

Figure S1. PTX resistance and DEG analysis. (A) Cell viability of A2780 and A2780/Taxol after treatment with PTX for 48 h. The IC₅₀ values of A2780 and A2780/Taxol cell were 18.92±0.52 and 636.44±16.22 ng/ml, respectively. The results were repeated three times, and the average was calculated. *P<0.05 and ***P<0.001 vs. A2780. (B) IC₅₀ and RI values of different PTX-resistant cell lines. (C) Venn diagram of DEGs in the RNA-seq data of the present study vs. gene expression in GEO data. (D) Venn diagram of DEGs in A.16PTX vs. A.32PTX vs. A.64PTX vs. A.128PTX cells. DEGs, differentially expressed genes; RI, RNA-seq, RNA-sequencing; GEO, Gene Expression Omnibus; PTX, paclitaxel.

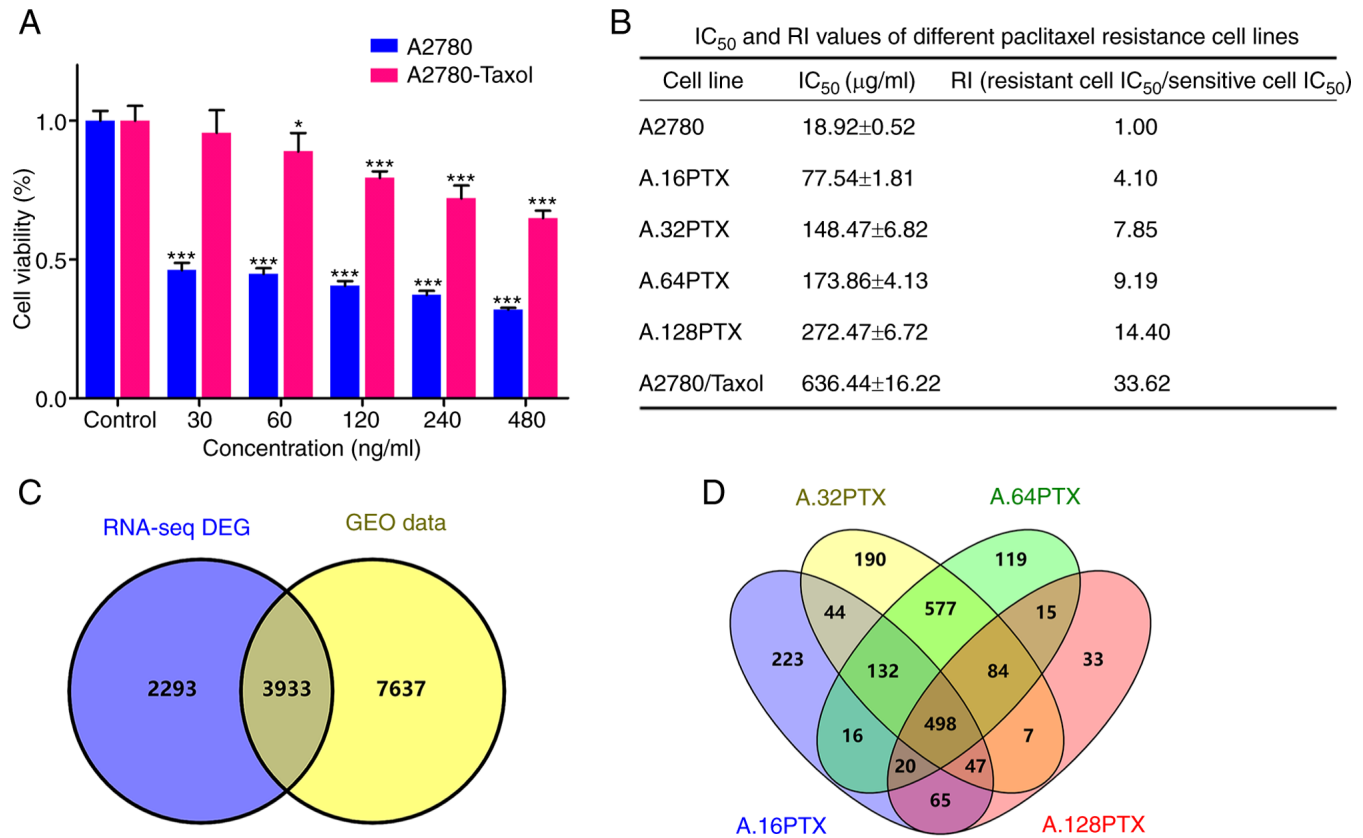


Figure S2. Survival curve of upregulated genes significantly related to patients with epithelial ovarian cancer treated with Taxol. ATF3, activating transcription factor 3; DHRS4L2, dehydrogenase/reductase 4 like 2; FLRT3, fibronectin-like domain-containing leucine-rich transmembrane protein 3; POLR3GL, RNA polymerase III subunit GL; GDF15, growth differentiation factor 15; ZNF239, zinc finger protein 239; PHLDA1, pleckstrin homology like domain family A member 1; SNCG, synuclein gamma; TPK1, thiamin pyrophosphokinase 1; NR1D2, nuclear receptor subfamily 1 group D member 2; SULF2, sulfatase 2.

