

Supplementary Figure S1. (A) Top 30 DEGs in **Figure 1B** was integrated with STRING database to establish a PPI network. (B) The PPI network integrated in **Supplementary Figure S1A** was calculated with Cytoscape software for the following analysis.

Supplementary Figure S2. (A) The relative mRNA of HJURP was detected by qRT-PCR to verify the efficiency of different siHJURP oligos. (B) Protein level of HJURP was detected by WB after silencing HJURP. (C) The relative mRNA of HJURP was detected by qRT-PCR to verify the efficiency of stable transfected HJURP knockdown cell lines. (D) The relative mRNA of HJURP was detected by qRT-PCR to verify the efficiency of stable transfected HJURP overexpression in SKOV3. (E) Protein level of HJURP in stable transfected cell lines was detected by WB. (F) Xenograft assay was performed in nude mice. The tumor images of control and HJURP overexpression group were captured. (G) Tumor weight in **Supplementary Figure S2F** was shown in scatter plot. (Quantitative data are described as mean±SD, ^{ns} $P>0.05$, * $P<0.05$, ** $P<0.01$ and *** $P<0.001$)

Supplementary Figure S3. (A) KEGG enrichment was analyzed based on all down-regulated DEGs in **Figure 3A** after silencing HJURP. (B) The union set of **Figure 3D** was integrated with STRING database to establish a PPI network. (C) The PPI network integrated in **Supplementary Figure S3B** was calculated with Cytoscape software for the following analysis.

Supplementary Figure S4. (A) Cell viability of A2780 with cisplatin treatment (0, 1, 2, 4, 8, 16 μg/ml) was detected by MTT assay. (B) IC₅₀ values of cisplatin were calculated using nonlinear regression equation by GraphPad Prism 7.0 software. (C) EdU assay was performed in control and siHJURP groups after corresponding cisplatin treatment (200 ×). Hoechst was used to label nucleus and determine total cell number. (D) EdU positive cell proportion was showed in histogram. (E) Clonogenic assay was performed in control and HJURP overexpression groups under the gradient treatment of cisplatin in SKOV3. (F) Cloning formation number of **Supplementary Figure S4E** was shown in histogram in the left. Cloning survival rate was shown in line chart in the right. (Quantitative data are described as mean±SD, ^{ns} $P>0.05$, * $P<0.05$, ** $P<0.01$ and *** $P<0.001$)

Supplementary Figure S5. (A) Clonogenic assay was performed in different conditions under the gradient treatment of cisplatin in SKOV3 and A2780. (B) Cloning formation number of **Supplementary Figure S5A** was shown in histogram, and cloning survival rate was shown in line chart. SKOV3 was laid above and A2780 was laid below. As for histogram, asterisks on blue-legend group meant the comparison between red-legend and blue-legend group, and asterisks on green-legend group meant the comparison between blue-legend and green-legend group. (C) Apoptosis assay was detected in A2780 and SKOV3 by flow cytometry to illustrate the rescued effect of siWEE1 after HJURP overexpression under cisplatin treatment. (D) The percentage of apoptotic cells was shown in histogram. A2780 was

laid in the left and SKOV3 was laid in the right. (Quantitative data are described as mean±SD, ^{ns} $P>0.05$, * $P<0.05$, ** $P<0.01$ and *** $P<0.001$)

Supplementary Figure S6. (A) Clonogenic assay was performed in control and HJURP overexpression groups under the gradient treatment of AZD1775 in SKOV3. (B) Cloning formation number of **Supplementary Figure S6A** was shown in histogram in the left. Cloning survival rate was shown in line chart in the right. (Quantitative data are described as mean±SD, ^{ns} $P>0.05$, * $P<0.05$, ** $P<0.01$ and *** $P<0.001$)

Supplementary Table S1. Primer sequences used in the present study.

Supplementary Table S2. Primary and secondary antibodies used in the present study.

Supplementary Table S3. Top 30 up-regulated genes of ovarian cancer generated by NGS.

