Figure S1. RBM15 expression in ovarian cancer. (A) Detection of RBM15 mRNA expression in normal ovarian epithelial tissues and ovarian malignant tumor tissues. Data were extracted from GEO datasets (GSE14407 and GSE12470) (https://www.ncbi.nlm.nih.gov/geo/). (B) Detection of RBM15 protein expression in normal ovarian epithelial tissues and ovarian primary malignant tumor tissues. Data were extracted from the CPTAC database (http://ualcan.path.uab.edu/index.html). (C) RBM15 protein was detected by immunohistochemistry staining. The SI of RBM15 was measured by the sum of the percentage of positive cells and the intensity score. The high and low expression groups were defined by SI of >5 and ≤5, respectively. Representative images are shown. Magnification, x400; scale bar, 20 μm. (D) Comparison of RBM15 expression in immunohistochemistry among 39 pairs of ovarian malignant tumor tissues and adjacent non-cancerous tissues. An unpaired Student's t-test was used in (A) and (B) and the Mann-Whitney test was used in (D). Data presented as mean ± SD. RBM15, RNA binding motif protein 15; GEO, Gene Expression Omnibus; SI, staining index; CPTAC, Clinical Proteomic Tumor Analysis Consortium.

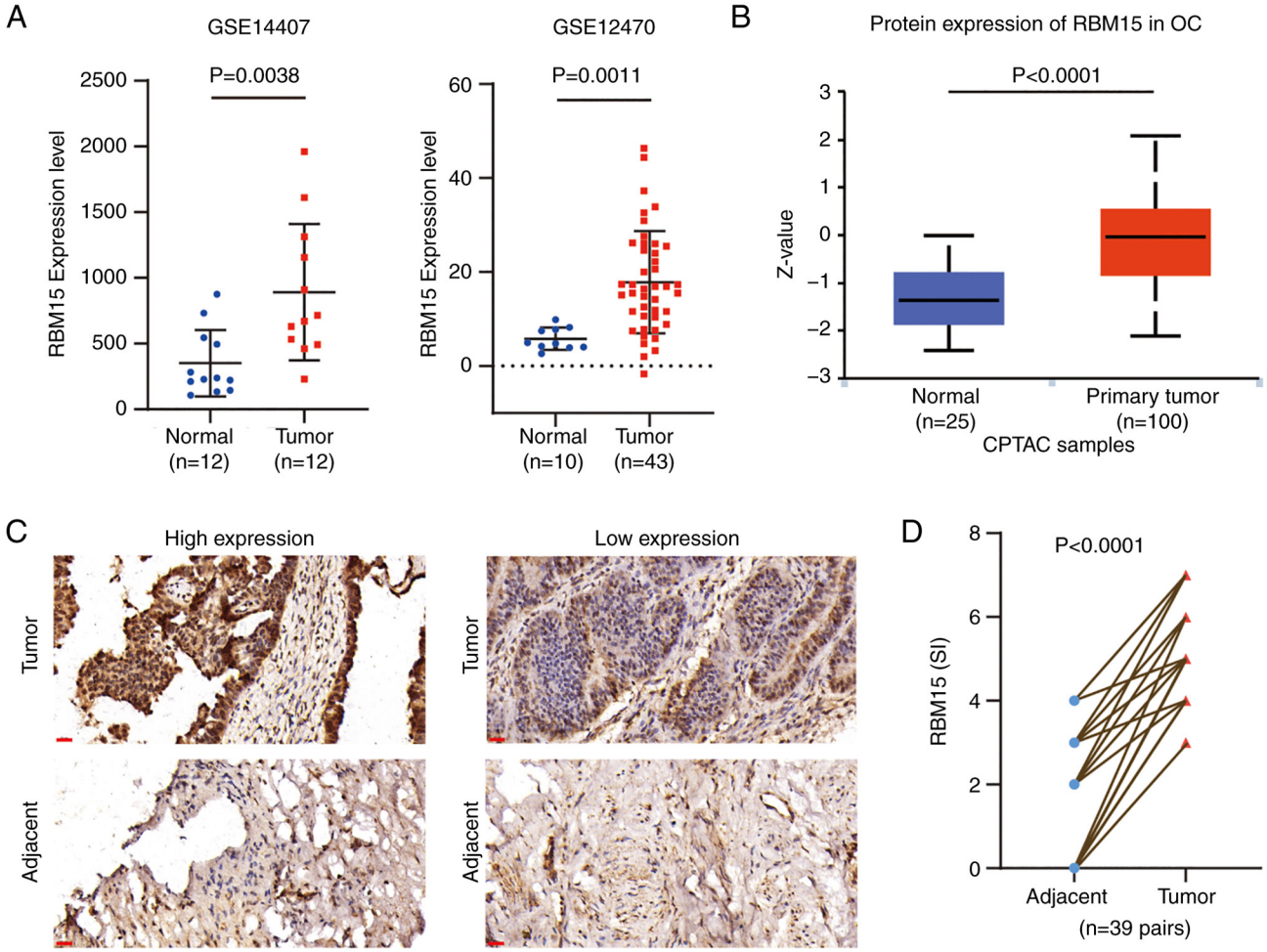

Figure S2. Association of RBM15 expression with the survival of ovarian cancer patients. (A) Kaplan-Meier curves showed the association between RBM15 expression and OS. (B) Kaplan-Meier curves showed the association between RBM15 expression and DFS time. (C and D) Survival analysis comparing the high expression to low expression of RBM15 from the dataset (1555760_a_at) by Kaplan-Meier Plotter. A Logrank test was used for statistical analysis. RBM15, RNA binding motif protein 15; OS, overall survival; DFS, disease-free survival; PFS, progression-free survival; HR, hazard ratio.

