

Supplementary Figure legends

Figure S1. The overall survival rates of melanoma patients with different expression levels of genes listed in a Venn diagram in Figure 1D. (A) The overall survival rates of melanoma patients with different *BIRC5* expression were not significantly different (p -value = 0.08). (B) The overall survival rates of melanoma patients with different *BUB1* expression were not significantly different (p -value = 0.91). (C) The overall survival rates of melanoma patients with different *CDCA5* expression were not significantly different (p -value = 0.24). (D) The overall survival rates of melanoma patients with different *CENPN* expression were not significantly different (p -value = 0.64). (E) The overall survival rates of melanoma patients with different *NDC80* expression were not significantly different (p -value = 0.62). (F) The overall survival rates of melanoma patients with different *NUF2* expression were not significantly different (p -value = 0.54).

Figure S2. Knocking down expression of *AURKB* mediates melanoma cell cycle. Knocking down expression of *AURKB* of (A) A375 and (B) A375R was established. The cells (2.5×10^5 /well) were seeded into 60-mm dishes. Samples were analyzed by using a FACSCalibur flow cytometer.

Figure S3. Knocking down of *AURKB* mediates expression of c-caspase 3 and c-PARP in xenograft melanoma specimens. Melanoma specimens from (A) A375, (B) A375R, (C) M249 and (D) M249R xenograft models were prepared for c-caspase

3 and c-PARP analysis by IHC staining; scale bars = 100 μ m. Statistical significance was determined by one-way ANOVA and the asterisks indicate a significant decrease compared with vehicle control mice (***, $p < 0.001$).

Figure S4. Knocking down expression of *AURKB* mediates EGF associated BRAF/MEK/ERKs and PI3-K/AKT pathways in melanoma. (A) The GSEA enrichment plot of the ERBB signaling pathway is associated with expression of *AURKB*; the expression data was from GSE: 4587. (B) Normalized expression profile with different *AURKB* expressing samples. Heat map was generated by GSEA. (C, D) Knocking down expression of *AURKB* decreased EGF level by ELISA kit in M249 and M249R. (E) Knocking down expression of *AURKB* increases in levels of cleaved PARP, cleaved caspase 3, Bax and decreases in Bcl-2 by Western blot. (F, G) Knocking down expression of *AURKB* mediates activation of histone H3, BRAF/MEK/ERKs and PI3-K/AKT in M249 and M249R cell lines. Statistical significance was determined by one-way ANOVA and the asterisks indicate a significant change compared with the control group (*, $p < 0.05$; **, $p < 0.01$).

Figure S5. HI-511 synthesis. The synthesis of HI-511 and NMR spectrum of the products.

Figure S6. HI-511 inhibits cell growth and mediates cell cycle in both A375 and A375R cells. (A) A375 (B) A375R (8×10^3 /well) cells were seeded into 96-well

plates. After incubation overnight, cells were treated with the indicated concentrations of HI-511 and incubated for 48 h. Viability was estimated using the MTS assay as described in Materials and Methods. **(C)** A375 and **(D)** A375R cells were seeded (2.5×10^5 /well) into 60-mm dishes. Treatment with DMSO or 5 μ M HI-511 for 48 h. Samples were analyzed by using a FACSCalibur flow cytometer. Statistical significance was determined by one-way ANOVA and the asterisks indicate a significant change compared with the control group (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$).

Figure S7. HI-511, a dual-target inhibitor against both AURKB and BRAF V600E, affects growth, apoptosis, and protein expression levels in M249 and M249R melanoma cells. (A, B) HI-511 inhibits anchorage-independent cell growth. Cells (8×10^3 /well) were seeded into 6-well plates with 0.3% Basal Medium Eagle agar containing 10% FBS and different concentrations of HI-511 and then cultured for 2 weeks. Colonies were scored under a microscope by using the Image-Pro PLUS (v6.) software program. Effect of HI-511 and the activation of histone H3, MEK, ERKs, and AKT was detected by Western blot in **(C)** M249 and **(D)** M249R cells. **(E, F)** M249 and M249R cells (2.5×10^5 /well) were incubated with HI-511 (1.25, 2.5, or 5 μ M) or vehicle control for 48 h. Cells were collected and apoptosis was detected by flow cytometry with Annexin V and propidium iodide staining. **(G, H)** The cells were incubated with HI-511 or vehicle control for 48 h, then the effect of HI-511 on apoptosis-associated protein expression was determined by Western blot. Statistical

significance was determined by one-way ANOVA. The asterisks indicate a significant change compared with untreated control cells (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). Vemu: vemurafenib.