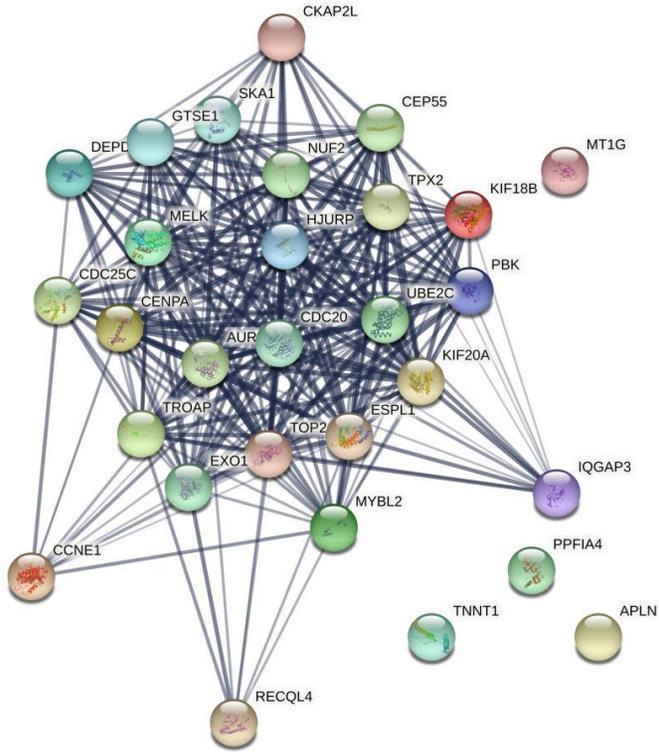
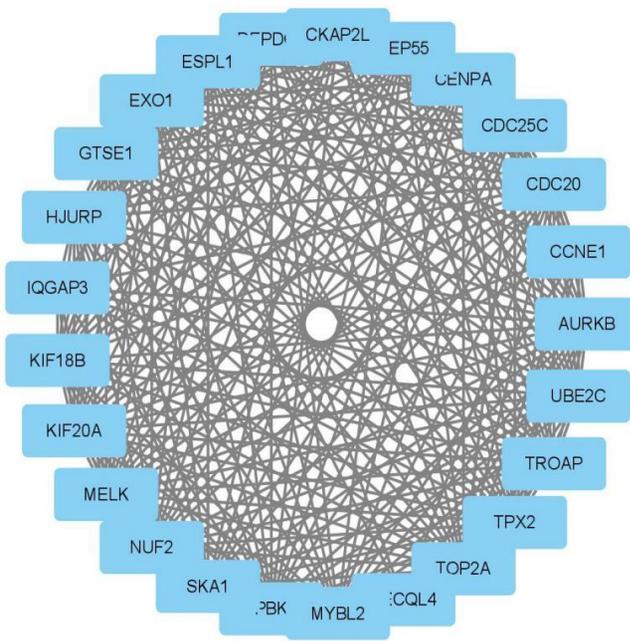
Supplementary Table S4. DEGs(P -adj<0.05) between siNC and siHJURP generated by NGS.

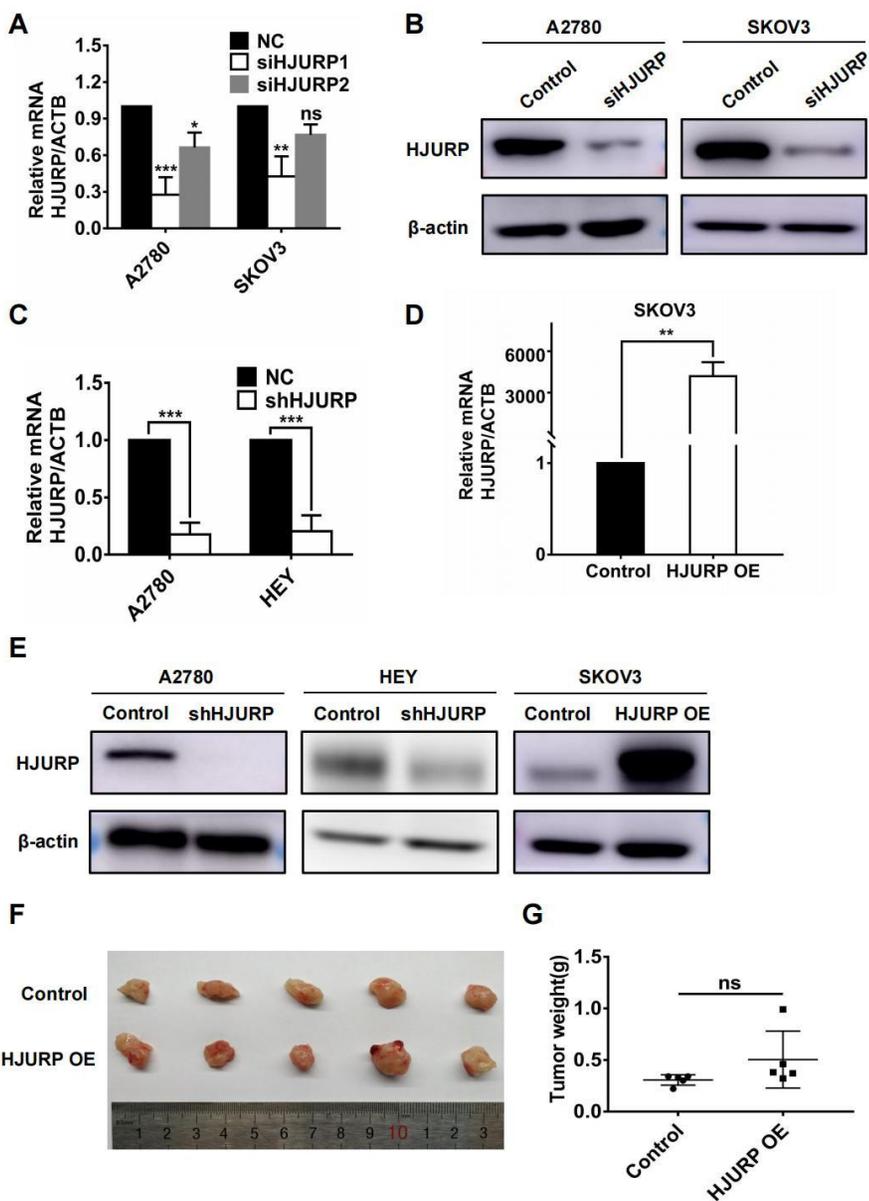
Supplementary Table S5. GO analysis of all DEGs(P -adj<0.05) between siNC and siHJURP.