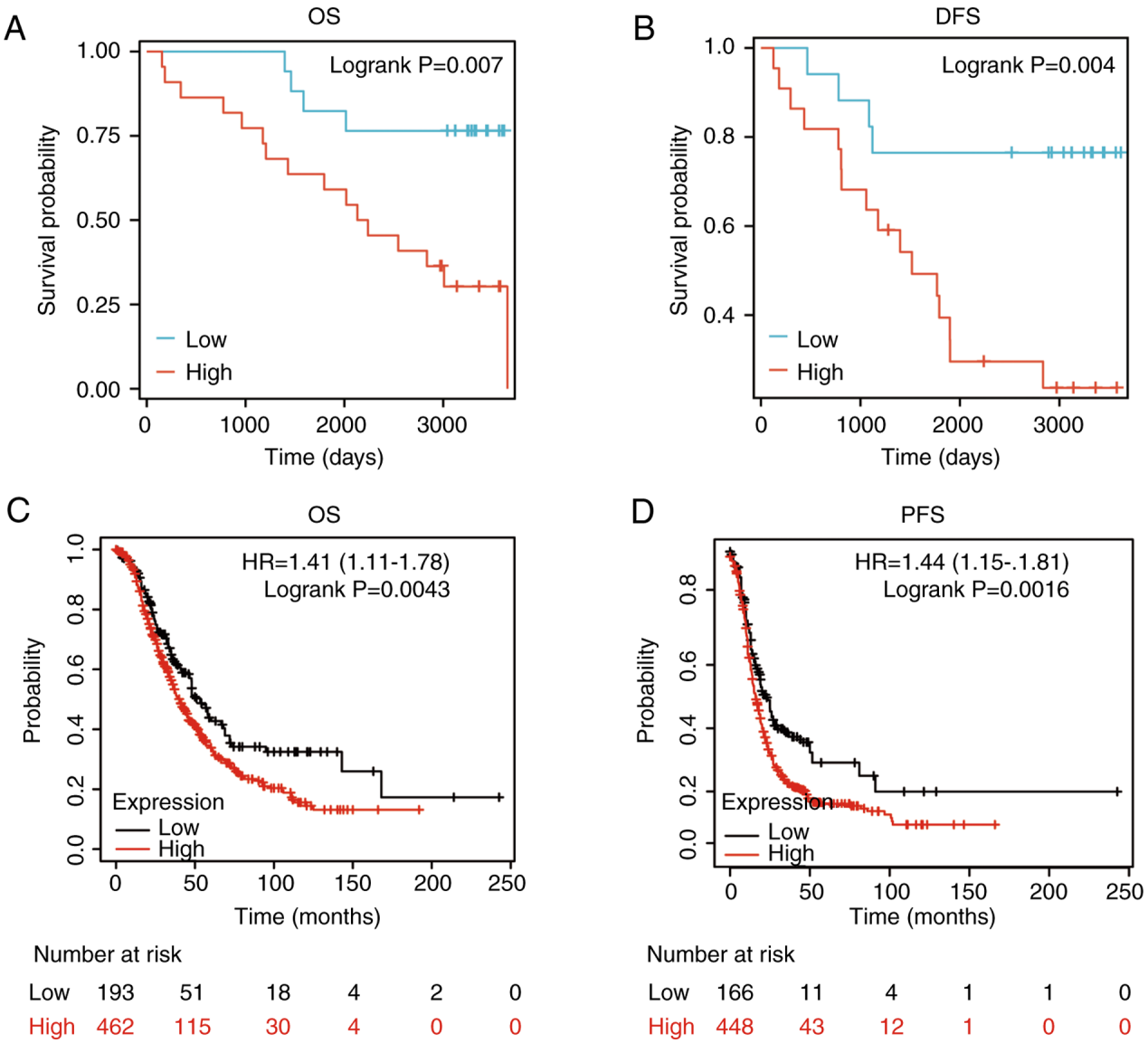

Figure S3. Expression of RBM15 in paclitaxel-sensitive (A2780, SK-OV-3) and -resistant (A2780-PTX, SK3R-PTX) cells. (A) RBM15 mRNA expression detected by RT-qPCR. One-way ANOVA followed by the Tukey test was used. Data presented as mean ± SD (n=3). (B) RBM15 protein expression detected by western blotting. Representative images are shown. (C) Semiquantitative analysis of membranes in (B); one-way ANOVA followed by the Tukey test was used. Data presented as mean ± SD (n-3). (D and E) Immunofluorescence staining of RBM15 protein. Magnification, x200. RBM15, RNA binding motif protein 15.

