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**Induction of apoptosis by thymoquinone in lymphoblastic leukemia  
Jurkat cells is mediated by a p73-dependent pathway which targets the  
epigenetic integrator UHRF1**

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## ABSTRACT

The salvage anti-tumoral pathway which implicates the p53-related *p73* gene is not yet fully characterized. We therefore attempted to identify the up- and down-stream events involved in the activation of the p73-dependent pro-apoptotic pathway, by focusing on the anti-apoptotic and epigenetic integrator UHRF1 which is essential for cell cycle progression. For this purpose, we analyzed the effects of a known anti-neoplastic drug, thymoquinone (TQ), on the p53-deficient acute lymphoblastic leukemia (ALL) Jurkat cell line. Our results showed that TQ inhibits the proliferation of Jurkat cells and induces G1 cell cycle arrest in a dose-dependent manner. Moreover, TQ treatment triggers programmed cell death, production of reactive oxygen species (ROS) and alteration of the mitochondrial membrane potential ( $\Delta\Psi_m$ ). TQ-induced apoptosis, confirmed by the presence of hypodiploid G0/G1 cells, is associated with a rapid and sharp re-expression of p73 and dose-dependent changes of the levels of caspase-3 cleaved subunits. These modifications are accompanied by a dramatic down-regulation of UHRF1 and two of its main partners, namely DNMT1 and HDAC1, which are all involved in the epigenetic code regulation. Knockdown of p73 expression restores UHRF1 expression, reactivates cell cycle progression and inhibits TQ-induced apoptosis. Altogether our results showed that TQ mediates its growth inhibitory effects on ALL p53-mutated cells via the activation of a p73-dependent mitochondrial and cell cycle checkpoint signaling pathway which subsequently targets UHRF1.

**Keywords:** Apoptosis; caspase; thymoquinone; tumor suppressor protein p73; UHRF1.

## 1. Introduction

The *p73* gene produces a protein homolog to p53 with similar functions [1]. p73 regulates the transcription of several p53 target genes, including the apoptosis-regulating gene *PUMA*, a Bax transactivator, and the cell cycle regulatory genes *p21<sup>Waf1/Cip1</sup>* [2] and *p16<sup>INK4A</sup>* [3]. Transcriptional activation of these genes leads to the induction of cell-cycle arrest and/or apoptosis [2]. It is therefore expected that many p53-responsive genes could also be targets of p73, especially those genes which respond to DNA damage and could initiate cell cycle arrest and/or apoptosis. This could explain that cells lacking functional p53 have the ability to undergo apoptosis through a p53-independent pathway when p73 is expressed [4]. Apart its p53-mimetic activity, p73 is also a major component of specific signaling cascades, like the caspase-independent cell death (CICD) [5].

Under physiological conditions, the basal expression of the *p73* gene is kept extremely low and is only up-regulated in response to cellular stress [1]. This explains that, in spite of extensive searches, mutations of the *p73* gene are rarely detected in primary tumors [6], but aberrant hypermethylation of the *p73* promoter region and subsequent inactivation of the *p73* gene have been reported in acute lymphoblastic leukemia (ALL) [7]. The consequences of this hypermethylation and its maintenance are not clearly understood but they likely target the expression of specific genes involved in the DNA damage response. We hypothesized that UHRF1 (Ubiquitin-like, containing PHD and RING Finger domains, 1) could be a major effector of the p73 deregulation, since this nuclear protein is known to be over-expressed in numerous cancer cell lines and tissues [8-11].

Several studies have shown that UHRF1 participates in the control of cell proliferation and cell cycle transition from G1 to S, by regulating the expression of several genes, including *RB1* and *p16<sup>INK4A</sup>* [12,13]. This suggests that pathological over-expression of UHRF1, by repressing permanently the expression of specific tumor suppressor genes, could induce disorders in the G1/S progression and consequently promote tumor development [10]. In agreement with our hypothesis, it has been shown that the activation of different cell cycle checkpoints during DNA damage-induced apoptosis leads to a down-regulation of UHRF1 [9]; such deregulation has been described to be dependent on the p53/p21<sup>WAF1/CIP1</sup> pathway [14]. It should be noted that reduction of UHRF1 expression solely can suppress proliferation and induce apoptosis of cancer cells whose p53 is inactivated [15]. This suggests that UHRF1 functions as a component in the DNA damage response pathways and that it plays a role in the maintenance of genomic stability. In this point of view, accumulating evidences have shown that UHRF1 acts as a multi-modular protein involved in the maintenance of the chromatin status and its propagation during cell division. Indeed, UHRF1 binds to methylated DNA and recruits DNA methyltransferase 1 (DNMT1) and histone deacetylase 1 (HDAC1) through the SRA (SET and RING finger Associated) domain [13,16-19]. These protein-protein interactions precede S phase entry and could be required for cell cycle progression [10,20]. UHRF1 therefore, ensures the crosstalk between DNA methylation and histone modifications, promoting the maintenance of the epigenetic code and its transmission from a mother cell to the descent cells [21]. For these reasons it is suspected that a down-regulation of UHRF1 in response to DNA damage has dramatic consequences on the cell viability.

A number of studies have shown that thymoquinone (TQ) is a potent cytotoxic and genotoxic drug over a broad range of human cancer cells [22]. It has been suggested that TQ, as a DNA damaging agent, is a potential reactive oxygen species (ROS) producer which exerts its anti-cancer effects by inhibiting cell growth, arresting cell cycle progression and inducing subsequently apoptosis [23-29]. p53-dependent [26] and p53-independent pathways [23,27] have been evidenced to explain the cellular actions of TQ. In HCT-116 colorectal cancer cells, TQ-induced apoptosis involves an up-regulation of both p53 and p21<sup>WAF1/CIP1</sup> expressions, concomitantly with a down-regulation of the expression of the anti-apoptotic protein Bcl-2 [26]. In p53-null myeloblastic leukemia HL-60 cells [27] and in p53-null osteosarcoma MG63 cells [28], the anti-cancer activities of TQ involve alterations of the Bax/Bcl2 ratio and caspase activations, but the precise mechanisms remain unknown.

The aim of the present study is to determine in the p53-deficient Jurkat cell line [30] whether an activation of the *p73* gene, via a TQ-induced DNA damage, could target the anti-apoptotic *UHRF1* gene with subsequent cell cycle arrest and apoptosis. Our results show that TQ produces intracellular ROS, promotes a DNA damage-related cell cycle arrest and triggers apoptosis through the activation of a p73-dependent mitochondrial and cell cycle signaling pathway, followed by a down-regulation of UHRF1. We hypothesize that this p73-dependent down-regulation of UHRF1 prevents epigenetic code replication and thus hinders the “cancer signature” to be inherited by the daughter cancer cells.

## 2. Material and methods

## 2.1. Cell Culture, Treatment and Transfection

The human leukemic T-cell line Jurkat (clone E6-1) was cultured as previously described [13]. A 100 mM solution of TQ (Sigma-Aldrich, St. Louis, MO, USA) was prepared in 100% DMSO (DiMethylSulfOxide; Millipore S.A.S., Molsheim, France) and appropriate working concentrations were prepared with the cell culture medium; the final concentration of DMSO was of 0.1% in both control and treated conditions. Transient transfections of p73 siRNA duplex (sc-36167; Santa Cruz Biotechnologies, Santa Cruz, CA, USA), UHRF1 siRNA duplex (5' - GGUCAAUGAGUACGUCGAUdTdT-3'; [13]) or scramble siRNA duplex (5' - GGACUCUCGGAUUGUAAGAdTdT-3'; [13]) were performed with lipofectamine 2000 (Invitrogen, Eugene, OR, USA), following the manufacturer's recommendations. Transient transfections with pSG5 or pSG5-UHRF1 plasmid were performed as previously described [31]. Experiments using a specific inhibitor of caspase-3 (Z-DEVD-FMK) were carried out according to the manufacturer's instructions (Millipore S.A.S.).

## 2.2. Cell proliferation, viability and apoptosis assays

Cells were seeded on 6-multiwell plates at a density of  $2 \times 10^6$  cells/well, grown for 24h and exposed to TQ at different concentrations for different times. Cell proliferation rate was then assessed by colorimetric assay using the CellTiter 96® AQueous One Solution Cell Proliferation Assay (MTS), following the manufacturer's recommendations (Promega, Charbonnières-les-Bains, France). Cell viability rate was determined by cell



counting using the trypan blue exclusion method (Invitrogen). The viability rate was obtained by dividing the number of trypan blue-negative cells by the total number of cells. Cell apoptosis rate was assessed by flow cytometer (BD FACSCalibur system, BD Biosciences, San Diego, CA, USA) using the Annexin V-FITC/propidium iodide (PI) apoptosis assay (BD Biosciences), following the manufacturer's recommendations. CellQuest software (BD Biosciences) was used for the analysis of the data. At least 10,000 events were recorded, iteratively increased if possible, and represented as dot plots.

### *2.3. Cell cycle phase distribution analysis and quantitation of hypodiploid sub-G0/G1 cell population*

Cells were plated in 80 cm<sup>2</sup> culture flasks at a density of  $1.5 \times 10^5$  cells/ml, grown for 24h and exposed to TQ at different concentrations for different times. Cells were then prepared as previously described [32]. Cellular DNA content was assessed by flow cytometry in either a Guava EasyCyte Plus HP system (Guava Technologies, Hayward, CA, USA) or a BD FACSCalibur system (BD Biosciences).

