1-BAX

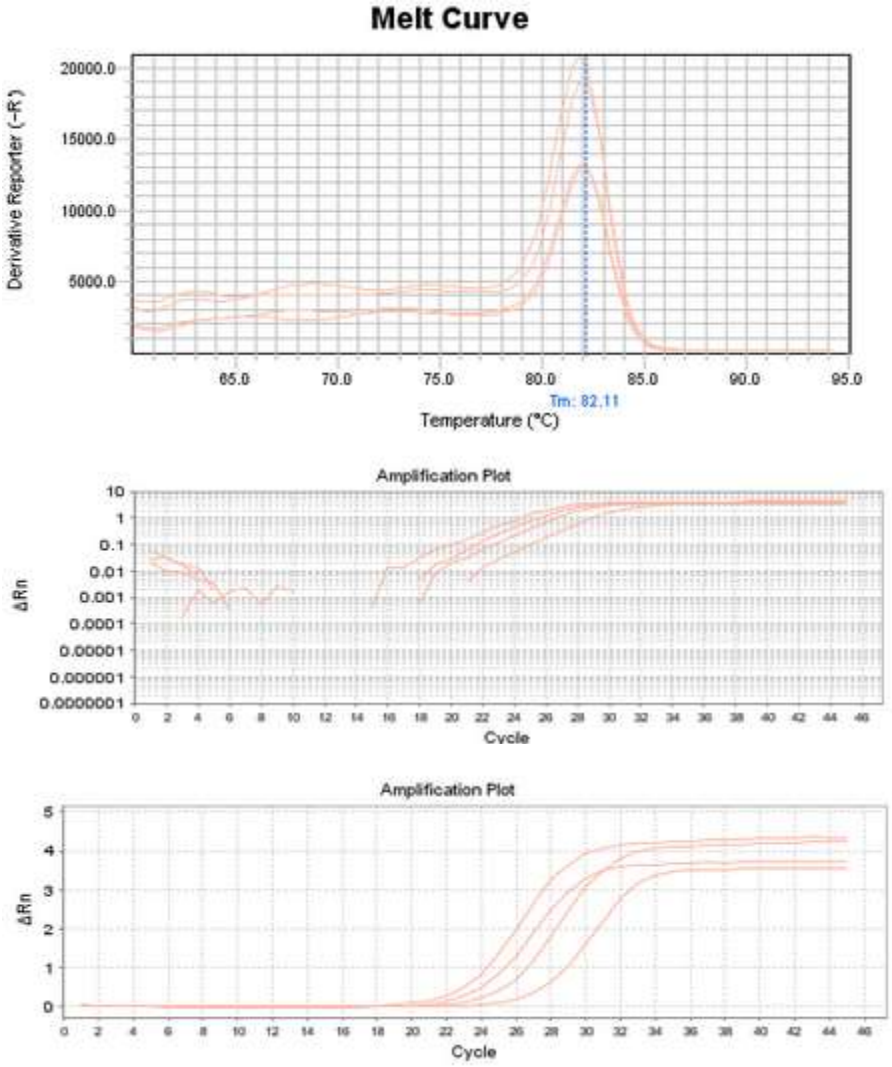

Figure 1. Expression of STAT6 in the CRC cell line. The HT-29 cell line has a higher level of STAT6 expression than other cell lines ($P<0.05$; $P<0.01$).

