

Figure S1 Hazard ratio for overall survival in TCGA-LUAD and the expression of *PPM1G* in LUAD cells. (A) The expression of *PPM1G* in LUSC and normal tissues. (B) Results of Cox proportional hazards regression analysis for survival in TCGA-LUAD patients. (C) Expression levels of *PPM1G* protein in normal and LUAD cell lines were detected via Western blotting. (D) *PPM1G* protein expression in H1299 and A549 cells was detected via Western blotting. *, $P < 0.05$; ***, $P < 0.001$ vs. 16HBE cells. **, $P < 0.01$; ***, $P < 0.001$ vs. si-NC group. ###, $P < 0.001$ vs. vector group. LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; NC, negative control; si, small interfering; TCGA, The Cancer Genome Atlas.

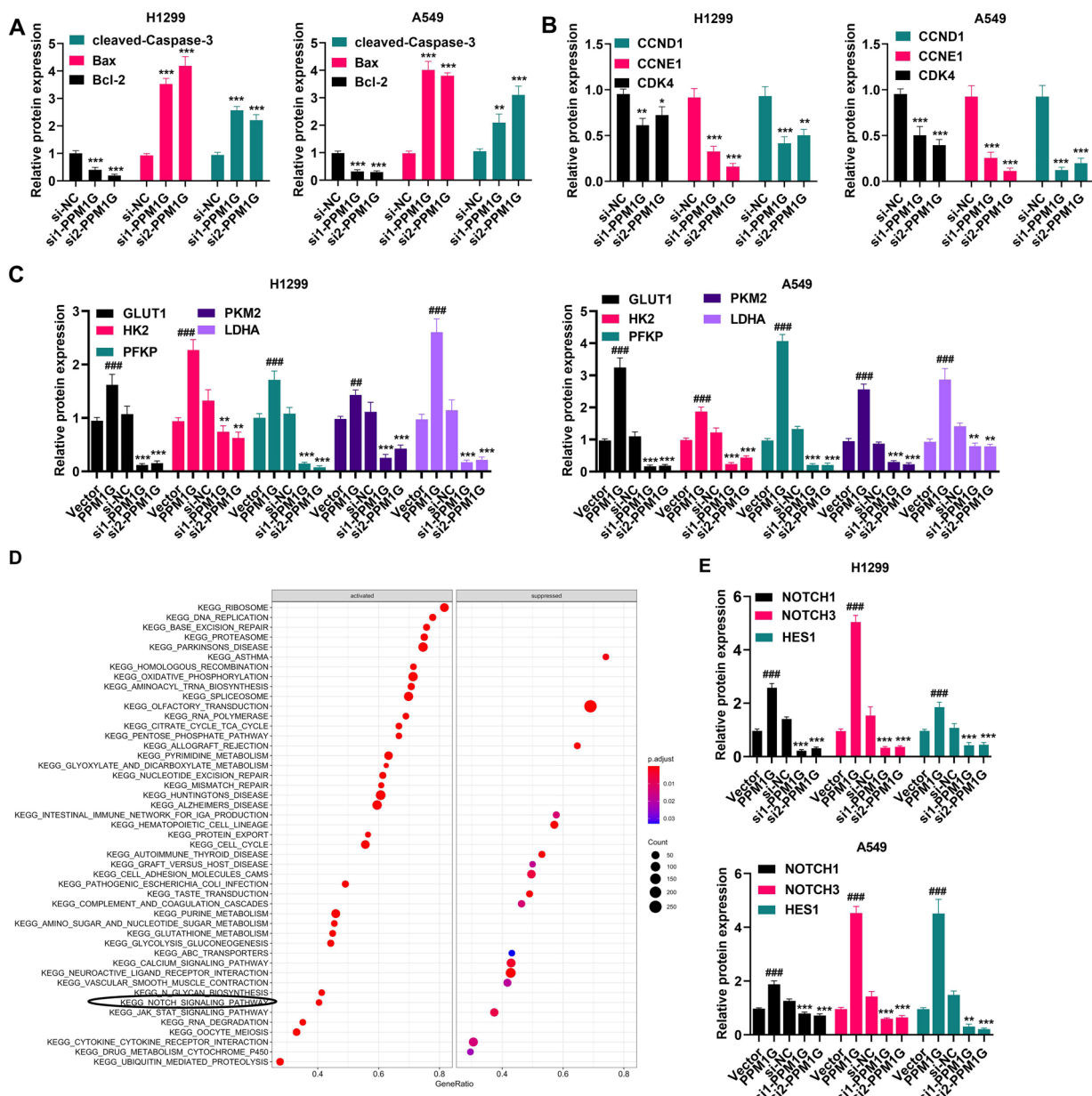


Figure S2 Quantification of Western blotting results and the bubble chart of *PPM1G*-enriched pathways. (A) Quantification analysis of Bax, Bcl-2, and cleaved caspase-3 protein levels in H1299 and A549 cells. (B) Quantification