Figure S1. RHOA mutations in digestive tract cancer cell lines. (A) Mutations in RHOA detected by Sanger sequencing. Arrows indicate mutations. (B) Electrophoresis of the amplified products of DNA isolated from CCK-81 cells (right) and a control human genomic DNA (left) using mutant specific primers for *RHOA*^{R5Q} and *RHOA*^{Y42C}, wild-type specific primers, and intron primers. (C) Sanger sequencing of the compound mutation of *RHOA*^{R5Q} and *RHOA*^{Y42C} in CCK-81, in which each mutant strand and wild-type strand was separately analyzed. Arrows indicate mutations. IF, intron forward; IR, intron reverse; MF, mutant specific forward; MR, mutant specific reverse; NC, negative control; WF, wild-type specific forward; WR, wild-type specific reverse.

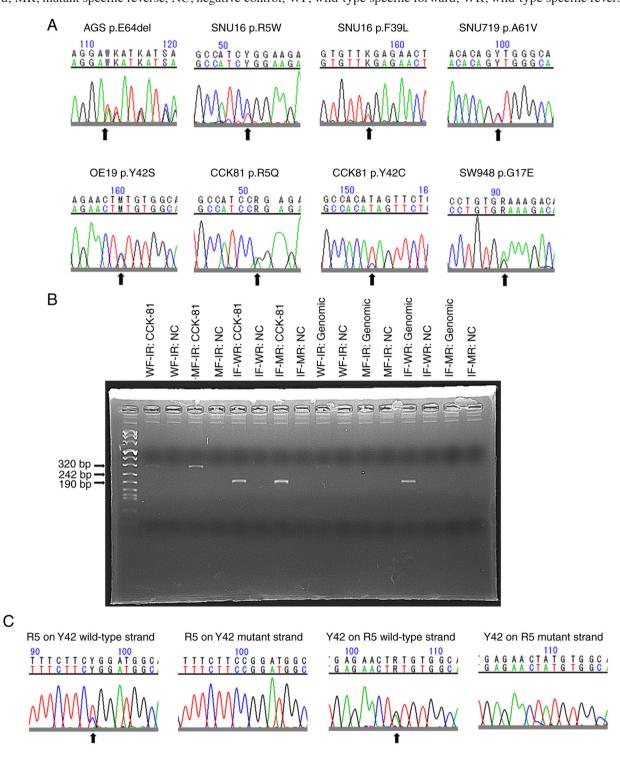


Figure S2. Pie charts indicate Gene Ontology analysis of significantly altered genes after RHOA knockdown. Ontologies are listed in Supplementary Table SV. These figures were generated by using PANTHER Classification System (http://pantherdb. org/).