2-BCL2

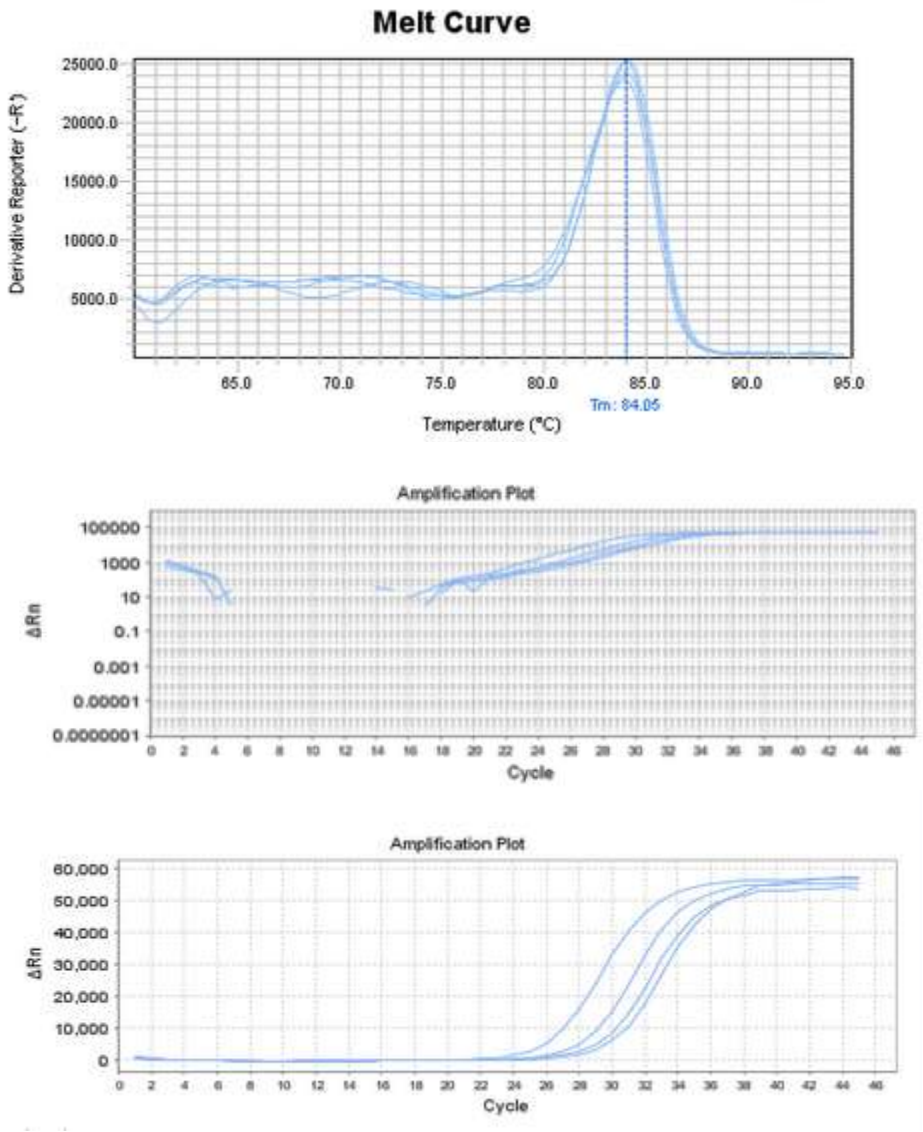

Figure 2. Impact of STAT6 siRNA at various periods and dosages on STAT6 expression. A) 100 pmol of siRNA significantly down-regulated STAT6 expression as compared to the control group and other dosages examined. B) 48 hr was selected as an optimum time (ns=not significant; $P<0.0001$).

