

## **5. Mechanisms of p14ARF induced chemosensitivity**

### **5.1 Introduction**

In the previous chapter we demonstrated that p14ARF increases the sensitivity of U2OS\_ARF cells to certain cytotoxic insults. Defining the mechanism(s) involved in p14ARF-mediated chemosensitivity may identify new drug targets as well as highlight the clinical settings in which p14ARF-induced chemosensitivity may be important.

The increase in chemosensitivity following p14ARF induction was associated with increased DNA fragmentation and phosphatidyl-serine exposure (as measured by increased sub-G1 content and annexin-V staining, respectively). These two features are markers of a classic apoptotic response, rather than necrosis or other forms of cell death (Clarke, 1990). The central mediators of apoptosis are a series of cysteine proteases, caspases, with initiator caspases (including caspase 2, 8, 9 and 10) cleaving and activating effector caspases. The effector caspases (caspase 3, 6 and 7) cleave substrates such as the inhibitor of caspase-activated DNase (iCAD) and poly(ADP-ribose) polymerase (PARP), leading to the phenotypic changes characteristic of apoptosis, including chromatin condensation, exposure of phosphatidyl-serine on the plasma membrane and DNA fragmentation (Clarke, 1990).

Initiation of apoptosis can occur via the intrinsic or extrinsic pathways. The extrinsic pathway activates caspase 8 and is initiated by death receptors such as fibroblast-associated receptor (Fas), tumour necrosis factor receptors (TNFR1/2) and TNF-related apoptosis inducing ligand receptor (TRAIL-R1). The intrinsic pathway is activated by

mitochondrial outer membrane permeabilisation, allowing release of pro-apoptotic proteins such as cytochrome c, second mitochondria-derived activator of caspases/direct IAP binding protein with low pI (SMAC/DIABLO) and apoptosis inducing factor (AIF) into the cytoplasm. Mitochondrial permeabilisation occurs when pores form in the mitochondrial outer membrane. These pores are formed via the assembly of pro-apoptotic Bcl-2-associated X protein (Bax) and Bcl-2 antagonist killer 1 protein (Bak) (Figure 5.1).

p53 is a key regulator of the intrinsic and extrinsic apoptotic pathways; p53 can transcriptionally activate several pro-apoptotic Bcl-2 family proteins, such as Bax, NOXA and PUMA, as well as death receptors such as Fas and the death domain containing protein PIDD (pro-apoptotic interacting domain), and also Fas ligand (FasL). Consequently, stabilisation of p53 by p14ARF may provide general pro-apoptotic signals to the cell via p53-dependent transactivation of PUMA, NOXA, Bax, Fas and FasL. Accordingly, p14ARF expression increased radio- and chemosensitivity in p53-intact cell lines (Gao *et al.*, 2001; Simon *et al.*, 2006). The impact of p53 on apoptosis is complex however, as p53 may preferentially transactivate pro-arrest rather than pro-apoptotic targets (eg p21<sup>Waf1</sup>, GADD45, 14-3-3 $\sigma$ ). The transcriptional program activated by p53 is influenced by post-translational modification of p53 and presence of co-stimulatory molecules such as hCas and hematopoietic zinc finger protein (Das *et al.*, 2007; Tanaka *et al.*, 2007; Xu, 2003).

An alternate mechanism by which ARF may chemosensitise cells involves the short isoform of ARF known as smARF (short mitochondrial ARF) (Reef *et al.*, 2006).

Ectopic expression of smARF reduces mitochondrial membrane potential without causing cytochrome c release or caspase activation. smARF induces autophagic cell death in a p53- and Bcl-2-independent manner and is a short-lived product derived from the internal initiation of translation at Met45 (Reef *et al.*, 2006) (reviewed in (Reef and Kimchi, 2006)). smARF lacks the amino-terminal ARF nucleolar targeting domain and localises to the mitochondria, where it interacts with and is stabilised by the mitochondrial protein, p32 (Reef *et al.*, 2007).

We investigated a number of key apoptotic effectors to determine the mechanism underlying p14ARF-mediated chemosensitivity. Our data show that p14ARF-mediated chemosensitivity is p53- and caspase-dependent, and is reliant on loss of mitochondrial potential. Inhibition of individual components of some apoptotic pathways showed that p14ARF-mediated cell death was not strictly dependent on Bax or Fas. Moreover, we found no evidence that smARF contributed to chemosensitisation by p14ARF in our cell models. These results reinforce the importance of p53 and caspases in the apoptotic programs facilitated by ARF.

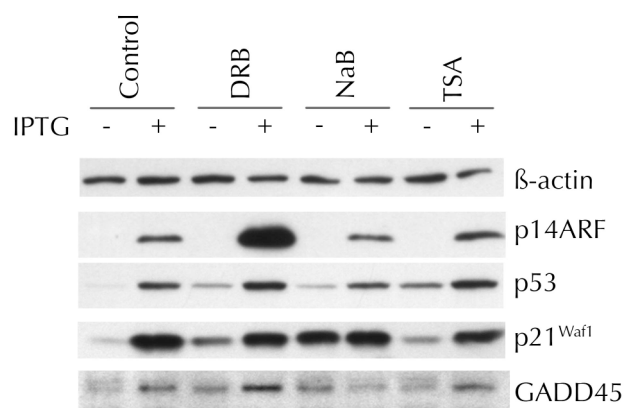


## 5.2 Results

To elucidate the mechanism responsible for p14ARF-mediated chemosensitivity, we focused on the effect of ARF expression on three separate cytotoxic agents - DRB, NaB and TSA. These drugs were selected because p14ARF expression significantly enhanced their killing capacity (see chapter 4).

### 5.2.1 p14ARF mediated chemosensitivity is p53-dependent

Considering that p14ARF-mediated cell cycle arrest requires p53, and p53 is a well-established apoptotic regulator, the role of p53 on p14ARF-mediated chemosensitivity was investigated. As shown in the previous chapter, p53 is stabilised in response to DRB, NaB or TSA treatment of U2OS\_ARF cells (Figure 5.2). As expected, induction of p14ARF expression alone also induced the accumulation of p53, to levels seen in the drug treated cells (Figure 5.2). These high levels of p53 were transcriptionally active as determined by increases in the levels of the p53 targets p21<sup>Waf1</sup> and, to a lesser extent, GADD45 (Figure 5.2).

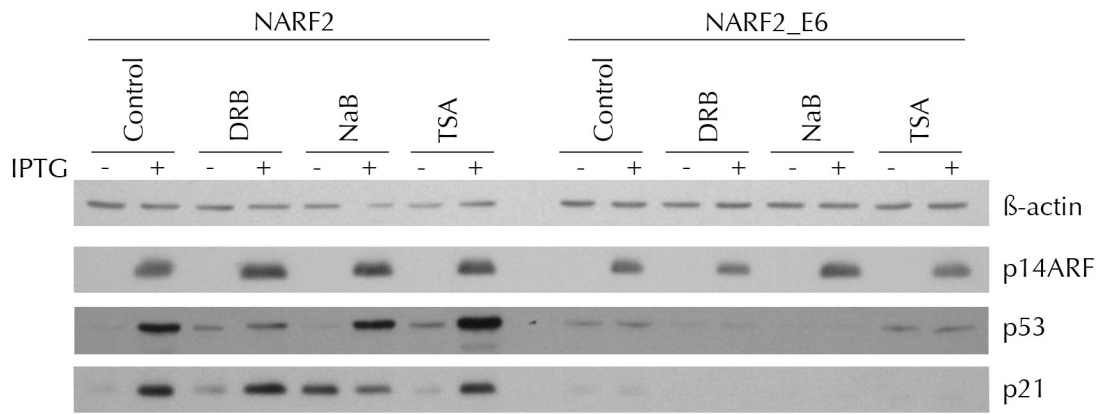


*Figure 5.2 Expression of p53, p21<sup>Waf1</sup>, and GADD45 in U2OS\_ARF cells treated with cytotoxic drugs and IPTG*

Expression of p14ARF, p53, p21<sup>Waf1</sup>, GADD45 and β-actin loading control was determined three days after treatment of U2OS\_ARF cells with 50μM DRB, 3mM NaB or 200nM TSA and PBS (-) or IPTG (+).

To investigate if p14ARF required p53 to increase chemosensitivity we initially compared the isogenic NARF2 (p53-intact) and NARF2\_E6 (p53-defective) osteosarcoma cell lines. Both these cell lines express IPTG inducible p14ARF but in the NARF2\_E6 cell line, p53 is degraded by constitutive expression of the human papilloma virus E6 ubiquitin ligase (Rodway *et al.*, 2004).

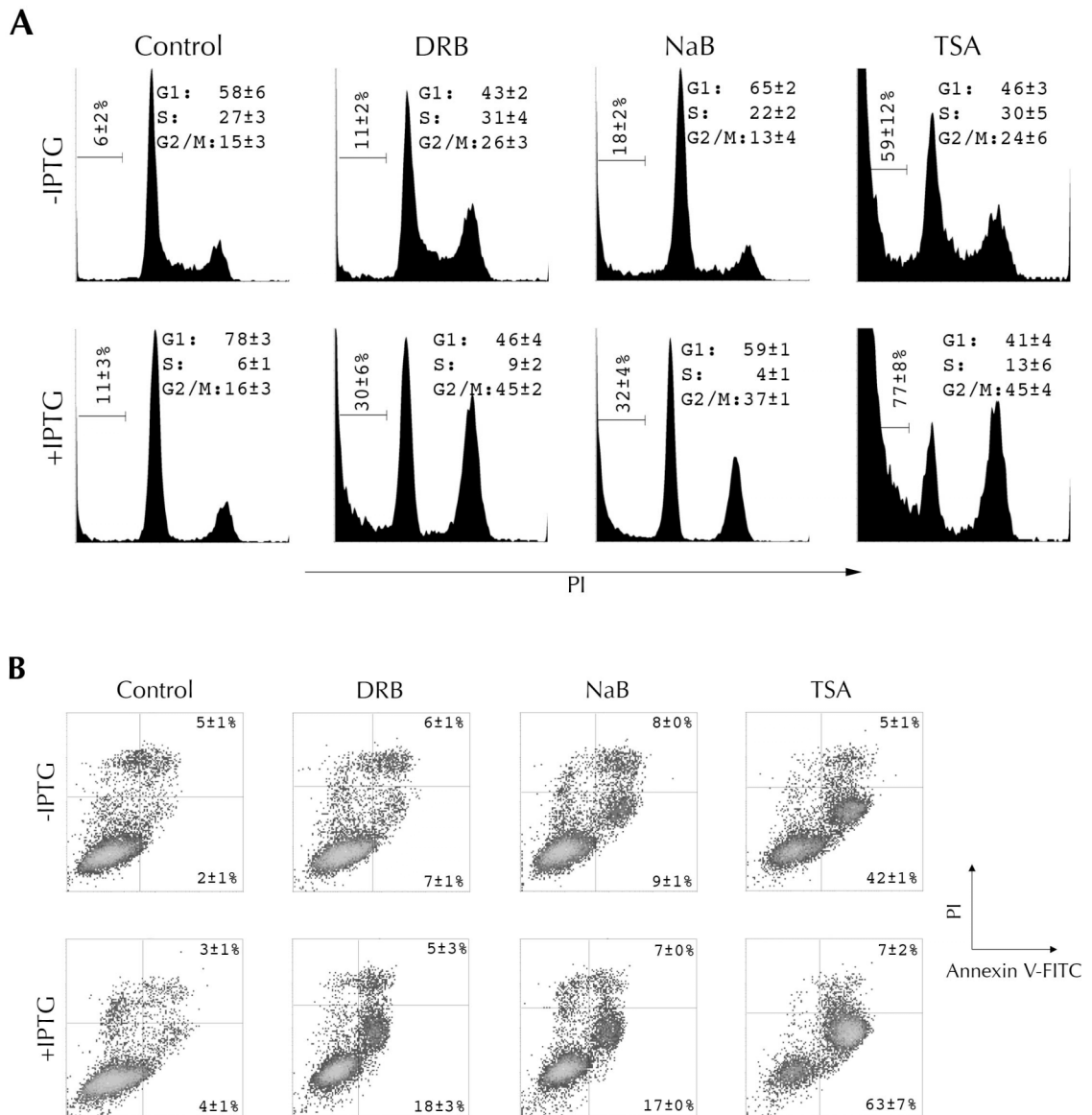
To ensure p14ARF expression enhanced chemosensitivity in the NARF2 cells, the cells were exposed to DRB, NaB or TSA or a DMSO carrier control for 72 hours in the presence or absence of IPTG. As expected, the NARF2 cells behaved as our U2OS\_ARF cells in response to IPTG and drugs (Figure 5.3, 5.4A & B). In particular, exposure of NARF2 cells to IPTG resulted in strong expression of p14ARF, and accumulation of p53 and p21<sup>Waf1</sup> (Figure 5.3) with concomitant cell cycle arrest (Figure 5.4A). IPTG treatment of NARF2\_E6 cells also resulted in strong accumulation of p14ARF in control and drug treated cells, but the low levels of p53 found in these cells did not increase with ARF expression and there was no change in the low levels of p21<sup>Waf1</sup> (Figure 5.3). These data confirm that p53 was effectively inactivated by constitutive E6 expression in these cells.



*Figure 5.3 Expression of p14ARF, p53, p21<sup>Waf1</sup> in NARF2 and NARF2\_E6 cells in response to cytotoxic drugs and p14ARF induction*

NARF2 and NARF2\_E6 cells were treated for three days with 50 $\mu$ M DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. p53 is inactivated in NARF2\_E6 cells by the E6 protein. Western blot was used to determine expression of p14ARF, p53, p21<sup>Waf1</sup> and  $\beta$ -actin loading control.

Accumulation of p14ARF in the p53-intact NARF2 cells increased cell death in response to the three cytotoxic drugs used. Specifically, the addition of IPTG increased the sub-G1 NARF2 population when cells were treated with DRB (11 $\pm$ 2% to 30 $\pm$ 6%), NaB (18 $\pm$ 2% to 32 $\pm$ 4%) and TSA (59 $\pm$ 12 to 77 $\pm$ 8%) (Figure 5.4A). Annexin-V staining confirmed that p14ARF induction increased levels of apoptosis in response to DRB, NaB and TSA (Figure 5.4B). Further, as was the case in our U2OS\_ARF cells, the induction of p14ARF also increased the G2/M population cells treated with DRB (26 $\pm$ 3% to 45 $\pm$ 2%), NaB (13 $\pm$ 4 to 37 $\pm$ 1%) and TSA (24 $\pm$ 6 to 45 $\pm$ 4%) (Figure 5.4A).



