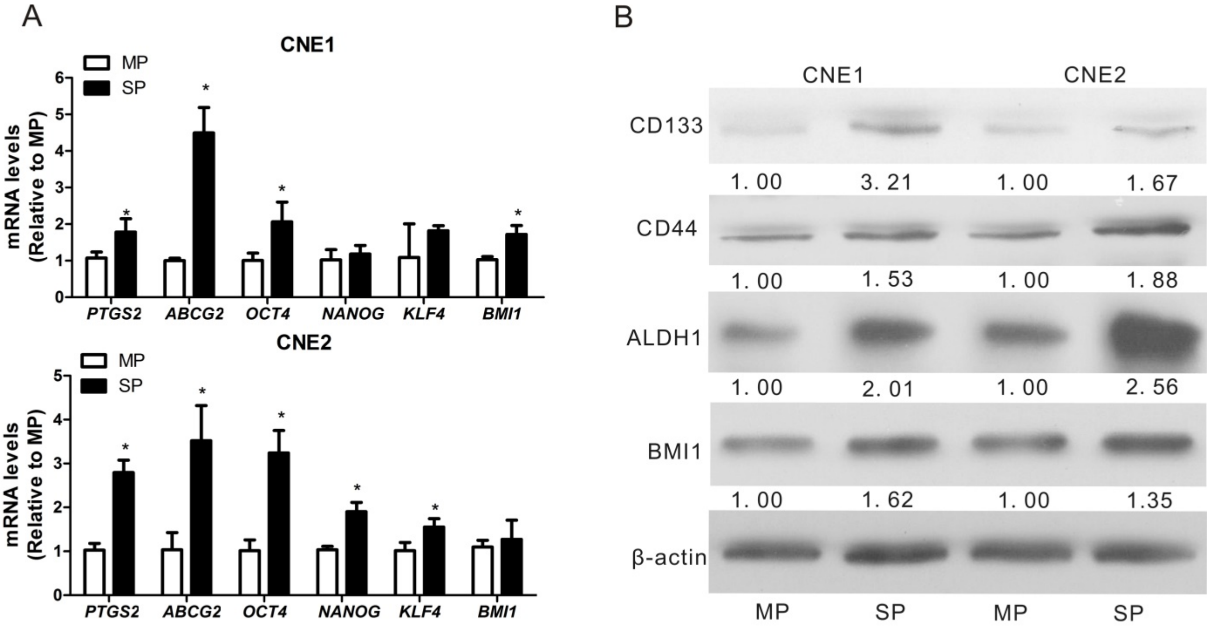

Fig.S1 (A) The mRNA levels of *PTGS2*, *ABCG2*, *OCT4*, *NANOG*, *KLF4*, and *BMI1* in side population (SP) and main population (MP) cells of CNE1 and CNE2 were detected with the quantitative real-time polymerase chain reaction (qRT-PCR). The target gene expression was normalized to *ACTB*. * $P < 0.05$ as compared with MP cells. (B) The protein levels of CD133, CD44, ALDH1, and BMI1 in SP and MP cells of CNE1 and CNE2 as detected by WB.

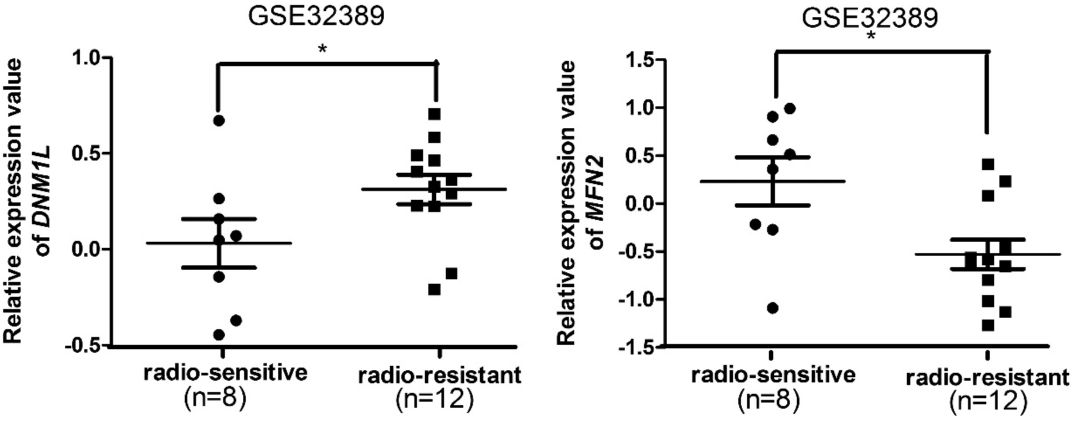

Fig.S2 *DNM1L* and *MFN2* expression levels in tumor tissues from cohorts of radio-sensitive and -resistant. NPC patients were shown by scatter plots. The relative expression values were obtained from NCBI, GEO database (Accession No. GSE32389). The light horizontal lines show the median values. * $P < 0.05$ as compared with radio-sensitive group.