Figure S8. HI-511 binds to and suppresses the activation of wild type BRAF. (A)

Computer docking model of HI-511 binding with wild type BRAF. **(B)** HI-511 inhibits wild type BRAF *in vitro*. Active kinase wild type BRAF and HI-511 (0, 1, 5, 10 μM) or vemurafenib (5 μM) were mixed with the substrate phosphatidylinositol.

(C) Knocking down of *AURKB* inhibits BRAF wild type melanoma cell (SK-MEL-

31) growth. **(D)** HI-511 suppresses BRAF wild type melanoma cell (SK-MEL-31)

growth. Statistical significance was determined by one-way ANOVA. The asterisks indicate a significant change compared with untreated control cells (**, $p < 0.01$; ***, $p < 0.001$).

Figure S9. HI-511 mediates the expression of apoptosis markers c-caspase 3 and

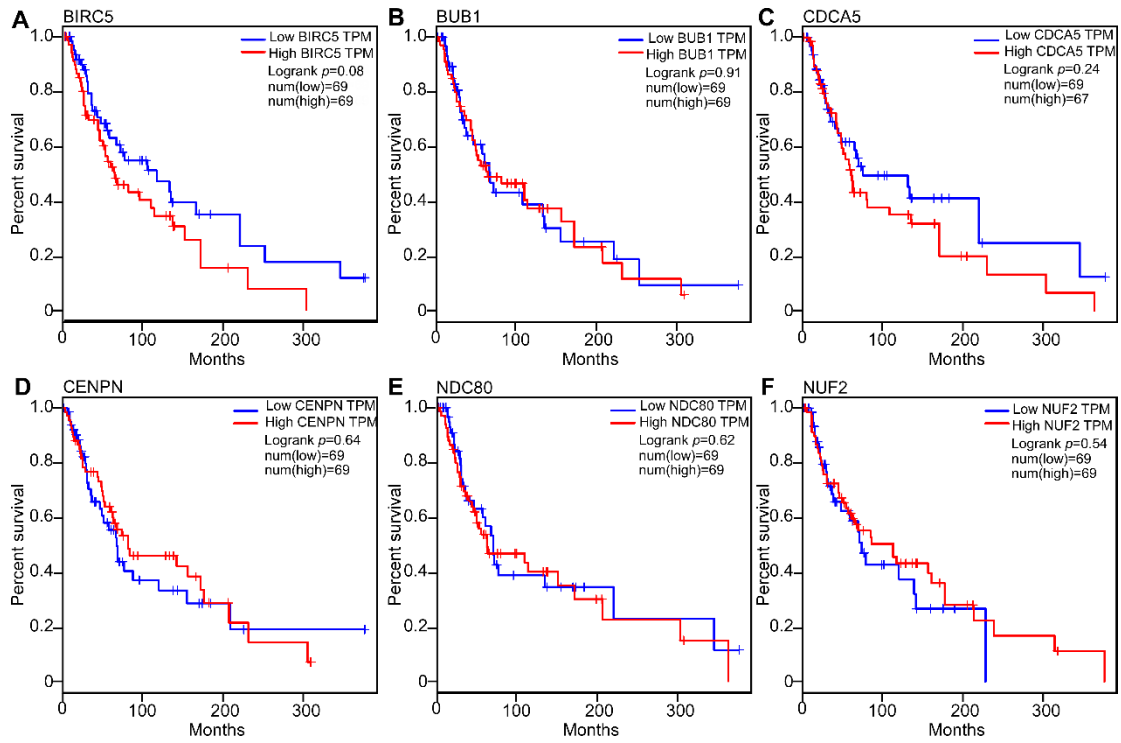
c-PARP. Melanoma specimens from **(A)** A375, **(B)** A375R, **(C)** M249 and **(D)**