**Figure 5.4** Expression of *p14ARF* sensitises *NARF2* cells to apoptosis in response to cytotoxic drugs

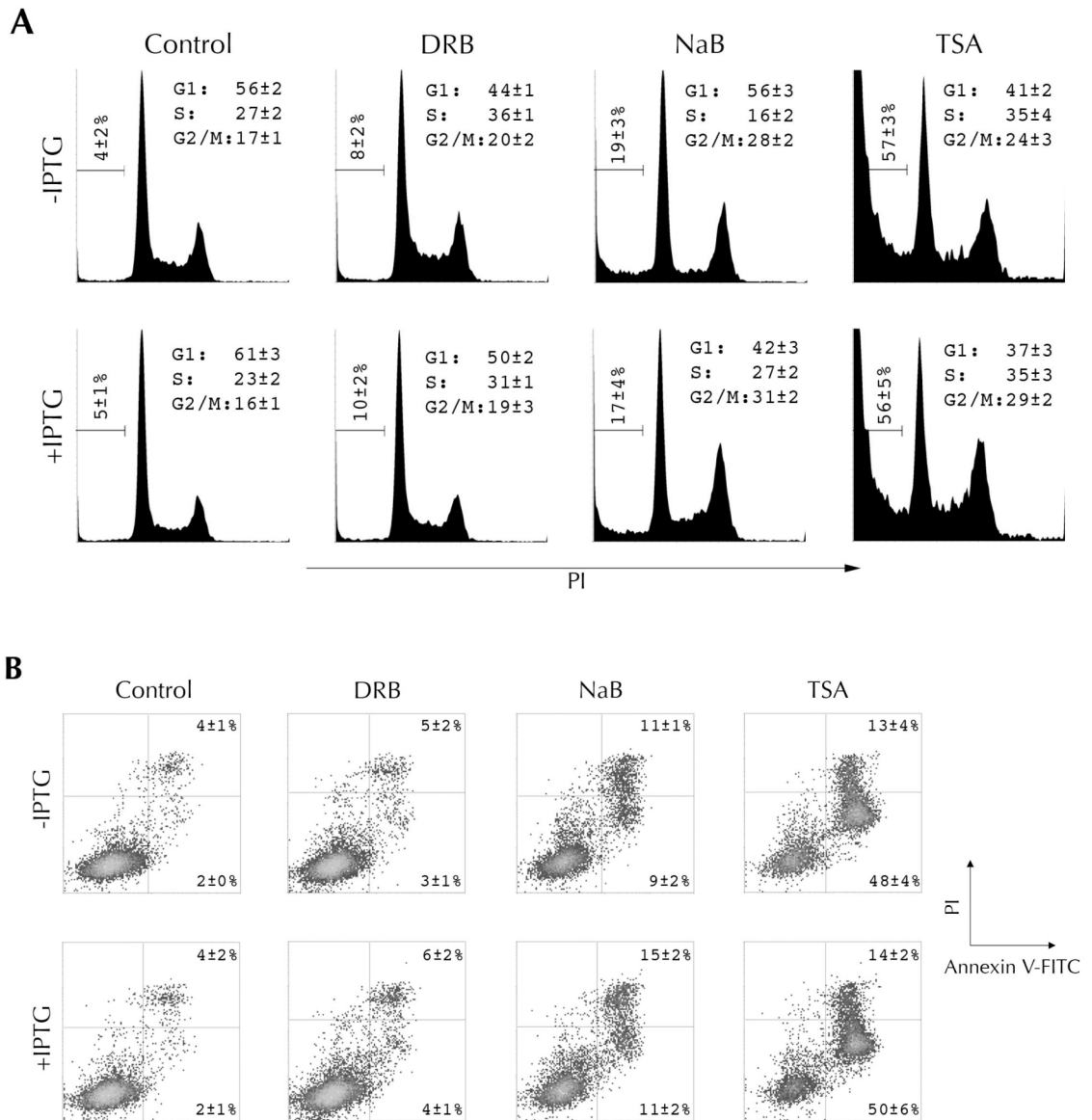
*NARF2* cells were treated for three days with 50 $\mu$ M DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce *p14ARF* expression.

(A) The cell cycle distribution and sub-G1 population of *NARF2* cells was examined using propidium iodide (PI) staining.

(B) Apoptotic *NARF2* cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

In contrast to the NARF2 cells, induction of p14ARF in NARF2\_E6 cells did not increase chemosensitivity. For instance, induction of p14ARF expression did not increase the sub-G1 population of NARF2\_E6 cells treated with DRB ( $8\pm 2\%$  to  $10\pm 2\%$ ), NaB ( $19\pm 3\%$  to  $17\pm 4\%$ ) or TSA ( $57\pm 3\%$  to  $56\pm 5\%$ ) (Figure 5.5A). Additionally, the annexin-V positive population was not increased by p14ARF induction in cells treated with DRB ( $8\pm 3\%$  to  $10\pm 3\%$ ), NaB ( $20\pm 2\%$  to  $26\pm 2\%$ ) or TSA ( $61\pm 1\%$  to  $64\pm 6\%$ ) (Figure 5.5B). Further, p14ARF accumulation did not lead to potent G1 arrest in these cells, although there was a slight decrease in S-phase cells in control ( $27\pm 2\%$  to  $23\pm 2\%$ ) and DRB treated cells ( $36\pm 1$  to  $31\pm 1\%$ ) and, surprisingly, an increase in S-phase in NaB treated cells ( $16\pm 2\%$  to  $27\pm 2\%$ ) (Figure 5.5A).

Although the NARF2 and NARF2\_E6 are isogenic cell clones, differing in their p53 status, they have increased ploidy (Figures 3.8A & B) which can affect cell response to cytotoxic insult (Castedo *et al.*, 2006) and the constitutive expression of E6 has p53-independent effects, including increased telomerase activity and enhanced vascular endothelial growth factor transcription (Clere *et al.*, 2007; Veldman *et al.*, 2003). To avoid non-specific E6 effects, we utilised a lentivirus system to stably and specifically silence p53 expression in the U2OS\_ARF cell line. U2OS\_ARF cells were infected with lentivirus expressing a short-hairpin-RNA (shRNA) molecule targeting the p53 transcript (U2OS\_ARF<sup>si-p53</sup>) or the luciferase transcript (U2OS\_ARF<sup>si-Luc</sup>) as a negative control. The co-expression of GFP confirmed that over 95% of cells stably expressed the shRNA molecules (data not shown).



**Figure 5.5** Expression of *p14ARF* does not sensitise *NARF2\_E6* cells to apoptosis in response to cytotoxic drugs

*NARF2\_E6* cells were treated for three days with 50µM DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce *p14ARF* expression. *p53* is inactivated in *NARF2\_E6* cells by the *E6* protein.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

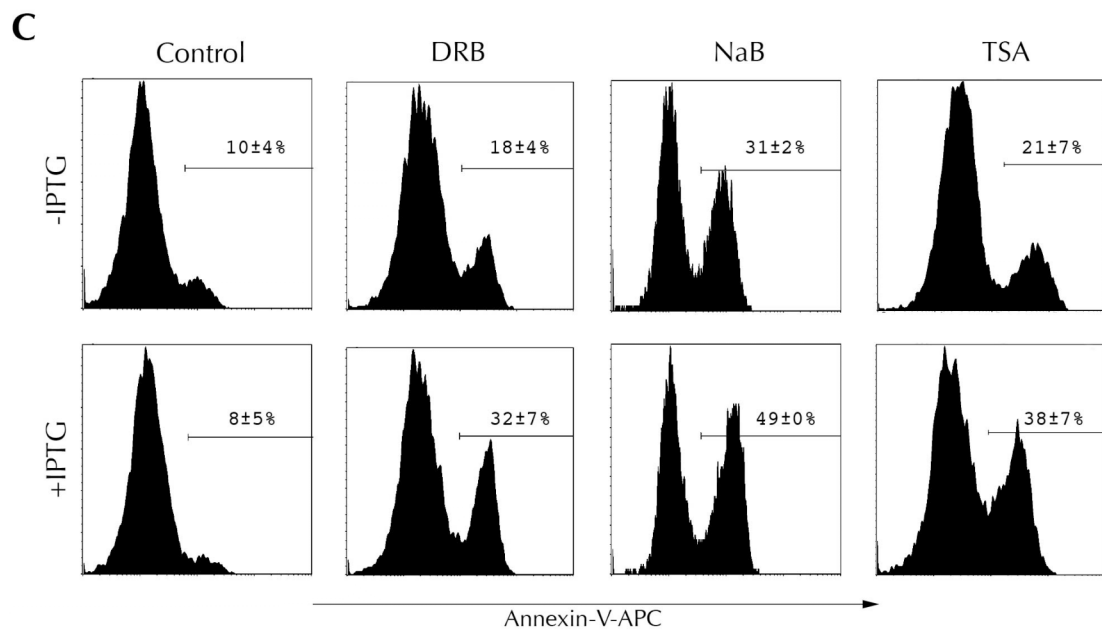
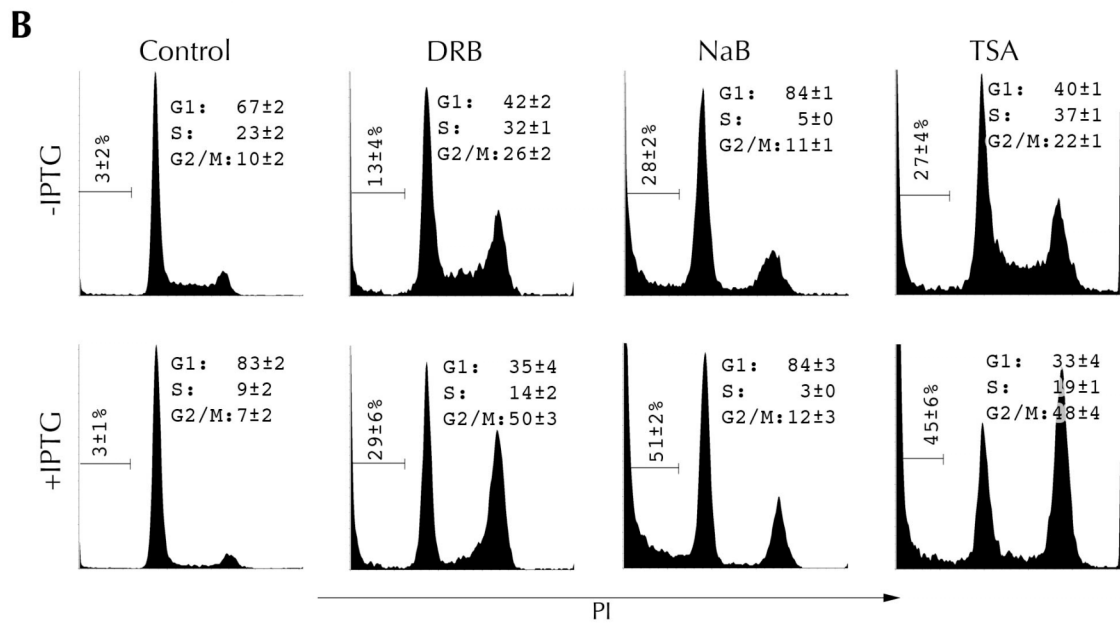
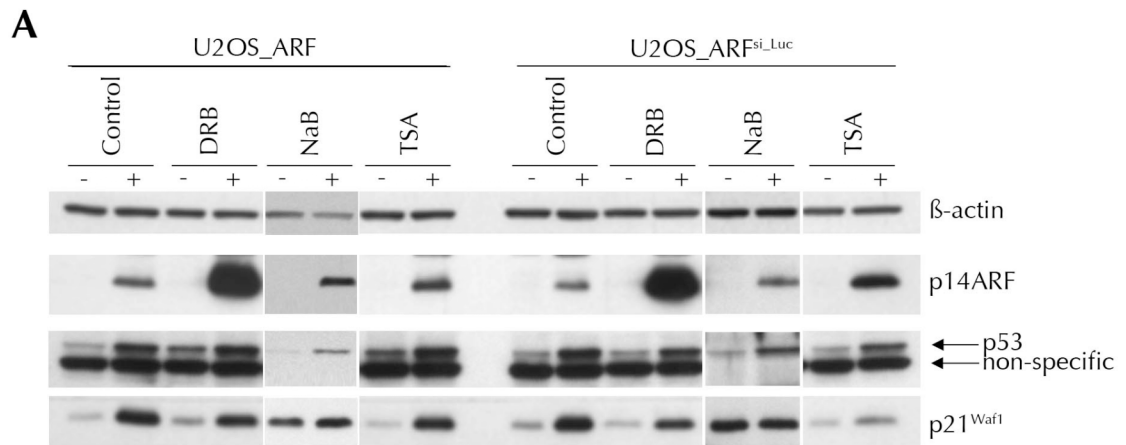
(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

U2OS\_ARF<sup>si-Luc</sup> cells were treated with DRB, NaB or TSA in the presence or absence of IPTG and protein expression, cell cycle distribution and annexin-V positive cells were analysed. To analyse chemosensitisation using annexin-V staining, U2OS\_ARF<sup>si-Luc</sup> cells were initially fixed for 10 minutes in 2% paraformaldehyde to inactivate any residual lentiviral particles and annexin-V positive cells were quantitated. Paraformaldehyde fixation prevented co-staining with propidium iodide, thus only one parameter could be analysed and the annexin-V results are presented as histograms rather than the usual 2-D dot plots. As expected, levels of p14ARF, p53 and p21<sup>Waf1</sup> were induced in the control U2OS\_ARF<sup>si-Luc</sup> cells as in the parental U2OS\_ARF cell line (Figure 5.6A). Cell cycle and apoptotic response of U2OS\_ARF<sup>si-Luc</sup> cells was also similar to the parental U2OS\_ARF cells. In particular, induction of p14ARF expression resulted in potent G1 arrest, no change in apoptotic sub-G1 cells or annexin-V positive cells (Figure 5.6B & 5.6C). As expected, cell death in response to cytotoxic drugs was also increased upon ARF induction in U2OS\_ARF<sup>si-Luc</sup> cells; the sub-G1 population increased in U2OS\_ARF<sup>si-Luc</sup> cells treated with DRB (13±4% to 29±6%), NaB (28±2% to 51±2%) and TSA (27±4% to 45±6%) (Figure 5.6B).

As mentioned above, annexin-V analysis of lentiviral infected cells is presented as 2D histograms, and it was evident that ARF induction increased the annexin-V positive population of U2OS\_ARF<sup>si-Luc</sup> cells treated with DRB (18±4% to 32±7%), NaB (31±2% to 49±0%) and TSA (21±7% to 38±7%) (Figure 5.6C).