analysis of CDK4, CCNE1, and CCND1 protein levels in H1299 and A549 cells. (C) Quantification analysis of GLUT1, HK2, PFKP, PKM2, and LDHA protein levels in H1299 and A549 cells. (D) Bubble chart of *PPM1G*-enriched pathways. (E) Quantification analysis of NOTCH1, NOTCH3, and HES1 protein levels in H1299 and A549 cells. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$ vs. si-NC group. #, $P < 0.01$; ###, $P < 0.001$ vs. vector group. NC, negative control; si, small interfering.

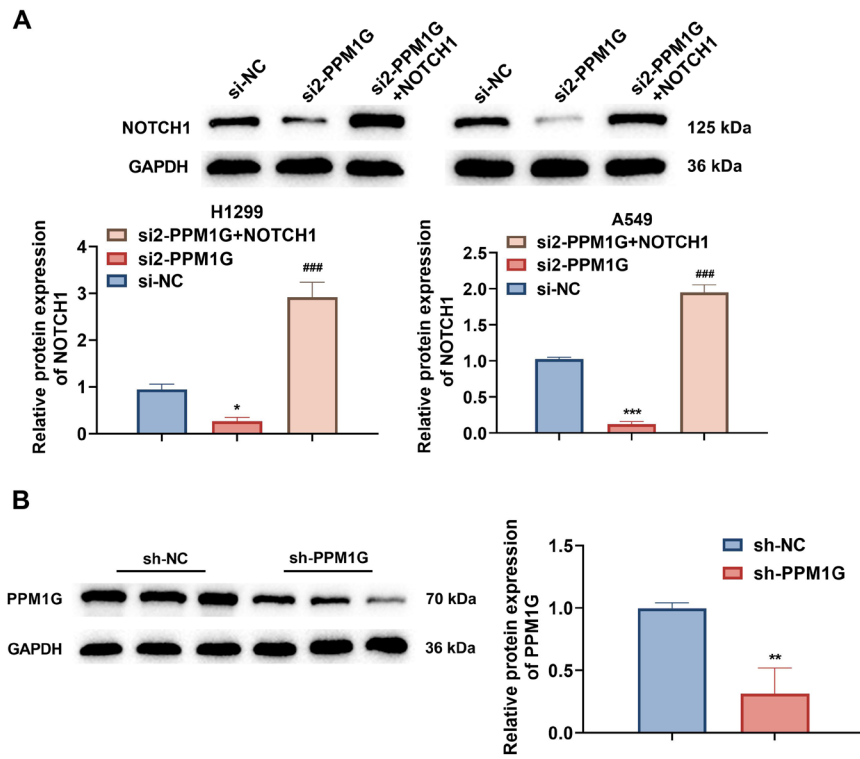


Figure S3 The transfection efficiency validation of *PPM1G*. (A) Expression levels of *PPM1G* protein in H1299 and A549 cells was detected via Western blotting. (B) Expression levels of *PPM1G* protein in xenograft tumor tissues was detected via Western blotting. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$ vs. si-NC or sh-NC group. ###, $P < 0.001$ vs. si2-*PPM1G* + NOTCH1 group. NC, negative control; si, small interfering; sh, short hairpin.