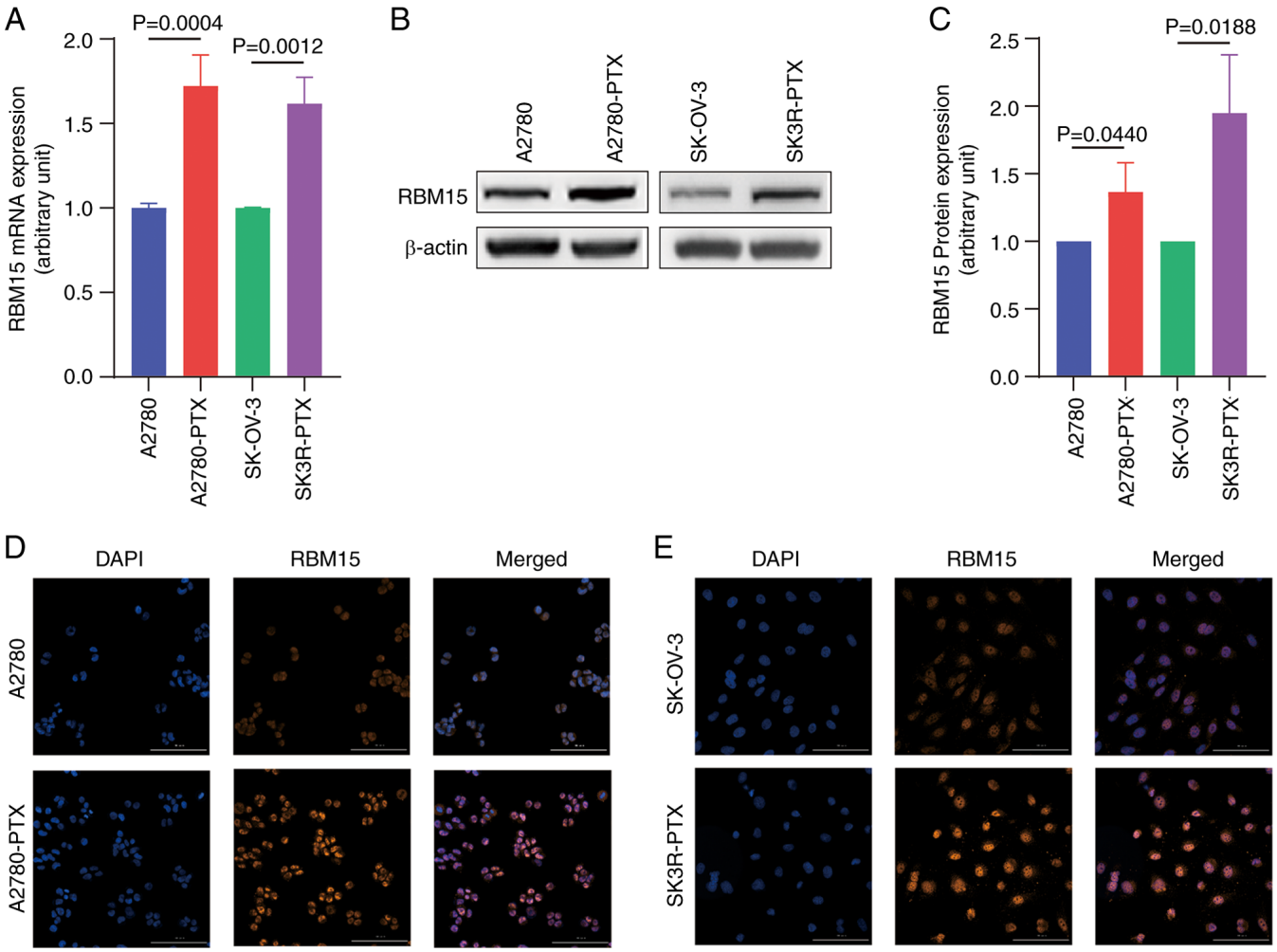

Figure S4. Validation of RBM15 knockdown and overexpression. (A) Validation of knockdown efficiency after transfection of three RBM15-siRNAs and detection of RBM15 protein expression in A2780/PTX cells by western blotting. (B) Validation knockdown efficiency after A2780-PTX and SK3R-PTX cells stably infected with sh-NC or sh-RBM15 and detection of RBM15 protein expression by western blotting. (C) Validation of overexpressed RBM15 mRNA by RT-qPCR after transfection of oe-NC or oe-RBM15. Two-way ANOVA followed by the Sidak test was used. Data presented as mean ± SD (n=3). ****P<0.0001. (D) Validation of