To confirm p14ARF increases chemosensitivity in a p53 dependent manner we applied a lentivirus expressing a p53-specific shRNA to create the U2OS\_ARF<sup>si-p53</sup> cell line. Silencing of p53 was very effective in these cells; p53 accumulation was barely

detectable and induction of p21<sup>Waf1</sup> was not evident in response to p14ARF induction (Figure 5.7A). While DRB treatment increased p14ARF levels in the parental U2OS\_ARF cells, the increase was not as prominent in the U2OS\_ARF<sup>si-p53</sup> cells, and in contrast to U2OS\_ARF cells, NaB and TSA treatment lowered p14ARF protein levels. This effect is presumably related to the lacswitch system of expression, as neither DRB, NaB nor TSA affected p14ARF accumulation in the Saos-2 and H1299 cells, that express endogenous p14ARF (see Figure 4.16C). Low levels of p21<sup>Waf1</sup> were detected in response to NaB treatment. This is not unexpected as the p21<sup>Waf1</sup> promoter has NaB responsive elements, that are less responsive in the absence of p53 (Xiao *et al.*, 1997). As expected, induction of p14ARF did not affect the cell cycle distribution in the U2OS\_ARF<sup>si-p53</sup> cells (Figure 5.7B). More importantly, p14ARF induction did not chemosensitise the U2OS\_ARF<sup>si-p53</sup> cells to DRB, TSA or NaB treatment. In particular, no change was noted in sub-G1 population following IPTG induction of cells treated with carrier control (3±1% to 3±2%), DRB (16±4% to 17±4%), NaB (27±3% to 27±4%) or TSA (27±4% to 27±4%) (Figure 5.7B). Nor did ARF induction change the proportion of annexin-V positive U2OS\_ARF<sup>si-p53</sup> cells treated with control (9±5% to 10±4%), DRB (19±5% to 19±6%), NaB (32±3% to 32±2%) or TSA (34±4% to 34±6%) (Figure 5.7C).



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*Figure 5.6 Expression of p14ARF sensitises U2OS\_ARF<sup>si-Luc</sup> cells to apoptosis in response to cytotoxic drugs*

U2OS\_ARF and U2OS\_ARF<sup>si-Luc</sup> cells were treated for three days with 50µM DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

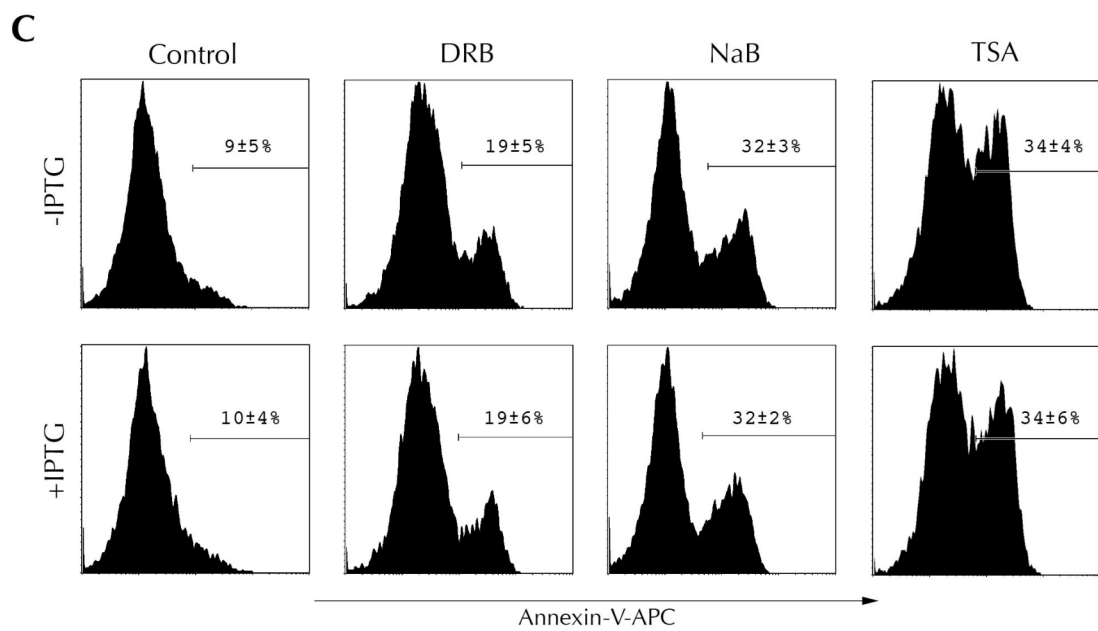
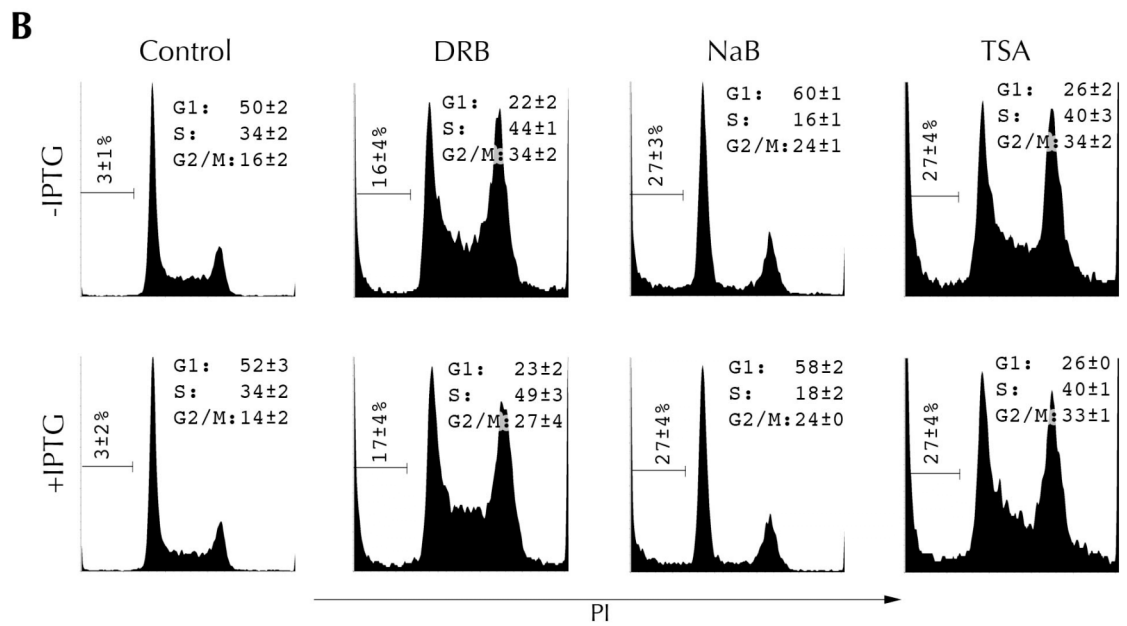
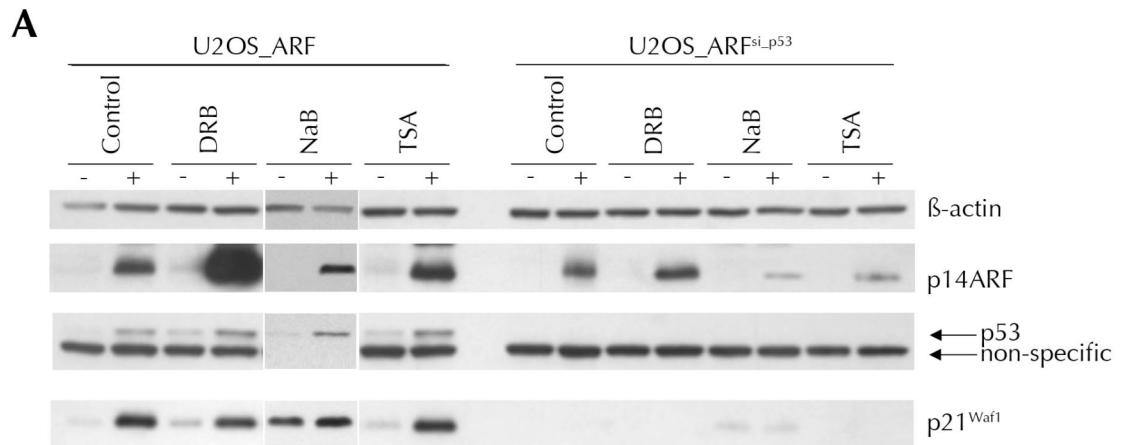
- (A) Western blot was used to compare expression of p14ARF, p53, p21<sup>Waf1</sup> and β-actin loading control.
- (B) The cell cycle distribution and sub-G1 population of U2OS\_ARF<sup>si-Luc</sup> cells was examined using propidium iodide (PI) staining.
- (C) Apoptotic U2OS\_ARF<sup>si-Luc</sup> cells were also analysed by flow cytometric staining of annexin-V.

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*Figure 5.7 Expression of p14ARF does not sensitise U2OS\_ARF<sup>si-p53</sup> cells to apoptosis in response to cytotoxic drugs*

U2OS\_ARF and U2OS\_ARF<sup>si-p53</sup> cells were treated for three days with 50µM DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. p53 is knocked down in U2OS\_ARF<sup>si-p53</sup> cells by RNA interference

- (A) Western blot was used to compare expression of p14ARF, p53, p21<sup>Waf1</sup> and β-actin loading control.
- (B) The cell cycle distribution and sub-G1 population of U2OS\_ARF<sup>si-p53</sup> cells was examined using propidium iodide (PI) staining
- (C) Apoptotic U2OS\_ARF<sup>si-p53</sup> cells were also analysed by flow cytometric staining of annexin-V.



### 5.2.2 Impact of p21<sup>Waf1</sup> on ARF induced chemosensitivity

As p14ARF mediated chemosensitivity was p53 dependent, we investigated whether the key p53 target that inhibits cell cycle, p21<sup>Waf1</sup>, was involved in p14ARF-mediated apoptosis. The cyclin dependent kinase inhibitor p21<sup>Waf1</sup> is essential in ARF and p53-mediated G1 arrest (Hemmati *et al.*, 2005) and also inhibits apoptosis via cell cycle arrest and indirect inhibition of caspase activity (Sohn *et al.*, 2006; Waldman *et al.*, 1995; Wendt *et al.*, 2006). Additionally, loss of p21<sup>Waf1</sup> via homozygous deletion in HCT116 colorectal cancer cells increases apoptosis in response to adenovirally-expressed p14ARF, as measured by DNA content, annexin-V positivity and caspase activation (Hemmati *et al.*, 2005). To investigate if p21<sup>Waf1</sup> was a component of ARF-mediated chemosensitivity we used the lentivirus system to generate a pool of U2OS\_ARF cells with silenced p21<sup>Waf1</sup>. Two previously published p21<sup>Waf1</sup> shRNA constructs were made that targeted different regions of the p21<sup>Waf1</sup> mRNA, but despite infecting over 99% of cells as demonstrated by GFP expression, they did not efficiently reduce p21<sup>Waf1</sup> expression levels (data not shown). Transducing U2OS\_ARF cells with a mixture of these lentiviral constructs resulted in p21<sup>Waf1</sup> knockdown of approximately 50%, and a pool of U2OS\_ARF<sup>si\_p21Waf1</sup> cells was generated using this method (Figure 5.8A). These cells were treated with DRB, NaB or TSA, in the presence or absence of IPTG, and analysed three days later. Unfortunately, even with a 50% knockdown in p21<sup>Waf1</sup> levels, the induction of p14ARF expression still induced G1 arrest (IPTG treatment increased cells in G1 from 69±0% to 81±2%) that was equivalent to the arrest induced in the parental U2OS\_ARF cell and lentiviral control U2OS\_ARF<sup>si\_Luc</sup> cells. Not surprisingly p14ARF-mediated chemosensitivity was also maintained, with induction of p14ARF expression approximately doubling in sub-G1 population of DRB,

NaB and TSA treated cells (Figure 5.8B & 5.8C), an increase that is similar to that seen in the control U2OS\_ARF<sup>si-Luc</sup> cells.

