

Figure S1. Effect of paraquat treatment on cellular viability. Equal numbers of (A) HT-29 and (B) HCT-116 cells were seeded in triplicates in 6-well plates and grown for 48 h. Media was replaced with indicated concentrations of paraquat and incubated for an additional 24 h. Scale bar, 50  $\mu$ m. Cellular viability was measured using trypan Blue staining and viability was presented relative to non-treated control. \*\*P<0.01 and \*\*\*P<0.001.

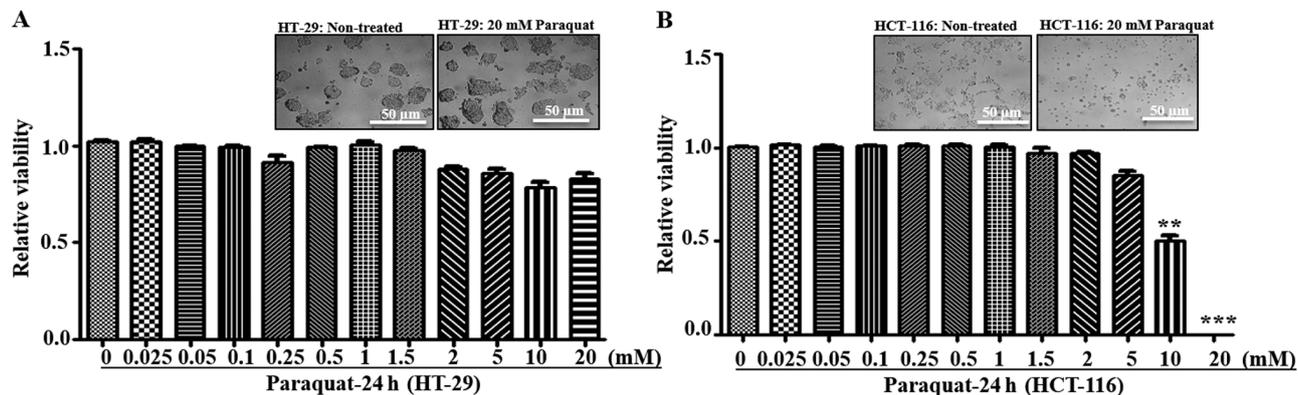


Figure S2. Analysis of mitochondrial C-I gene expression, mitochondrial functions and mitochondrial biogenesis. (A) mRNA expression of mtDNA encoded C-I subunit genes (ND-1, 2, 4 4L, 6) was measured using RT-qPCR. (B) Mitochondrial functions such as (B-a) ROS levels were measured via staining with 2',7'-dichlorodihydrofluorescein diacetate, (B-b) mitochondrial superoxide levels were measured by MitoSOX™ Red staining. In both of these measurements, cells were counterstained with Hoechst and used for normalization. (B-c) Total cellular ATP content was measured using ATP detection kit and normalized with total protein levels. (B-d) MMP was measured after tetramethylrhodamine methyl ester perchlorate staining and normalization with Hoechst-33342 reading. (C-a) Mitochondrial DNA copy number was determined using SYBR green qPCR. mRNA expression levels of (C-b) mitochondrial biogenesis markers PGC1- $\alpha$  and (C-c) *TFAM* were analyzed via RT-qPCR. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\* $P < 0.001$ . RT-qPCR, reverse transcription-quantitative PCR; PGC1- $\alpha$ , Peroxisome proliferator-activated receptor  $\gamma$  coactivator  $\alpha$ ; TFAM, mitochondrial transcription factor A; mtDNA, mitochondrial DNA; C-, complex; ROS, reactive oxygen species; MMP, mitochondrial membrane potential.