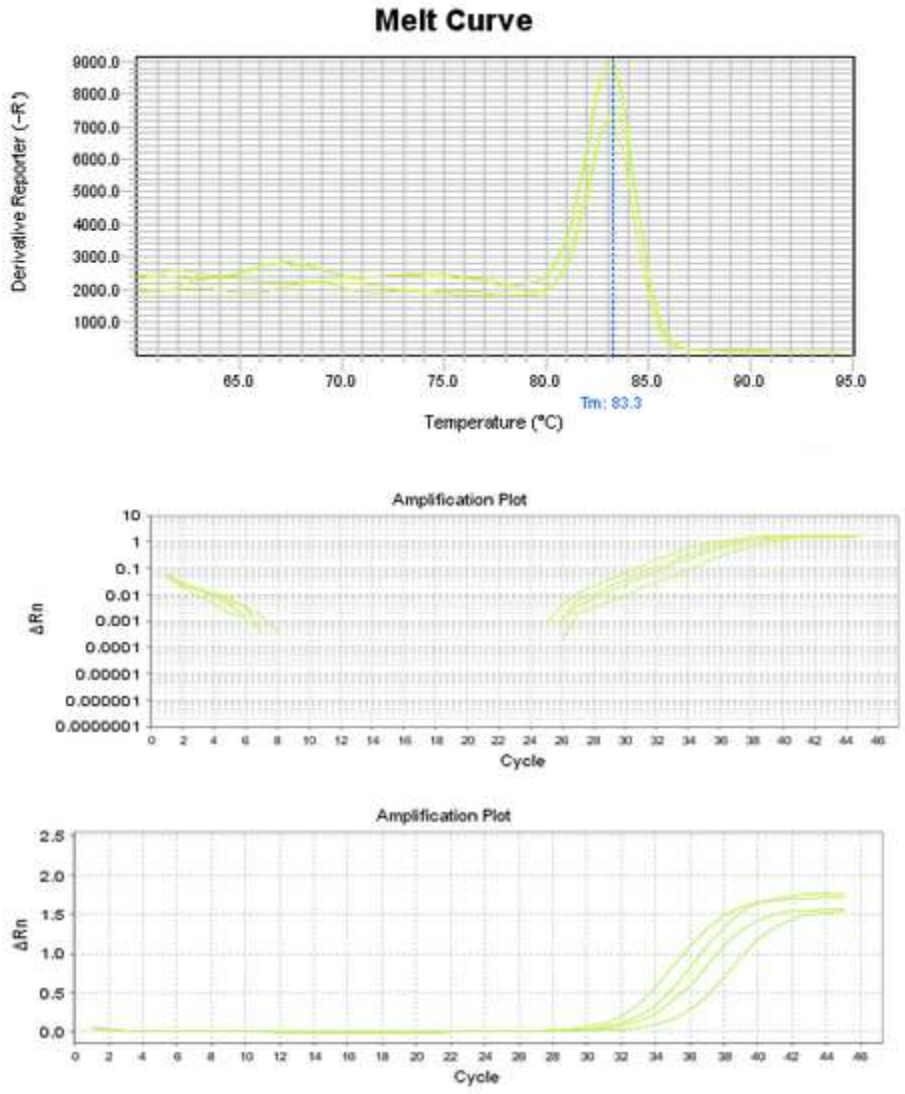

Figure 3. Effect of STAT6-siRNA separate and in combination with 5-FU on cell proliferation. A) STAT6 silencing reduced HT-29 cell proliferation compared with the control. B) In HT-29 cells, STAT6-siRNA silencing enhances chemosensitivity to 5-FU in a dose-dependent manner. The data were shown as mean±SD (ns= not significant; *P*< 0.01; *P*<0.001).