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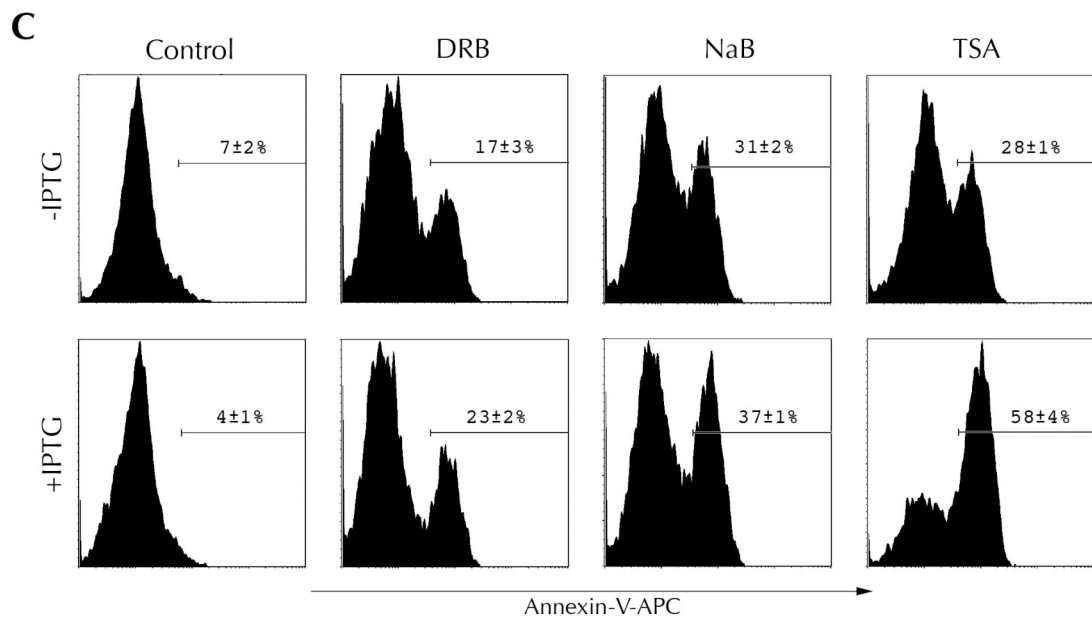
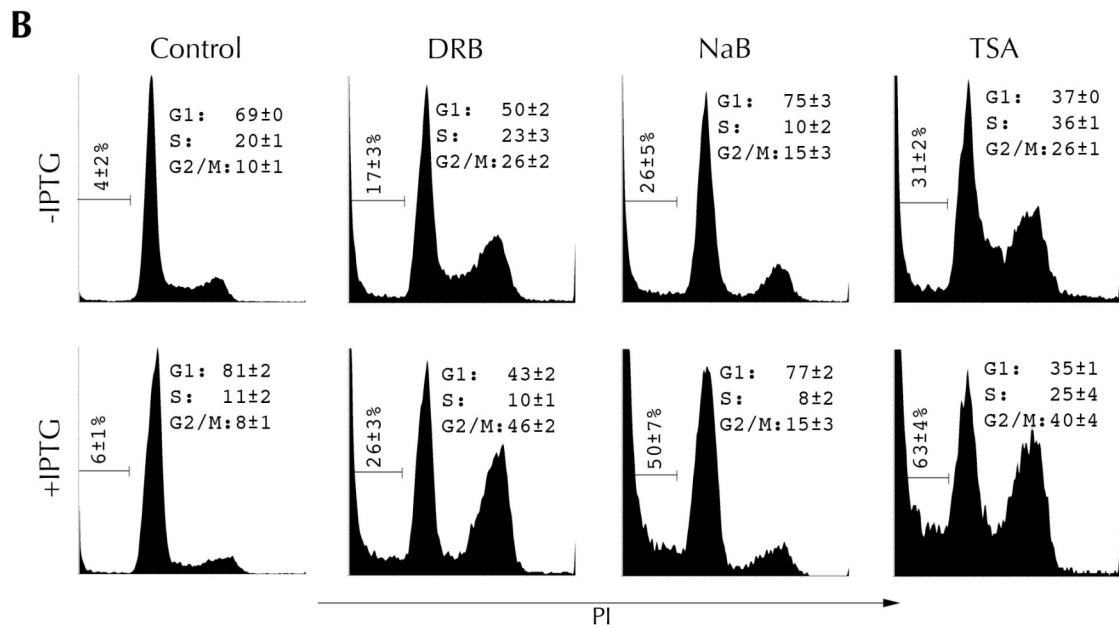
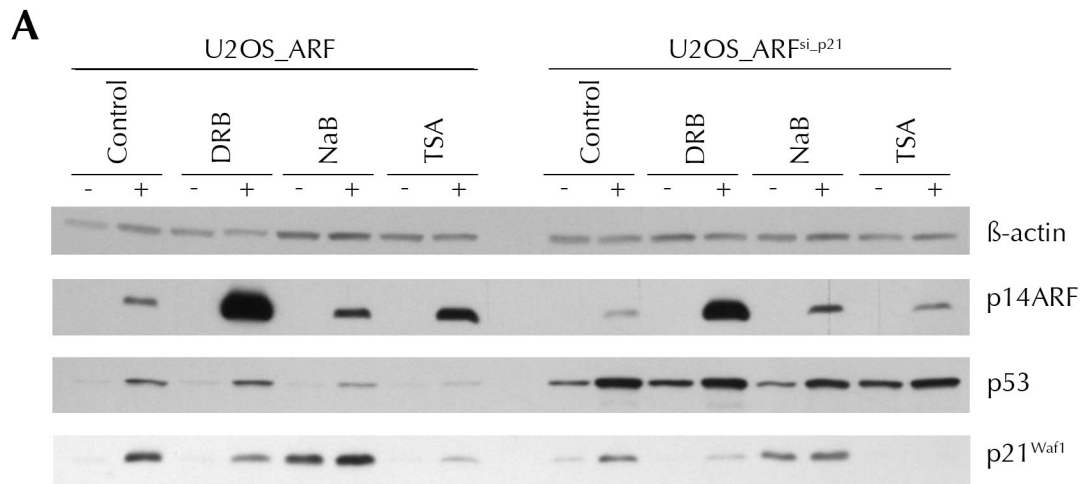
*Figure 5.8 Expression of p14ARF sensitises U2OS\_ARF<sup>si-p21</sup> cells to apoptosis in response to cytotoxic drugs*

U2OS\_ARF and U2OS\_ARF<sup>si-p21</sup> cells were treated for three days with 50µM DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. p21<sup>Waf1</sup> is partially knocked down in U2OS\_ARF<sup>si-p21</sup> cells by RNA interference.

(A) Western blot was used to compare expression of p14ARF, p53, p21<sup>Waf1</sup> and β-actin loading control.

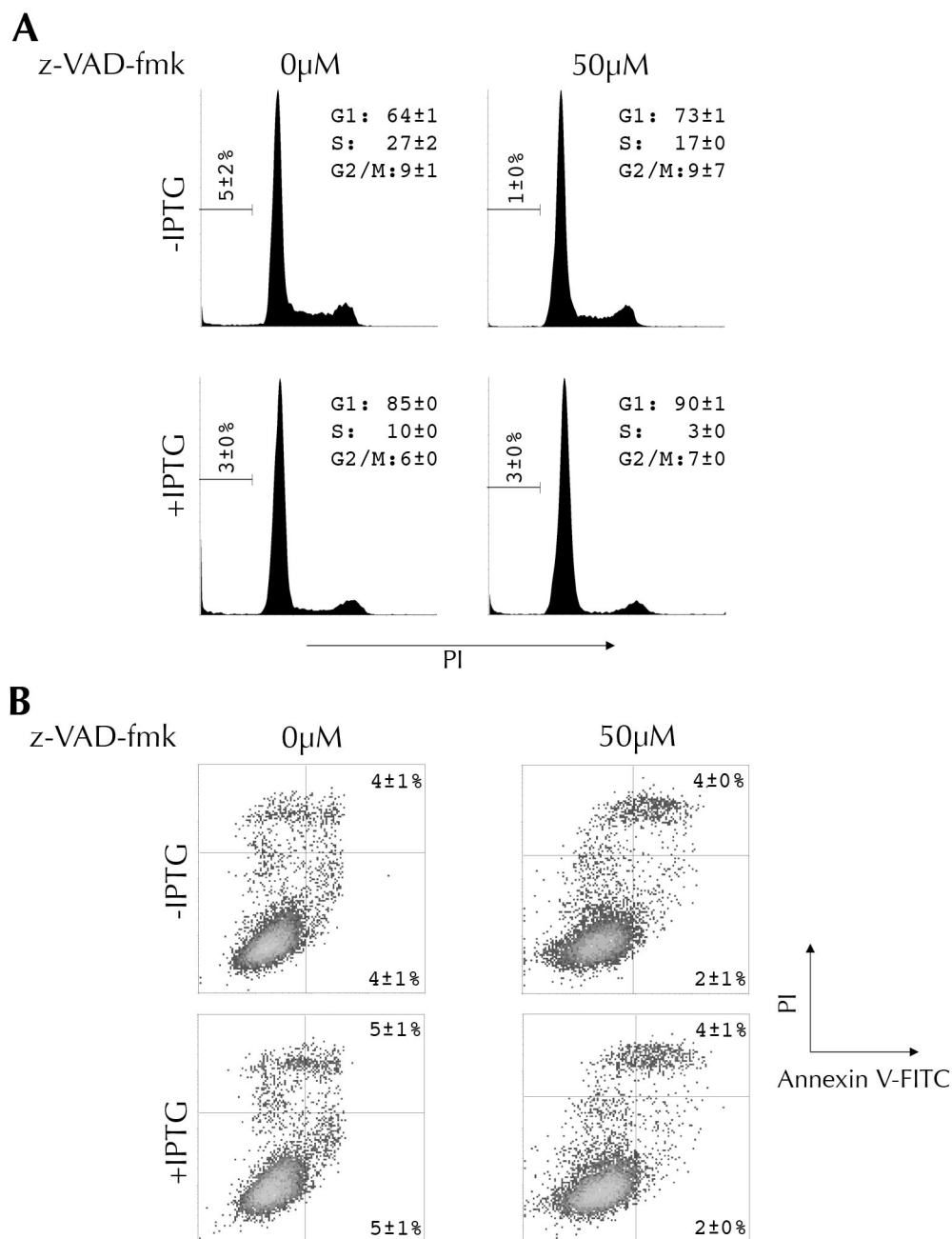
(B) The cell cycle distribution and sub-G1 population of U2OS\_ARF<sup>si-p21</sup> cells was examined using propidium iodide (PI) staining.

(C) Apoptotic U2OS\_ARF<sup>si-p21</sup> cells were also analysed by flow cytometric staining of annexin-V.



5.2.3 *p14ARF* does not sensitise U2OS\_ARF cells to apoptosis in the presence of the pan-caspase inhibitor z-VAD-fmk.

The increased annexin-V population and cleavage of genomic DNA as a result of p14ARF induction (observed as an increase in sub-G1 population of propidium iodide stained nuclei) in drug treated U2OS\_ARF cells suggested the involvement of caspase-mediated apoptosis. To determine if p14ARF mediated chemosensitivity was caspase dependent, U2OS\_ARF cells were pre-treated with z-VAD-fmk, a pan-caspase inhibitor that irreversibly binds to the catalytic site of caspases (Medina-Palazon *et al.*, 2004). After 3 h of treatment with 50 $\mu$ M z-VAD-fmk, DRB, NaB or TSA was added, along with IPTG or PBS control and the cells analysed 72 hours later. Treatment of U2OS\_ARF cells with this caspase inhibitor resulted in slight S-phase reduction (27 $\pm$ 0% to 17 $\pm$ 0%) and G1 arrest (64 $\pm$ 1% to 73 $\pm$ 1%) and decreased the low percentage of sub-G1 cells (5 $\pm$ 2% to 1 $\pm$ 0% of cells) and annexin-V positive cells (Figure 5.9A & 5.9B). Similarly, treatment of U2OS\_ARF cells with z-VAD-fmk prevented apoptosis in response to DRB, TSA or NaB regardless of IPTG-induced p14ARF expression. For example, the annexin-V positive population of DRB treated U2OS\_ARF cells remained at 11 $\pm$ 1% (without IPTG) and 10 $\pm$ 2% (with IPTG) (Figure 5.10B). z-VAD-fmk treatment increased the G1 population in uninduced DRB treated cells from 63 $\pm$ 2% to 84 $\pm$ 0% and in induced cells from 45 $\pm$ 3% to 66 $\pm$ 5% (Figure 5.10A), presumably as suppression of caspase activity can lead to changes in cell cycle distribution (Jorquera and Tanguay, 1999; Piekarz *et al.*, 2004). The apoptotic sub-G1 population of DRB treated cells was also reduced by z-VAD-fmk to 1 $\pm$ 0% (without IPTG) and 4 $\pm$ 1% (with IPTG) (Figure 5.10A). Similarly, results demonstrating the requirement of caspase activation for p14ARF-mediated chemosensitisation were obtained for NaB and TSA (Figure 5.11A, 5.11B, 5.12A & 5.12B).

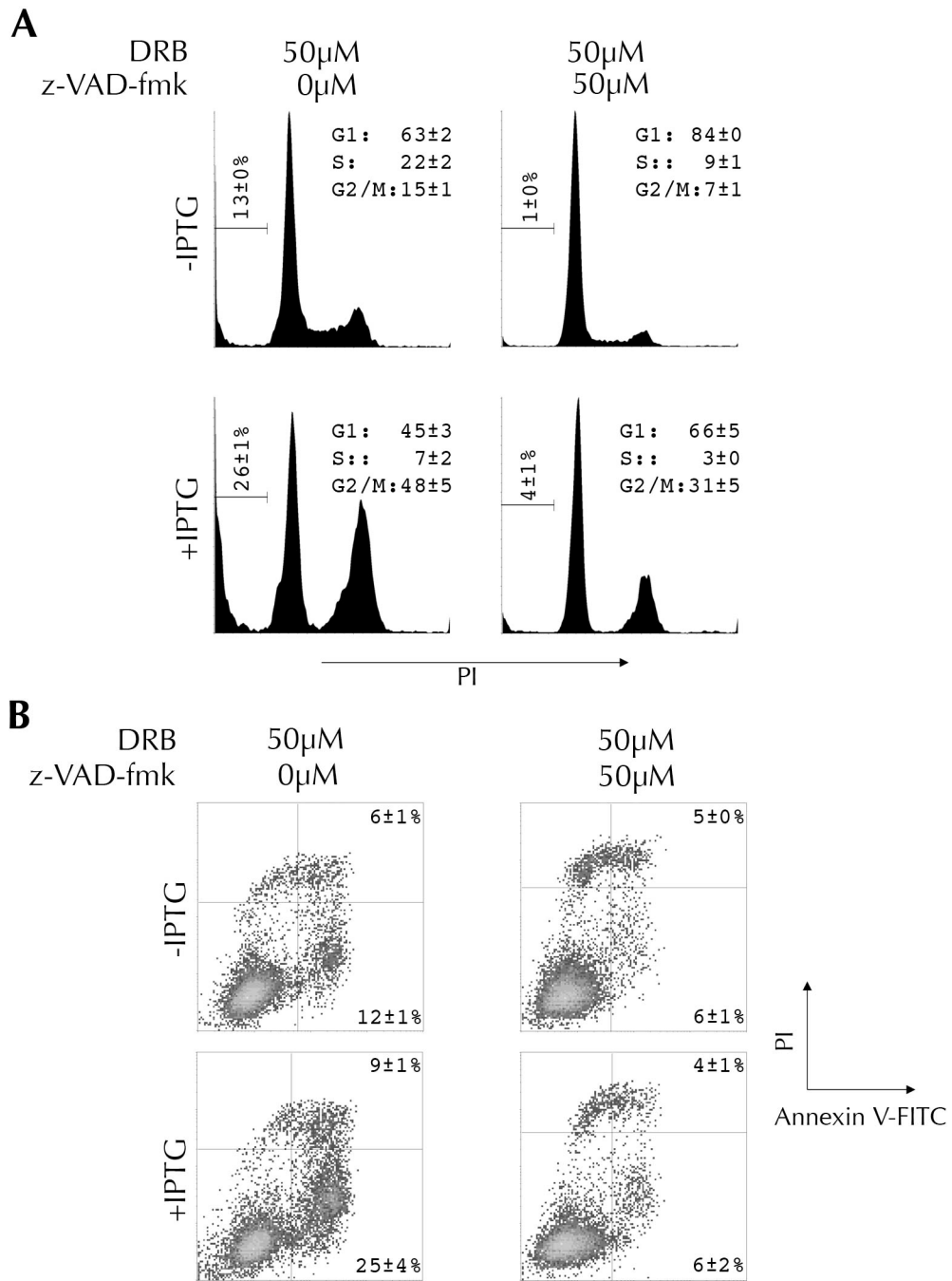


*Figure 5.9 Analysis of the effect of pan-caspase inhibition on U2OS\_ARF cells*

U2OS\_ARF cells were pre-treated with the pan-caspase inhibitor z-VAD-fmk then treated for three days with 0.1% DMSO carrier control and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