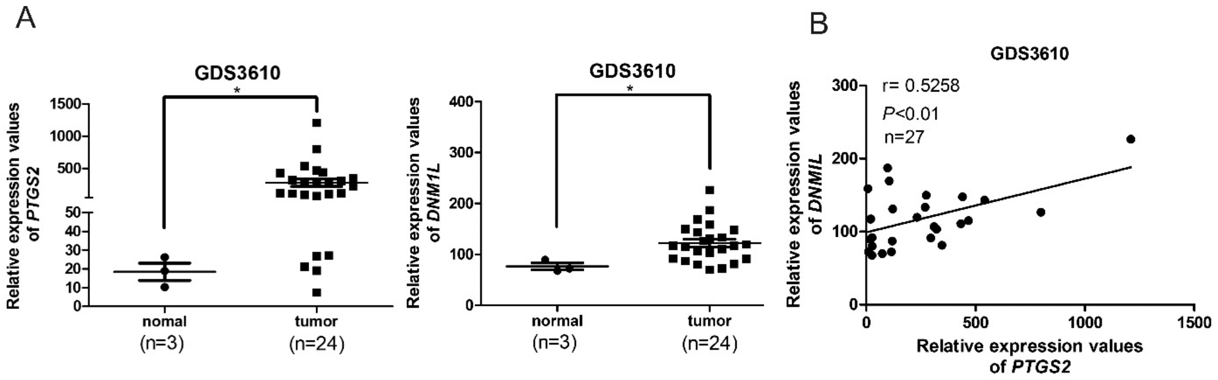

Fig.S3 (A) *PTGS2* and *DNM1L* expression levels in cohorts of NPC patients were shown by scatter plots. The relative expression values were obtained from NCBI, GEO database (Assession No. GDS3610). * $P < 0.05$ as compared with normal group. (B) Pearson's correlation analysis of *PTGS2* and *DNM1L* mRNA levels.

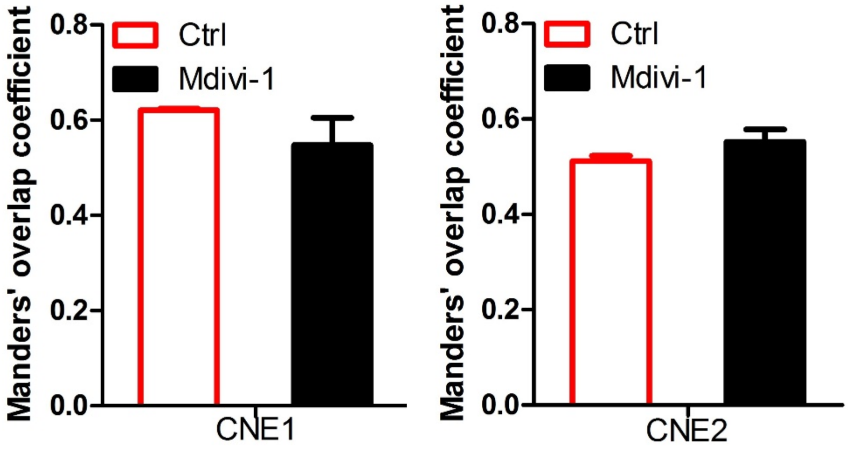

Fig.S4 CNE1 and CNE2 cells were treated with 20 μM Mdivi-1 for 24 h. Manders' overlap coefficients for the co-localization of COX-2 with mitochondria is shown in bar graphs.