4-CDK4

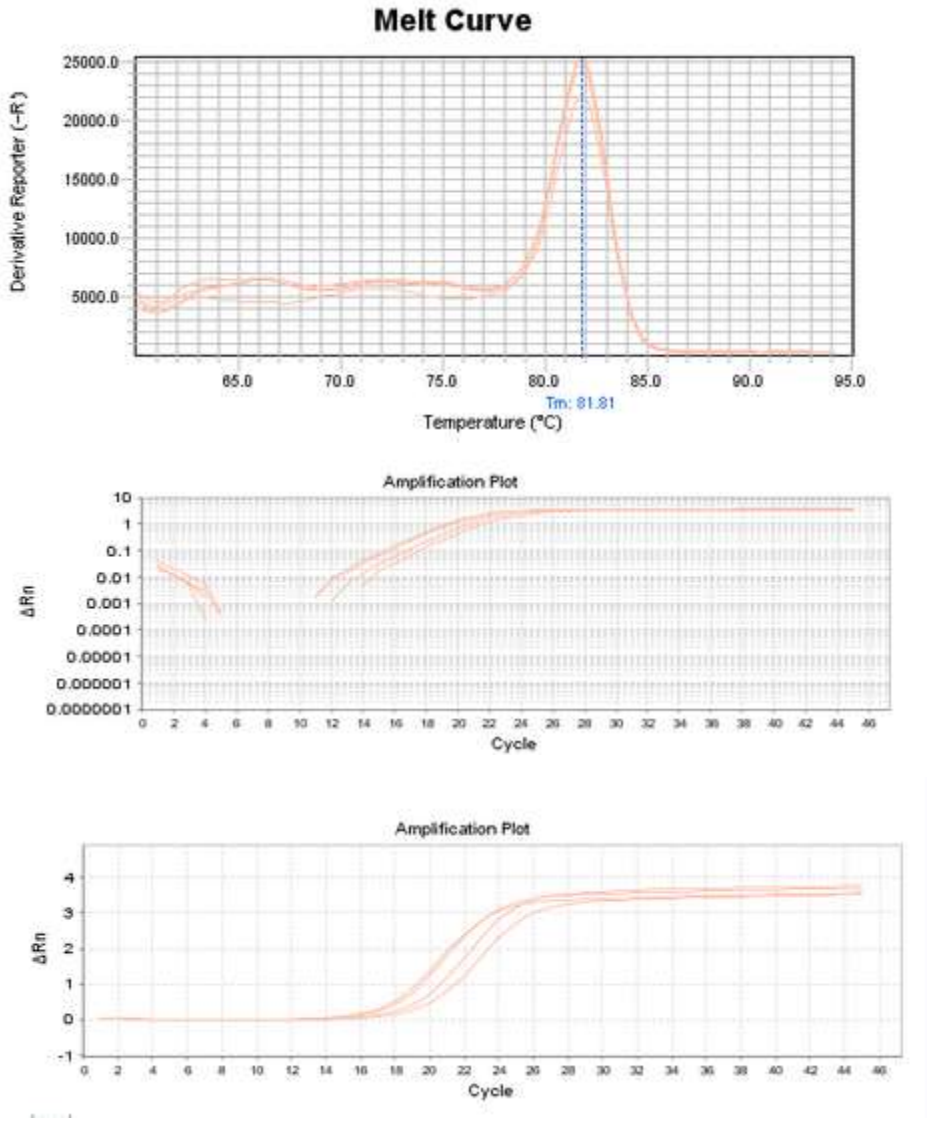

Figure 4. A) Annexin V-FITC/PI test revealed that STAT6-siRNA-transfected cells that were treated with 5-FU had higher apoptotic activity than STAT6-siRNA-transfected cells with no 5-FU treatment. B) The combined group qRT-PCR results showed a significantly higher expression of *caspase9* and *Bax* but a significantly lower expression of *Bcl2* ($P<0.05$, $P< 0.01$, $P<0 .001$, $P<0.0001$).

