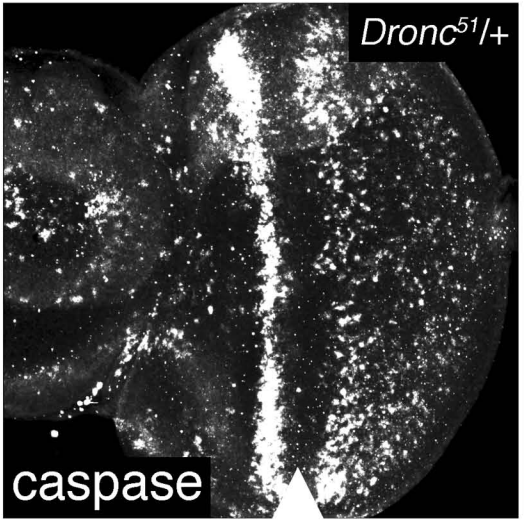
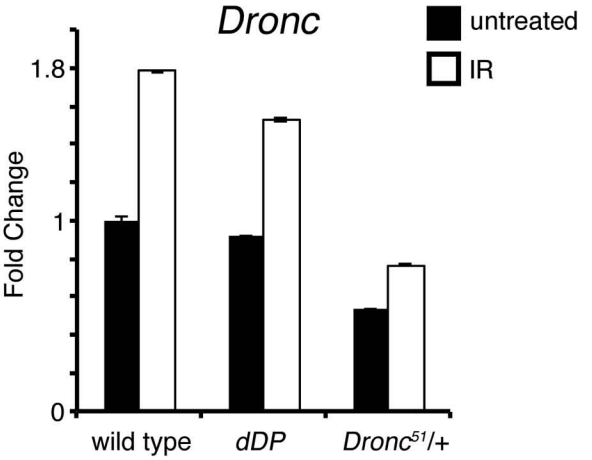
Ambrus Supplemental Figure S1

