

Table S1 IC50 values of shKCNQ1OT1-transfected cells were measured with CCK-8 assays after exposure to ADM, DDP, and VP-16

	H69AR			H446DDP		
	Control	shRNA1#	shRNA2#	Control	shRNA1#	shRNA2#
ADM (μg/ml)	120.15±8.98	91.46±7.55	87.78±4.54	0.86±0.11	0.46±0.03	0.62±0.08
DDP (μg/mL)	14.93±0.49	11.26±0.73	12.25±0.38	8.10±0.06	7.26±0.48	6.62±0.12
VP-16 (μg/mL)	593.70±17.49	540.03±13.94	481.42±39.70	39.20±0.72	28.18±1.85	36.89±0.57

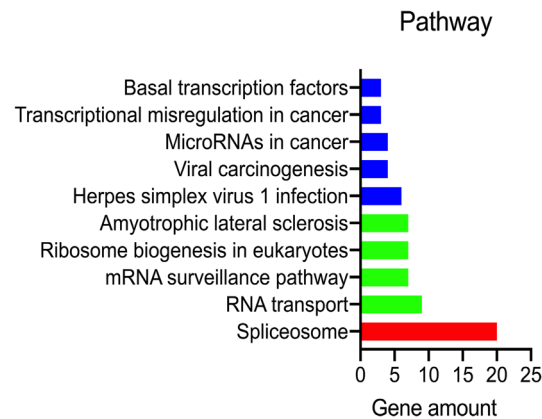


Figure S1 The top 10 KEGG pathways including the target mRNAs of KCNQ1OT1.

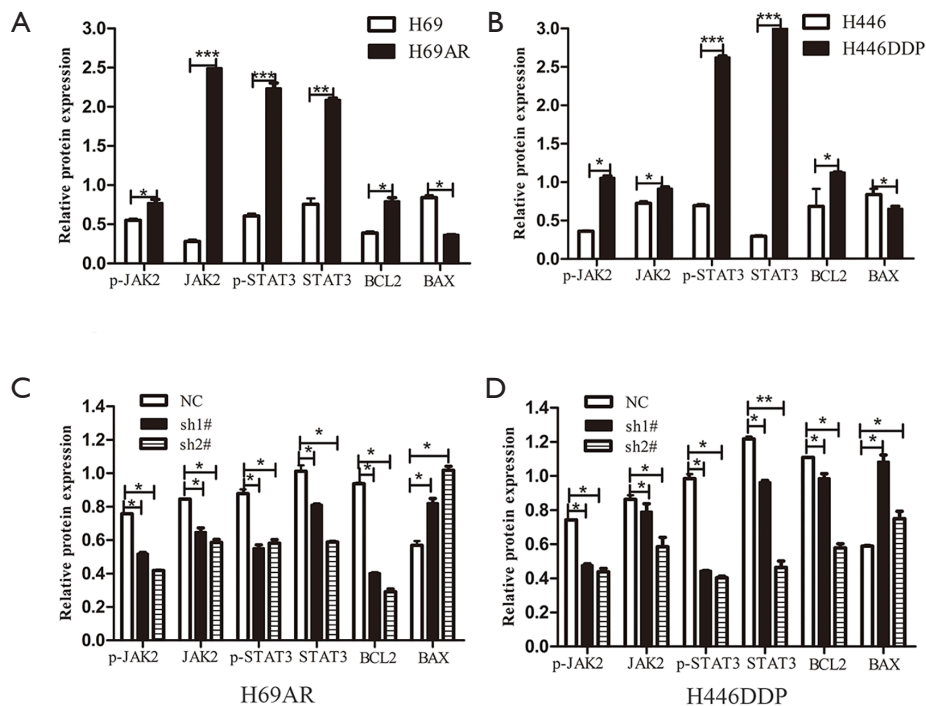


Figure S2 The quantitative statistics for western blot (A) P-JAK2, JAK2, P-STAT3, BCL2, and BAX expression in H69 and H69AR. (B) P-JAK2, JAK2, P-STAT3, BCL2, and BAX expression in H446 and H446DDP. (C) P-JAK2, JAK2, P-STAT3, BCL2, and BAX expression in H69AR after shKCNQ1OT1. (D) P-JAK2, JAK2, P-STAT3, BCL2, and BAX expression in H446DDP after shKCNQ1OT1. *, P<0.05; **, P<0.01; ***, P<0.001.