Supplementary Table S1. Summary of shRNA and siRNA Oligos

Name	Oligo Sequence
ARRB1 shRNA 1	CCGGGGAGAGTCTATGTGACGCTGACTCGAGTCAGCGTCACATAGACTCTCCTTTTTG
ARRB1 shRNA 2	CCGGGCAGGAACGCCTCATCAAGAACTCGAGTTCTTGATGAGGCGTTCCTGCTTTTTG
ARRB1 shRNA 3	CCGGTGGAACTGCCCTTCACCCTAACTCGAGTTAGGGTGAAGGGCAGTTCCATTTTTG
Sh-NC	GGATCCGTTCTCCGAACGTGTCACGTTTCAAGAGAACGTGACACGTTCGGAGAATTTTTT
TAK1 siiRNA	GUAAACACCAGCUCAUGGCAUGAGC

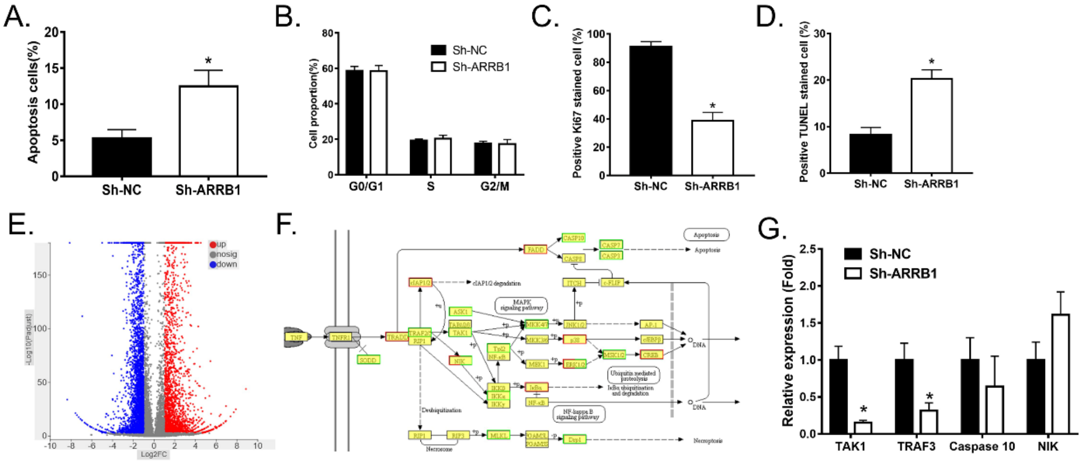

Figure Supplementary 1.

A. Percentage of apoptotic cells in ARRB1 knockdown NOZ cells, compared with sh-NC group. **B.** Cell cycle percentage distribution in cells mentioned above. **C and D.** The positive stained cells of Ki67 and TUNEL in subcutaneous tumors after silencing the ARRB1 and control. **E.** Volcano plot (fold change > 2.5 and P value < 0.01) detected by RNA-seq analysis. **F.** TNF signaling pathway showed upregulated (red) and downregulated (green) differentially expressed genes between the sh-NC and shARRB1. **G.** The mRNA levels of the aforementioned genes (TAK1, TRAF3, Caspase 10 and NIK) were measured by RT-PCR**.** * $P < 0.05$.