### *2.4. Assessment of DNA fragmentation pattern*

Genomic DNA was prepared according to the manufacturer's instructions (Qiagen, Courtaboeuf, France), separated by electrophoresis on a 1% agarose gel and visualized under UV light with ethidium bromide.

## 2.5. Analysis of the production of ROS metabolites

Treated and untreated cells, seeded at an initial density of  $2 \times 10^6$  cells/well in 6-well plates, were stained for 30min at room temperature with a  $1 \mu\text{mol/l}$  dihydroethidium (DHE; Sigma Aldrich) solution and then subjected to flow cytometric analyses (BD FACSCalibur, BD Biosciences). 10,000 events were recorded per experiment.

## 2.6. Mitochondrial membrane potential measurement

Cells grown as described above, were incubated for 15 min at  $37^\circ\text{C}$  in PBS supplemented with 40 nM of [3,3' - Dihexyloxacarbocyanine iodide] –DiOC6; Sigma Aldrich- and  $1 \mu\text{g/ml}$  PI, followed by FACS analysis (BD FACSCalibur, Becton Dickinson). At least, 5,000 cells were analyzed for each sample.

## 2.7. Western blot analysis

Proteins from cell lysates were extracted, separated on 10-15% SDS-polyacrylamide gels and transferred to membranes as previously described [13,33]. Immunoblotting was performed by using either a mouse monoclonal anti-p73 antibody (BD Biosciences Pharmingen), a rabbit polyclonal anti-p16 antibody (Proteogenix, Oberhausbergen,

France), a rabbit polyclonal anti-cleaved caspase-3 antibody (Cell Signaling Technology, Danvers, MA, USA), a mouse monoclonal anti-UHRF1 antibody [31], a mouse monoclonal anti-DNMT1 antibody (Stressgen Biotechnologies, Victoria, BC Canada), a rabbit polyclonal anti-HDAC1 antibody (USBiological, Swampscott, MA, USA), or a mouse monoclonal anti-beta actin antibody (Abcam, Paris, France), according to the manufacturer's instructions. Membranes were then incubated with the appropriate horseradish peroxidase-conjugated secondary antibody. Signals were visualized as previously described [13] and subjected to optical densitometric (OD) quantification by using NIH's Image J software.

## 2.8. Statistical analysis

Data were presented in a bar graph form, expressed as means  $\pm$  S.E.M. from at least three independent experiments and statistically subjected to the one-way ANOVA test. Significance levels were defined in accordance with the standard notation.

## 3. Results

### 3.1. TQ inhibits cell growth and induces cell cycle arrest of Jurkat cells

The Jurkat cell line was used to identify and characterize the molecular mechanisms induced by TQ. We first analyzed the effects of TQ on the growth parameters of this cell line. Cell proliferation (Fig. 1A) and cell viability (Fig. 1B) following TQ treatment, were decreased in a concentration-dependent manner. In our experimental

conditions, calculated concentrations of TQ-induced half-maximal effects on cell proliferation and viability were respectively of  $24.2 \pm 0.3 \mu\text{M}$  and  $24.3 \pm 0.2 \mu\text{M}$  for 24h of treatment. When treated with TQ for 48h, these values were  $23.3 \pm 0.2 \mu\text{M}$  and  $23.1 \pm 0.4 \mu\text{M}$  respectively (data not illustrated). These results indicate that Jurkat cells respond to TQ within 24h and at the previously published concentrations [24-28].

Because cell growth is a result of the progression of the cells through the different phases of the cell cycle, we next determined the effects of TQ on the cell cycle distribution (Fig. 1C). Slight modifications were already detectable at  $10 \mu\text{M}$  of TQ and a significant accumulation of the cell population in G0/G1 phase was observed for higher concentrations. It appears therefore that TQ is able to inhibit the growth of Jurkat cells by promoting cell cycle arrest at the G0/G1 phase.

### 3.2. TQ induces apoptosis in Jurkat cells

We next investigated whether TQ could induce apoptosis in Jurkat cells. As shown in Fig. 2A, increasing concentrations of TQ are associated with increasing number of apoptotic cells. TQ began to trigger apoptosis at  $10 \mu\text{M}$  while at  $30 \mu\text{M}$ , a major proportion of cells was concerned. As expected, the calculated half-maximal effect of TQ on apoptosis was  $24.7 \pm 0.3 \mu\text{M}$  (24h treatment). For 48h of treatment with TQ, this value was  $23.2 \pm 0.3 \mu\text{M}$  (results not illustrated). Hence, these data were consistent with those obtained from cell proliferation assays. As a next step, cell cycle phase distribution analysis was focused on the detection of specific G0/G1 apoptotic cells; as shown in Fig. 2B, increasing concentrations of TQ led to increasing number of hypodiploid sub-G0/G1 cells. In agreement with these data, the intensity of the genomic

DNA smears of the TQ-treated Jurkat cells increased in a concentration-dependent manner (Fig. 2C). Finally all these results demonstrate the occurrence of a p53-independent DNA damage-related apoptosis in the p53-mutated Jurkat cells, when exposed to TQ.

### *3.3. TQ induces the generation of ROS and the breakdown of $\Delta\Psi_m$ in Jurkat cells*

We suspected that TQ, like many quinone compounds (e.g. denbinobin), can trigger apoptosis by generating ROS [34], that in turn should induce mitochondrial membrane disruption. We therefore determined by flow cytometry the levels of the DNA intercalating fluorescent marker ethidium which is produced after intracellular oxidation of DHE. As shown in Fig. 3A, cells exposed to increasing concentrations of TQ exhibited enhanced accumulation of intracellular ROS. When compared to untreated cells, a 77% increase of the fluorescence emitted by the ROS-induced oxidation of DHE was detected in cells treated with 100  $\mu\text{M}$  of TQ (Fig. 3A, Fig. 3B). In parallel, the effects of TQ on the mitochondrial membrane potential status were investigated by determining the uptake rate of DiOC6, a mitochondrial specific and voltage-dependent fluorescent dye. Fig. 4 shows that the number of cells, emitting high fluorescence levels, decreases when 20  $\mu\text{M}$  or higher concentrations of TQ were used, indicating a dramatic drop of  $\Delta\Psi_m$ . These results suggest that the DNA-damaging agent TQ induces apoptosis by producing ROS metabolites and triggering mitochondrial membrane potential loss in the p53-mutated Jurkat cells.

### *3.4. p73 is up-regulated and UHRF1 is down-regulated in TQ-treated Jurkat cells*

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4 In order to define the nature of the cell cycle checkpoint signaling pathway which could  
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6 be activated in response to the TQ-induced DNA damage, we first examined the  
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8 expression status of p73. In the absence of TQ, the expression of p73 in Jurkat cells was  
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10 faintly detectable; however when concentrations of TQ reached 10  $\mu$ M, a sharp increase  
11  
12 in the expression of p73 was observed after either 24h or 48h of treatment (Figs. 5A &  
13  
14 5B). This up-regulation, observed in a concentration-dependent manner, concerned both  
15  
16  $\alpha$  and  $\beta$  isoforms of p73 and was correlated with increasing expression levels of the  
17  
18 tumor suppressor protein p16<sup>INK4A</sup> (Fig. 5A). Interestingly, p73 re-expression was  
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20 accompanied by a transient over-expression of caspase-3 cleaved subunits, only  
21  
22 observed in cells exposed to 10  $\mu$ M of TQ. At higher concentrations of TQ however,  
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24 caspase-3, became undetectable in their active conformation (Fig. 5A).  
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31 There are several lines of evidence that UHRF1 deregulation may impair the  
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33 control of G1/S transition during cell cycle checkpoint activation [8, 9, 14]. Since such  
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35 activation is known to occur during the DNA damage-related apoptosis of TQ [23-26],  
36  
37 we analyzed the expression levels of UHRF1 and its partners DNMT1 and HDAC1 in  
38  
39 TQ-treated Jurkat cells. As shown in Fig. 5A, treatment of Jurkat cells with TQ (up to  
40  
41 10  $\mu$ M) resulted in a faint decrease in the expression levels of UHRF1 and DNMT1. In  
42  
43 contrast, the expression levels of HDAC1 appeared to increase. However at higher  
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45 concentrations of TQ, all the three proteins became undetectable. Taken together, these  
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47 results also observed after 48h of TQ treatment (Fig. 5B), indicate that TQ-induced  
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49 apoptosis in Jurkat cells is associated with an activation of the cell cycle checkpoint  
50  
51 regulator p73 and a down-regulation of the UHRF1/DNMT1/HDAC1 complex.  
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### 3.5. TQ rapidly induces apoptosis, cell cycle arrest and deregulation of p73 and UHRF1 expressions in Jurkat cells

In order to determine more precisely the chronology of the cellular and molecular events induced by TQ, we analyzed the time-course effects of TQ on Jurkat cells, at a concentration corresponding to its half-maximal activity (25  $\mu$ M). As shown in Fig. 6A and 6B, a notable number of cells in apoptosis appeared within 3h of treatment, suggesting that the cell cycle progression is rapidly slowing down after TQ exposition. Accordingly, significant accumulation of cells in G0/G1 phase could be evidenced after 6h of treatment (Fig. 6C). Interestingly, increased levels of p73 could be detected within 3h of TQ exposition (Fig. 6D); this up-regulation is accompanied with a progressive down-regulation of UHRF1, in association with the appearance of a lower molecular weight form (Fig. 6D). Moreover the up-regulation of p73 was also correlated with a marked over-expression of caspase-3 cleaved subunits. Thus, for the concentrations of TQ above 10 $\mu$ M that showed an absence of cleaved caspase-3 after 24h or 48h (Figs. 5A & 5B), there was an increased expression of the activated caspase-3 in the early hours of treatment. These results suggest that TQ-induced apoptosis is linked to a rapid deregulation of p73 and UHRF1 expressions in Jurkat cells.