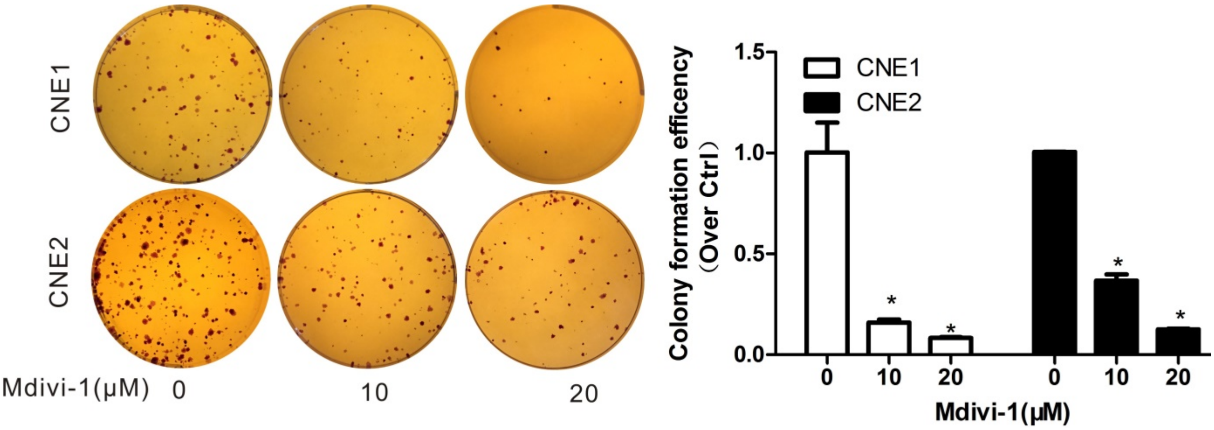

Fig.S5 The colony formation assay was conducted with treatments of 0, 10, or 20 μM Mdivi-1 for 24 h in CNE1 and CNE2 cells. Representative images of colonies are shown and the right-hand panel is bar chart of colony formation efficiency (CFE). * $P < 0.05$ as compared with Ctrl group.

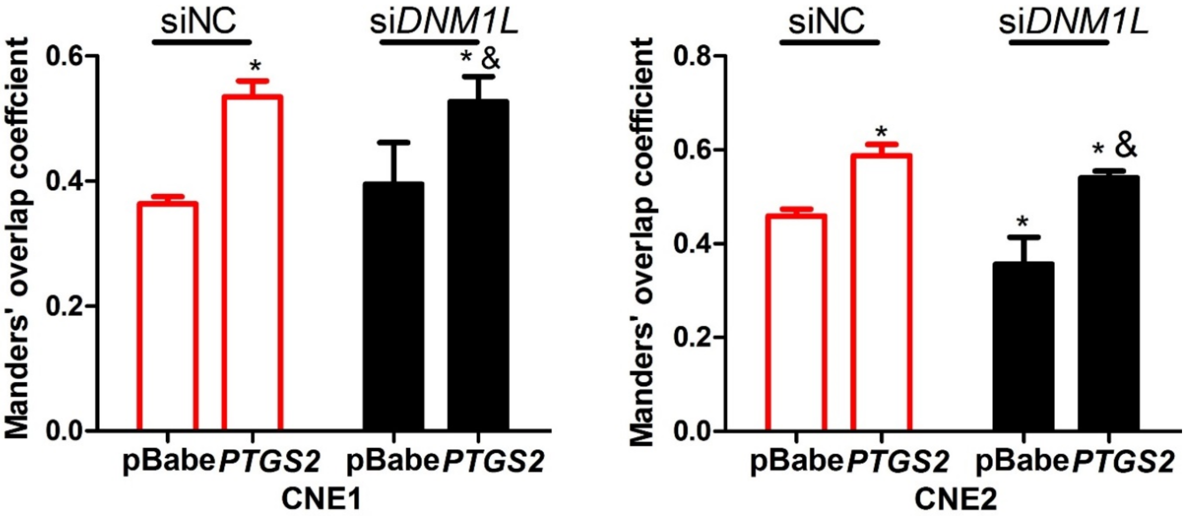

Fig.S6 CNE1-pBabe, CNE1-*PTGS2*, CNE2-pBabe, and CNE2-*PTGS2* cells were transfected with siNC or si*DNM1L* (50 nM) for 12 h. The co-localization of COX-2 (green) and mitochondria (red) was determined by confocal microscopy. Manders' overlap coefficient for the co-localization of COX-2 with mitochondria is shown in bar graphs. * $P < 0.05$ as compared with -pBabe (siNC) cells. $^{\&}$ $P < 0.05$ as compared with -pBabe (si*DNM1L*) cells.