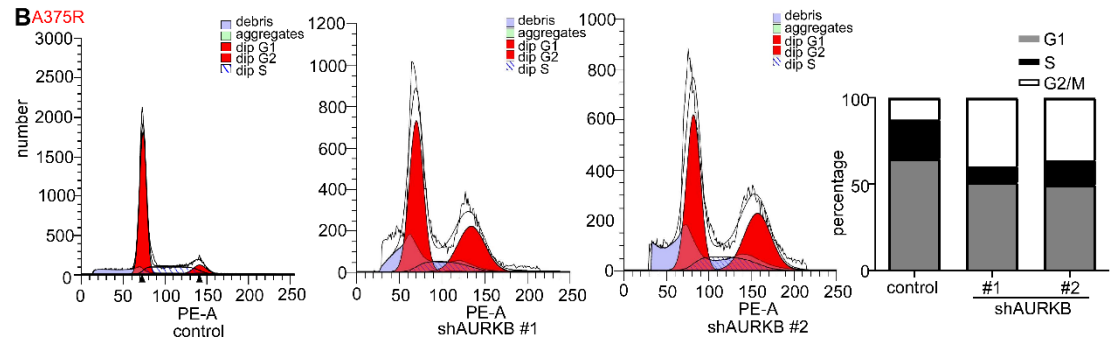
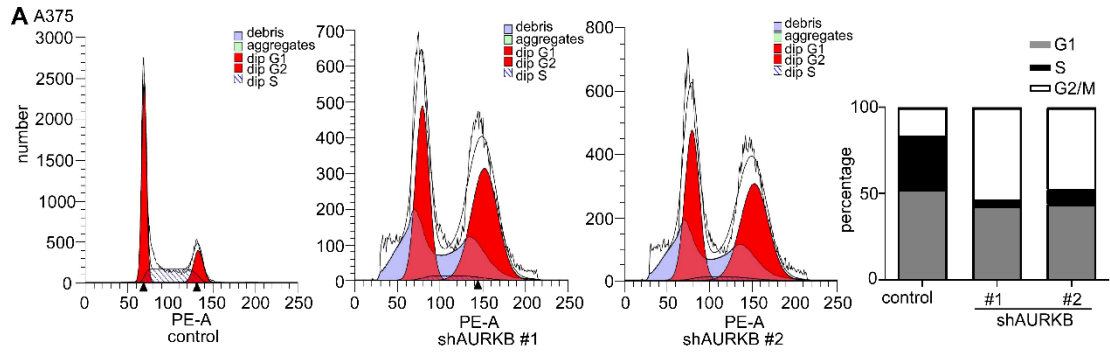
M249R xenograft models were prepared for IHC staining for c-caspase 3 and c-