### 3.6. Knockdown of p73 counteracts TQ-induced UHRF1 down-regulation, cell cycle arrest and apoptosis in Jurkat cells

To determine whether p73 could act in Jurkat cells as a main regulator of the apoptotic signaling pathway activated by TQ, we attempted an acute depletion of p73 by

transfecting TQ-treated cells with specific siRNA against p73. As shown in Fig. 7A, p73 knockdown restored UHRF1 expression at levels similar to those observed for untreated cells; accordingly a normalization of the expression level ratio of the two proteins could be evidenced (Fig. 7B). The knockdown of p73 also allowed reactivation of cell cycle progression since the percentage of the cell populations in G0/G1 and S phase is significantly inversed when compared to that of TQ-treated cells transfected with scramble siRNA (Fig. 7C). Consistently, a significant decrease in the number of apoptotic cells could be observed (Fig. 7D). These data clearly demonstrated that UHRF1 is down-stream of p73 in the TQ-induced apoptotic pathway. In order to address unambiguously whether UHRF1 is targeted by p73 and is involved in the apoptotic process, we further determined the direct relationships between a p73 deregulation, modulations of UHRF1 expression and apoptosis in Jurkat cells, in the absence of TQ. As shown in Fig. 8A, siRNA-induced decrease of the basal expression levels of p73 upregulated UHRF1 expression. Moreover UHRF1 siRNA which induced the decrease of the basal expression levels of UHRF1 (Fig. 8B) significantly increased the number of apoptotic cells when compared to the controls (Fig. 8C), showing that UHRF1 exhibits anti-apoptotic properties. Altogether these results indicate that TQ triggers apoptosis in Jurkat cells through a DNA damage response involving the activation of the tumor suppressor protein p73, which is able to induce a down-regulation of the expression of the anti-apoptotic protein UHRF1.

### *3.7. UHRF1 down-regulation in TQ-treated Jurkat cells leads to apoptosis via a caspase-dependent mechanism*



We suspected that TQ, at a concentration corresponding to its half-maximal effects, could activate a p73-dependent caspase-dependent pathway which could then trigger the down-regulation of UHRF1 and subsequently apoptosis. We therefore examined the effects of a caspase-3 specific inhibitor on TQ activity in Jurkat cells. Indeed, Z-DEVD-FMK was able to counteract the decrease of UHRF1 expression (Fig. 9A) and the apoptotic process (Fig. 9B) induced by 25  $\mu$ M of TQ. Moreover, an acute overexpression of UHRF1 after TQ treatment can partially rescue the cells from apoptosis, thus mimicking the effects of a caspase-3 inhibitor (Fig. 9C). The results suggest that the TQ-activation of the p73-dependent mitochondrial caspase-dependent pathway induces UHRF1 down-regulation which explains, at least in part, the observed apoptosis.

## Discussion

It has been reported that the pro-apoptotic activity of TQ on cancer cells occurs in p53 wild-type cells through an up-regulation of both the tumor suppressor protein p53 and the cyclin dependent kinase inhibitor p21<sup>Waf1/Cip1</sup> which in turn induces G1 cell cycle arrest and apoptosis [26]. In p53-null cells however, the molecular mechanisms leading to TQ-induced mitochondrial reactivity are poorly documented.

The present study demonstrates that TQ triggers apoptosis in the p53-deficient Jurkat cell line through the production of ROS and the activation of the cell cycle checkpoint regulator p73. Accordingly it has been shown that ROS production can be an efficient activator of p73 expression [35]. On the other hand, different point mutations in the *p53* gene have been evidenced in Jurkat cells, mostly at the C-terminal

1 basic domain [30], which is required for the activation of the  $p21^{Waf1/Cip1}$  gene, for cell  
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3 cycle arrest and for apoptosis [36]. Thus, the p53-dependent pathway is not involved in  
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5 the effects of the ROS producer TQ on Jurkat cells.  
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8 Similarly to p53, the structural and functional homolog p73 can promote cell  
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10 cycle arrest and apoptosis when over-expressed [4]. Moreover, it has been reported that  
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12 cellular stress signals can induce endogenous expression of p73 in p53 null or mutant  
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14 cells, engaging a p53-independent apoptotic pathway [37,38]. Accordingly p73 seems to  
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16 act as a cellular gatekeeper by preventing the proliferation of TQ-exposed Jurkat cells;  
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18 obviously the sharp re-expression of p73 that we observed in response to TQ, triggers  
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20 G0/G1 cell cycle arrest and apoptosis. This cell reactivity is likely a down-stream effect  
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22 of p73 since the knockdown of p73 in TQ-treated cells restored cell cycle progression  
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24 and proliferation. It has been observed that early increased expression of p73 in  
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26 response to cell stress is a consequence of an accumulation at the protein level [39]. It  
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28 could therefore be hypothesized that the proteasome-mediated proteolytic degradation  
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30 of p73 is rapidly blocked after TQ-treatment, leading to a stabilization of the protein.  
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37 To determine whether the cell cycle checkpoint regulator p73 possesses an  
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39 operative activity, we analyzed the expression of some of its down-stream effectors in  
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41 TQ-treated Jurkat cells. Interestingly, a transient TQ concentration-dependent up-  
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43 regulation of caspase 3 cleaved subunits has been shown. First of all, this suggests that  
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45 TQ exerts its apoptotic activity through caspase-dependent and caspase-independent  
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47 pathways. p73, like p53, is known to promote the activation of caspases [2]. However,  
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49 only p73 is involved in a caspase-independent cell death (CICD), which protects cells  
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51 from aneuploidy by inducing their death when chromosome missegregation occurs [5].  
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57 Interestingly it has been observed that the switch from a caspase-dependent to a  
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1 caspase-independent pathway allows the progression from a specific cell death state to  
2 another [40]. Jurkat cells treated with high concentrations of TQ likely switch to a  
3 particular cell death program which involves the p73-dependent CICD pathway.  
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8 We have previously shown in HCT116 cells, a colon cancer cell line, that the  
9 activation of the p53-dependent p21<sup>Waf1/Cip1</sup> pathway is able to down-regulate UHRF1  
10 [14]. Here we show in Jurkat cells, the most abundant known source of UHRF1 ([31];  
11 personal laboratory observations), that a p73-dependent pathway also regulates UHRF1.  
12  
13 Indeed, TQ induces the activation of the cell cycle checkpoint regulator p73, which in  
14 turn represses UHRF1 expression in the p53 mutant Jurkat cells. The knockdown of p73  
15 in either untreated or TQ-treated cells modulates UHRF1 expression, indicating that  
16 UHRF1 is a down-stream effector of p73 in this cell type. Our data also show that TQ  
17 down-regulates DNMT1, which is not surprising considering that DNMT1 is a  
18 privileged partner of UHRF1 [13]. Otherwise the variations of HDAC1 expression  
19 levels after TQ treatment, at least during the first 24h, remain to be elucidated.  
20 Interfering effects between direct and indirect actions of TQ could however be invoked.  
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22

23  
24 We have previously observed that UHRF1 reduction after activation of the p53-  
25 dependent pathway is consecutive of both a transcriptional suppression and a protein  
26 degradation enhancement [14]; this suggests that the p73-dependent down-regulation of  
27 UHRF1 we evidenced, likely results from the same processes. Accordingly the lower  
28 molecular weight form we observed within few hours after TQ-treatment could be  
29 related to increased UHRF1 degradation after caspase activation. Indeed a specific  
30 inhibitor of caspase-3 can recover UHRF1 expression and rescue cells from apoptosis  
31 induced by TQ. Interestingly it has been shown that repression of UHRF1 expression  
32 after treatment with different inducers of cell cycle checkpoints regulators is associated  
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with cell cycle arrest in G0/G1 and cell proliferation inhibition [9]. Although accumulating data have highlighted a correlation between the reduction of UHRF1 expression and cell cycle arrest or apoptosis, the molecular mechanisms which clearly explains this correlation remains unknown [10]. In view of the important role that the epigenetic integrator UHRF1 plays in the maintenance of the chromatin status, its down-regulation should necessarily lead to the loss of genome integrity and cell death. Accordingly, we observed that UHRF1 knockdown in untreated cells, as well as an acute overexpression of UHRF1 in TQ-treated cells, have direct incidences of the cell apoptosis rate. UHRF1 appears therefore to have in our experimental settings anti-apoptotic properties, in agreement with previous observations [10,15,21]. One interesting idea therefore is that preventing the epigenetic code to be replicated after UHRF1 deregulation leads to the activation of an apoptotic pathway. But this hypothesis needs further investigations.

In conclusion, this is the first report which shows that a natural compound induces apoptosis by acting on the epigenetic integrator UHRF1. By using a p53 mutant cell line, we have shown that TQ produces ROS metabolites and acts through a p73-dependent mitochondrial pathway which targets UHRF1 and likely DNMT1. This pathway could involve either a caspase-dependent or caspase-independent activation (see graphical abstract). However the role of CICD on UHRF1 expression and activity remains unclear and its study is currently under investigation. Our data also highlight a new property of TQ which could be used to prevent the epigenetic code to be transmitted from a mother cell to the daughter cells.