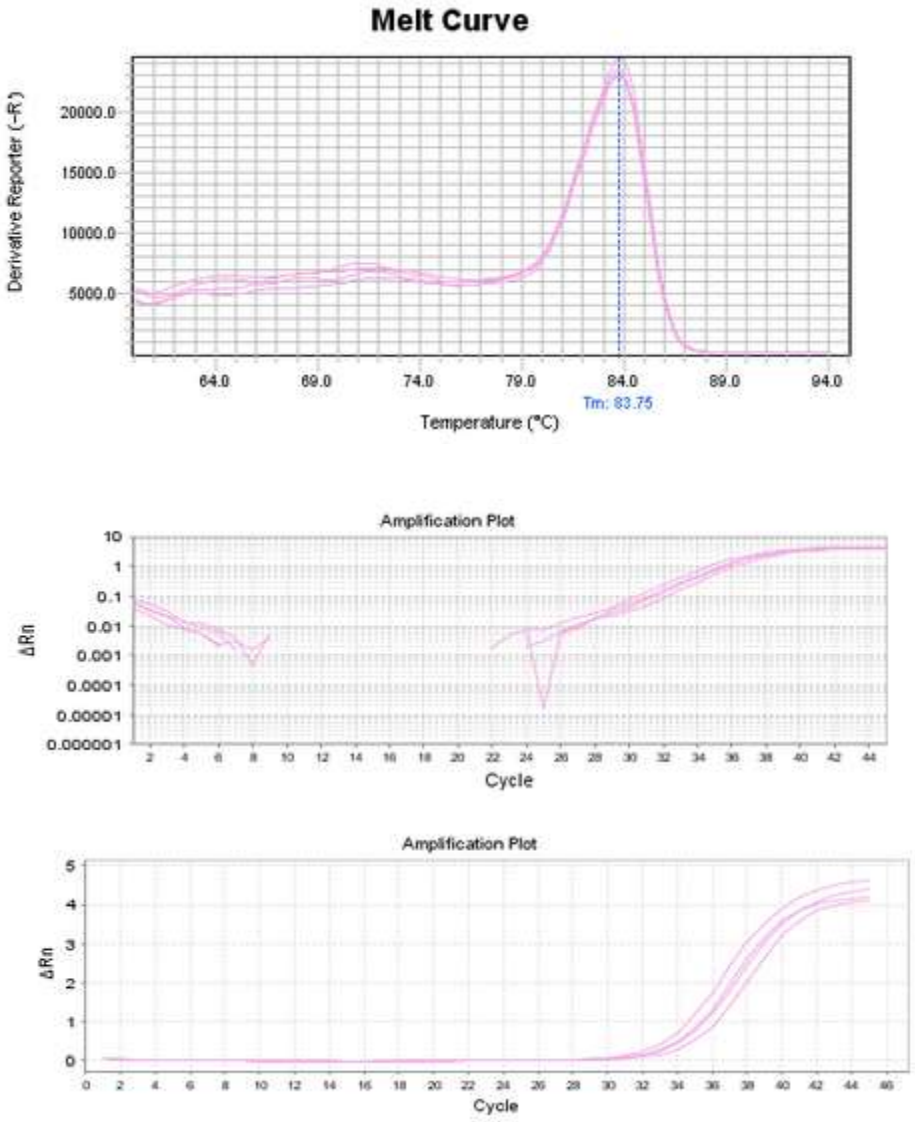

Figure 5. Effects of STAT6-siRNA and 5-FU combined therapy on HT-29 cell cycle distribution. A) Flow cytometry revealed a significant sub-G1 phase population in the combination group. B) In the combined group, *CDK4* and *cyclin D1* expression were significantly decreased by qRT-PCR. The findings were given as the mean of the experiments' standard deviations (ns= not significant; *P*<0 .001, *P*< 0.0001).