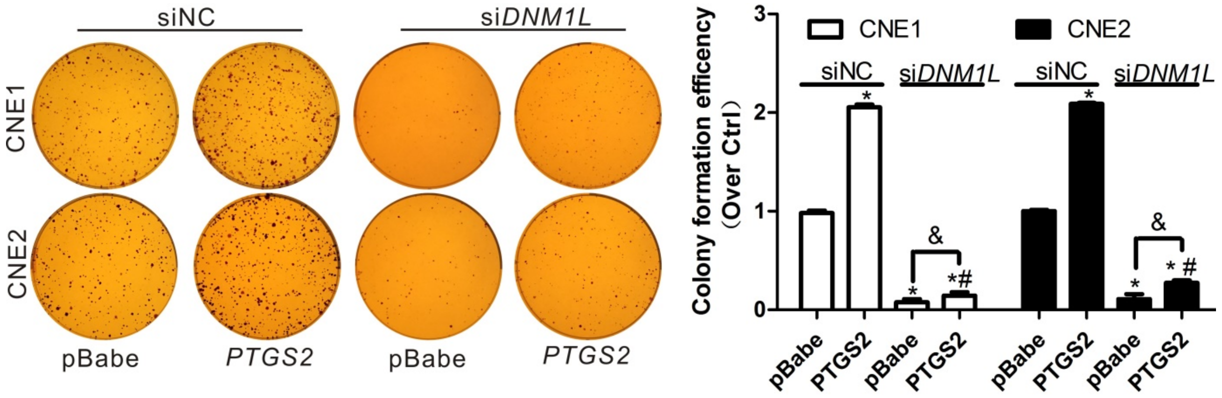

Fig.S7 CNE1-pBabe, CNE1-*PTGS2*, CNE2-pBabe and CNE2-*PTGS2* cells were transfected with siNC or si*DNM1L* (50 nM) for 12 h. The colony formation assay was conducted. Representative images of colonies are shown. The right-hand panel is bar chart of colony formation efficiency (CFE). * $P < 0.05$ as compared with -pBabe (siNC) cells. $^{\#}$ $P < 0.05$ as compared with -*PTGS2* (siNC) cells. $^{\&}$ $P < 0.05$ as compared with -pBabe (si*DNM1L*) cells.

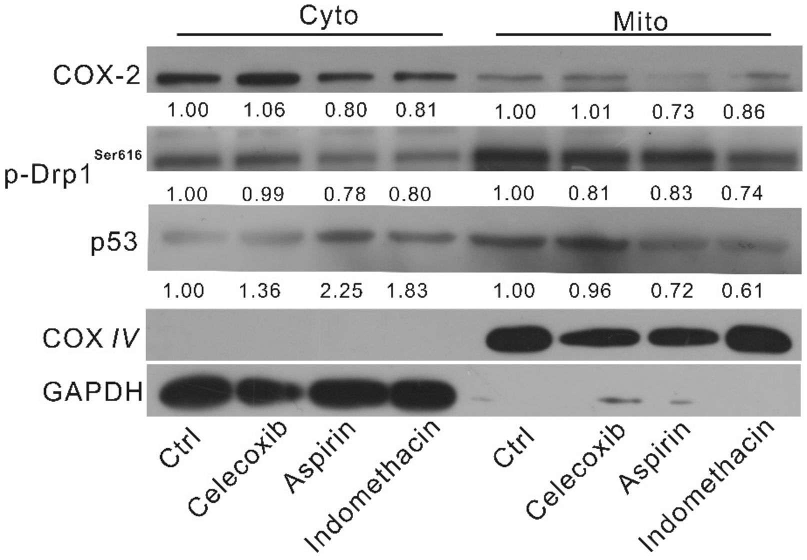

Fig.S8 CNE2 cells treated with or without 20 μM aspirin, celecoxib or indomethacin for 24 h. Cytosolic (Cyto) and mitochondrial (Mito) fractions were subjected to WB assay. Expressions of COX-2, p-Drp1^{Ser616}, p53 are shown.