## Acknowledgments

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## Figure captions

**Fig. 1.** Concentration-dependent effects of TQ on proliferation, cell viability and cell cycle of Jurkat cells. Cells were exposed to TQ at the indicated concentrations and incubated for 24h. **(A)** Cell proliferation rate was assessed by colorimetry using the MTS assay. **(B)** Cell viability rate was assessed by cell counting using trypan blue dye exclusion assay. The absolute value obtained for each TQ-treated sample is expressed in a second step as percent relative to the corresponding absolute value obtained for the untreated sample and set at 100. **(C)** Cell cycle distribution was assessed by a capillary cytometry detection assay. Cell number in G0/G1, S or G2/M phase was determined and expressed as percent relative to the total cell number. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$  (versus the corresponding untreated group).

**Fig. 2.** Concentration-dependent apoptosis induced by TQ in Jurkat cells. Cells were exposed to TQ at the indicated concentrations and incubated for 24h. **(A)** Cell apoptosis rate was assessed by capillary cytometry using the Annexin V-FITC staining assay. The number of apoptotic cells is expressed as percent relative to the total cell number. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*\*\*,  $p < 0.001$  (versus untreated group). **(B)** Hypodiploid sub-G0/G1 cell rate was assessed by cytometry detection assay. Cell number was determined and expressed as percent relative to the total cell number. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*,  $p < 0.05$ ; \*\*\*,  $p < 0.001$  (versus untreated group). **(C)**

Genomic DNA fragmentation was analyzed on an agarose gel, as described in “Material and methods”. The observed patterns are representative of three different experiments.

**Fig. 3.** Concentration-dependent ROS production induced by TQ in Jurkat cells. Cells were exposed to TQ at the indicated concentrations and incubated for 24h. ROS accumulation was assessed by flow cytometry after DHE incubation. **(A)** shows in each histogram the levels of fluorescence. **(B)** shows the overlapping fluorescence curves obtained for untreated and TQ-treated (100  $\mu$ M) cells. The data are representative of three independent experiments.

**Fig. 4.** Concentration-dependent  $\Delta\Psi_m$  disruption induced by TQ in Jurkat cells. Cells were exposed to TQ at the indicated concentrations and incubated for 24h.  $\Delta\Psi_m$  alteration was assessed by flow cytometry using the DiOC6 staining assay. The percentage of damaged cells with depolarized mitochondrial membranes is indicated in each histogram. The results are representative of three independent experiments.

**Fig. 5.** Effects of TQ on UHRF1, DNMT1, HDAC1, p73, p16 and cleaved caspase-3 expressions in Jurkat cells. Cells were exposed to TQ at the indicated concentrations and incubated for 24h **(A)** or 48h **(B)**. Immunoblotting analyses were performed as described in “Material and methods” with the corresponding antibodies. Specific bands were detected with their expected apparent molecular weight. The data are representative of at least three independent experiments.

**Fig. 6.** Time-course of the effects of TQ on the number of apoptotic cells, cell cycle distribution and p73, UHRF1 and cleaved caspase-3 expressions in Jurkat cells. Cells were exposed to 25  $\mu$ M of TQ for the indicated times. **(A)** shows the results of a representative apoptosis assay, as explained in the legend of Fig. 2A. Cells of the lower left quadrant are viable; cells of the lower right quadrant are in apoptosis. The number of cells in apoptosis, expressed as percentage relative to the total cell number, is indicated. **(B)** recapitulates the percentage of cells in apoptosis. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$  (versus untreated group). **(C)** shows the cell cycle distribution, as explained in the legend of Fig. 1C. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*\*\*,  $p < 0.001$  (versus the corresponding untreated group). **(D)** shows representative immunoblotting results, as explained in the legend of Fig. 5.

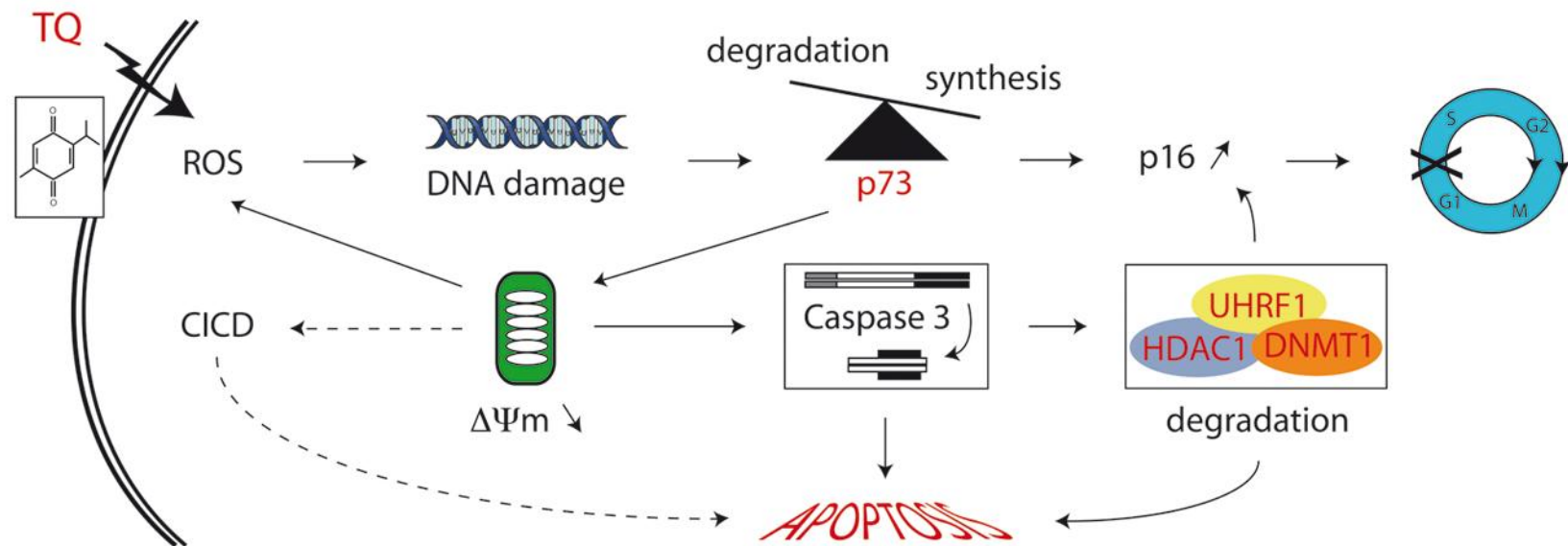
**Fig. 7.** Effects of p73 knockdown on TQ activity in Jurkat cells. Untransfected cells (2; TQ), scramble siRNA (80 pmol) transfected cells (3; TQ + scr. siRNA) or p73 siRNA (80 pmol) transfected cells (4; TQ + siRNA p73), seeded at a density of  $2 \times 10^5$  cells/ml were grown 18h before exposure to 10  $\mu$ M TQ and further cultured for 54h. As a control, untransfected cells were cultivated without TQ for 72h (1; Control). **(A)** shows representative immunoblotting results, as explained in the legend of Fig. 5. **(B)** shows UHRF1/p73 expression level ratio, determined as described in “Material and methods”. **(C)** shows the cell cycle distribution, as explained in the legend of Fig. 1C. **(D)** shows the percentage of cells in apoptosis, as explained in Fig. 2A. Values are means  $\pm$  S.E.M. of three experiments (n=3); statistically significant: \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ .

0.001 (versus the corresponding cell condition 1); °°,  $p < 0.01$  (versus the corresponding cell condition 3).

**Fig. 8.** Direct relationships between p73 knockdown, UHRF1 deregulation and apoptosis in Jurkat cells. Cells were seeded at a density of  $2 \times 10^5$  cells/ml and grown after different transfection treatments for 48h. **(A)** and **(B)** show representative immunoblotting results, as explained in the legend of Fig. 5, and obtained with protein extracts of untransfected cells (control) or cells transfected with 80 pmol of either a scramble siRNA, a siRNA against p73 or a siRNA against UHRF1. **(C)** shows the percentage of cells in apoptosis after the different treatments, as explained in legend of Fig. 2A. Values are means  $\pm$  S.E.M. of three experiments ( $n=3$ ); statistically significant: \*\*\*,  $p < 0.001$  (versus control); °°,  $p < 0.001$  (versus scramble siRNA).