6-MMP9

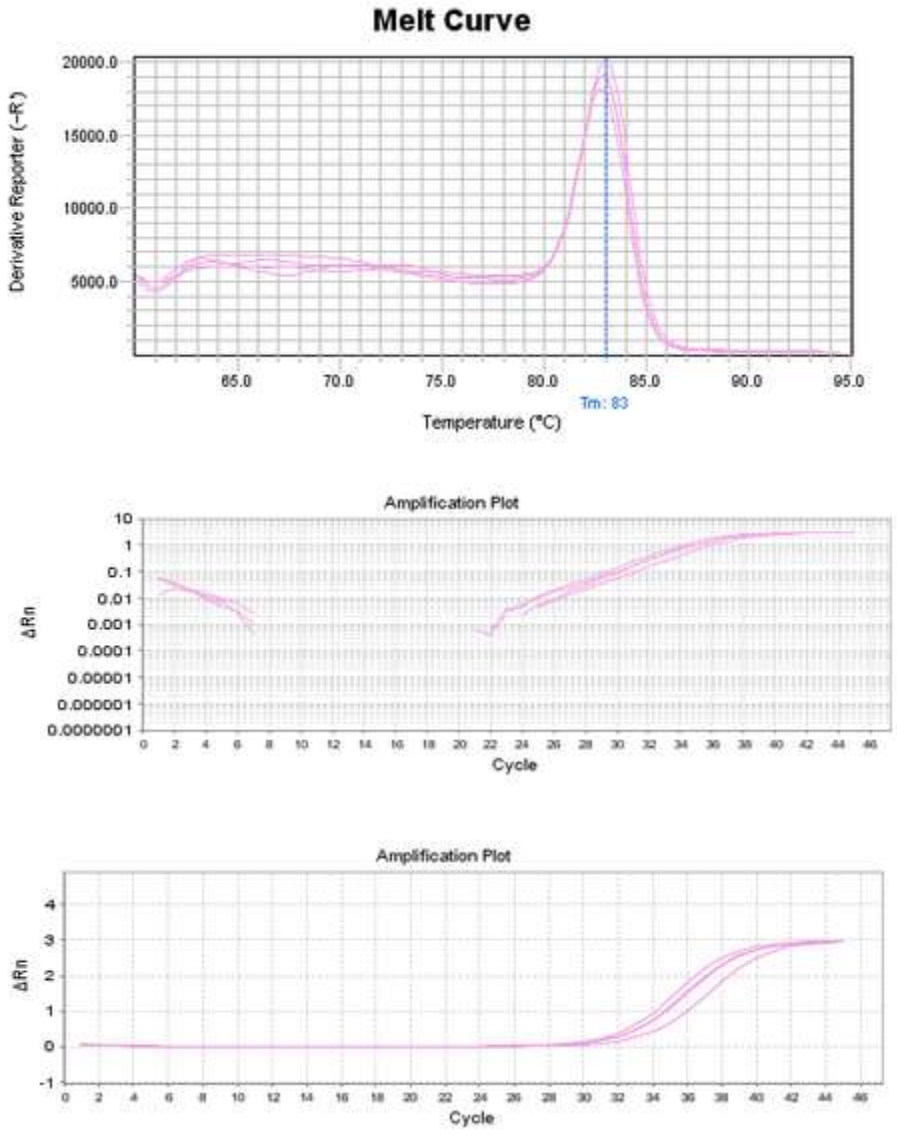

Figure 6. Combined effects of STAT6-siRNA and 5-FU treatment on HT-29 cell migration in a wound-healing assay. A) The rate of HT-29 cells migrated to the wound area showed that STAT6-siRNA suppression combined with 5-FU therapy reduced HT-29 cell migration. B) In the combination group, the results of qRT-PCR demonstrated a substantial decrease in the mRNA expression levels of *MMP9* (P<0.0001).