overexpressed RBM15 protein by western blotting after transfection of oe-NC or oe-RBM15. (E) Effect of si-RBM15 on cyclin D1 expression in SK3R-PTX and A2780-PTX cells. RBM15, RNA binding motif protein 15; si, small interfering; PTX, paclitaxel; NC, negative control; sh, short hairpin; oe, overexpressing.

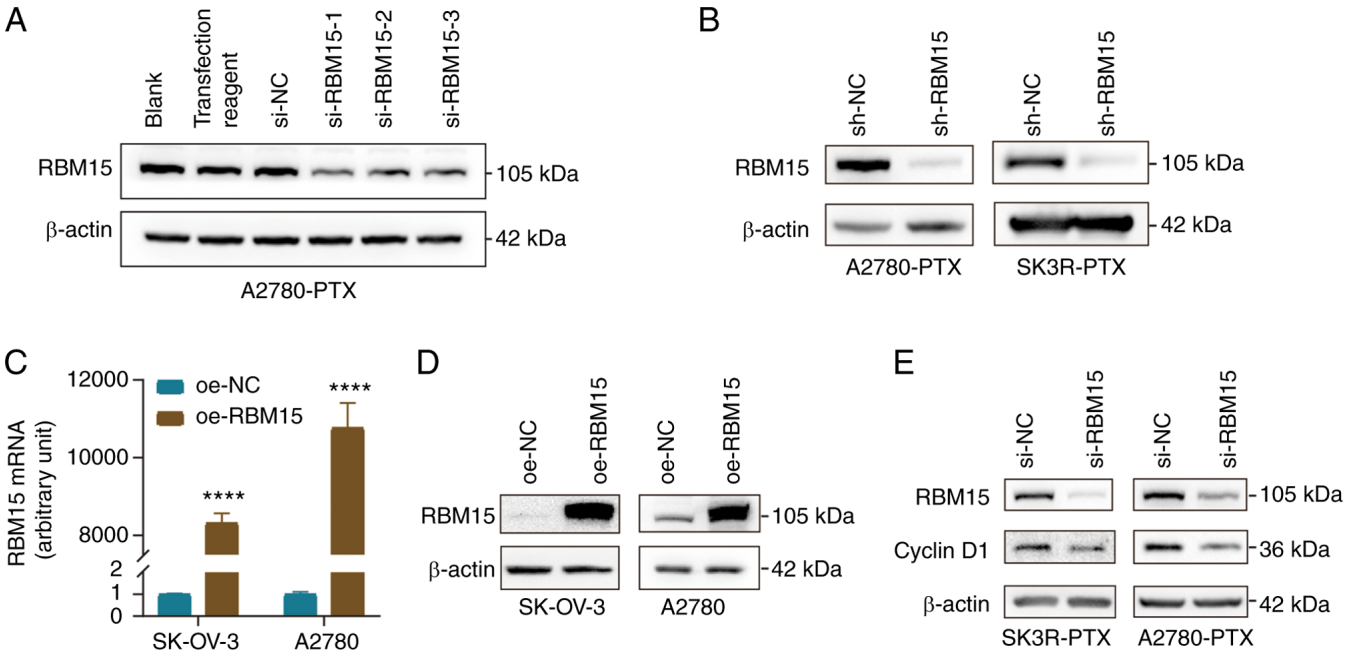

Figure S5. The sensitivity (IC_{50}) analysis of anti-cancer drugs on ovarian cancer treatment. The expression of RBM15 was associated with the sensitivity of (A) veliparib, (B) cyclopamine, (C) elesclomol, (D) pictilisib, (E) lapatinib, (F) temsirolimus and (G) vinblastine. RBM15, RNA binding motif protein 15.