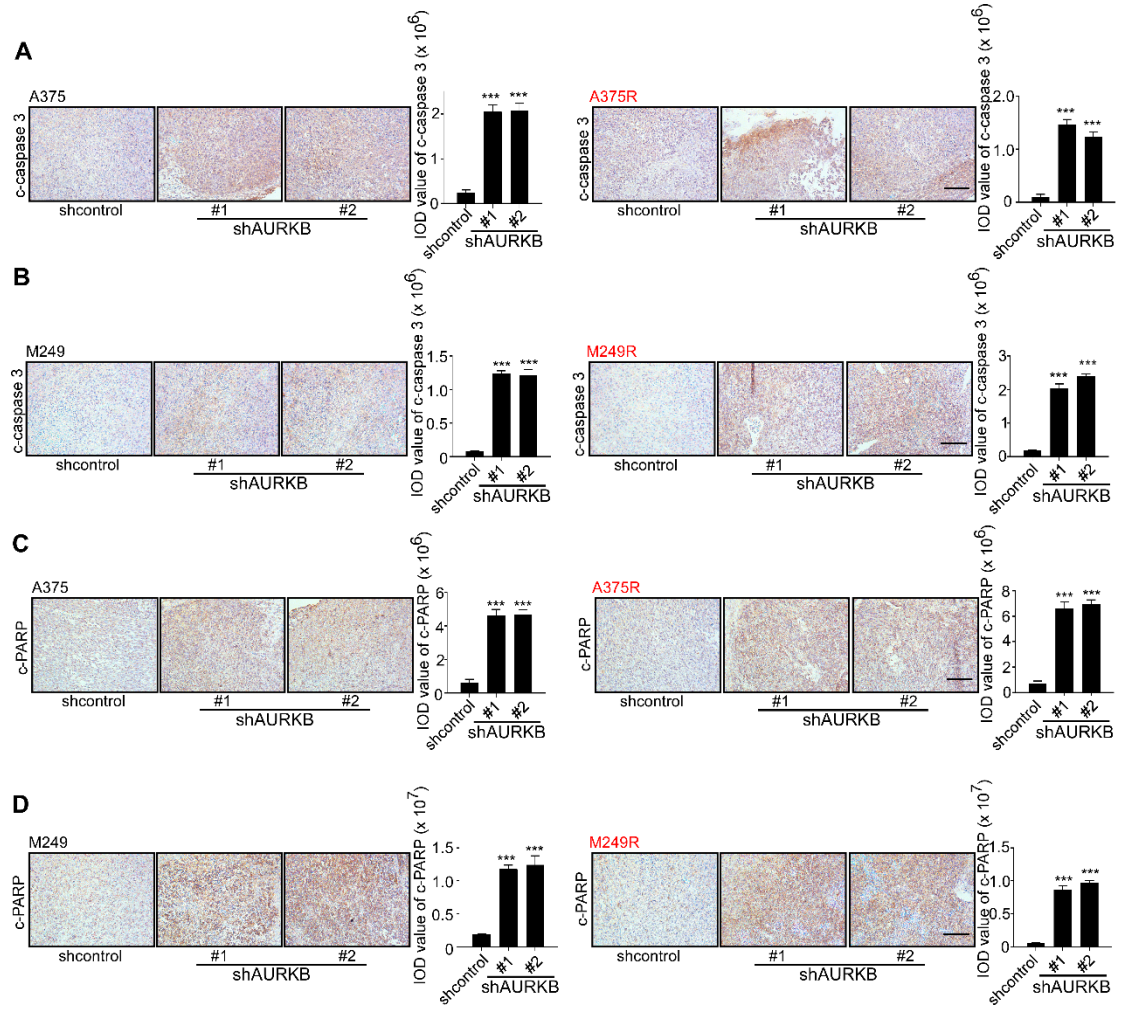
PARP; scale bars = 100 μm . Statistical significance was determined by one-way