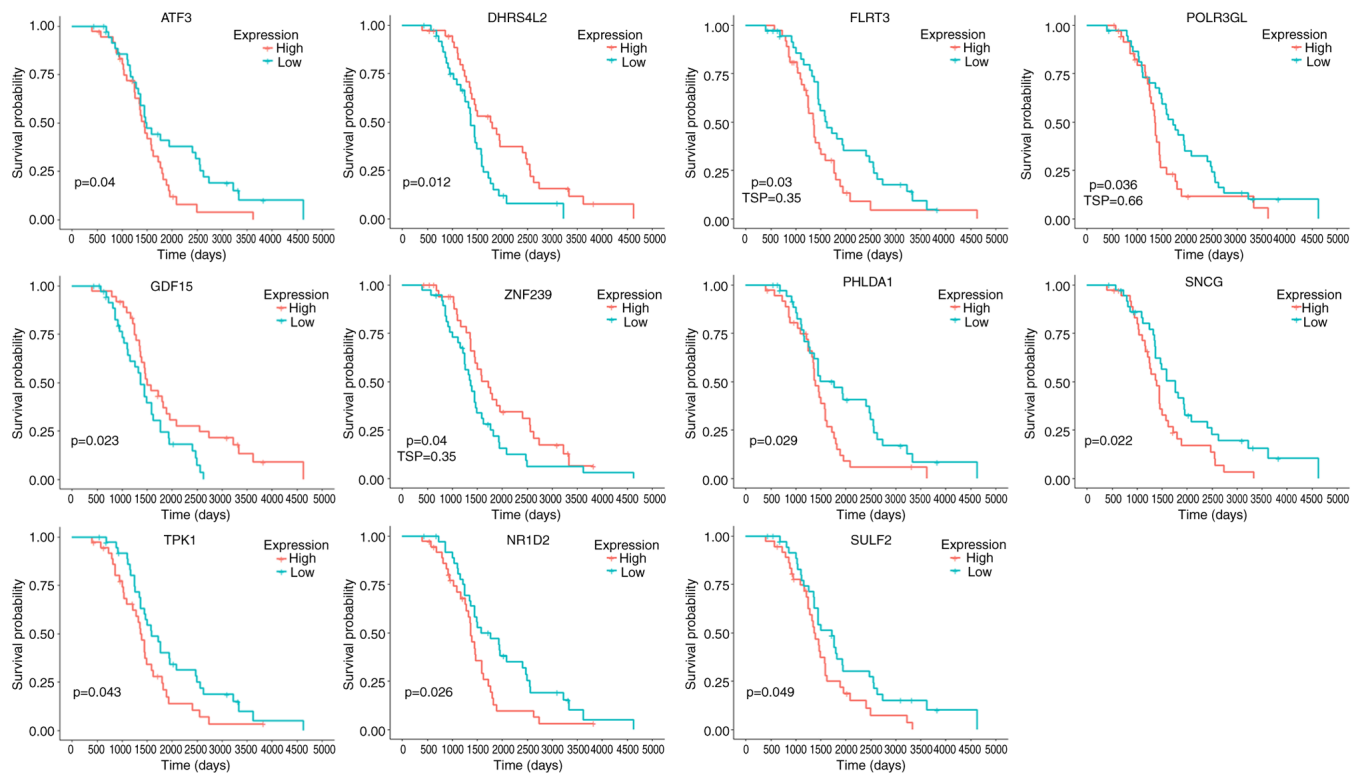


Figure S3. Survival curve of downregulated genes significantly related to patients with epithelial ovarian cancer treated with Taxol. ABCA5, ATP binding cassette subfamily A member 5; DSE, dermatan sulfate epimerase; FBXO22, F-box protein 22; ZFHX4, zinc finger homeobox 4; SSBP2, single stranded DNA binding protein 2; SVIL, supervillin; FBXL7, F-box and leucine rich repeat protein 7; SUN3, Sad1 and UNC84 domain containing 3; EXOC6B, exocyst complex component 6B; NCAM2, neutral cell adhesion molecule 2; ONECUT2, one cut homeobox 2; MTRNR2L1, MT-RNR2 like 1; SERPING1, serpin family G member 1.