**Fig. 9.** Rescue effects after treatment with a caspase-3 inhibitor or an acute overexpression of UHRF1 on TQ-induced apoptosis of Jurkat cells. **(A)** shows representative immunoblotting results, as explained in the legend of Fig. 5, and obtained with protein extracts of cells, seeded at a density of  $2 \times 10^5$  cells/ml, exposed or not after 24h to the caspase-3 inhibitor Z-DEVD-FMK for 1h and then grown for further 6h in the presence or absence of 25  $\mu$ M of TQ. **(B)** shows the percentage of cells in apoptosis after the different treatments, as explained in the legend of Fig. 2A. Values are means  $\pm$  S.E.M. of three experiments ( $n=3$ ); statistically significant: \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$  (versus control); °,  $p < 0.05$  (versus TQ). **(C)** shows the apoptosis rate, as explained in the legend of Fig. 2A. Cells, seeded at a density of  $2 \times 10^5$  cells/ml, transfected or not after 24h with 6  $\mu$ g of either a pSG5 or pSG5-UHRF1 plasmid for 24h, were grown for

1 further 6h in the presence or absence of 25  $\mu$ M of TQ. Values are means  $\pm$  S.E.M. of  
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4 three experiments (n=3); statistically significant: \*\*\*,  $p < 0.001$  (versus control); °,  $p <$   
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6 0.05 (versus TQ + pSG5).  
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Hypothetical model of TQ p53-independent apoptotic activity involving a caspase-dependent or -independent pathway

Figure 1

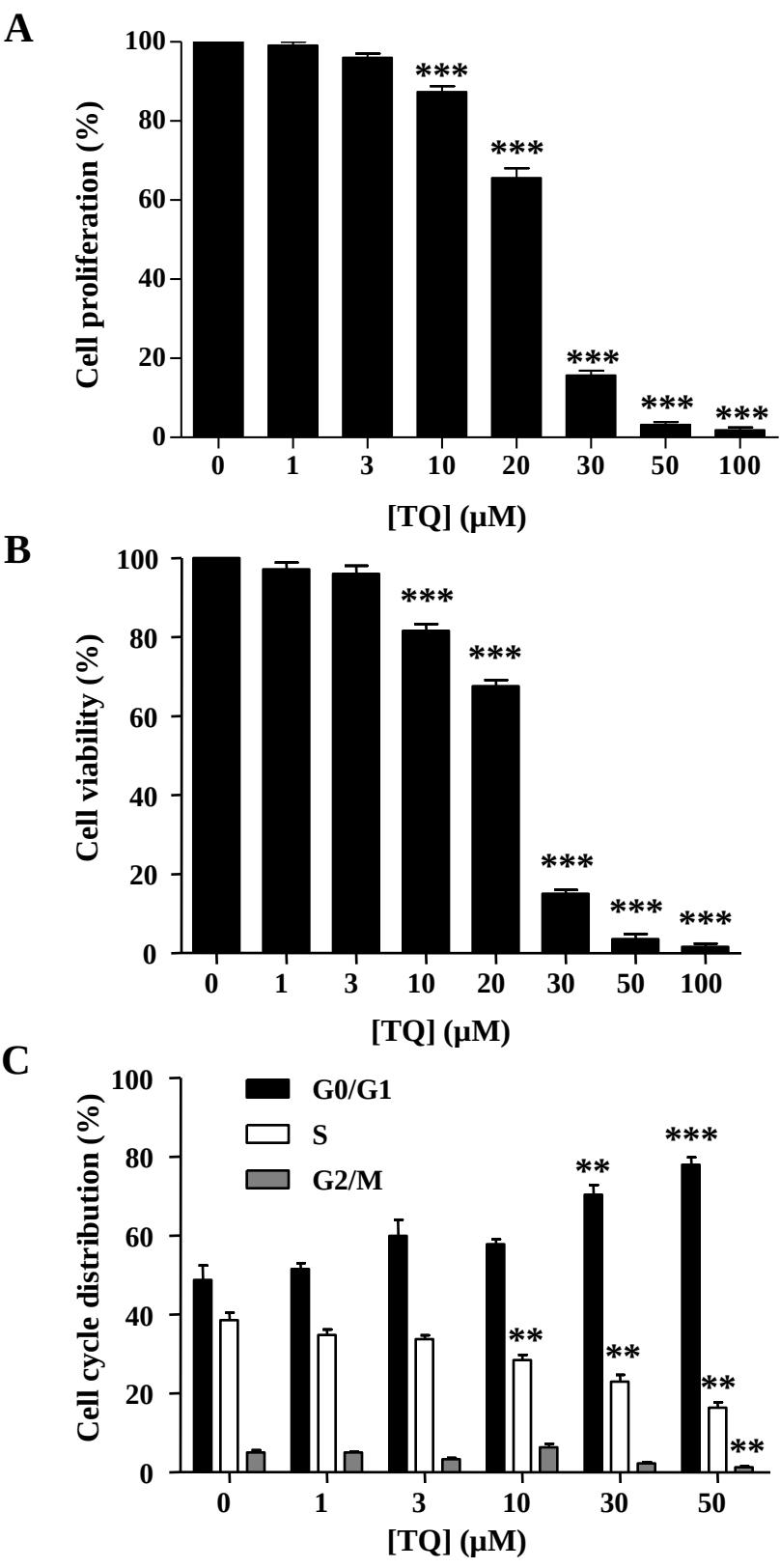


Fig. 1.



Figure 2

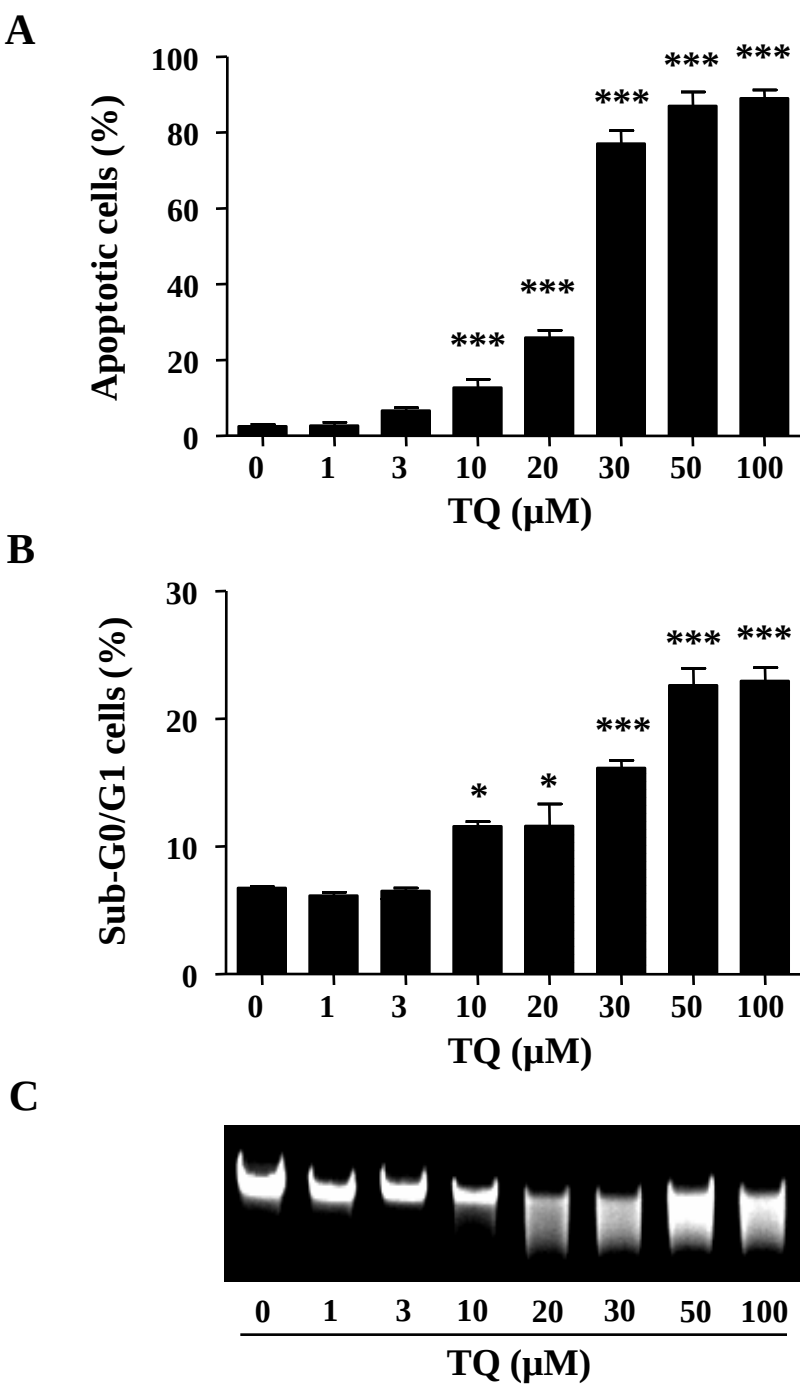


Fig. 2.

