## Supplementary Table S1. Summary of shRNA and siRNA Oligos

| Name       | Oligo Sequence                                                                 |
|------------|--------------------------------------------------------------------------------|
| ARRB1 shRNA 1 | CC GG GG AG AG TG CT AT TG AC GCT G ACT CG  
|             | AG TC AG CG TG AC AT GA CT GG ACT TG CT C T C T T T T T G                  |
| ARRB1 shRNA 2 | CC GG GC AG GA AC GC CT CAT CA AG GA ACT CG  
|             | AG TT CT TG AT GA GG CG T T C T G C T T T T T T G                        |
| ARRB1 shRNA 3 | CC GG TG GA ACT GC C C T T C ACC CT A A C T CG  
|             | AG TT AG GG GT GA AG GG CG AT T C C A T T T T T T G                   |
| Sh-NC      | GG AT CC GT TT CT CC GA AC GT GC AC AC TT T T CA  
|             | AG GA AA CG TG AC AC GT T C GC GA AG A AT T T T T T T T                  |
| TAK1 siRNA | GU AA AC ACC AG CU CA UGG CA UG AG C                                                  |
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.