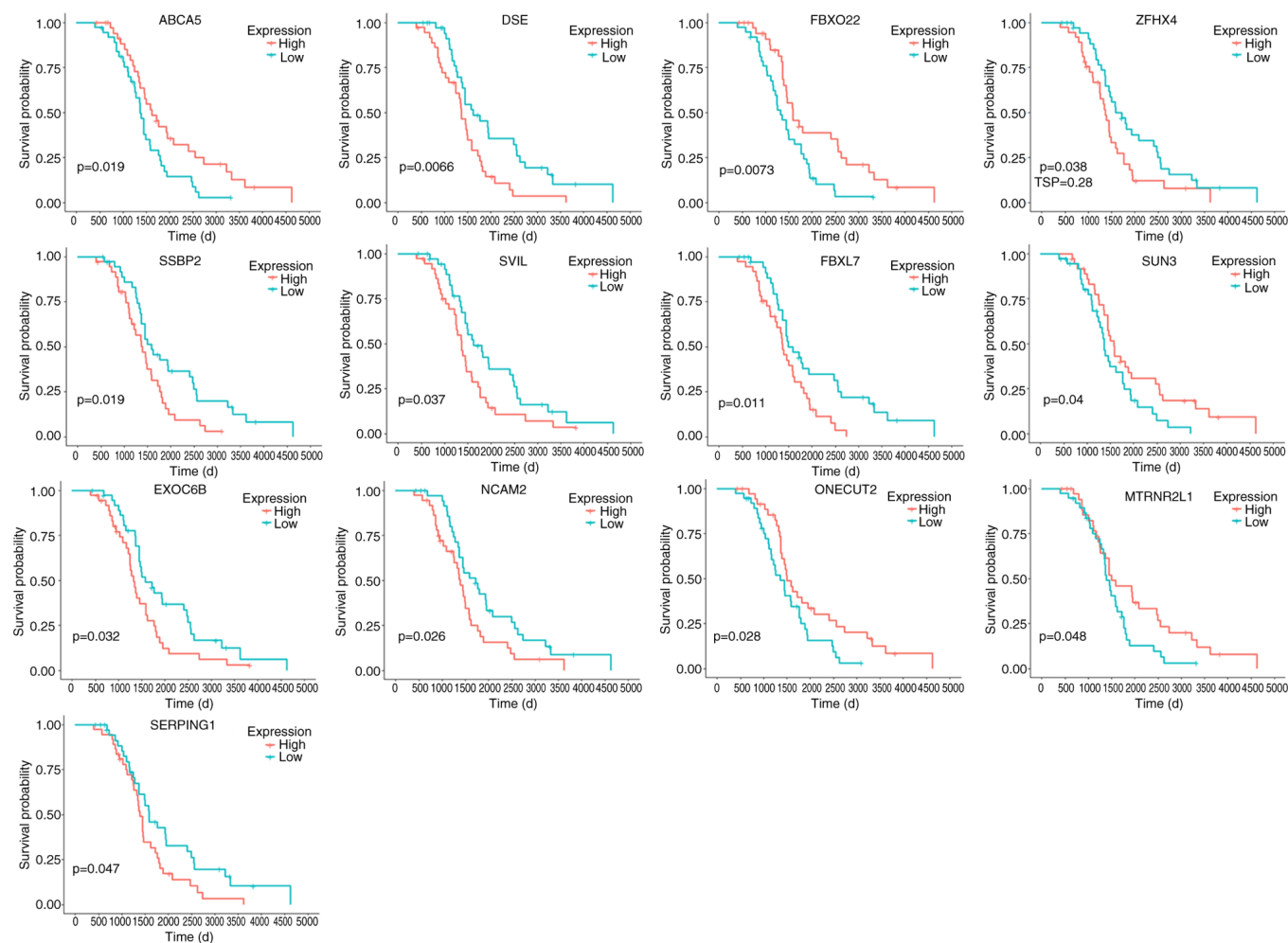


Figure S4. GO enrichment and correlation of target gene with stage of patients with EOC treated with Taxol. (A) Top 15 significant enrichment GO terms in cellular component. (B) Top 15 significant enrichment GO terms in molecular function. (C) Top 15 significant enrichment GO terms in biological process. (D) Correlation between MMP1 and EOC patient stage. (E) Correlation between ZYX and EOC patient stage. (F) Correlation between UNC5C and EOC patient stage. ZYX, zyxin; GO, Gene Ontology; EOC, epithelial ovarian cancer; MMP, matrix metalloprotease; UNC5C, Unc-5 netrin receptor C.