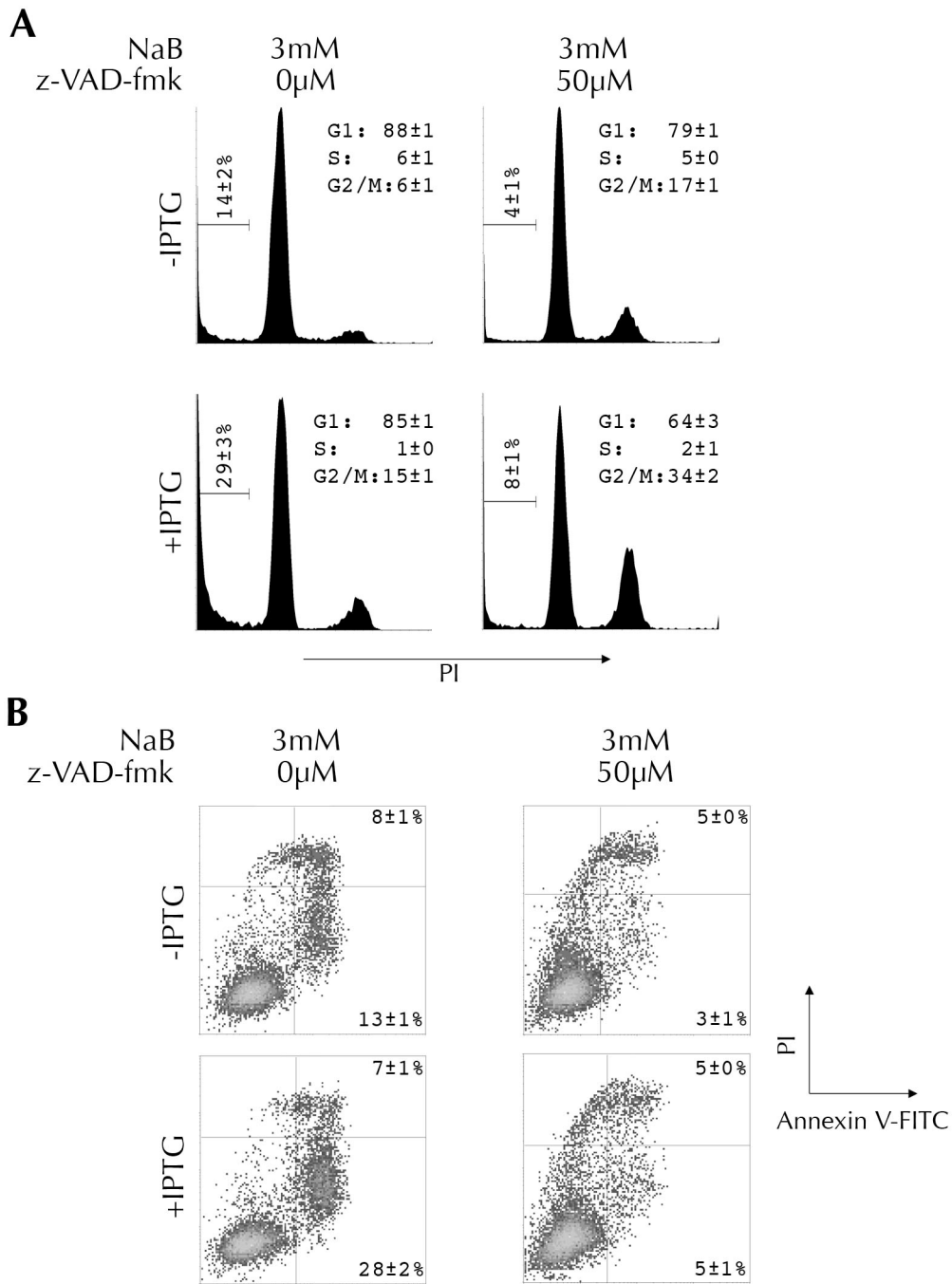


**Figure 5.10** Pan-caspase inhibition prevents apoptosis and chemosensitivity induced by *p14ARF* expression in DRB treated U2OS<sub>ARF</sub> cells

U2OS<sub>ARF</sub> cells were pre-treated with the pan-caspase inhibitor z-VAD-fmk or 0.1% DMSO carrier control, then treated for three days with 50µM DRB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion

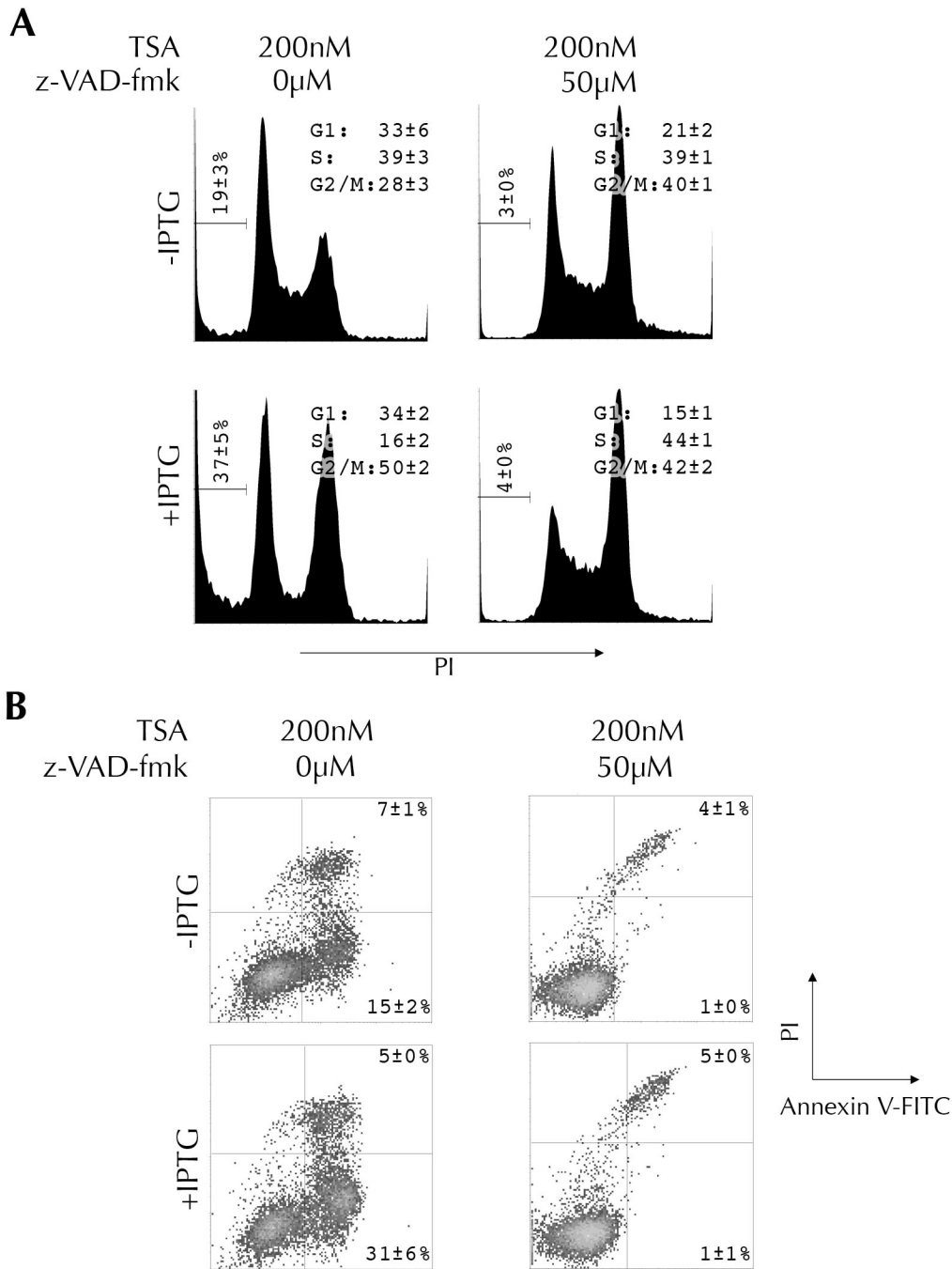


**Figure 5.11** Pan-caspase inhibition prevents apoptosis and chemosensitivity induced by *p14ARF* expression in sodium butyrate (NaB) treated U2OS\_ARF cells

U2OS\_ARF cells were pre-treated with the pan-caspase inhibitor z-VAD-fmk or 0.1% DMSO carrier control, then treated for three days with 3mM NaB and PBS (-) or 1mM IPTG (+) to induce *p14ARF* expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.



**Figure 5.12** Pan-caspase inhibition prevents apoptosis and chemosensitivity induced by p14ARF expression in trichostatin A (TSA) treated U2OS\_ARF cells

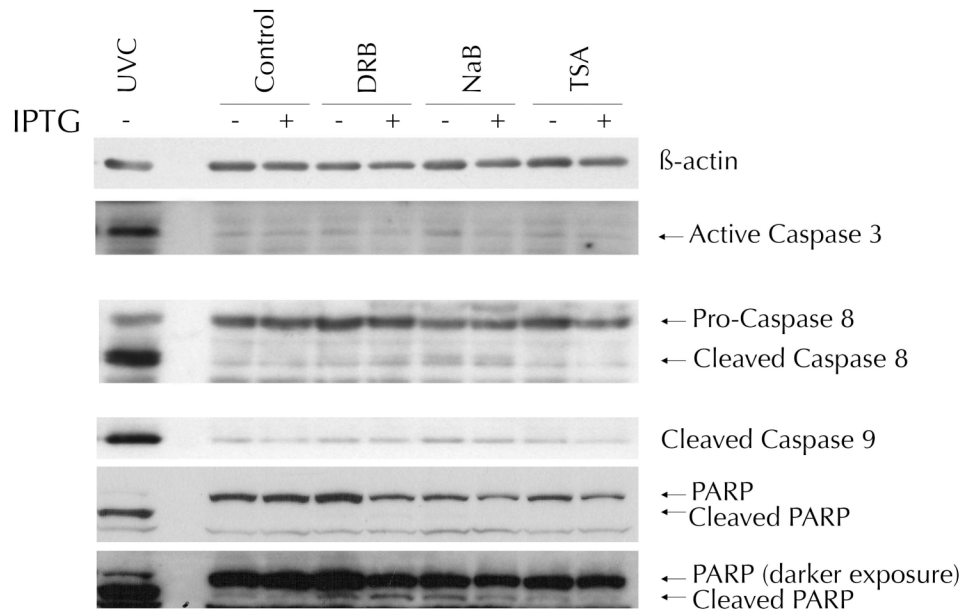
U2OS\_ARF cells were pre-treated with the pan-caspase inhibitor z-VAD-fmk or 0.1% DMSO carrier control, then treated for three days with 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

*5.2.4 Active caspases are not detected in U2OS\_ARF cells treated with cytotoxic drugs and induced to express p14ARF*

As z-VAD-fmk prevented ARF-mediated chemosensitivity, we investigated changes in caspase 3, 8 and 9 as well as PARP, a target of caspase 3 proteolytic activity. U2OS\_ARF cells were treated with DRB, NaB or TSA in the presence or absence of IPTG to induce p14ARF expression. Three days later cells were harvested and subject to western blotting. To detect cleaved caspase 3 we used an antibody that specifically detects active, cleaved caspase 3. Surprisingly, activated caspase 3 was not detected in induced or uninduced U2OS\_ARF cells treated with DRB, NaB, TSA or carrier control (Figure 5.13). Detection of activated caspase 3 in a caspase positive control (U2OS\_ARF cells 24 hours post 80J/m<sup>2</sup> UVC treatment) demonstrated the antibody could detect activated caspase 3 in these cells. Similarly, we did not detect cleaved caspase 8 or 9, even though the cleaved form of these proteins could be detected in UVC-treated U2OS\_ARF cells (Figure 5.13). To investigate alterations in downstream targets of effector caspases, we used a PARP antibody that detects both full length and the 85kDa cleaved fragment of PARP. Full length PARP was not significantly lost in drug treated U2OS\_ARF cells, regardless of the presence of p14ARF (Figure 5.13). Levels of cleaved PARP increased in U2OS\_ARF cells treated with DRB and NaB, but were very low compared to levels of full length PARP. ARF induction did not affect the levels of PARP cleavage.



*Figure 5.13 p14ARF induction in cytotoxic drug treated U2OS\_ARF cells does not lead to activation of caspase 3, 8 or 9*

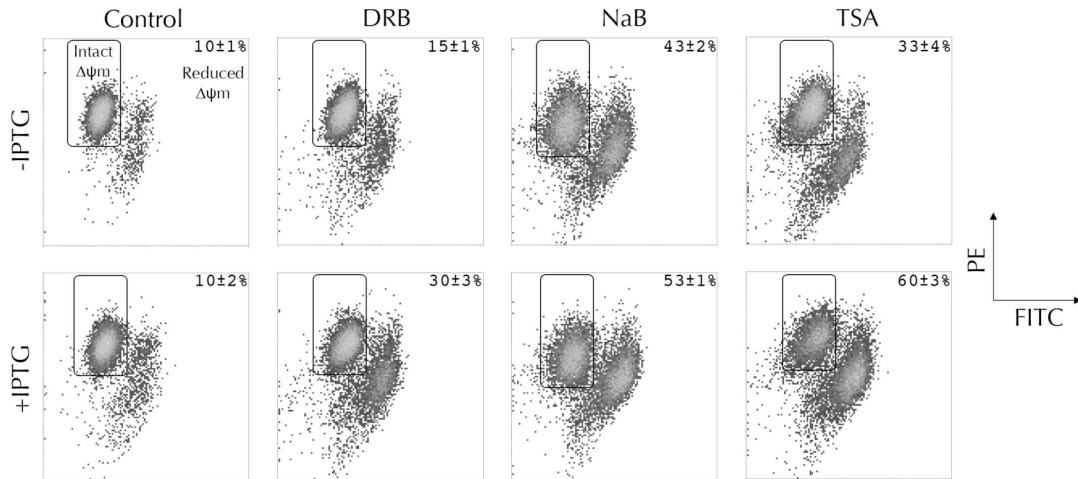
Expression of active caspase 9, caspase 8, active caspase 3, PARP and  $\beta$ -actin loading control was determined three days after treatment of U2OS\_ARF cells with 50 $\mu$ M DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. Arrows indicate the full length and cleaved protein bands where relevant.