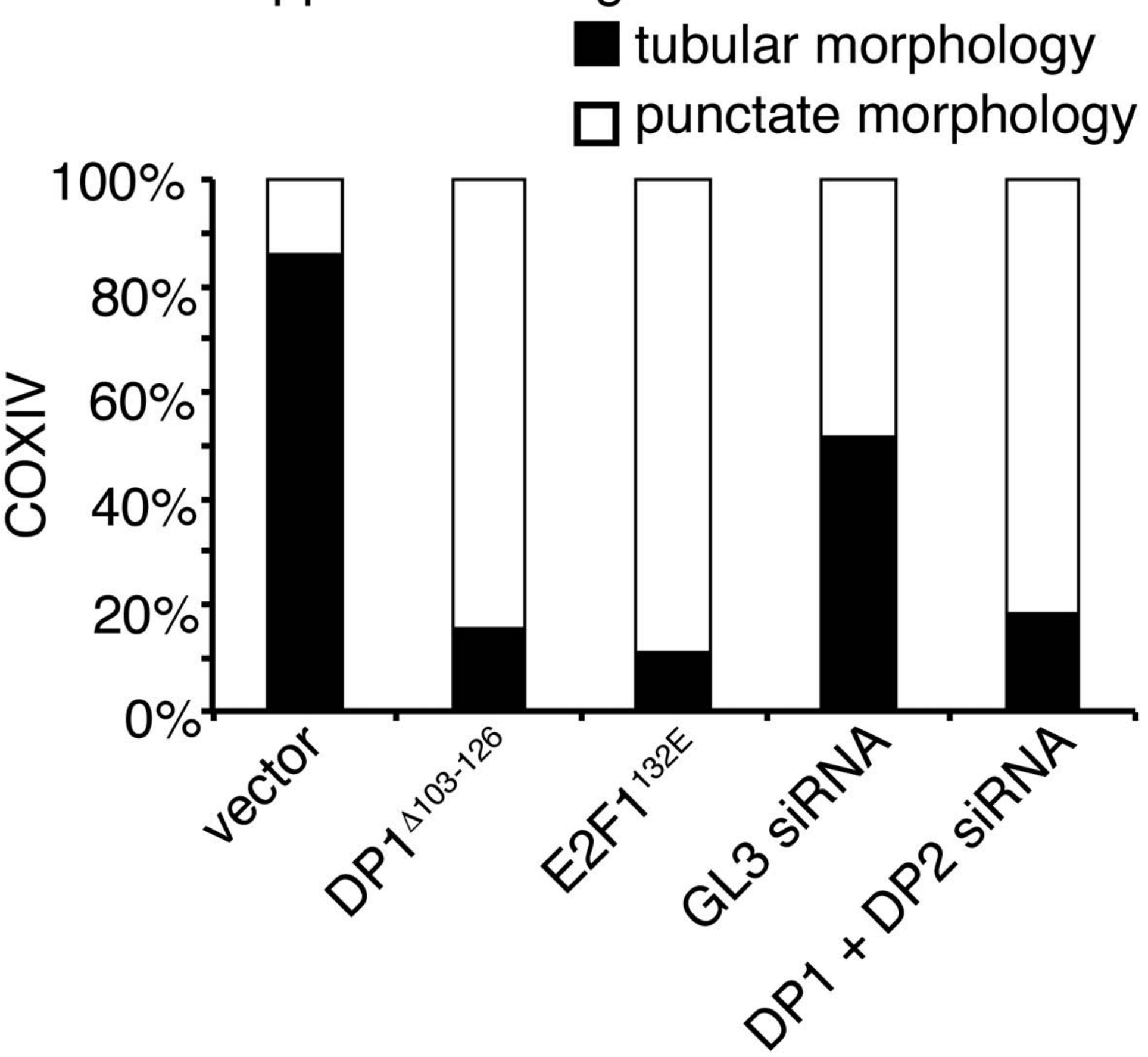
A



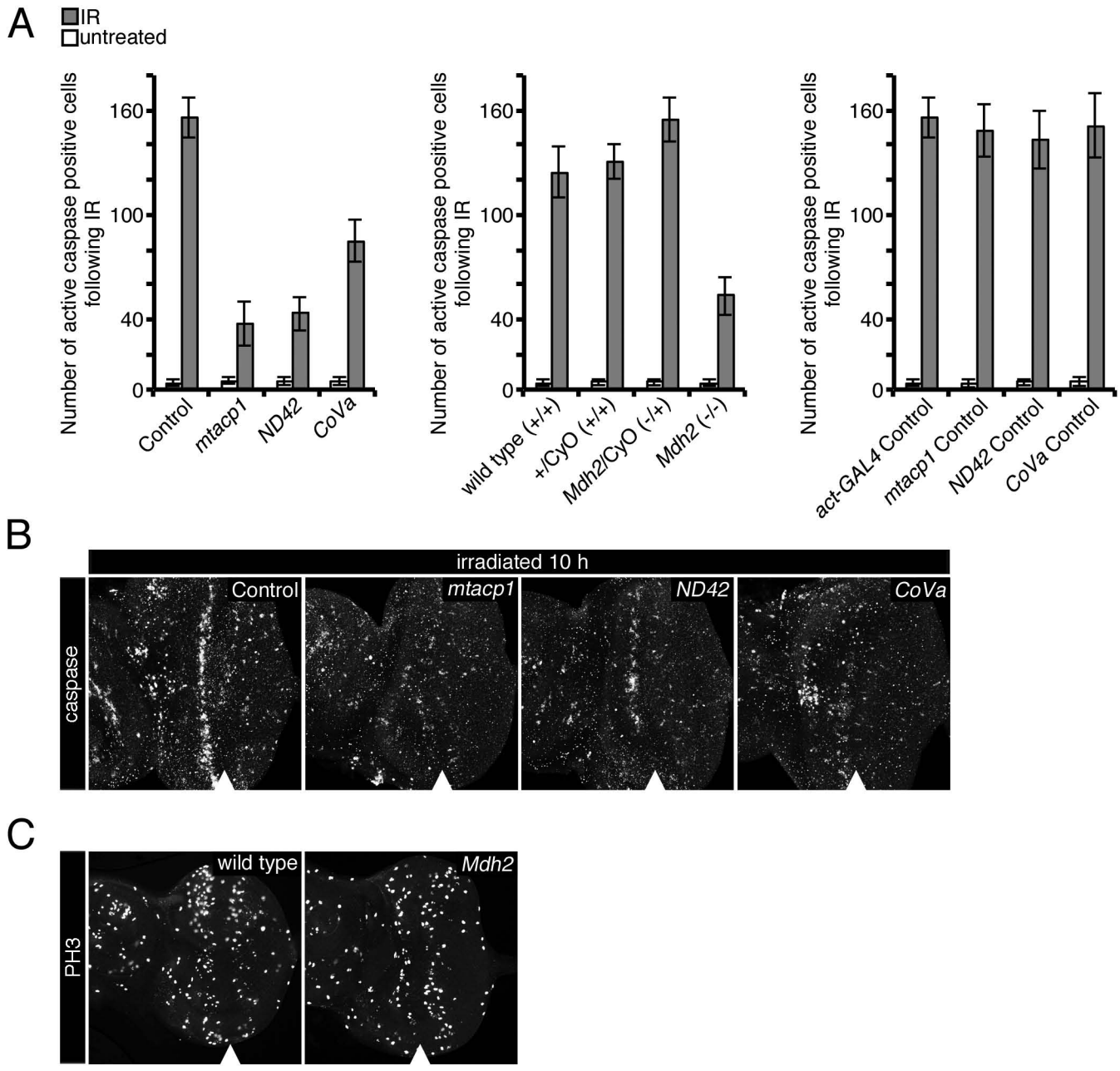
B



Ambrus Supplemental Figure S2



Ambrus Supplemental Figure S3



SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Eye discs with reduced expression of Dronc efficiently undergo irradiation-induced apoptosis, related to Figure 1.

(A) Active caspase immunostaining was used to detect apoptotic cells 4h after IR in *Dronc*^{51}/+ eye discs. The eye disc is oriented with the posterior to the right. An arrowhead indicates the morphogenetic furrow. (B) RNA was isolated from wild type, *dDP* mutant, and *Dronc*^{51}/+ larvae which were either untreated or IR. Quantitative real-time PCR was used to measure the expression of *Dronc*. Expression levels of *Dronc* for untreated (black bars) or IR (white bars), for wild type, *dDP* mutant, and *Dronc*^{51}/+ eye discs are normalized to wild type untreated (± SD, using 3 replicates for each genotype and treatment).

Supplemental Figure S2. Mitochondria display structural abnormalities in SAOS-2 cells deficient in E2F1 activity, related to Figure 5.

SAOS-2 cells were either transfected with empty vector, dominant negative DP1 (DP1$^{\Delta 103\text{-}126}$), dominant negative E2F1^{132E}, unrelated GL3 siRNA, or DP1 and DP2 siRNA. Two days after transfection cells were immunostained for mitochondrial marker COXIV and scored for displaying a tubular or punctate mitochondria phenotype.