Figure 3

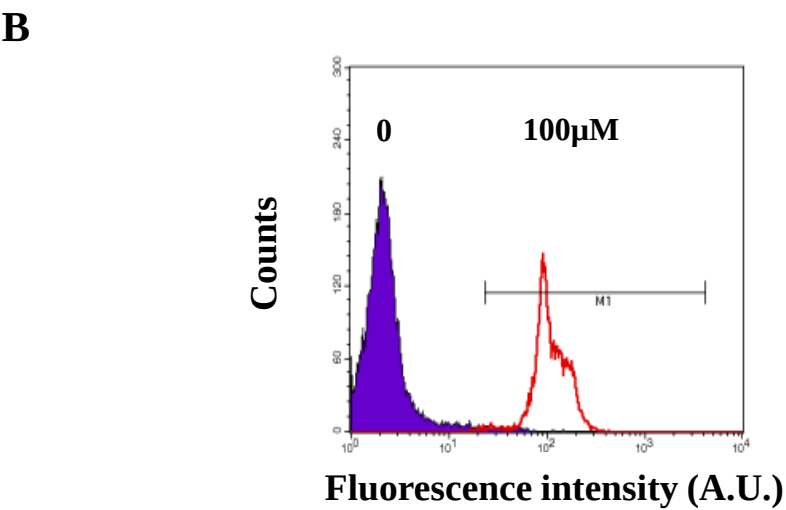
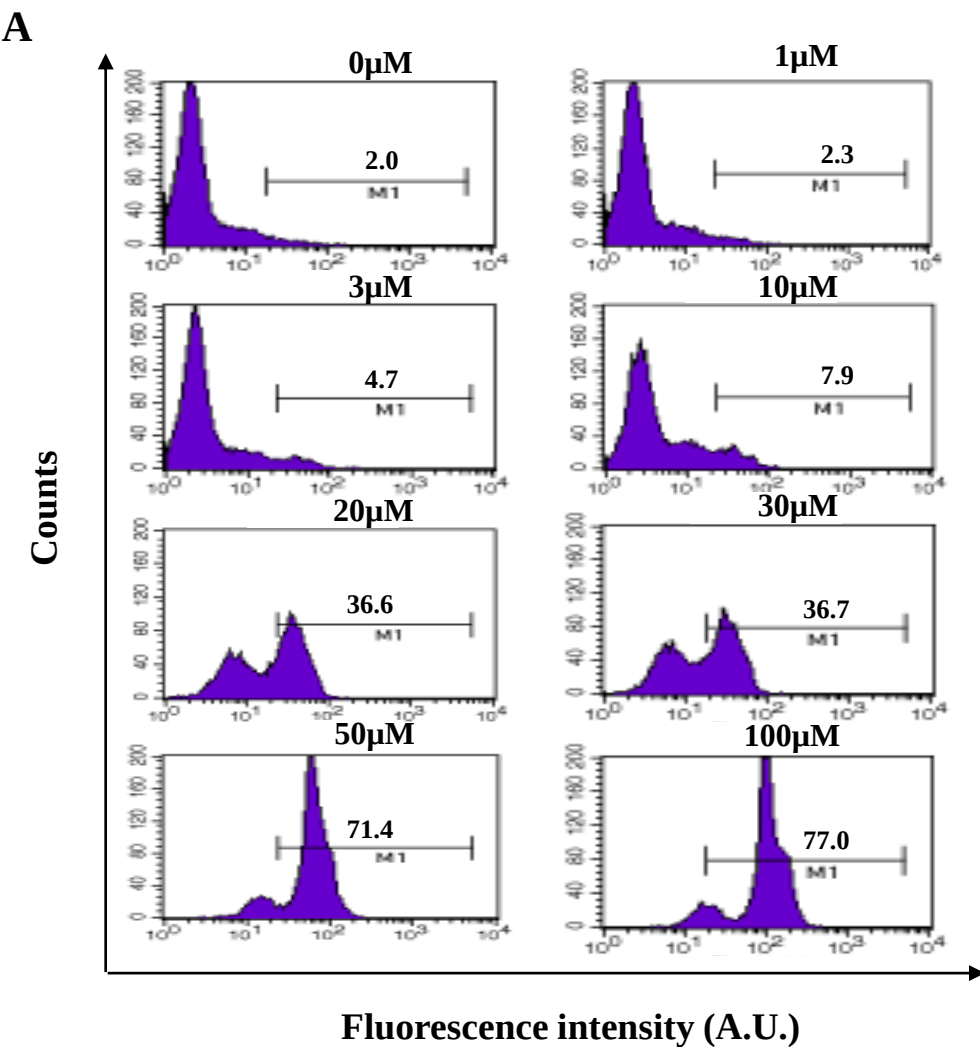


Fig. 3.

Figure 4

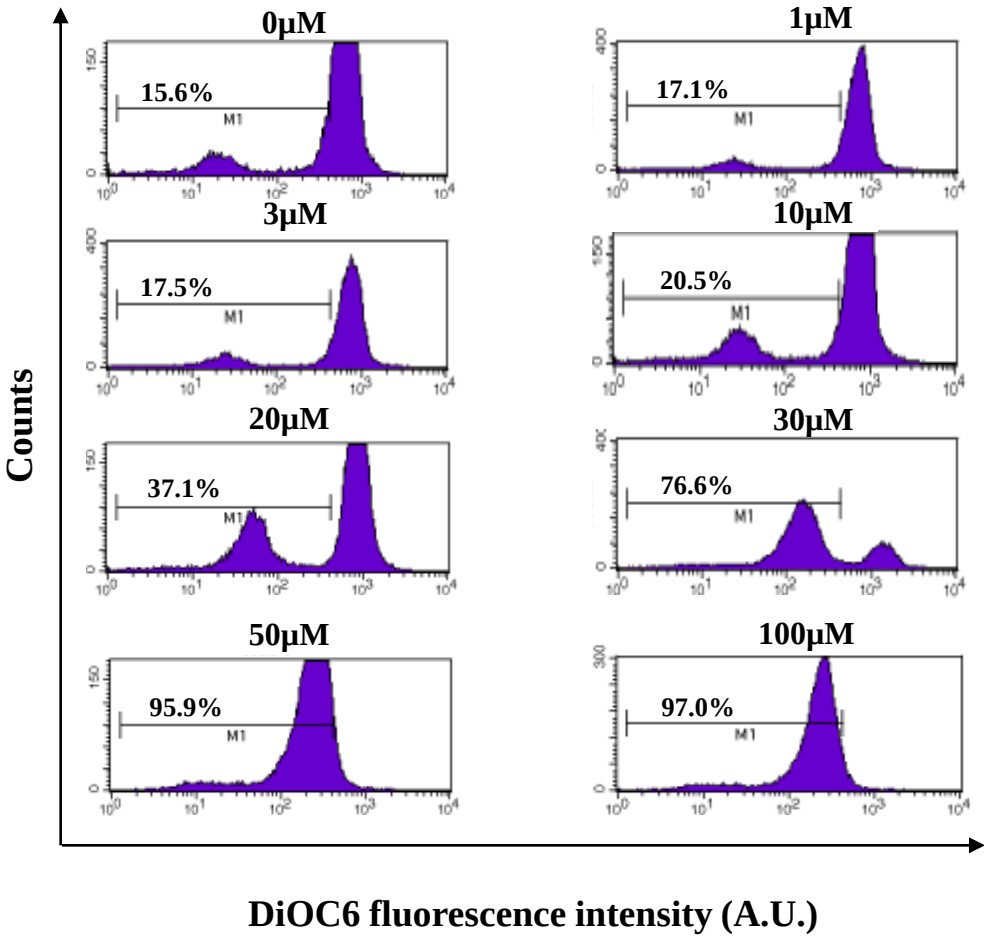


Fig. 4.

Figure 5

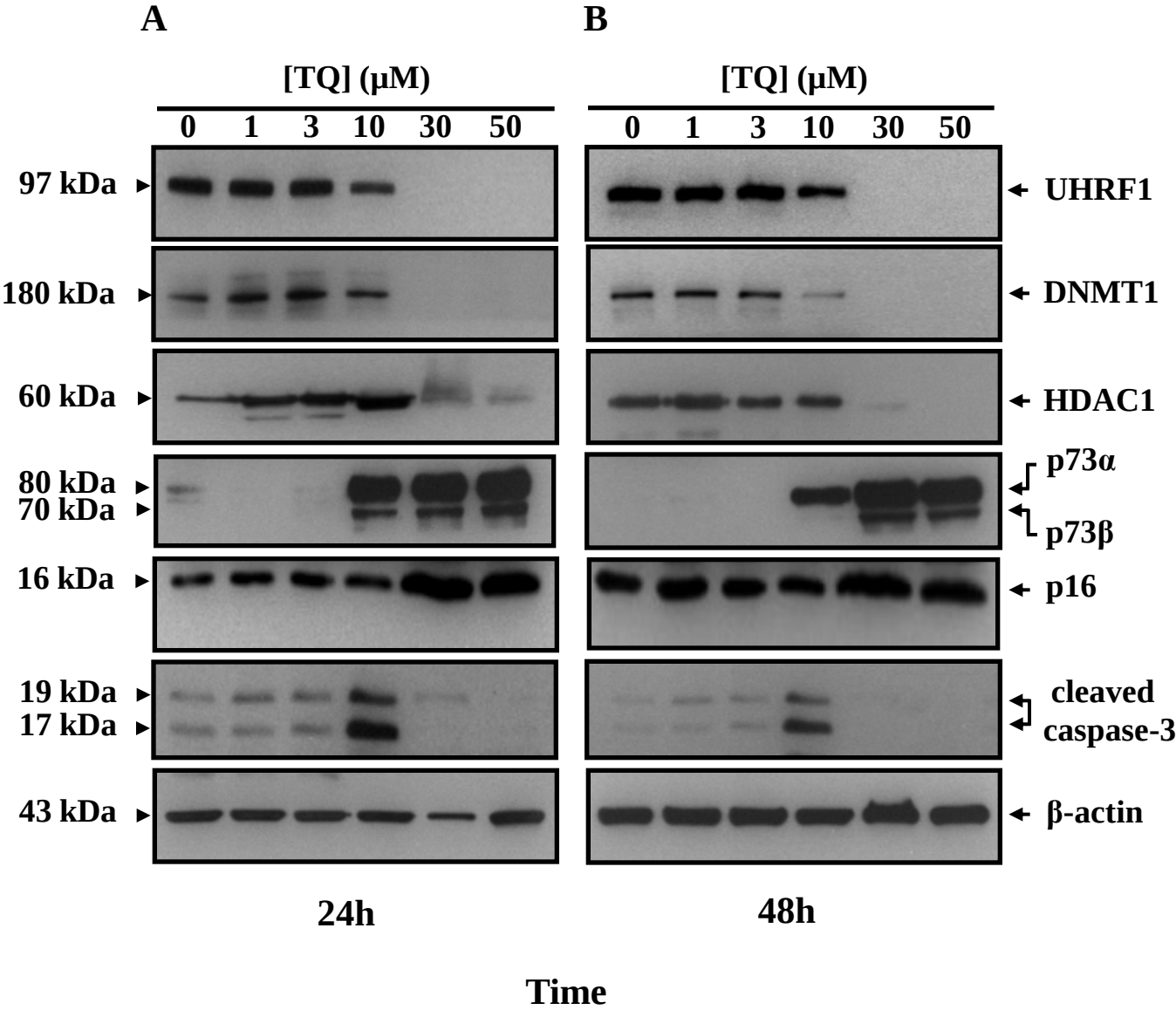


Fig. 5.