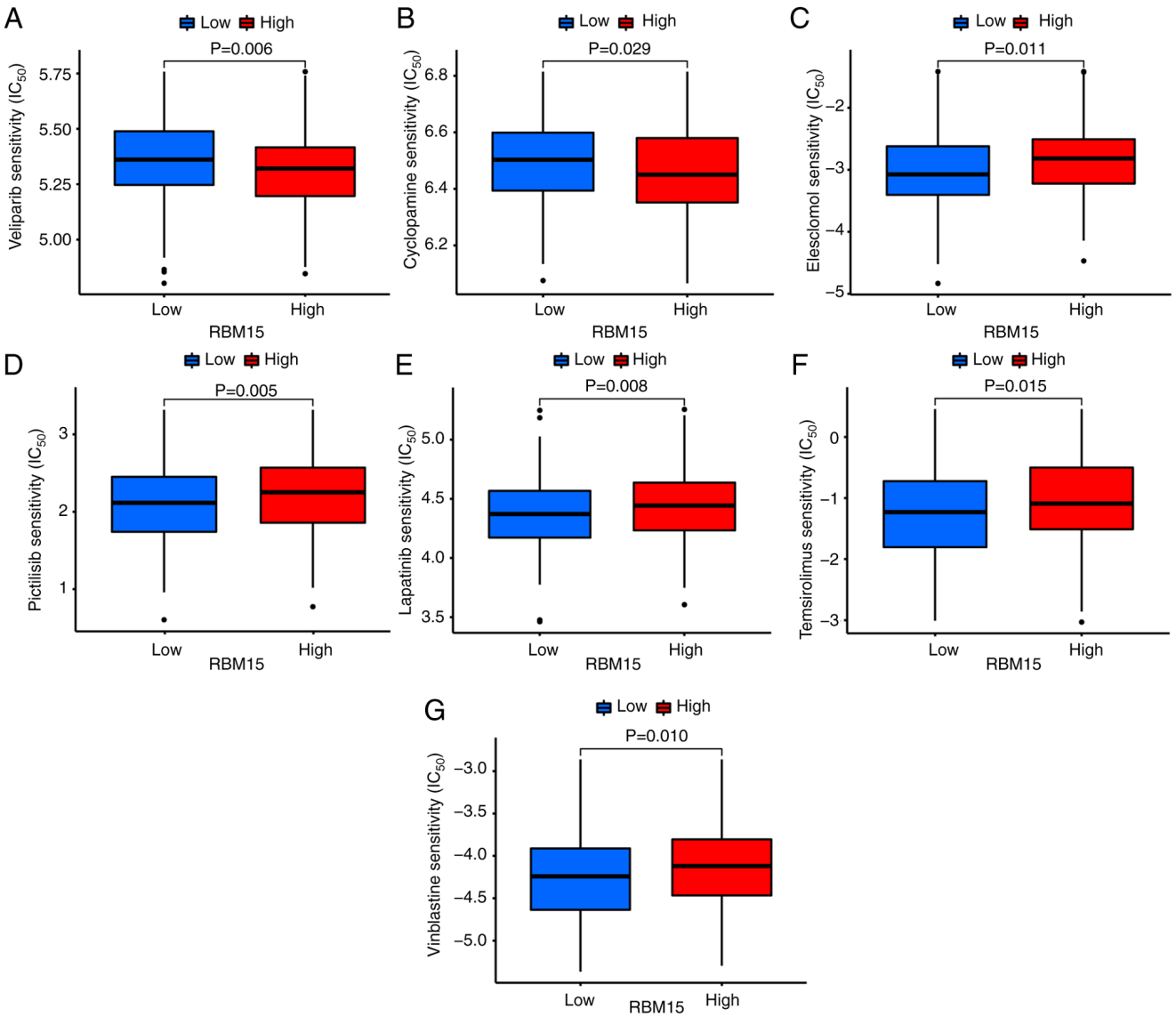

Figure S6. Effect of RBM15 on cell apoptosis detected by flow cytometry. (A) Measurement of apoptotic cells after si-RBM15 and PTX treatment in A2780-PTX and SK3R-PTX cells. (B) Measurement of apoptotic cells after oe-RBM15 and PTX treatment in A2780 and SK-OV-3 cells. (C-F) Histograms show the statistical analyses. One-way ANOVA followed by the Tukey test was used. Data presented as mean ± SD (n=3). ns, not significant (P>0.05). RBM15, RNA binding motif protein 15; si, small interfering; PTX, paclitaxel; oe, overexpressing.