Supplemental Figure S3. Analysis of mitochondria associated dE2f1/dDP targets in irradiation-induced apoptosis, related to Figure 6.

(A) The effect of depletion of selected mitochondria associated genes on irradiation-induced apoptosis was examined in third instar larval eye discs. For each gene indicated, the corresponding dsRNA under *Gal4-UAS* control (of the indicated lines) was expressed in the eye disc with *ey-FLP*;

Act>>*Gal4* except for the *Malate dehydrogenase 2* (*Mdh2*) gene for which a mutant allele was used instead of RNAi. Active caspase immunostaining was used to detect and quantify apoptotic cells when eye discs were untreated (white bars) or 4h after irradiation (gray bars) (± SD, with at least 5 discs quantified for each genotype). For RNAi experiments several genetic backgrounds were used as controls: *ey-FLP*; *Act>>Gal4/CyO GFP* (Control or *act-GAL4* Control), *ey-FLP*; *+/CyO GFP*; *UAS-mtacp1*^{RNAi} (*mtacp1* Control), *ey-FLP*; *+/CyO GFP*; *UAS-ND42*^{RNAi} (*ND42* Control), *ey-FLP*; *+/CyO GFP*; *UAS-CoVa*^{RNAi} (*CoVa* Control). (B) *ey-FLP*; *Act>>Gal4/CyO GFP* (Control) and the indicated RNAi lines of third instar larval eye discs were untreated or irradiated (IR) with 40 Gy of ionizing radiation. Active caspase immunostaining was used to detect apoptotic cells 10h after IR. All eye discs are oriented with the posterior to the right. An arrowhead indicates the morphogenetic furrow (MF).