Figure 6

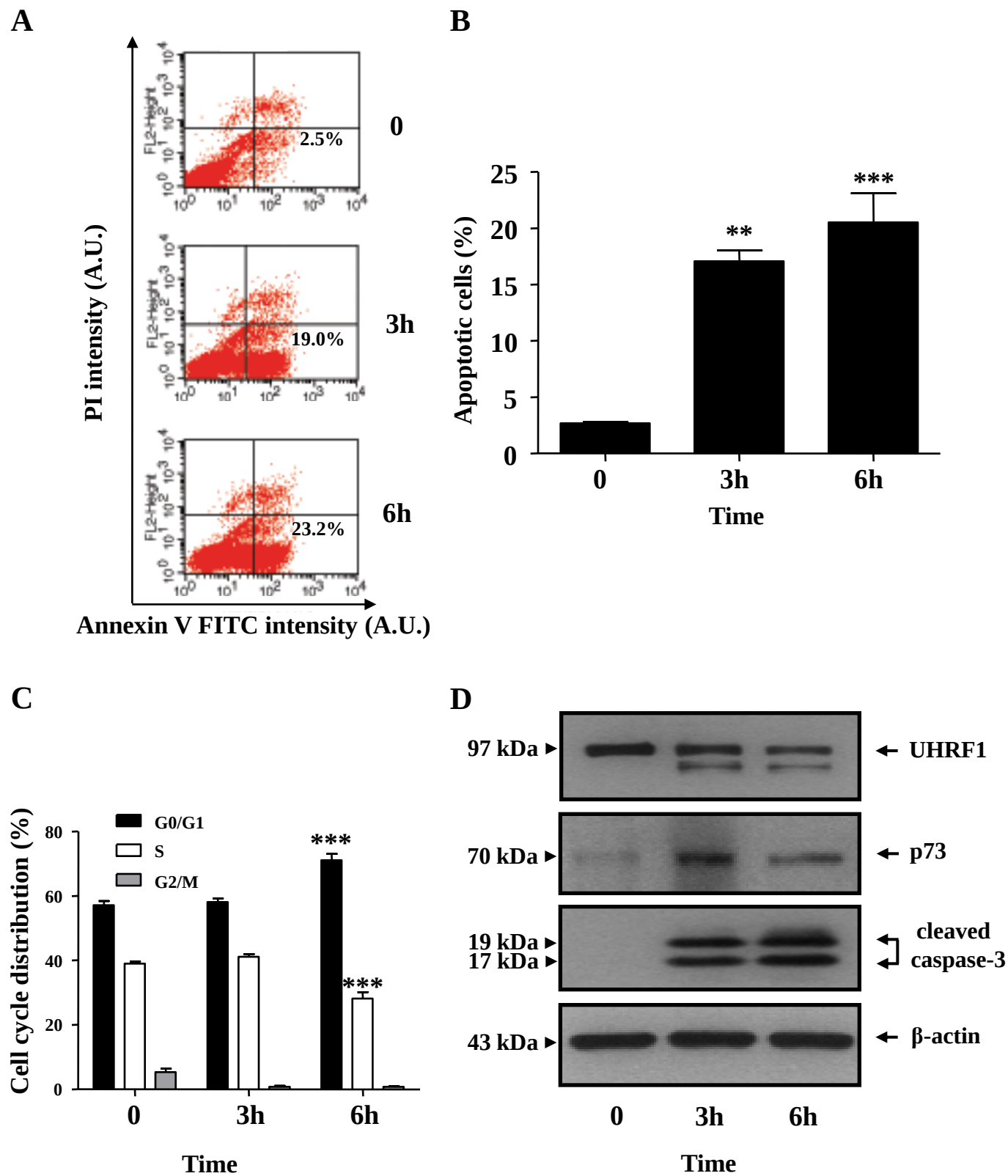


Fig. 6.

Figure 7

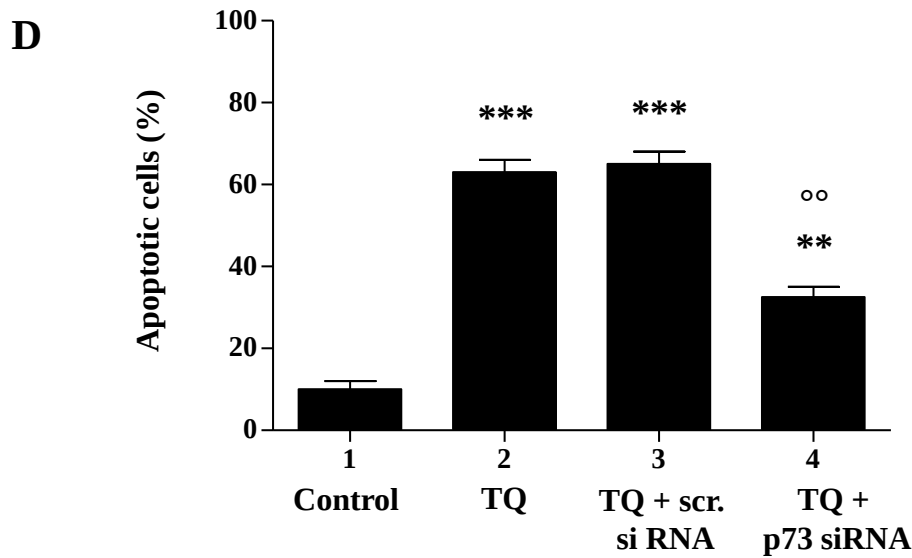
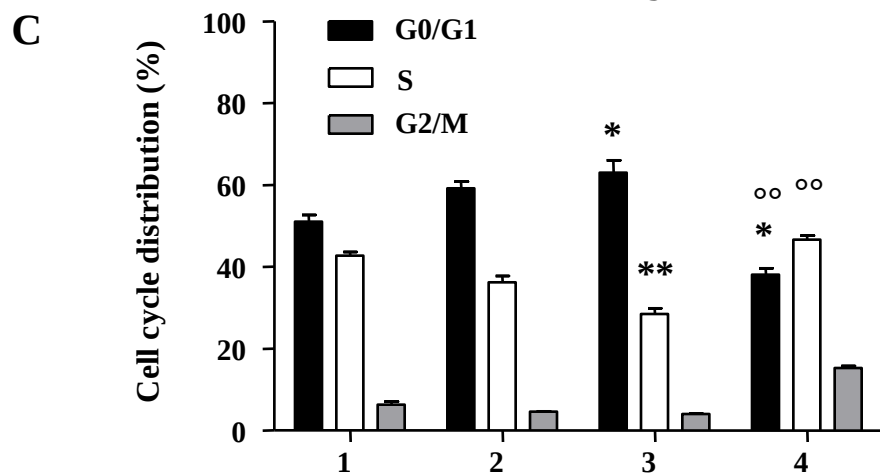
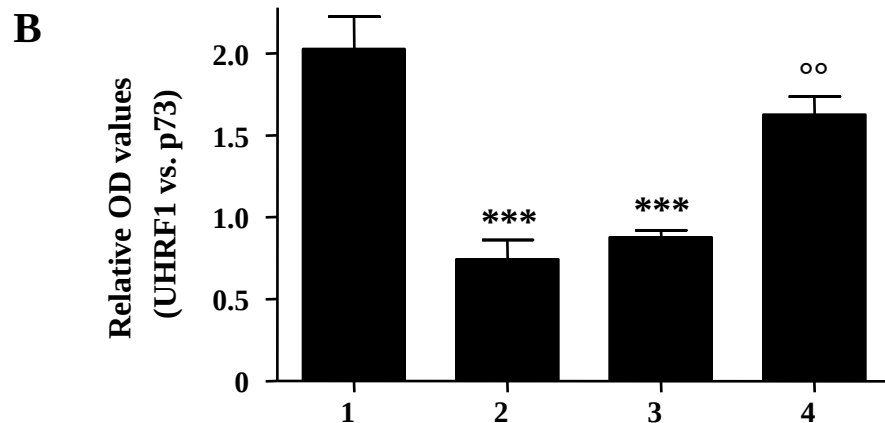
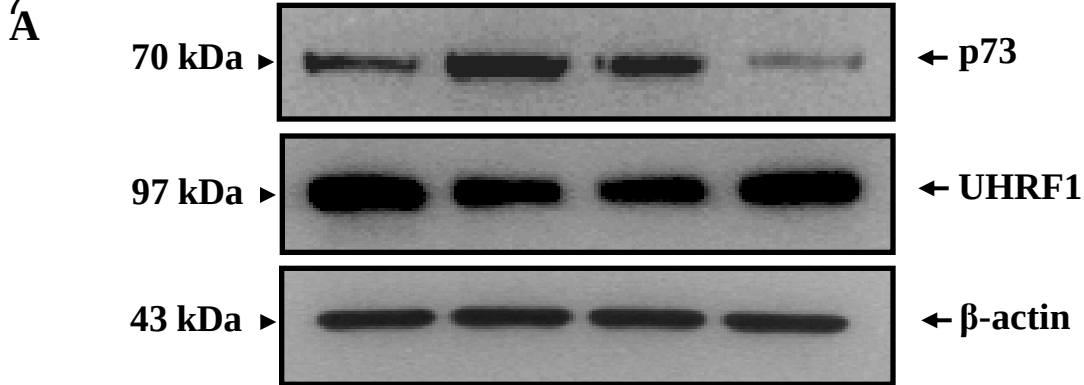
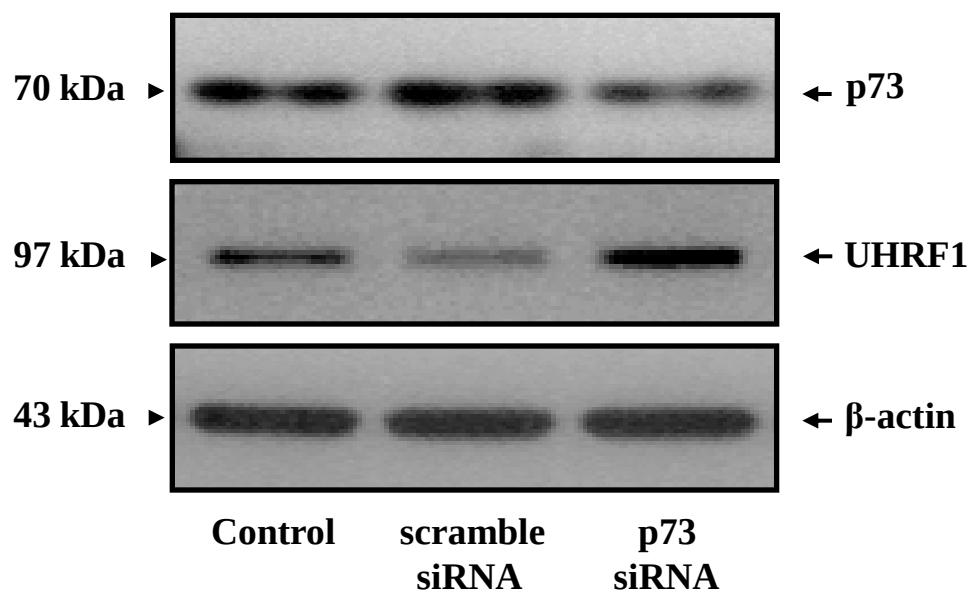