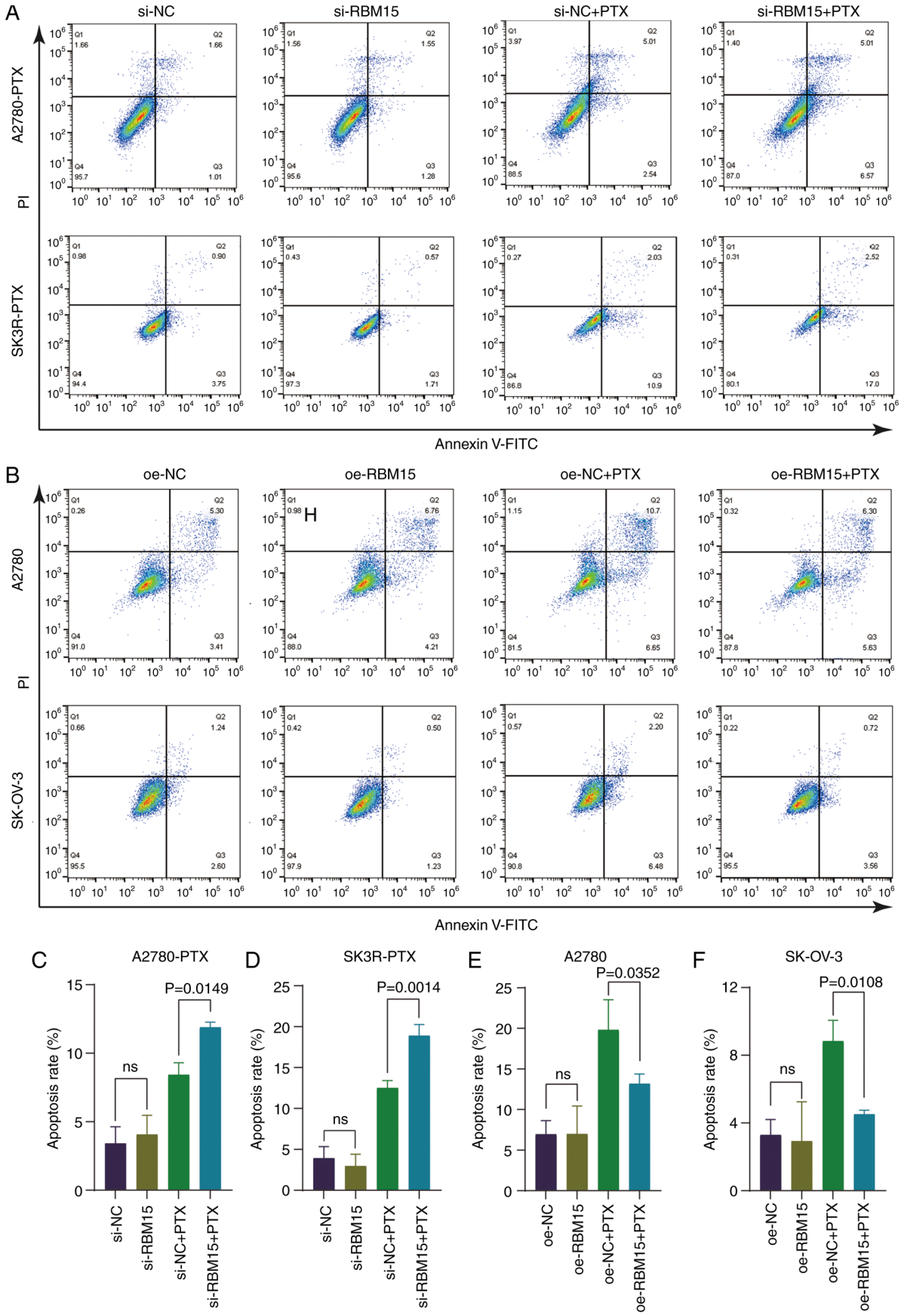

Figure S7. Spheroid formation in A2780-PTX and SK3R-PTX cells. (A) Stable cells were cultured in serum-free DMEM/F12 medium with EGF, bFGF, heparin and B27 supplements for 11 days. Images were captured every two days. Representative images are shown. Magnification, x100; scale bar, 100 μm. (B and C) Measurement of the diameter of each spheroid in (A). Two-way ANOVA followed by the Sidak test was used. Data presented as mean ± SD (n=3). *P<0.05; ****P<0.0001. PTX, paclitaxel; EGF, epidermal growth factor; bFGF, basic fibroblast growth factor; si, small interfering; sh, short hairpin.