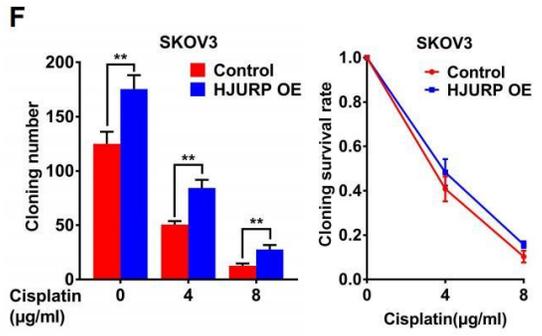
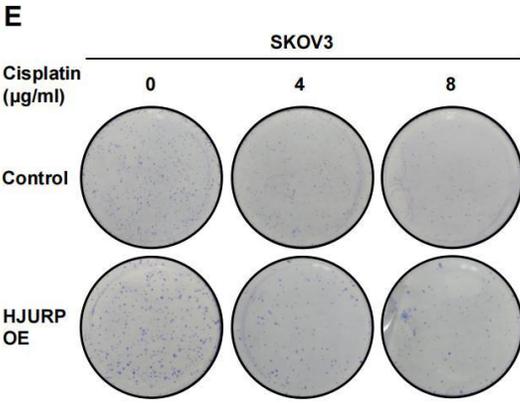
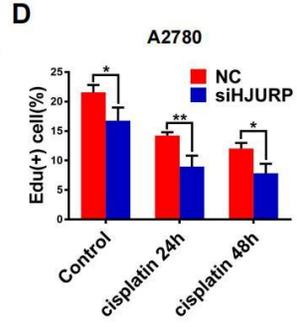
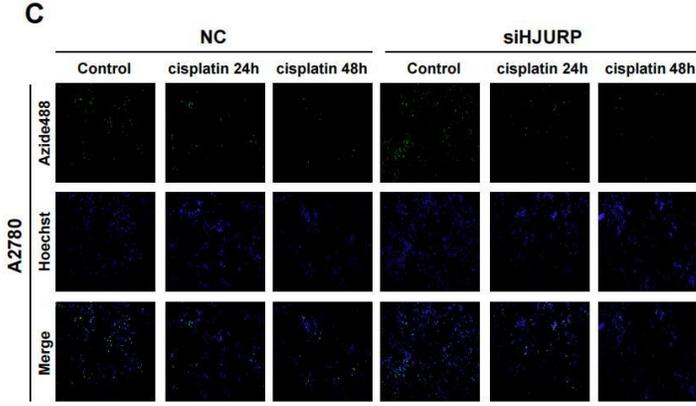
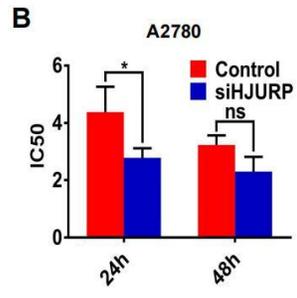
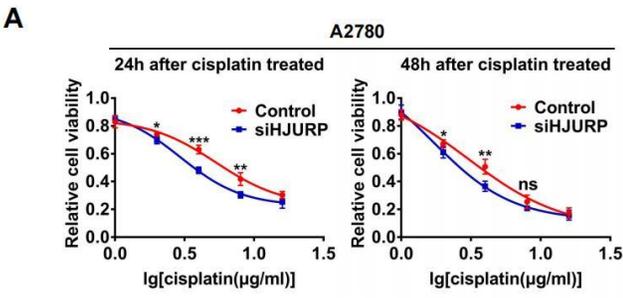
Supplementary Table S6. KEGG analysis of all down-regulated genes(P -adj<0.05) along with siHJURP.

Supplementary Table S7. GO analysis of restricted DEGs(\log_2 FoldChange>0.5 and P -adj<0.05) between siNC and siHJURP.

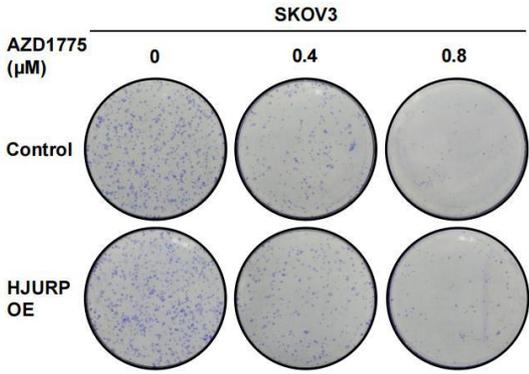
Supplementary Table S8. Cell-cycle-related DEGs(\log_2 FoldChange>0.5 and P -adj<0.05) between siNC and siHJURP from GO analysis.

A**B**





A



B