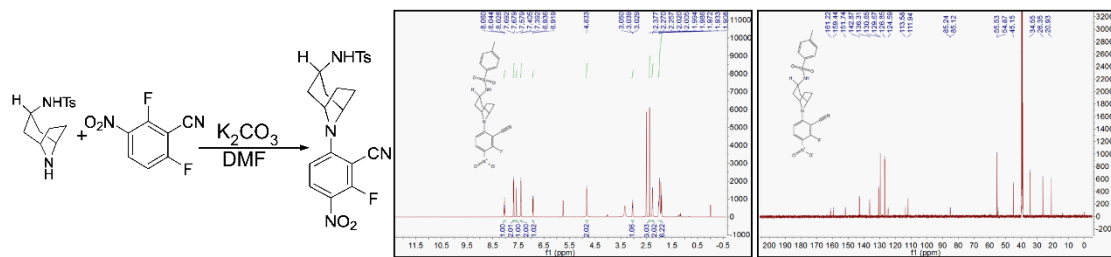
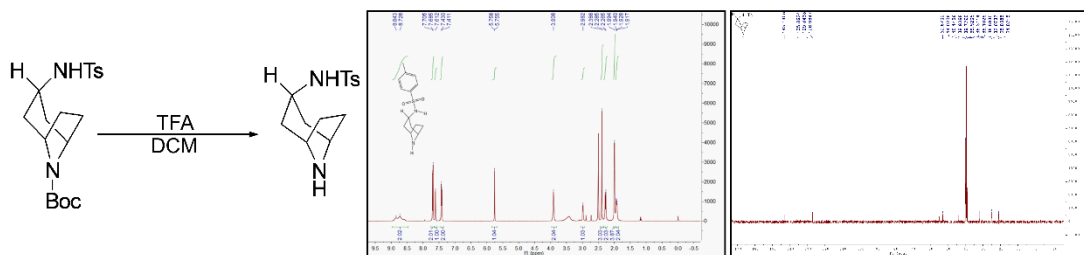
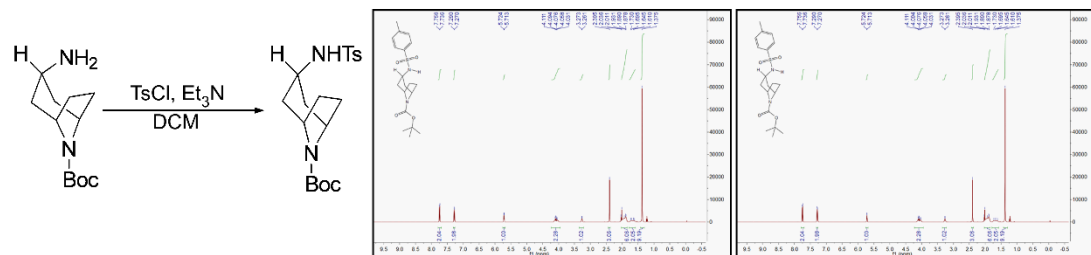
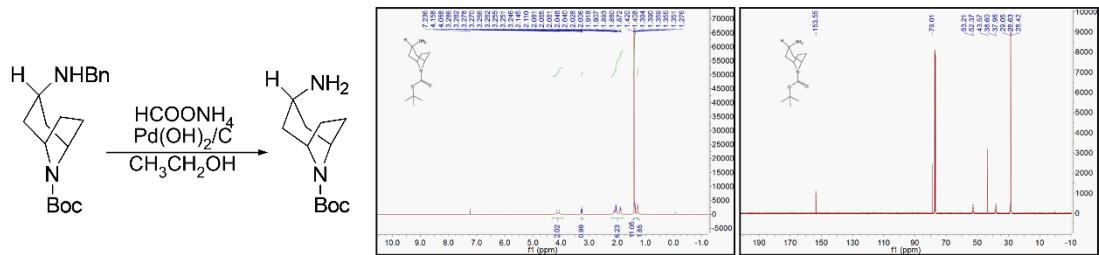
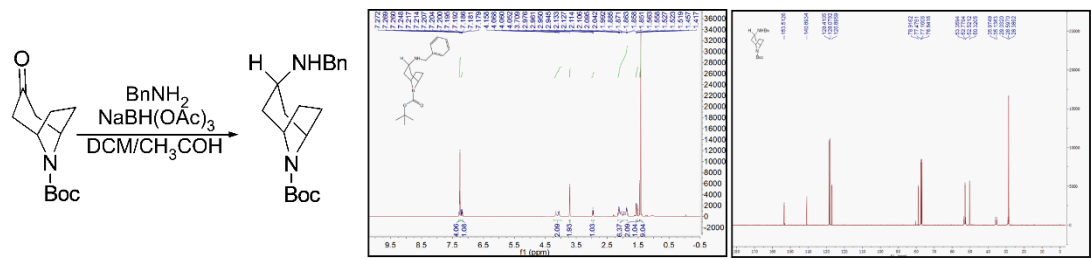
ANOVA and the asterisks indicate a significant decrease compared with vehicle