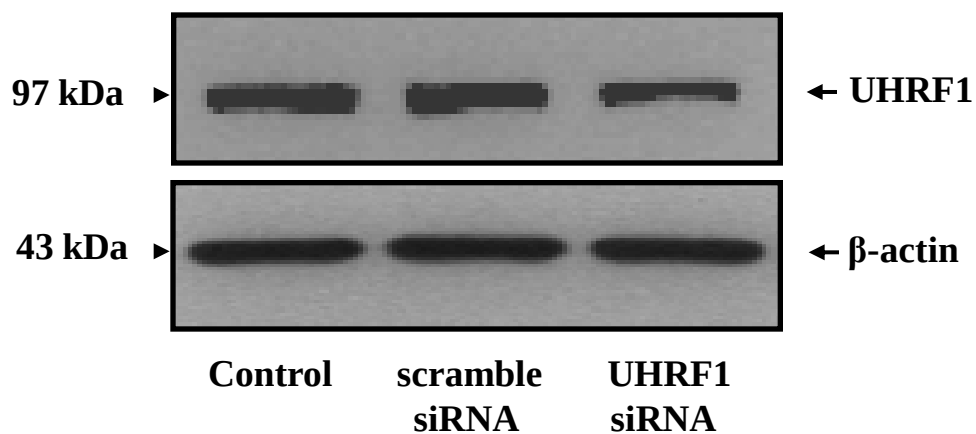
Fig. 7.

Figure 8

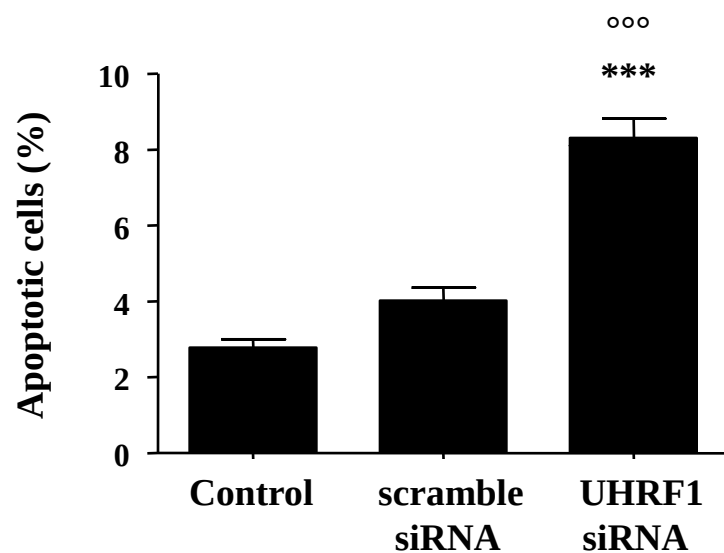
**A**



**B**



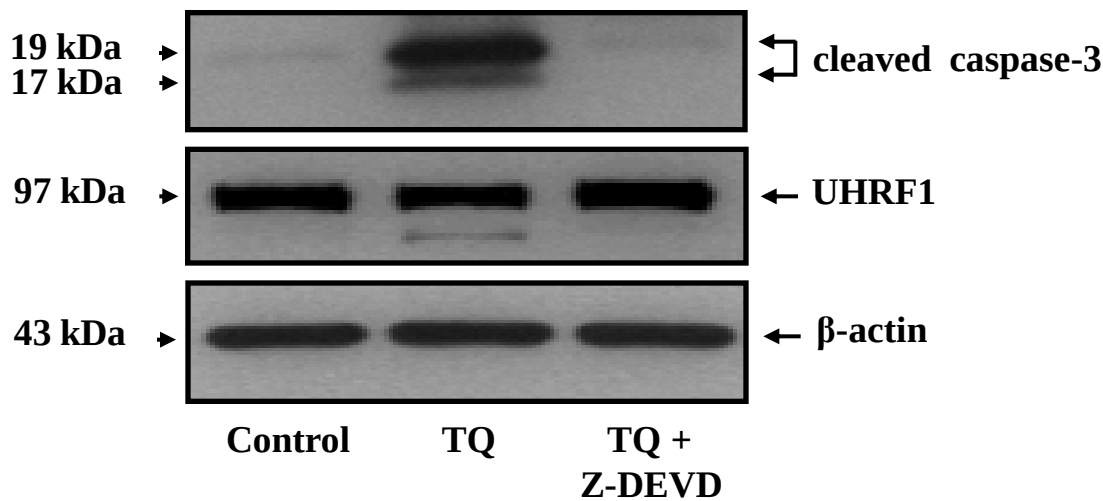
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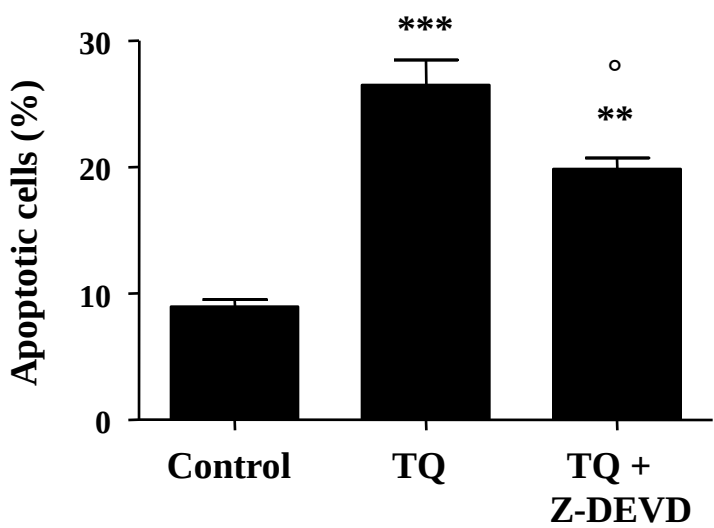
**Fig. 8.**

Figure 9

A



B



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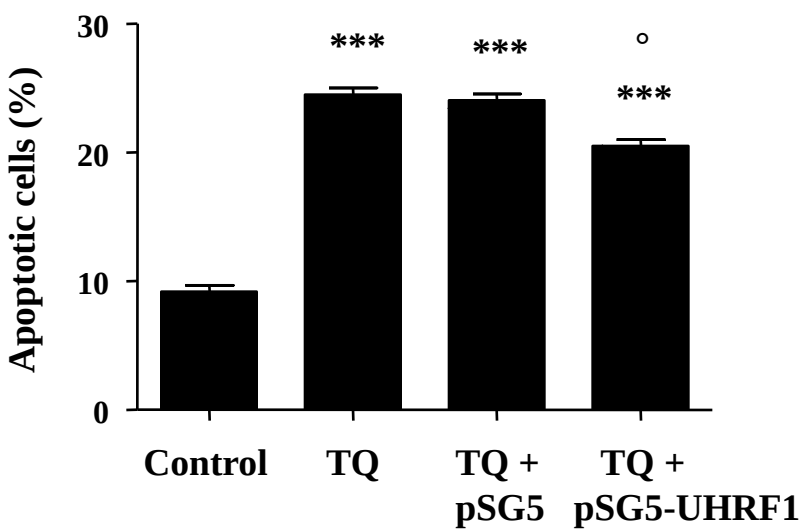


Fig. 9.