7-CD44

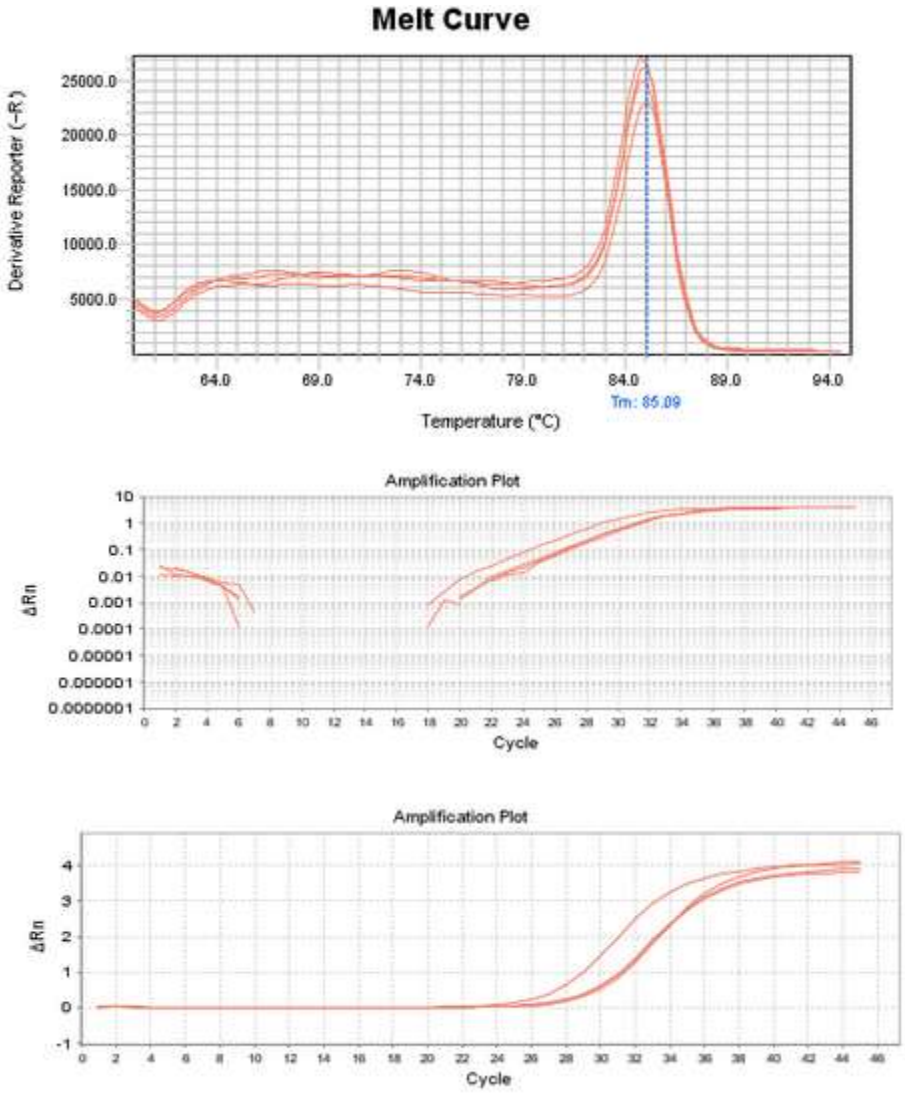

Figure 7. Effect of STAT6-siRNA combined with 5-FU on stemness properties in HT-29 cells. A) Compared with single groups, the combined treatment had fewer colonies. B) After inhibiting STAT6-siRNA with 5-FU, qRT-PCR revealed a significant reduction in *Sox2* and *CD44* mRNA expression. ($P < 0.0001$).

8-SOX2

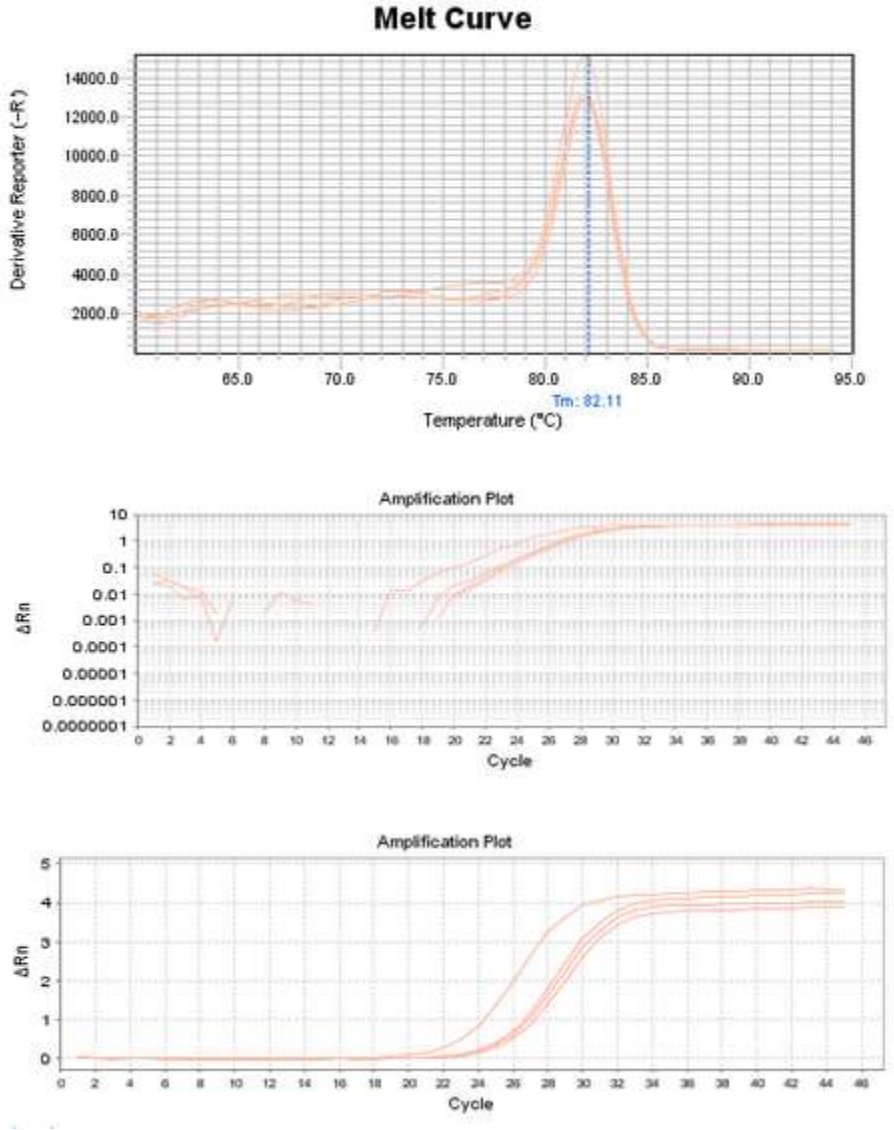

Figure 8. Co-expression networks.

