Figure S1. TRAP1 mRNA expression in human colorectal cancer from public databases and the efficiency of transfection of HCT116 cells and transduction of p9T organoids. (A) Boxplot graph of TRAP1 gene expression in colorectal cancer comparing normal human colorectal mucosa (n=160) and primary colorectal cancer (n=160), based on gene chip data of TNMplot. The statistical significance of differential expression (P<0.001=3.02e-25) was evaluated using the Kruskal-Wallis test. (B) Reverse transcription-quantitative PCR for TRAP1 in HCT116 cells transiently silenced or not for TRAP1 and exposed to hypoxia (0.5% O_2) or normoxia (20% O_2) for 8 and 24 h. (C) Reverse transcription-quantitative PCR for TRAP1 in 293T and HCT116 cells, respectively transduced with four different shTRAP1 lentiviruses (#1, #2, #3 and #4) and control vector pMOCK. (D) Reverse transcription-quantitative PCR for TRAP1 in p9T organoids transduced with shTRAP1 #1 and shTRAP1 #3 lentiviruses. (E) Reverse transcription-quantitative PCR for TRAP1 in p9T organoids exposed to hypoxia (0.5% O_2) or normoxia (20% O_2) for 8 and 24 h. TRAP1 #3 lentiviruses. (E) Reverse transcription-quantitative PCR for TRAP1 in p9T organoids exposed to hypoxia (0.5% O_2) or normoxia (20% O_2) for 8 and 24 h. TRAP1 #3 lentiviruses.