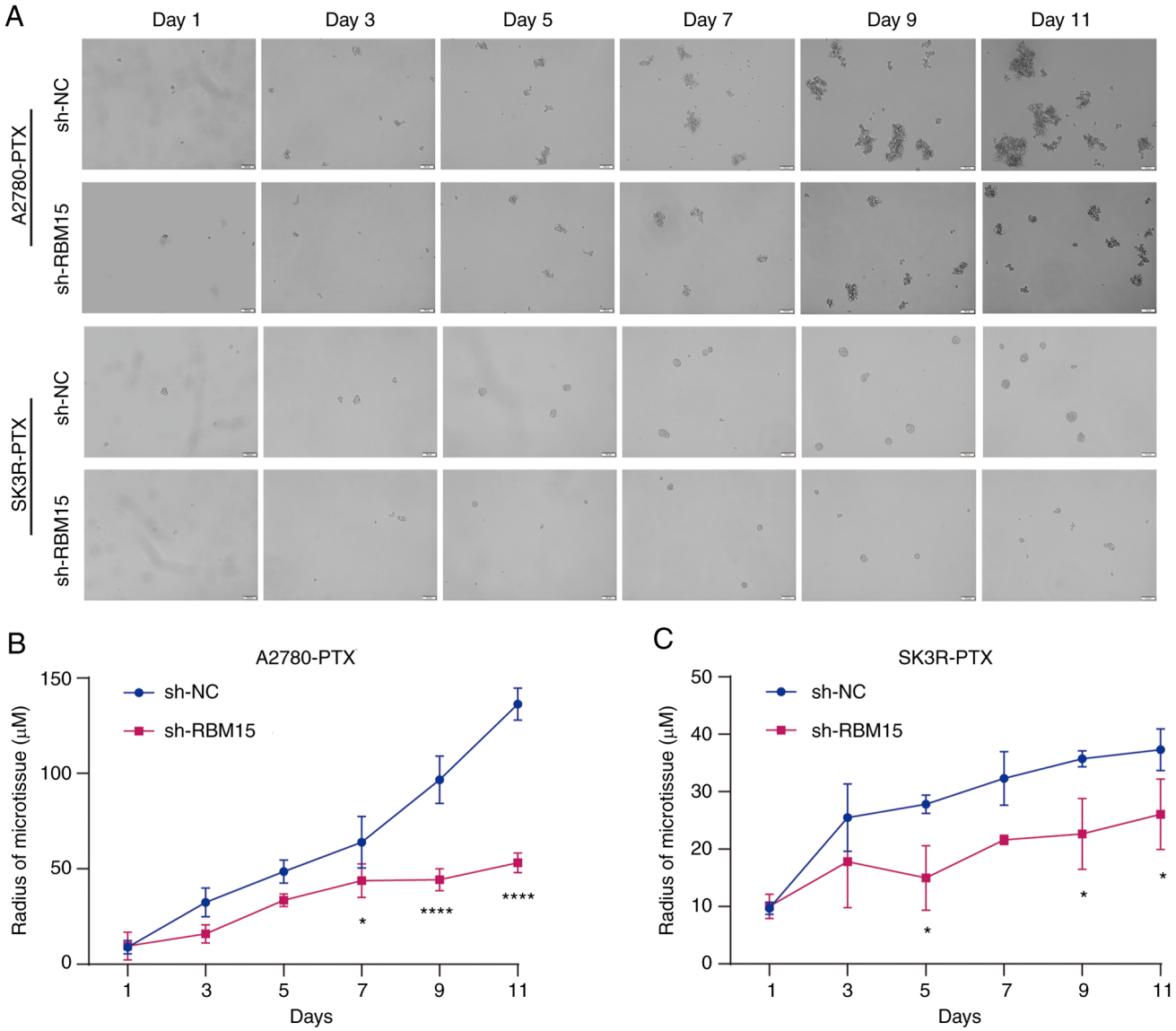

Figure S8. GO and KEGG enrichment analyses. (A) Functional enrichment analysis of intersecting genes positively or negatively correlated with RBM15. The bubble plot showed the top 10 elements significantly enriched in the GO categories: BP, CC and MF. GeneRatio refers to the ratio of the number of genes enriched in the term/pathway to the total number of genes in the terms/pathways. (B) A total of six pathways were acquired from KEGG pathway enrichment analysis. The Spearman test was used for statistical analysis. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cellular component; MF, molecular function.