### *5.2.5 p14ARF induced chemosensitivity is associated with mitochondrial depolarisation*

Pore formation in the outer mitochondrial membrane as a result of Bax or Bak activation, and subsequent mitochondrial outer membrane permeability is a crucial step in the activation of the intrinsic apoptotic pathway. Pore formation allows release of cytochrome c, SMAC/DIABLO and AIF into the cytosol, which enable caspase dependent and caspase independent cell death to occur. Additionally, p53 increases transcription of a number of pro-apoptotic Bcl-2 members that facilitate activation of Bax and Bak, including PUMA, Noxa, Bid and Bax itself (Chipuk and Green, 2006). With this in mind, we determined if p14ARF mediated chemosensitivity is associated

with mitochondrial depolarisation by using JC-1, a cell permeable stain that fluoresces red in intact mitochondria but fluoresces increasingly green and less red in depolarised mitochondria. While mitochondrial depolarisation is not a direct measure of Bax/Bak pore formation, mitochondrial outer membrane permeabilisation is usually associated with permanent loss of mitochondrial membrane potential ( $\Delta\Psi_m$ ) (Heiskanen *et al.*, 1999), and thus loss of  $\Delta\Psi_m$  is used as a surrogate marker for mitochondrial outer membrane permeabilisation

U2OS\_ARF cells were treated with DRB, NaB, TSA or DMSO carrier control in the presence or absence of IPTG, and mitochondrial potential measured by JC-1 staining after 72 hours. IPTG treatment had no effect on cells that were not exposed to cytotoxic drugs, with  $10\pm 1\%$  of uninduced cells exhibiting depolarised mitochondria, compared to  $10\pm 2\%$  of IPTG treated cells (Figure 5.14). In DRB treated cells,  $15\pm 1\%$  of cells had depolarised mitochondria, which was increased to  $30\pm 3\%$  by p14ARF induction (Figure 5.14). Enforced expression of p14ARF also increased mitochondrial depolarisation in NaB treated cells from  $43\pm 2\%$  to  $53\pm 1\%$  and TSA treated cells from  $33\pm 4\%$  to  $60\pm 3\%$  (Figure 5.14), demonstrating p14ARF mediated chemosensitivity is associated with mitochondrial outer membrane permeabilisation.



*Figure 5.14 p14ARF induction increases mitochondrial depolarisation in cytotoxic drug treated U2OS\_ARF cells*

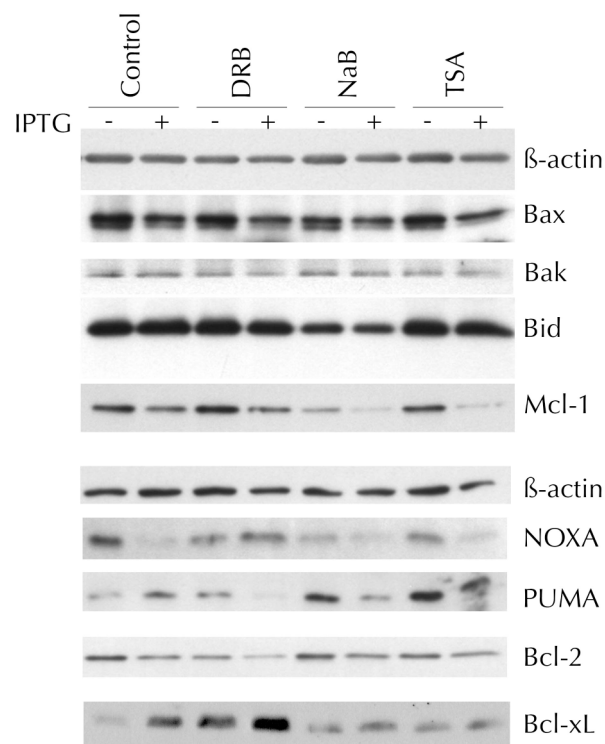
JC-1 staining was used to determine U2OS\_ARF cells with intact (boxed) or depolarised mitochondria, three days after treatment with 50 $\mu$ M DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. The percentage of depolarised cells is indicated.

### 5.2.6 Changes in Bcl-2 family members

As p14ARF mediated chemosensitivity was associated with mitochondrial depolarisation, we investigate the levels of a number of Bcl-2 family proteins, which control the initiation of pore formation in the outer mitochondrial membrane. We analysed expression level of several members of the Bcl-2 family, including pro-apoptotic members Bax, Bak, Bid, Noxa, PUMA, and anti-apoptotic Bcl-2, Bcl-x<sub>L</sub> and Mcl-1 (Figure 5.15).

Induction of p14ARF expression decreased Bax levels slightly in drug treated and untreated cells. The reduction in Bax following ARF induction of drug treated cells was unexpected, especially given Bax is a transcriptional target of p53 (Miyashita and Reed, 1995). One explanation is Bax may be cleaved, generating an 18kDa C-terminal

fragment that potently promotes apoptosis (Gao and Dou, 2000; Wood *et al.*, 1998). However we did not detect the cleaved form of Bax, despite using an antibody (Bax clone B9, Santa Cruz Biotechnology, Santa Cruz, CA) that can detect activated cleaved Bax (Gao and Dou, 2000). Levels of Bak were not changed by drug treatment or p14ARF induction (Figure 5.15).



**Figure 5.15 Analysis of Bcl-2 family proteins in U2OS<sub>ARF</sub> cells treated with cytotoxic drugs and IPTG**

Western blot was used to determine levels of Bcl-2 family proteins in U2OS<sub>ARF</sub> cells three days after treatment with 50μM DRB, 3mM NaB or 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. Top β-actin was probed as a loading control for Bax, Bak, Bid and Mcl-1. Middle β-actin was probed as a loading control for NOXA, PUMA, Bcl-2 and Bcl-x<sub>L</sub>,

The active form of the BH-3 only protein Bid (truncated Bid, tBid) is generated by caspase 8 cleavage, thus linking the extrinsic and intrinsic apoptotic pathways. Levels of full length, inactive Bid were unchanged by p14ARF induction or DRB and TSA

treatment, although they were reduced in NaB treated cells (Figure 5.15). Truncated Bid was not detected in any treatment, suggesting that NaB may reduce overall Bid levels, rather than promote Bid cleavage.

The pro-apoptotic proteins Noxa, PUMA are p53 targets and promote apoptosis by inhibiting anti-apoptotic Bcl-2 members. Contrary to expectations, Noxa levels were reduced by ARF induction in U2OS\_ARF cells, and ARF caused a slight reduction or no detectable change in Noxa levels in cells treated with DRB, NaB or TSA (Figure 5.15). In contrast, PUMA accumulation was enhanced in response to p14ARF induction, but decreased in cells expressing ARF and treated with DRB or NaB. PUMA levels remained high in TSA treated cells in the presence of ARF.

Accumulation of the anti-apoptotic Bcl-2 was decreased by p14ARF induction alone and in cells expressing ARF and treated with DRB, NaB or TSA. Similarly, levels of anti-apoptotic Mcl-1 also decreased as a result of p14ARF induction in untreated and drug treated cells. Mcl-1 was also decreased by NaB treatment alone, but not by DRB or TSA treatment. Induction of p14ARF increased levels of the anti-apoptotic Bcl-x<sub>L</sub> protein. Levels of Bcl-x<sub>L</sub> increased in DRB treated cells and were further increased by ARF induction. Bcl-x<sub>L</sub> levels were low in U2OS\_ARF cells treated with NaB or TSA and were not altered by ARF expression in these cells (Figure 5.15).

Changes in the level of Bcl-2 family proteins is summarised in Table 5.1.

Table 5.1 p14ARF-induced changes in the protein level of Bcl-2 family members.

	ARF	Drug	Drug+ARF
<b><i>Pro-apoptotic</i></b>			
Noxa	↓	↔	↓
PUMA	↑	↑	↓/↑ <sup>1</sup>
Bax	↓	↔	↓
Bak	↔	↔	↔
Bid	↔	↔/↓ <sup>2</sup>	↔/↓ <sup>2</sup>
<b><i>Anti-apoptotic</i></b>			
Bcl-2	↓	↔	↓
Mcl-1	↓	↔/↓ <sup>2</sup>	↓
Bcl-x <sub>L</sub>	↑	↑/↔ <sup>3</sup>	↑↑/↔ <sup>3</sup>

↓ protein expression decreased, ↑protein expression increased, ↔protein expression was unchanged

1 TSA and ARF increased PUMA levels

2 NaB decreased Bid and Mcl-1 expression

3 NaB or TSA treated cells did not show altered Bcl-x<sub>L</sub> levels

### 5.2.7 Loss of mitochondrial outer membrane potential is required for increased sensitivity to apoptosis caused by p14ARF induction

We then investigated if increased mitochondrial depolarisation was required for p14ARF-mediated chemosensitivity. As both Bax and Bak may cooperate to cause mitochondrial outer membrane permeability, we blocked activation of both proteins by ectopically expressing EGFP-tagged Bcl-2, which sequesters BH-3 only proteins, preventing Bax and Bak oligomerisation and the formation of the mitochondrial permeability pore (Cheng *et al.*, 2001).

We used CMX-Ros to ensure Bcl-2 expression prevented mitochondrial outer membrane permeabilisation. CMX-Ros is a lipophilic, cationic dye that is concentrated in the mitochondria due to the negative matrix charge in the same manner as JC-1. Unfortunately JC-1 could not be used, due to fluorescent interference from the EGFP-tagged Bcl-2 molecule. Cells with depolarised mitochondria do not absorb as much

CMX-Ros and can be detected by flow cytometry as a population with reduced fluorescence.

U2OS\_ARF cells transfected with Bcl-2\_EGFP or the control spectrin\_EGFP showed a similar CMX-Ros staining, indicating intact mitochondria and this was not affected by p14ARF induction (Figure 5.16A). As expected these cells also had a low percentage of apoptotic cells as measured by the sub-G1 population and annexin-V positive population (Figure 5.16B & C). Treatment of U2OS\_ARF cells with 3mM NaB resulted in mitochondrial depolarisation, as indicated by reduced CMX-Ros uptake (Figure 5.17A). The mitochondria were protected by the overexpression of Bcl-2, which also reduced the percentage of sub-G1 cells from  $43\pm 1\%$  to  $26\pm 4\%$  and annexin-V positive cells from  $38\pm 4\%$  to  $21\pm 2\%$  (Figure 5.17B & 5.17C). Complete inhibition of apoptosis was not observed, as has been previously reported in cells treated with a low dose of a histone deacetylase inhibitor for extended periods (Lucas *et al.*, 2004). As expected, induction of p14ARF expression increased mitochondrial depolarisation in NaB treated cells but the loss of  $\Delta\Psi_m$  was largely prevented by expression of Bcl-2\_EGFP (Figure 5.17A). In cells expressing Bcl-2 and treated with NaB, p14ARF induction did not affect the levels of cell death, with uninduced/induced cells having a sub-G1 population of  $26\pm 4\%$  vs.  $26\pm 2\%$ , and annexin-V positive population of  $21\pm 3\%$  vs.  $26\pm 2\%$ . These data indicate that mitochondrial outer membrane permeabilisation is a crucial step for p14ARF-induced chemosensitivity.



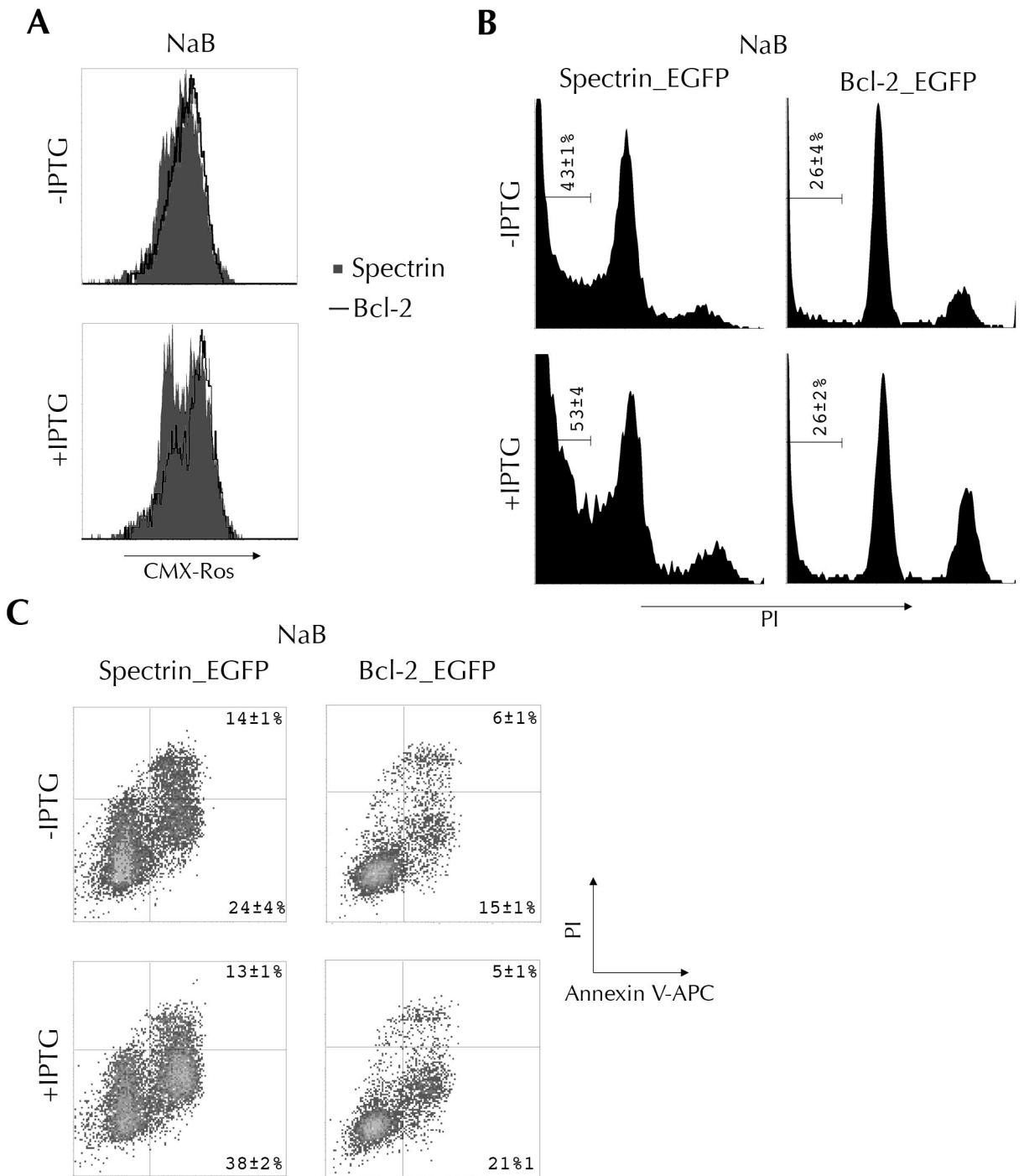
**Figure 5.16 Analysis of the effect of Bcl-2 over expression in U2OS\_ARF cells**

U2OS\_ARF cells were transfected with Bcl-2\_EGFP or control Spectrin\_EGFP. After 24 hours incubation, cells were treated for three days with PBS carrier control and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. Green cells expressing the transgene were selected by flow cytometry.