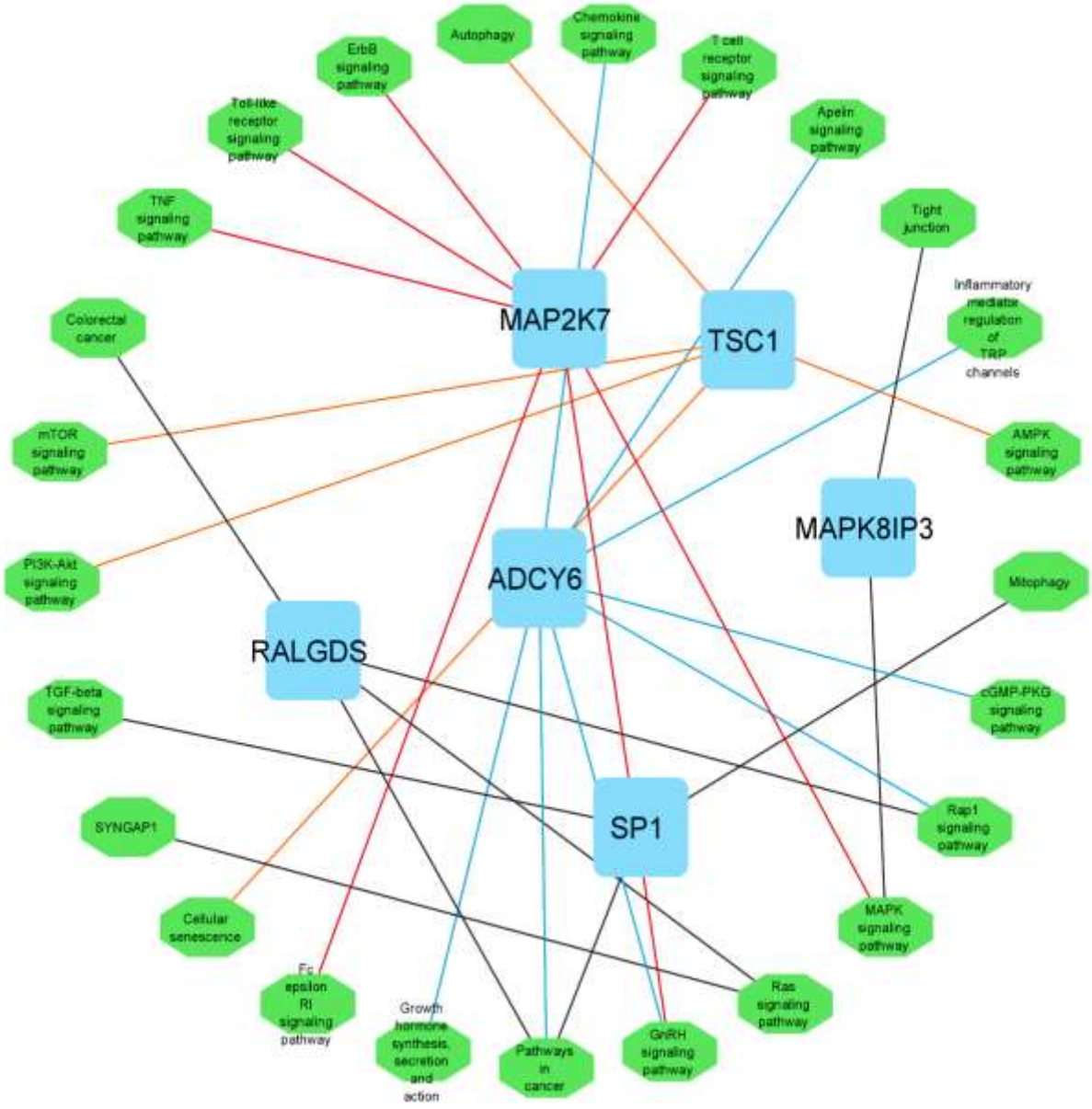

Figure 9. Pathways and the genes related to these pathways.