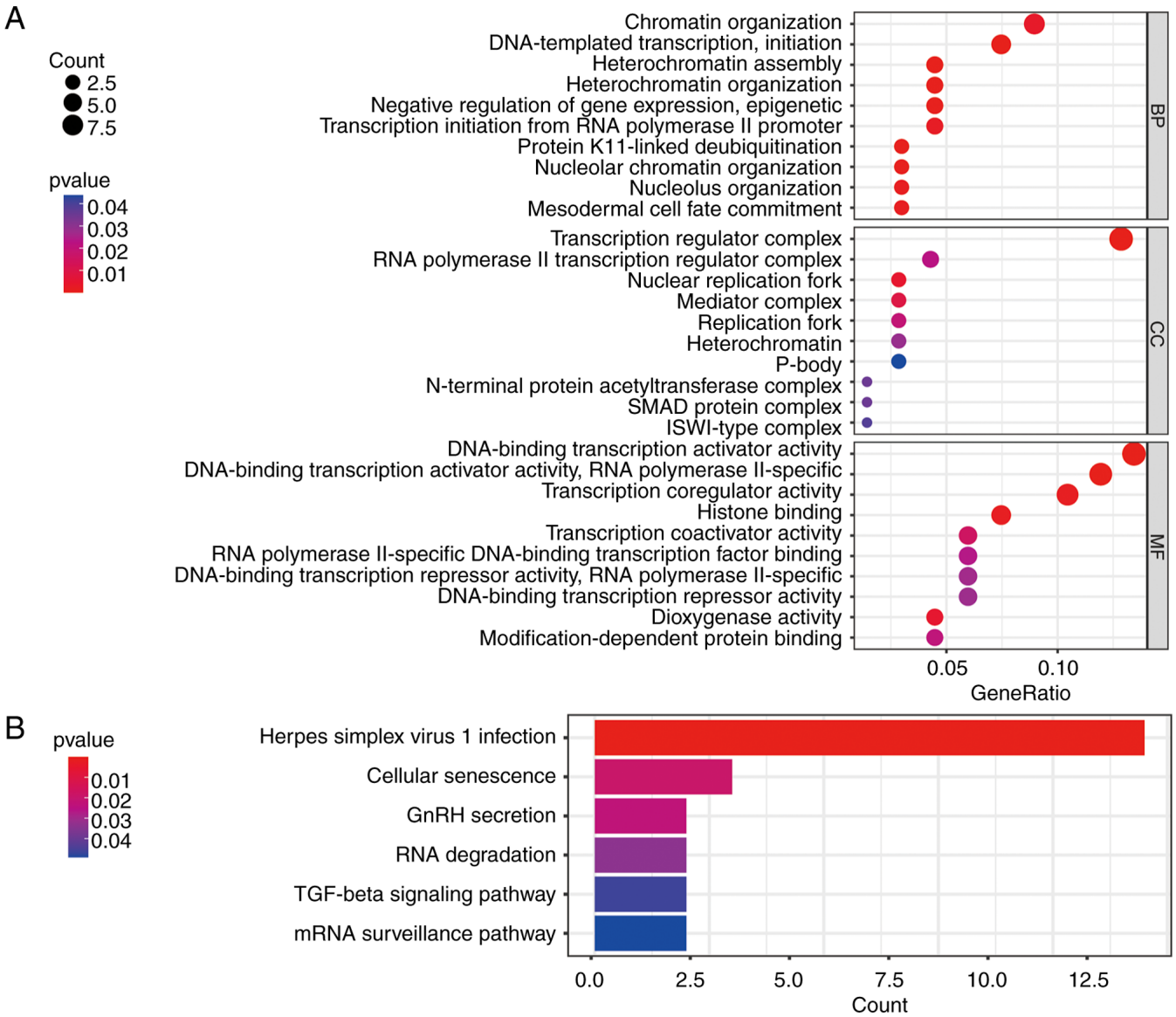

Figure S9. Detection of p-Smad2 and Smad2 protein in SK-OV-3 and SK3R-PTX cells by western blotting. p-, phosphorylated; PTX, paclitaxel.