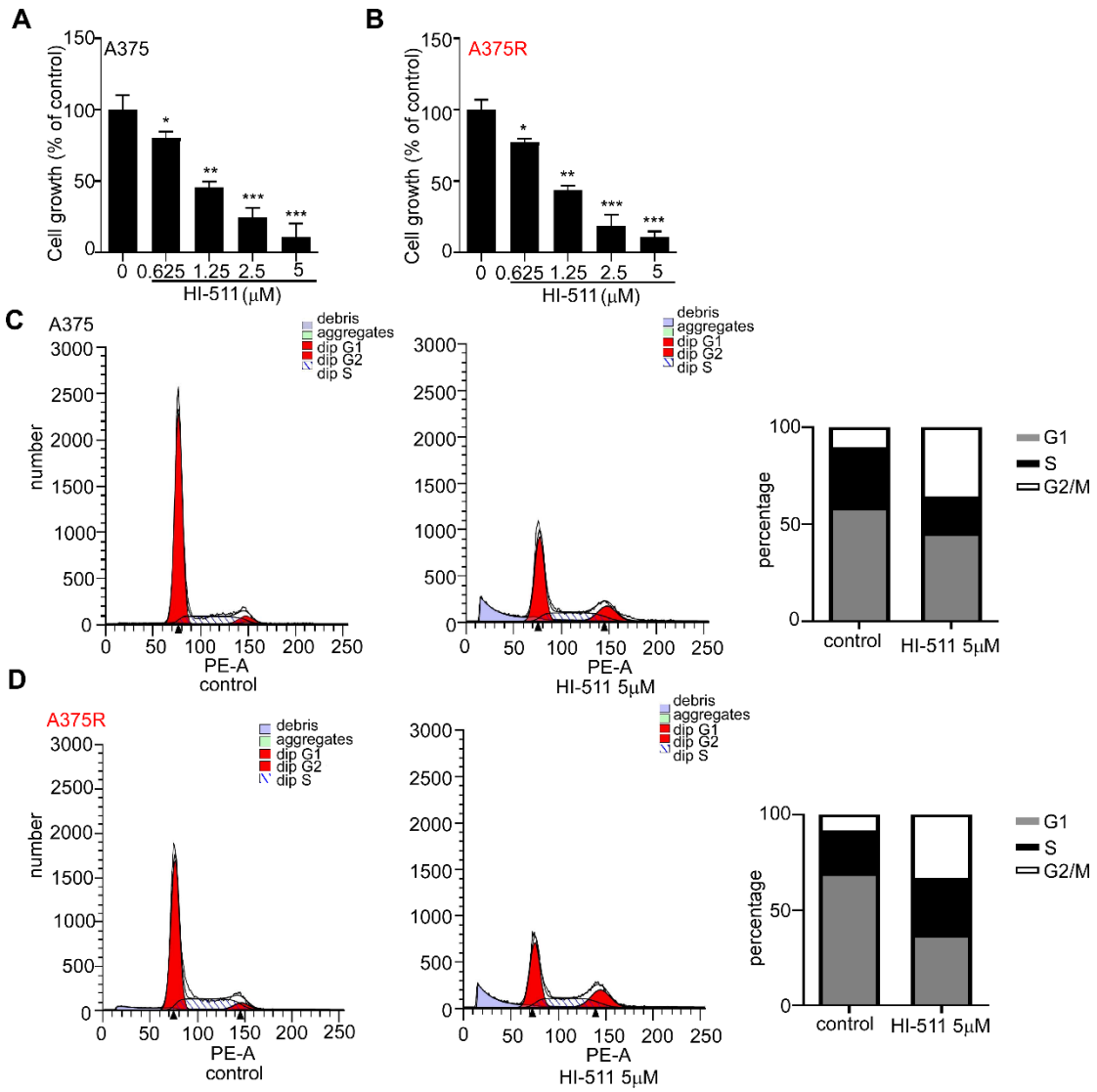
control mice (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). Vemu: vemurafenib.

