid (oe-CROT) for 48 h.

Figure S7

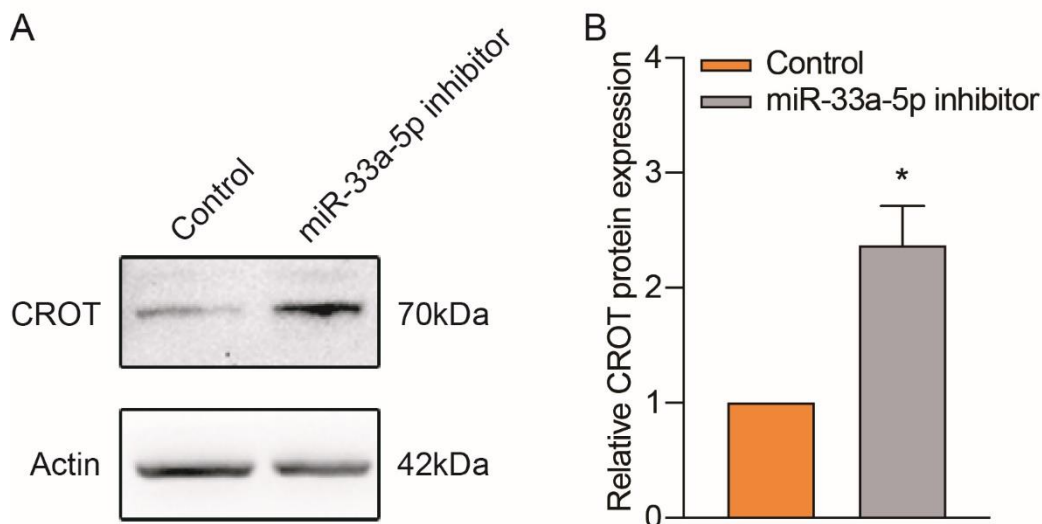


FIGURE S7 | Detection of CROT protein in SK-OV-3 cells. (A) Protein was detected by Western blot after the treatment of miR-33a-5p inhibitors for 48 h. (B) The histogram shows the densitometric analyses of protein bands in A (n=3). Data were presented as mean \pm SEM. *, $P < 0.05$.

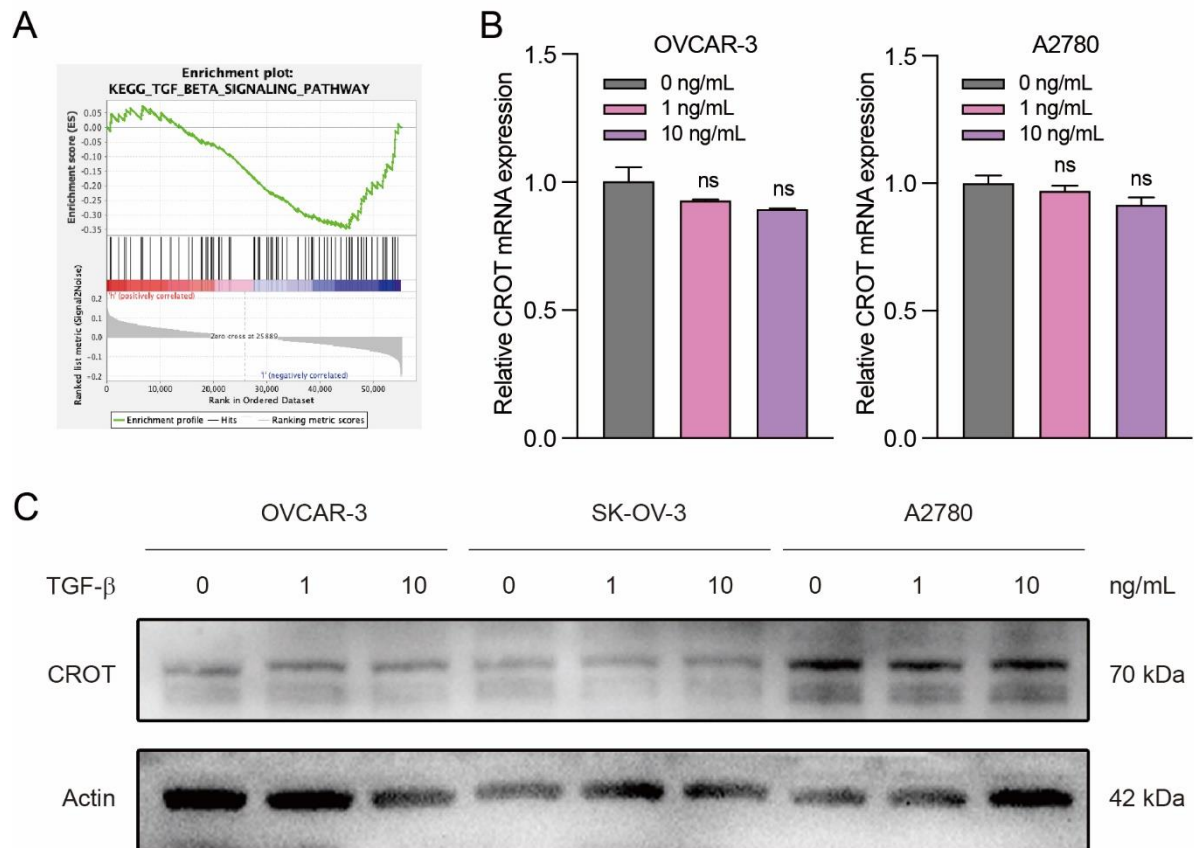


FIGURE S8 | Effect of TGF- β on CROT expression. **(A)** GSEA analysis of the association between the enrichment of the TGF- β signaling pathway and CROT expression based on the data from the TCGA-OV database. **(B-C)** Detection of CROT mRNA and protein expression in OVCAR-3 and A2780 cells after the administration of TGF- β 1 (0, 1, or 10 ng/ml) by qRT-PCR and Western blot. Data were presented as mean \pm SEM. GSEA, gene set enrichment analysis; ns, not significant.