(C) Wild type and *Mdh2*^{2} mutant third instar larval eye discs were dissected and phosphorylated histone H3 (PH3) immunostaining was used to detect mitotic cells. All eye discs are oriented with the posterior to the right. An arrowhead indicates the morphogenetic furrow.

SUPPLEMENTAL TABLES

Supplemental Table S1. DE genes and statistics of GOBP for WT, WT IR, dDP, and dDP IR conditions. See corresponding separate Excel file.

Supplemental Table S2. Statistics of KEGG, GOBP, and GOCC for dDP IR vs. dDP DE genes. See corresponding separate Excel file.

Supplemental Experimental Procedures

qPCR primers for detection of gene expression

Gene Symbol	Primer 1	Primer 2
Buffy	ATACTCCGGATGCTGTGAGC	CTTGGCGTACACAATCAACG
cyt-c-d	TTCTGGTGATGCAGAGAACG	ACTTGTATCCCGCTGCTGTG
cyt-c-p	TGCTGGTGATGTTGAGAAGG	CGATCAGACCATGCAGATTG
Dark	TCGCCAAGTACAATGTGAGC	AGGCACACATCCAAGGCTAC
Dcp-1	GACCTGCTCACCCTGCTTAC	AGGCACGGTATTTGCTTCTG
debcl	CACAAACATATCGCGACAGC	CGAAAAAGATCCTTGGCAAC
DIAP1	TTGTGCAAGATCTGCTACGG	AATATACGCGCATCACATCG
dOmi	CCGGTGTTACACAGTCATGC	ATCGAACCAATCGTCTCCAG
Dredd	TGCACTACTTGCCGCATATC	GCGAACATCTAGGAGCAAGC
drICE	TCAACCATGAGCACTTCGAG	ATGTCCTTGTAGCGGCAGTC
Dronc	ATTTGGTGAACAAGCCGAAG	GTGTCAGGCCACTTCTCCTC
Drp1	GTCTCCGACAAGAGCCAGAC	TTCCGTGGTCTCGATATTCC
grim	ACATCATCATCAGCAACAG	CAGAGCGTAGCAGAAGAT
hid	AGAGCTCCAATAGCCACTCG	CTTCGCCTTTTGTCGTTCTC
rpr	CCAGTTGTGTAATTCCGAACGA	GGATCTGCTGCTCCTTCTGC
skl	GCACCAACTAAGGCTCCTA	TGTCACTGTCTCGCTCATT

qPCR primers for ChIP validations

Gene Symbol	Primer 1	Primer 2	Amplified genomic region relative to translation start site
Acon	GATTTAAGTTTTAACGCCATAGAGTCC	GTTTCCCGCCAAAATTGGGTCG	-313 to -187
CG5599	AGACCGCCAGTGCGGAATTC	CTATTTTACGCGATTCGACGAGG	-877 to -729
CoVa	CGAGCCATTAGTCACATTCACG	GATGACCAGTACAACGAAGATGG	-1004 to -857
Mdh2	CATAAAATGTTCCCCCCAAATCAAAAC	TCCCACGGGCCAATGAAACAG	-219 to -71
mtacp1	GCTATTGTCGCCGAAAGTTGGC	GTTGGCAATAAACTCTTCATTGAAGC	-1763 to -1627
ND23	GACGATGAGGGGGAAGAGAC	AATAATGACTACCGGATGAGCATTG	-767 to -918
ND42	CATCTAGTCGCTACCAGCGG	CTTTGCCCTGCTGGATGTGC	-1889 to -1739

qPCR primers for measuring mitochondrial DNA content

Gene Symbol	Primer 1	Primer 2
mt:CoI	GCAGGTTTTATTCACTGATACCC	TCGAGGTATTCCAGCCAATC
mt:CoII	GCTGCTGATGTTATTCATTCTTG	AGCCCCACAGATTTCTGAAC
mt:CoIII	CCACGGAATTCATGTATTAATCG	TCATGCAGCTGCTTCAAAAC
mt:Cyt-b	GAAAATTCCGAGGGATTCAA	AACTGGTCGAGCTCCAATTC
mt:ND4	CCCAGAAGAACATAAACCATGA	TTGCTTATTCATCTGTTGCTCA
mt:ND5	CGTTAAAACAAGCTGAAGTTAAAGG	TGCTGGGGCTATTATTCACA
mt:srRNA	AACGACGGTATATAAACTGATTACAA	AAAAATTTGGCGGTATTTTAGTCT