(A) Mitochondrial depolarisation was assessed by CMX-Ros staining. Loss of CMX-Ros fluorescence indicates mitochondrial depolarisation. Bcl-2\_EGFP transfected cells is overlaid on control, spectrin\_EGFP expressing cells.

(B) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(C) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.



(Previous page)

*Figure 5.17 Bcl-2 over-expression prevents p14ARF-mediated mitochondrial depolarisation and chemosensitivity in sodium butyrate treated U2OS\_ARF cells*

U2OS\_ARF cells were transfected with Bcl-2\_EGFP or control Spectrin\_EGFP. After 24 hours incubation, cells were treated for three days with 3mM sodium butyrate (NaB) and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. Green cells were selected by flow cytometry.

(A) Mitochondrial depolarisation was assessed by CMX-Ros staining. Loss of CMX-Ros fluorescence indicates mitochondrial depolarisation. Bcl-2\_EGFP transfected cells are overlaid on control, spectrin\_EGFP expressing cells.

(B) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(C) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

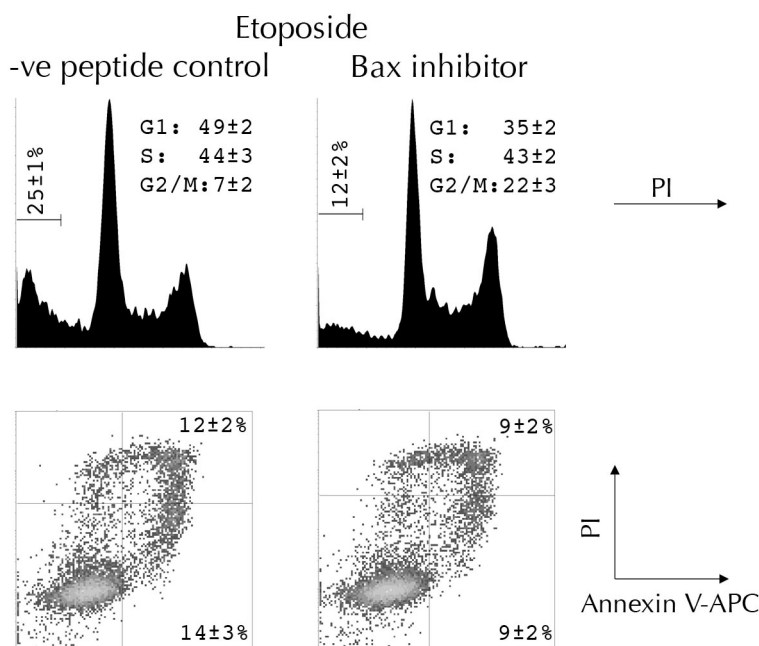
*5.2.8 p14ARF does not require Bax to sensitise cells to apoptosis*

As the increased death resulting from p14ARF induction in drug treated cells was dependent on loss of mitochondrial potential, we investigated if Bax, an important mediator of mitochondrial depolarisation, was essential for this process. Although Bax levels decreased slightly as a result of p14ARF induction in drug treated cells (Figure 5.15), it is the conformation of Bax, rather than its expression that regulates its activity (Lalier et al., 2007; Miyashita and Reed, 1995). Additionally, loss of Bax alters the tumour spectrum of ARF-null mice, resulting in tumours uncommon in Bax<sup>+/+</sup>/ARF<sup>-/-</sup> mice such as osteosarcoma and hemangiosarcoma, as well as multiple primary tumours (Eischen et al., 2002). Furthermore, Bax is required for apoptosis caused by ectopic p19ARF expression, and Bax loss abrogates apoptosis caused by adenovirally-expressed p14ARF in human HCT116 colorectal cells (Hemmati *et al.*, 2006; Suzuki *et al.*, 2003).

To examine if p14ARF increased chemosensitivity is Bax-dependent, Bax activity was inhibited by adding the Bax inhibiting peptide V5 (BIP-V5) to U2OS\_ARF cells. After five hours of pre-incubation, cells were exposed to DRB, NaB or TSA in the presence

or absence of IPTG and cell cycle and annexin-V staining analysed by flow cytometry after three days.

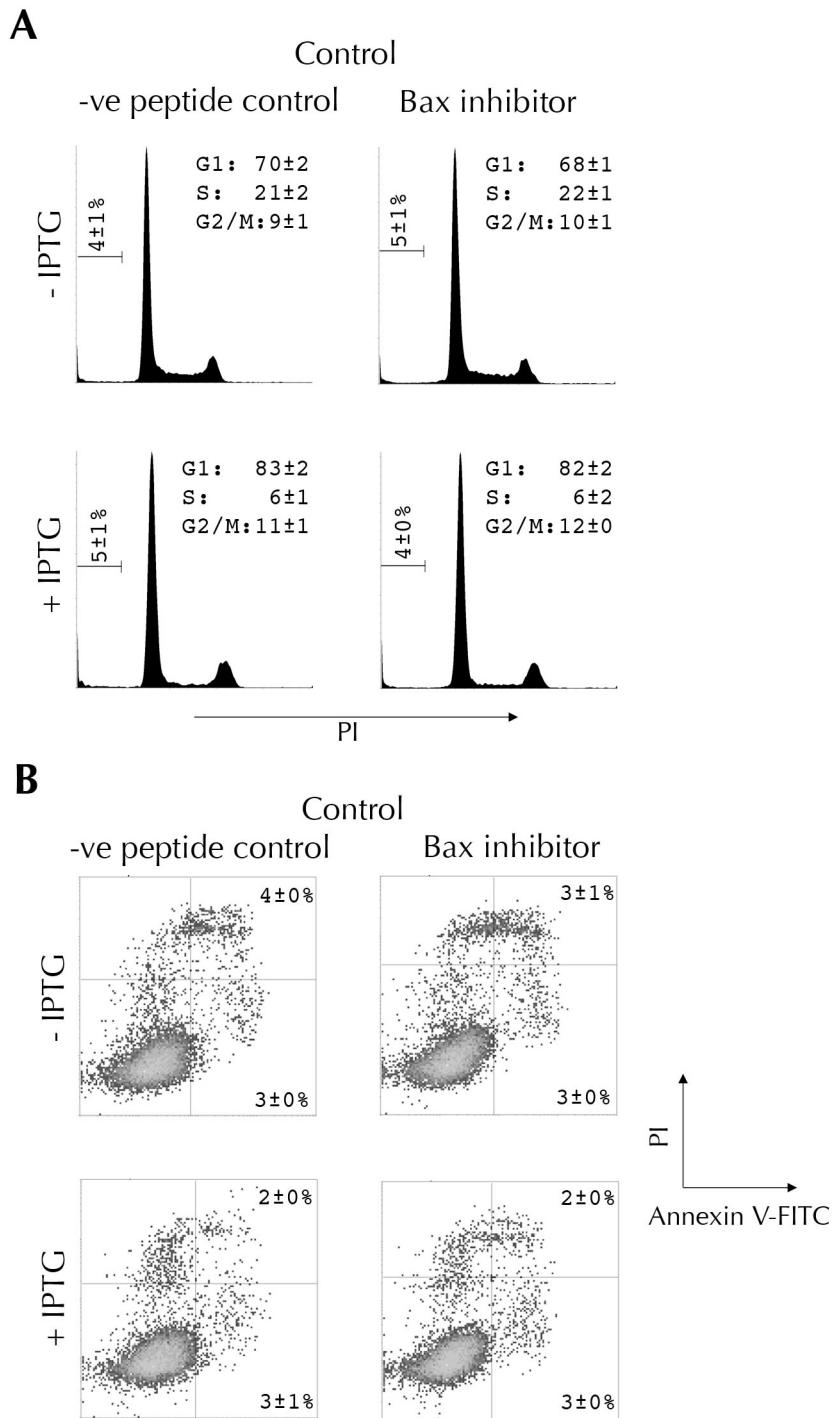
To confirm the Bax inhibitor was effective, U2OS\_ARF cells were treated with BIP-V5 or the negative peptide control (BIP-NC) for 5 hours, then etoposide added and cells incubated for 72 hours. Etoposide killing of U2OS is partly Bax dependent (Taylor *et al.*, 2000) and BIP-V5 reduced apoptosis, with the sub-G1 population decreasing from  $25\pm 1\%$  to  $12\pm 2\%$  and the percentage of annexin-V positive cells decreasing from  $26\pm 3\%$  to  $18\pm 2\%$  (Figure 5.18 A & B).



**Figure 5.18** *The Bax inhibitor BIP-V5 reduces apoptosis caused by etoposide*

U2OS\_ARF cells were pre-treated with the Bax inhibiting peptide BIP-V5 or control peptide BIP-NC then treated with  $30\mu\text{M}$  etoposide for three days. The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining. Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion .

BIP-V5 had no effect on the cell cycle distribution or apoptosis of uninduced or induced U2OS\_ARF cells, as measured by PI and annexin-V staining (Figure 5.19A & B). In cells treated with DRB, NaB or TSA, the Bax inhibitor reduced the total levels of apoptosis but did not prevent IPTG induction from increasing the level of apoptosis. Although the Bax inhibitor reduced overall levels of apoptosis, this was not associated with a change in cell cycle distribution. Specifically, in DRB plus BIP-NC treated cells, induction of IPTG increased the sub-G1 population from  $15\pm 2\%$  to  $26\pm 3\%$ , and annexin-V positive cells from  $12\pm 3$  to  $27\pm 1\%$ , while in DRB plus BIP-V5 treated cells IPTG changed the sub-G1 population from  $13\pm 4\%$  to  $19\pm 2\%$ , and annexin-V positive cells from  $10\pm 2\%$  to  $17\pm 1\%$  (Figure 5.20A & B). BIP-V5 acted in a similar fashion in cells treated with NaB (Figure 5.21A & B) and TSA (Figure 5.22A & B), reducing overall levels of apoptosis but not preventing p14ARF-mediated chemosensitivity. Thus, although Bax contributes to death as a result of drug treatment, with or without ARF induction, it is not essential for p14ARF-mediated chemosensitivity.

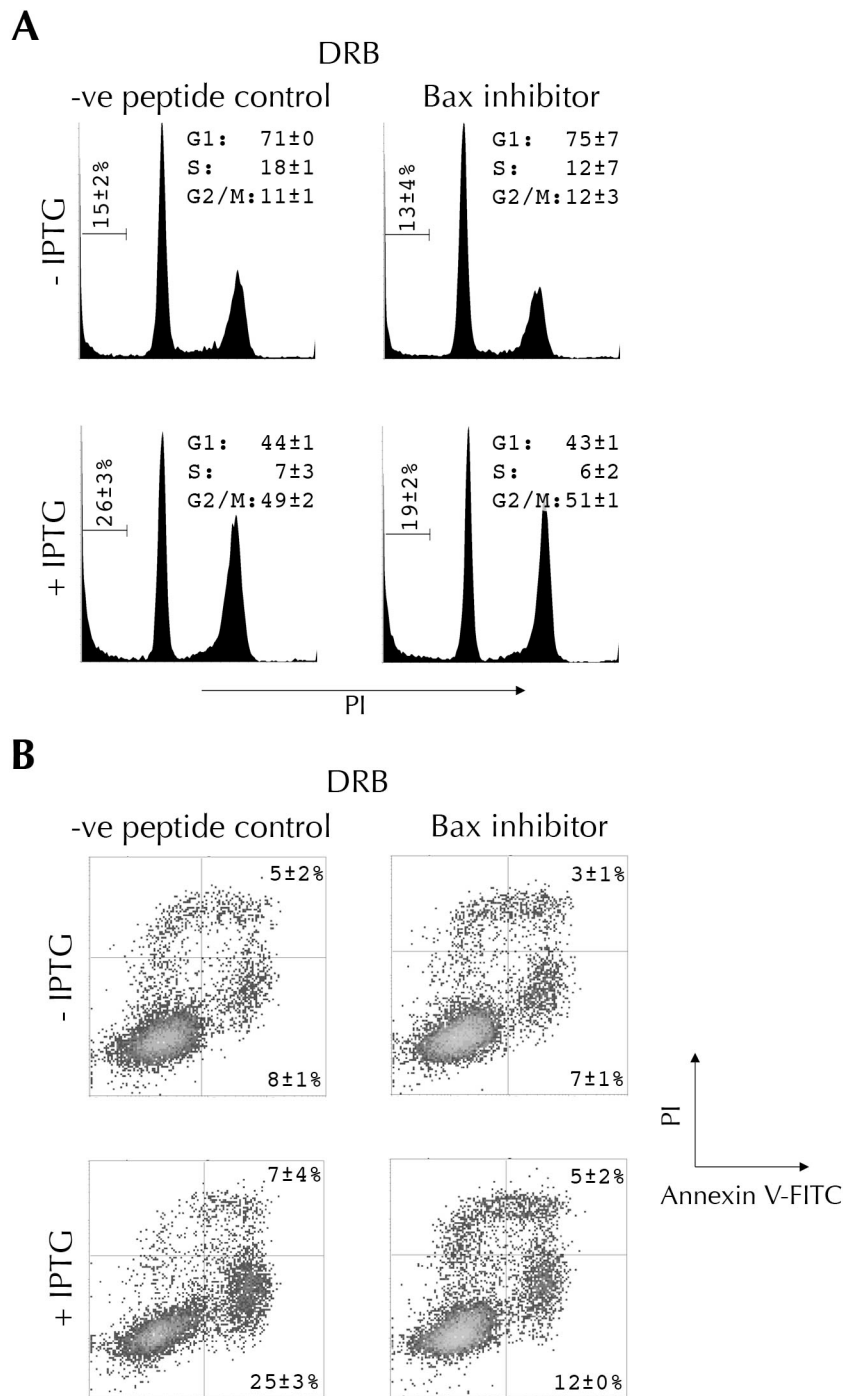


**Figure 5.19 Analysis of the effect of Bax inhibition in U2OS\_ARF cells**

U2OS\_ARF cells were pre-treated with the Bax inhibiting peptide BIP-V5 or control peptide BIP-NC then treated for three days with DMSO carrier control and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

