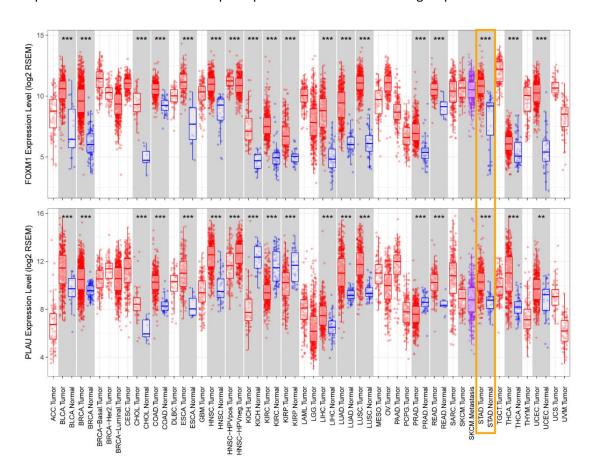
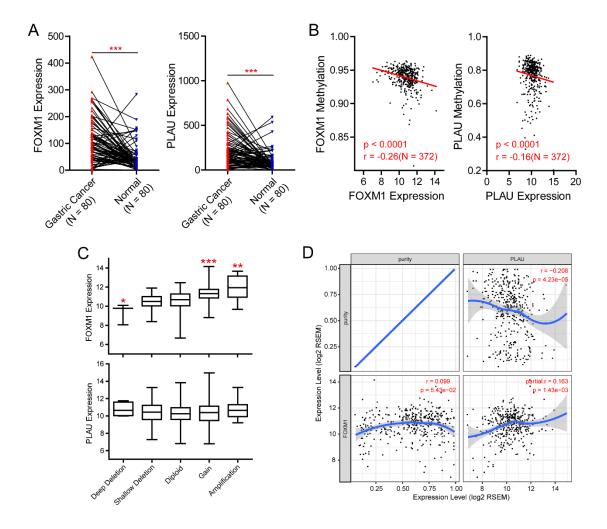
## **Supplementary Materials**

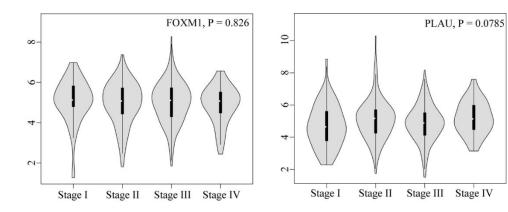
**Supplementary Figure 1.** Box plot of FOXM1 and PLAU expression in 32 cancer types. FOXM1 and PLAU are overexpressed in gastric cancer (marked in yellow box). \*\*\*: p<0.001, \*\*: p<0.01, \*: p<0.05. Red represents expression value in cancer while blue represents expression in normal control. Purple represents SKCM metastases group.



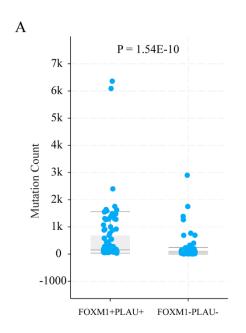
**Supplementary Figure 2.** FOXM1 and PLAU are overexpressed in gastric (A, data from GSE27342, red represents cancer, blue represents normal control); FOXM1 and PLAU expression are negatively correlated with methylation level, Pearson r and p values are presented (B); FOXM1 and PLAU expression and copy number variation, FOXM1 expression is associated with CNV (C); Correlation of FOXM1 and PLAU expression adjusted by tumor cell proportion (D). \*\*\*: p<0.001, \*\*: p<0.01, \*: p<0.05.

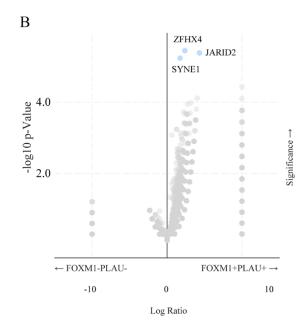


**Supplementary Figure 3.** The expression of FOXM1 and PLAU are not associated with tumor stages, P = 0.826 and 0.0785, respectively.

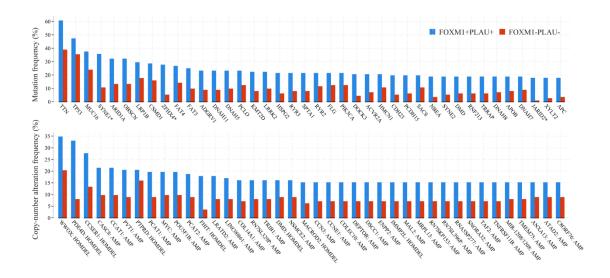


**Supplementary Figure 4.** The mutation count in FOXM1+PLAU+ group is significantly higher than FOXM1-PLAU- group (A). JARID2, ZFHX4 and SYNE1 mutations are significantly enriched in FOXM1+PLAU+ group (B).

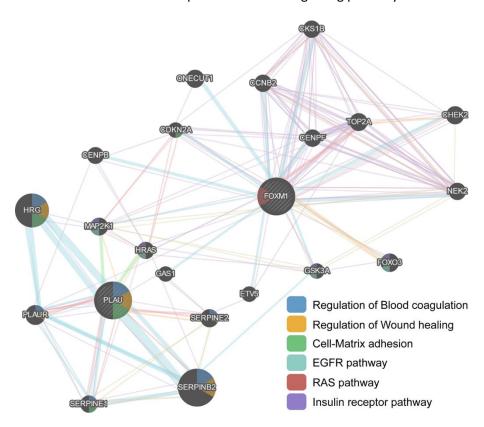




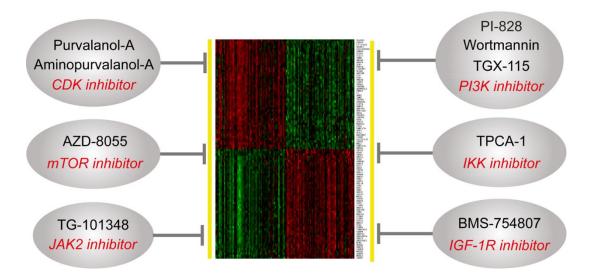
**Supplementary Figure 5.** Mutation frequency and CNA frequency comparison between FOXM1+PLAU+ and FOXM1-PLAU- groups. As is shown in this graph, blue represents FOXM1+PLAU+ group and red represents FOXM1-PLAU- group.



**Supplementary Figure 6.** Gene interaction network and function enrichment of FOXM1 and PLAU. Different line colors represent different signaling pathways.



**Supplementary Figure 7.** Data mining results from LINCs dataset suggests several inhibitors that could reverse the expression pattern of genes differentially expressed in FOXM1+/PLAU+ subgroup compared with FOXM1-/PLAU- subgroup.



## **Supplementary Tables**

**Supplementary Table 2.** Top 50 up/down genes in FOXM1+PLAU+ group compared with FOXM1-PLAU- group.

**Supplementary Table 1.** Number of patients in each group in figure 1.

**Supplementary Table 3.** The differences of Mutation and clinical attributes between FOXM1+PLAU+ and FOXM-PLAU- groups.

**Supplementary Table 4.** Mutations enriched in FOXM1+PLAU+ and FOXM1+PLAU+ group.

**Supplementary Table 5.** Protein changes of key signaling pathways from RPPA data of TCGA.

**Supplementary Table 6.** Drugs targeting genes expression patterns of FOXM1+PLAU+ group.