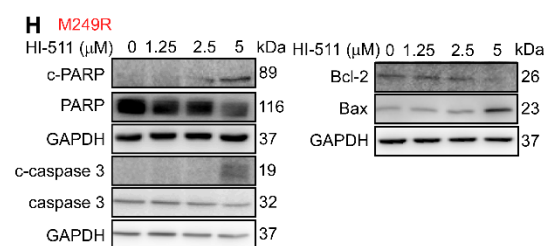
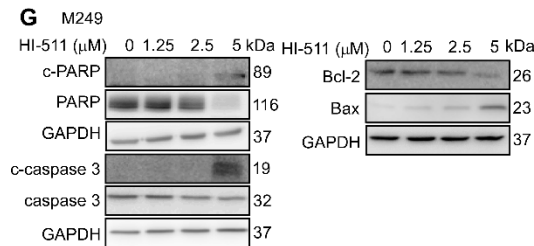
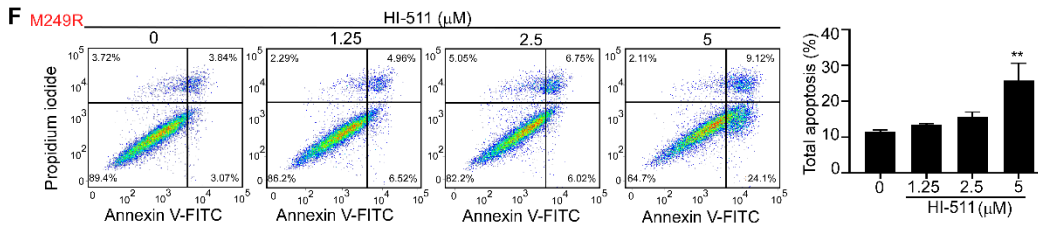
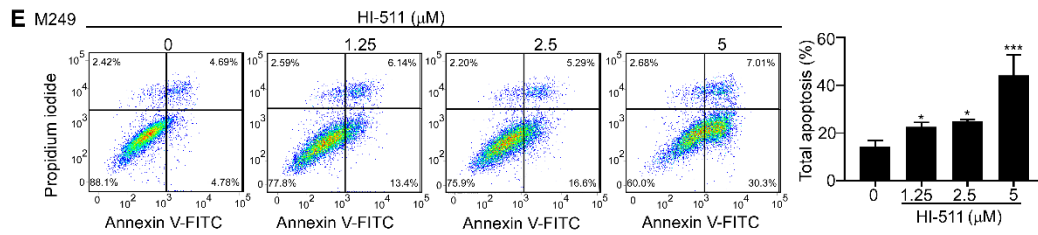
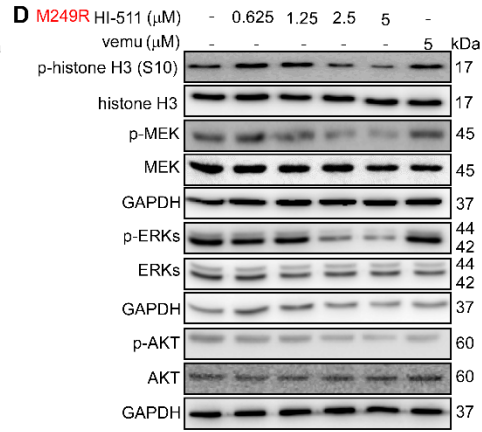
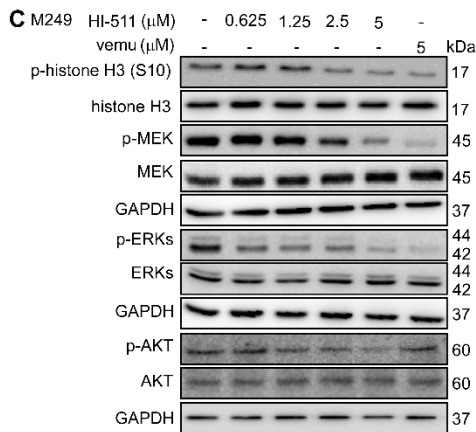
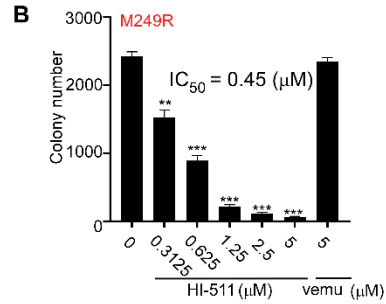
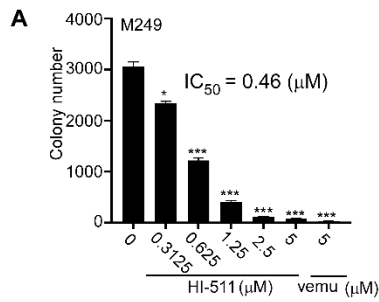




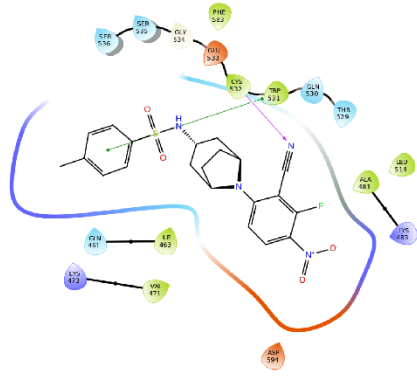








A



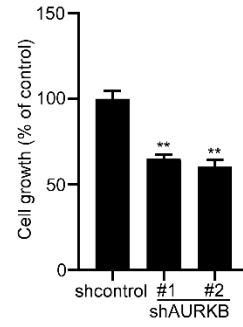
B

HI-511 binding with BRAF

BRAF binding residue	interaction	HI-511 binding area
Cys 532	H-bond	nitrile group
Trp 531	π - π stacking	phenyl ring

Active BRAF	-	+	+	+	+	+	+
MEK1	+	-	+	+	+	+	+
HI-511(μ M)	-	-	-	1	5	10	-
Vemurafenib(μ M)	-	-	-	-	-	-	5
p-MEK							
BRAF							
Coomassie Brilliant Blue							

C SK-MEL-31



D SK-MEL-31