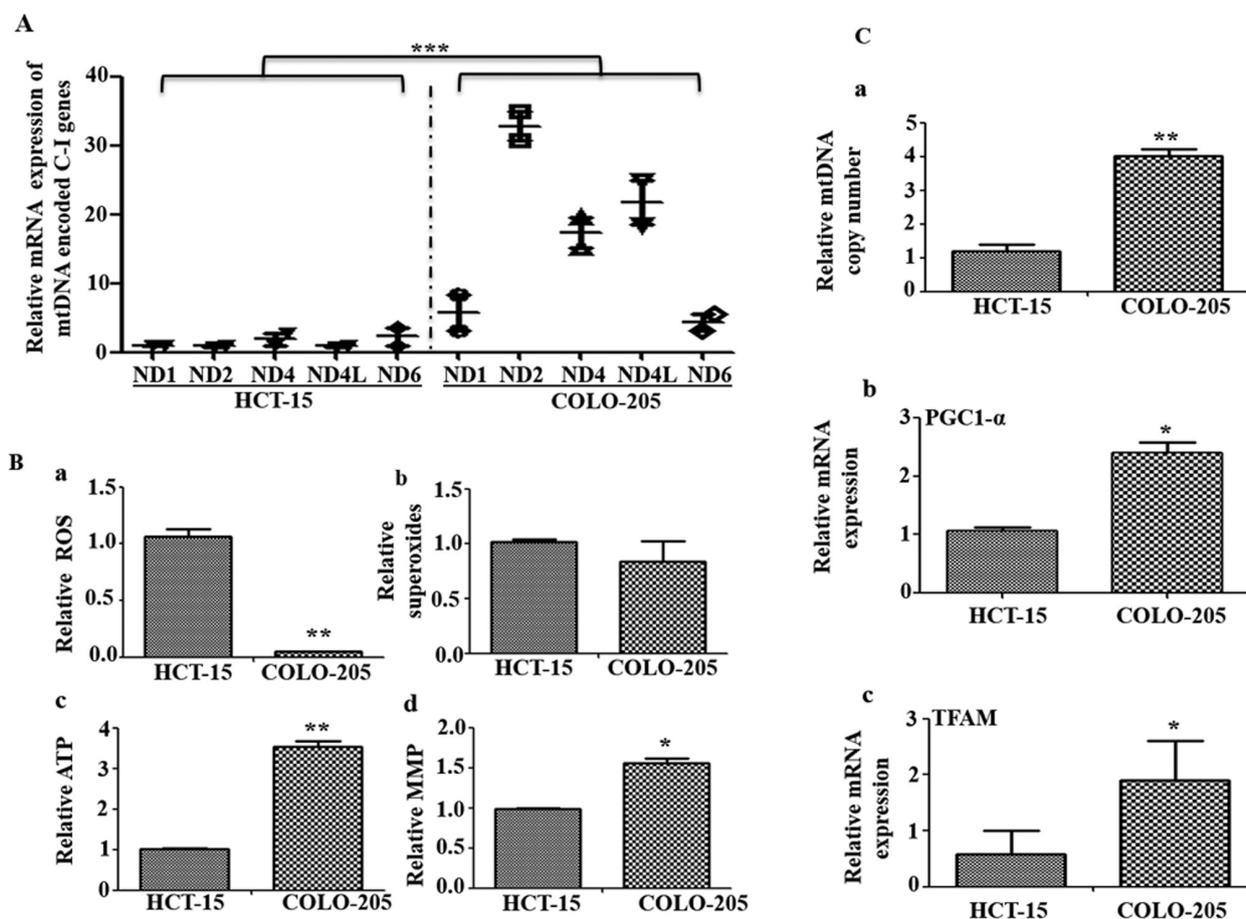


Figure S3. Effect of paraquat treatment on signaling pathways in HCT-116 cells. HCT-116 cells were treated with paraquat (10 mM) for indicated time points and RNA was isolated for cDNA preparation followed by RT-qPCR. mRNA expression levels of (A) AKT-1, (B) HIF1- $\alpha$ , (C) cMyc, (D) Survivin, (E) *SLC2A1*, (F) *CA-9* and (G) *VEGF* were analyzed using RT-qPCR. Fold changes were calculated relative to non-treated control at 0 h. \* $P < 0.05$  and \*\* $P < 0.01$ . HIF1- $\alpha$ , hypoxia inducible factor 1 subunit  $\alpha$ ; SLC2A1, solute carrier family 2 member 1; CA-9, carbonic anhydrase-9; RT-qPCR, reverse transcription-quantitative PCR.