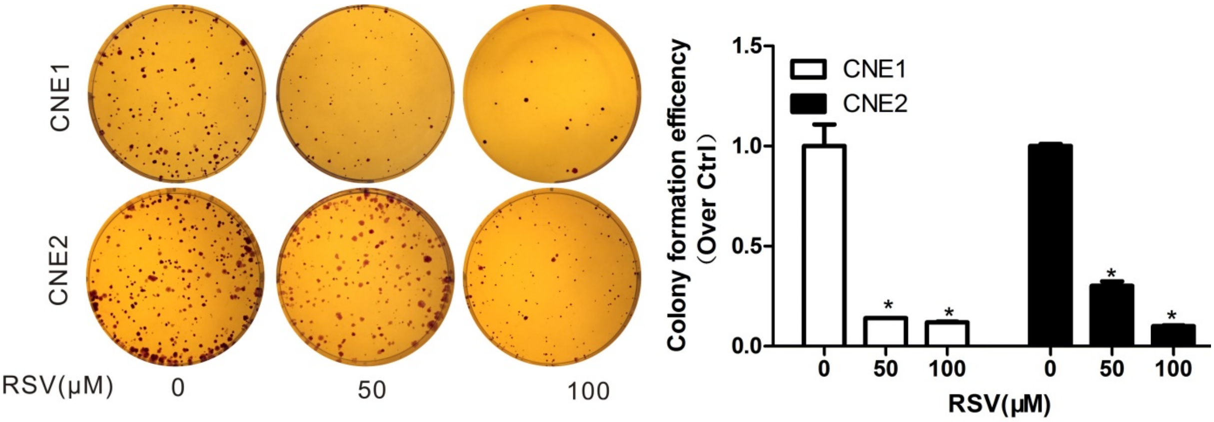

Fig.S9 Colony formation efficiencies of the CNE1 and CNE2 cells treated with 0, 50, or 100 μM resveratrol (RSV) for 24 h. The right-hand panel is bar chart of colony formation efficiency (CFE). * $P < 0.05$ as compared with Ctrl group.

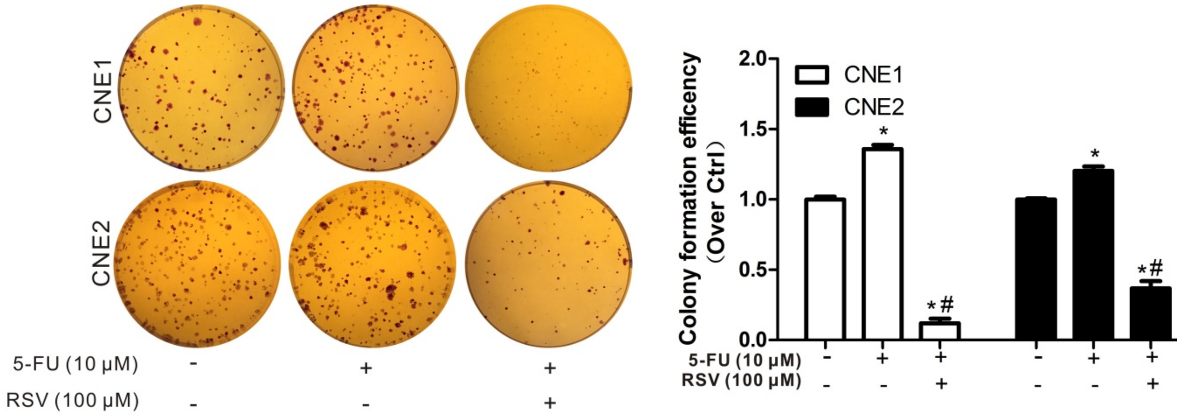

Fig.S10 Colony formation efficiencies of the CNE1 and CNE2 cells treated with 10 μM 5-FU in the presence or absence of 100 μM resveratrol (RSV) for 24 h. The right-hand panel is bar chart of colony formation efficiency (CFE). * $P < 0.05$ as compared with Ctrl. $^{\#}P < 0.05$ for combination treatment vs. 5-FU alone.

Table S1. Primers used for qRT-PCR in this study

Gene	Forward primer	Reverse primer
PTGS2	5'-CAG CCA TAC AGC AAA TCC TTG-3'	5'-CAA ATG TGA TCT GGA TGT CAA C-3'
ABCG2	5'-ATA TTA TCG AAT ATC AAT GGG ATC A-3'	5'-CAA TGA AAA TCT TCA GGA GAT A-3'
OCT4	5'- CAC CAG GGC GTG ATG GT -3'	5'-ACC ACA CTC GGA CCA CAT C-3'
NANOG	5'-AAC CTC AGC TAC AAA CAG GT-3'	5'-AGG TCT GGT TGC TCC ACA T-3’
KLF4	5'-CTC CAT TAC CAA GAG CTC AT-3'	5'-GGT AAG GTT TCT CAC CTG T-3
BMI1	5'-ACA TTC CTT CTG TAA AAC GTG-3'	5'-CAT TGG CAG CAT CAG CAG-3'
ACTB	5’-CAC CAG GGC GTG ATG GT-3’	5’-CTC AAA CAT GAT CTG GGT CAT-3

Table S2 GEO Datasets used in this study

Data source	**Platform**	**Probes/Genes**	**NPC Sample No.**	**Patient Ethnicity**	**Etiology**	**Source URL**
GEO (GDS3341)	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	54694/47,000	41	Asian	EBV	http://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS3341
GEO (GDS3610)	[HG-U133A] Affymetrix Human Genome U133A Array	39,000/ 33,000	28	Chinese	EBV	http://www.ncbi.nlm.nih.gov/sites/GDSbrowser?acc=GDS3610
GEO (GSE32389)	UGI Human 14112 V1.0	14112/8220	20	Chinese	-	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32389