qPCR control primers

Gene Symbol	Primer 1	Primer 2
ß-Tubulin	ACATCCCGCCCCGTGGTC	AGAAAGCCTTGCGCCTGAACATAG
RpP0	GTCAACCAGGTCTACGACTCC	GCCCACGGACAAACAAACG

qPCR primers for detection of gene expression in SAOS-2 cells

Gene Symbol	Primer 1	Primer 2	Ensembl Gene ID
ACO2	AGCCAGGAAATTGAGCGAGG	ATGGTCACAGTGGATGGTGG	ENSG00000100412
APOO2884.2	TTGGAAAGTGCTAGGCCTGG	TTCCTGGTGATGTCTTGGGC	ENSG00000255292
COX5A	TTCGCTGCTATTCCCATGGG	ACGCAATTCCCAGGCATCTA	ENSG00000178741
DBT	TGGCTCAGGAAAAGATGGCA	TGGGTTCTGTTTTGTCTTTGCC	ENSG00000137992
MDH2	ACGGTGACATTTCTCTTGTGGG	GAGGTACCAGACAAGGCTTTCA	ENSG00000146701
NDUFA7	CTGTGGGTCCTAGCCACAAG	GCCTTCTGCGACGACATGAT	ENSG00000167774
NDUFA10	CAAGGTGTTGTGTTGGAGCG	ACAGTAAGTGCAAGGTGAGTCT	ENSG00000130414
NDUFAB1	GCTCCTTTCTTGCAGCTTTCA	AGACGCCCACCACTTCTTTC	ENSG00000004779
NDUFS8	TGAGGAGCTGCTGTACAACAA	TGGGGTCGGAGTGGTTTTATT	ENSG00000110717
POLR2A	ATCTCCCAGGTCATTGCTGTCGTT	GCTTGAAGCCAAATGGAATCCGCT	ENSG00000181222
SDHD	GCTTCGAACTCCAGTGGTCA	TGGCTCGGTGACAAGTGTAT	ENSG00000204370
TFDP1	ATGGCCATGAACATCATCTC	CCTCTGTCTTTCCACCTCTA	ENSG00000198176
TFDP2	GGCGGATAGAACGGATAAAG	CGATTTCTCTGTACCAGGTTT	ENSG00000114126

qPCR primers for ChIP in SAOS-2 cells

Gene Symbol	Primer 1	Primer 2	Ensembl Gene ID
ACO2	TCTTCTCATCAGAGGCCACA	GGGTTCCCGTCTCTTCCTTA	ENSG00000100412
AP002884.2	GACCACCAAGGAAGGTGAAA	CAGCAGAAGGCGCAGTTTA	ENSG00000255292
COX5A	CCTCGCCTCCATTCCTACTT	GCGCTGAGGACAAACTGTTA	ENSG00000178741
DBT	GCTCGTTTCTTCCCTCCCTA	GCCGCAAACTGGAGAGACT	ENSG00000137992
FH	TGAATCCGAAGGCCTTACAC	TCCAATCAACAGCCTCACAC	ENSG00000091483
Int20D, Int26E			as described in Beshiri et al. 2012
MDH2	GGTCTCTGCAACTTGGGAAA	TCTGAGCTCCGGAAAGGTAG	ENSG00000146701
NDUFA7	ACCGGAGTGGAGGAAGAAGT	TCTGATGGTTCCCTTTAACGA	ENSG00000167774
NDUFA10	TGGTGAAACCCCGTCTCTAC	CCCGAGTAGCTGGGACTACA	ENSG00000130414
NDUFAB1	GTGCTAGGATTAAAGGCGTCA	ACACGGCACGAGAAACCTAC	ENSG00000004779
NDUFA7	ACCGGAGTGGAGGAAGAAGT	TCTGATGGTTCCCTTTAACGA	ENSG00000167774
NDUFS8	GGTCTACCATGCGTGTCCTC	TCTGCGCTGAGGGTAGGTAG	ENSG00000110717
SDHD	GACCACCAAGGAAGGTGAAA	CAGCAGAAGGCGCAGTTTA	ENSG00000204370

siRNA primers

Gene Symbol	Primer
DP1	GCCAACGGAGAACUCAAGGdTdT
DP2	GCUACUGGCUGGGUCCCUGdTdT