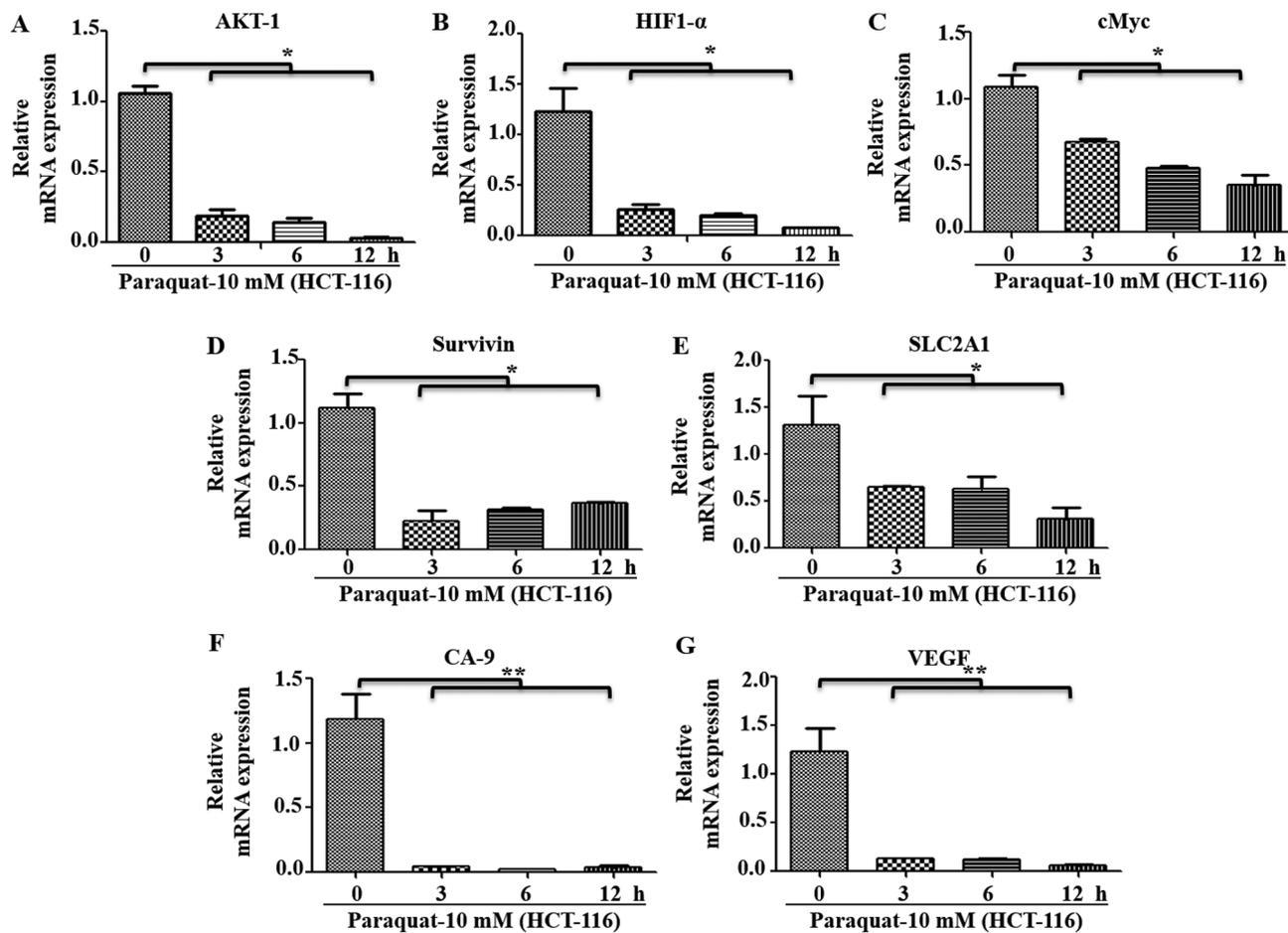


Table SI. List of primers used for gene expression profiling of various signaling pathway genes.

Gene	Primer	Sequence (5'→3')	(Refs.)
PGC1- $\alpha$	Fwd	GGCAGAAGGCAATTGAAGAG	Onishi <i>et al</i> (23)
	Rev	TCAAAACGGTCCCTCAGTTC	
TFAM	Fwd	CCGAGGTGGTTTTTCATCTGT	
	Rev	GCATCTGGGTTCTGAGCTTT	
$\beta$ -actin	Fwd	GATCATTGCTCCTCCTGAGC	
	Rev	ACATCTGCTGGAAGGTGGAC	
AKT-1	Fwd	GTCATCGAACGCACCTTCCAT	Spandidos <i>et al</i> (24)
	Rev	AGCTTCAGGTACTCAAATCTCGT	
HIF1- $\alpha$	Fwd	CCAGCAGACTCAAATACAAGAACC	Li <i>et al</i> (22)
	Rev	TGTATGTGGGTAGGAGATGGAGAT	
cMyc	Fwd	GTCAAGAGGGCGAACACACAAC	Spandidos <i>et al</i> (24)
	Rev	TTGGACGGACAGGATGTATGC	
Survivin	Fwd	AGGACCACCGCATCTCTACAT	
	Rev	AAGTCTGGCTCGTTCTCAGTG	
SLC2A1	Fwd	ATTGGCTCCGGTATCGTCAAC	
	Rev	GCTCAGATAGGACATCCAGGGTA	
CA-9	Fwd	CCGAGCGACGCAGCCTTTGA	Wheaton <i>et al</i> (25)
	Rev	GGCTCCAGTCTCGGCTACCT	
VEGF	Fwd	TACCTCCACCATGCCAAGTG	
	Rev	GATGATTCTGCCCTCCTCCTT	

Fwd, forward; Rev, reverse; HIF1- $\alpha$ , hypoxia inducible factor 1 subunit  $\alpha$ ; SLC2A1, solute carrier family 2 member 1; CA-9, carbonic anhydrase-9; ATG5, autophagy related 5; PGC1- $\alpha$ , Peroxisome proliferator-activated receptor  $\gamma$  coactivator  $\alpha$ ; TFAM, mitochondrial transcription factor A.