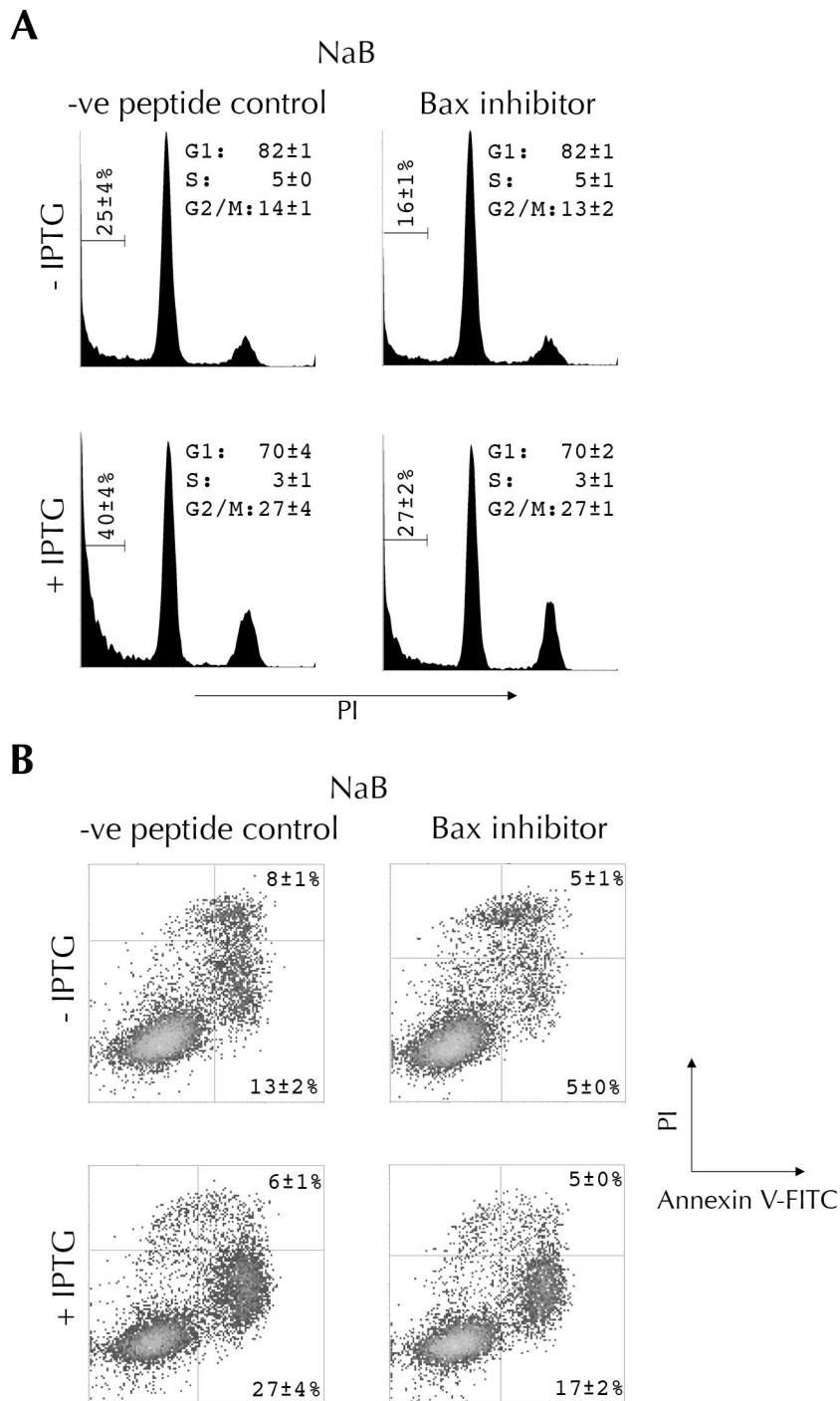


**Figure 5.20** *Bax inhibition does not prevent p14ARF increasing sensitivity of U2OS\_ARF cells to DRB*

U2OS\_ARF cells were pre-treated with the Bax inhibiting peptide BIP-V5 or control peptide BIP-NC then treated for three days with 50µM DRB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

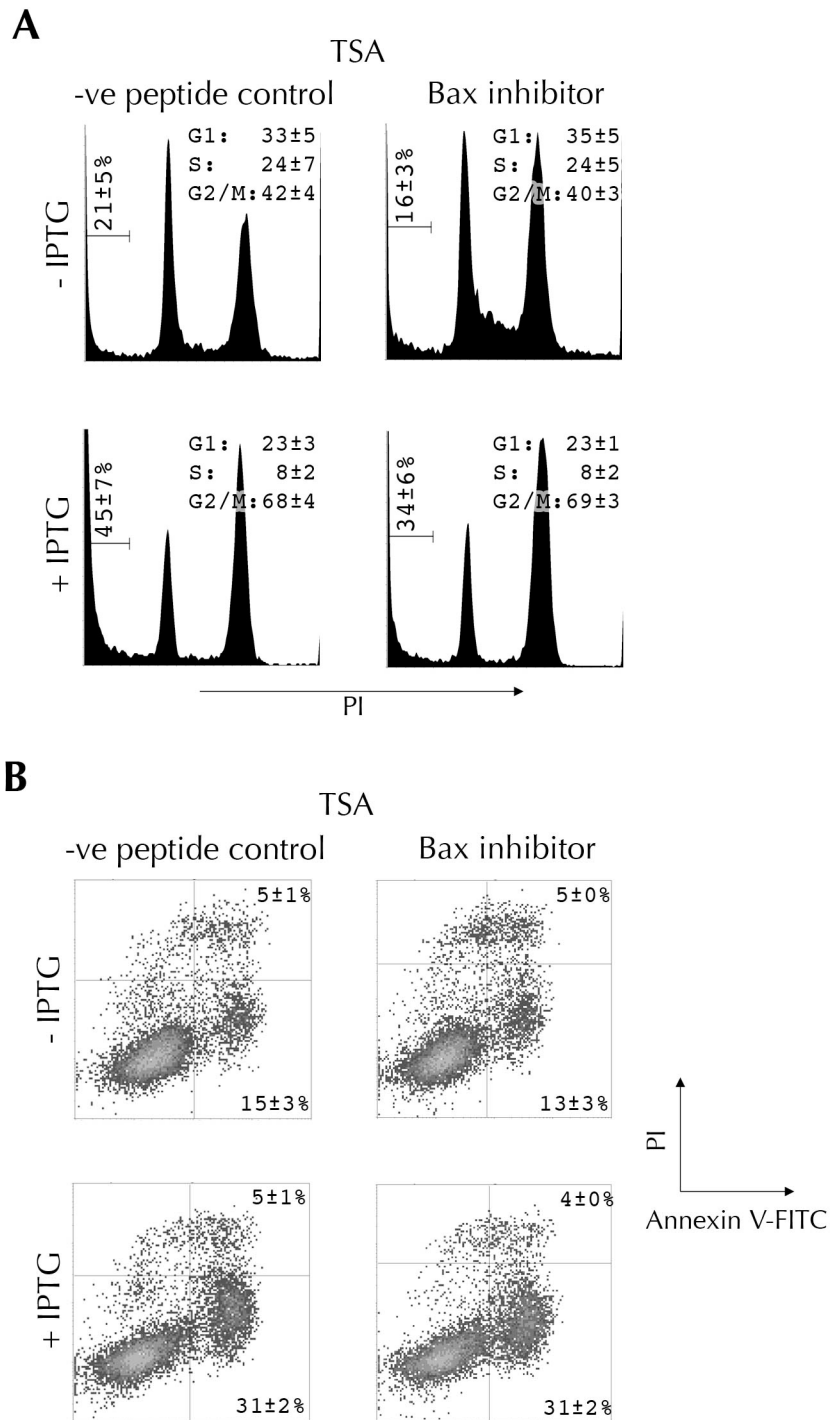


*Figure 5.21 Bax inhibition does not prevent p14ARF increasing sensitivity of U2OS<sub>ARF</sub> cells to sodium butyrate (NaB)*

U2OS<sub>ARF</sub> cells were pre-treated with the Bax inhibiting peptide BIP-V5 or control peptide BIP-NC then treated for three days with 3mM NaB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.



**Figure 5.22** Bax inhibition does not prevent p14ARF increasing sensitivity of U2OS\_ARF cells to trichostatin A (TSA)

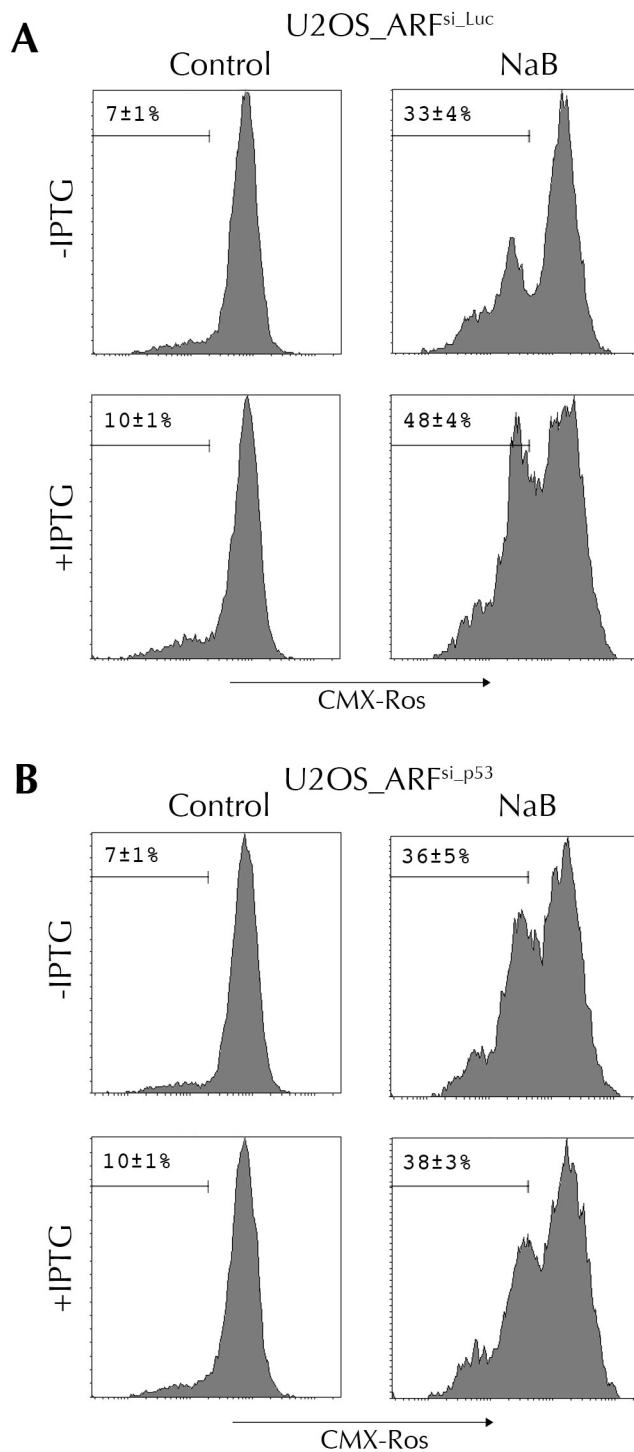
U2OS\_ARF cells were pre-treated with the Bax inhibiting peptide BIP-V5 or control peptide BIP-NC then treated for three days with 200nM TSA and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

### *5.2.9 p14ARF requires p53 to increase mitochondrial permeabilisation*

As both p53 and mitochondrial depolarisation were required for p14ARF-mediated chemosensitivity, we investigated whether p53 was acting upstream of the mitochondria. We treated the p53 depleted U2OS\_ARF<sup>si-p53</sup> cells (see Figure 5.7A) and control U2OS\_ARF<sup>si-Luc</sup> cells with NaB in the presence or absence of IPTG and measured mitochondrial depolarisation with CMX-Ros, which was suitable to use in these GFP expressing cells. As expected p14ARF induction of NaB treated cells increased the population of cells with depolarised mitochondria (Figure 5.23A). However ARF did not affect mitochondrial depolarisation in NaB treated U2OS\_AR<sup>si-p53</sup> cells, demonstrating p14ARF requires p53 to increase mitochondrial depolarisation (Figure 5.23B).



**Figure 5.23** *p53* is required for *p14ARF* to increase mitochondrial depolarisation in sodium butyrate (NaB) treated cells

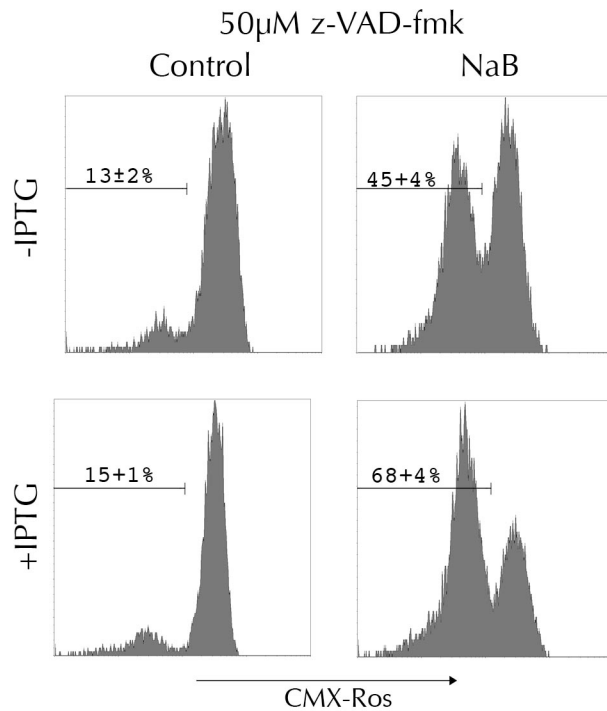
U2OS\_ARF<sup>si\_Luc</sup> and U2OS\_ARF<sup>si\_p53</sup> cells were treated for 3 days with 3mM NaB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. p53 is ablated in U2OS\_ARF<sup>si\_p53</sup> cells by RNA interference.

(A) Mitochondrial depolarisation in U2OS\_ARF<sup>si\_Luc</sup> cells was assessed by CMX-Ros staining. Loss of CMX-Ros fluorescence indicates mitochondrial depolarisation.

(B) Mitochondrial depolarisation in U2OS\_ARF<sup>si\_p53</sup> cells was assessed by CMX-Ros staining.

### *5.2.9 z-VAD-fmk does not inhibit loss of mitochondrial depolarisation induced by ARF expression*

Although active caspases were not detected by western blotting, the pan-caspase inhibitor z-VAD-fmk prevented cell death induced by DRB, NaB and TSA, with or without p14ARF expression. To investigate if z-VAD-fmk protected these cells by preventing mitochondrial depolarisation, we pre-treated U2OS\_ARF cells with 50 $\mu$ M z-VAD-fmk, then exposed them to NaB in the presence or absence of IPTG to induce p14ARF expression. Mitochondrial depolarisation was measured by CMX-Ros staining after three days of incubation. z-VAD-fmk treatment did not prevent p14ARF accumulation from increasing mitochondrial depolarisation (Figure 5.24), although these cells displayed a very low sub-G1 and annexin-V population (similar to Figure 5.11A & B). Thus p14ARF does not require caspases to promote mitochondrial depolarisation, but the apoptotic morphology that results is suppressed by z-VAD-fmk.



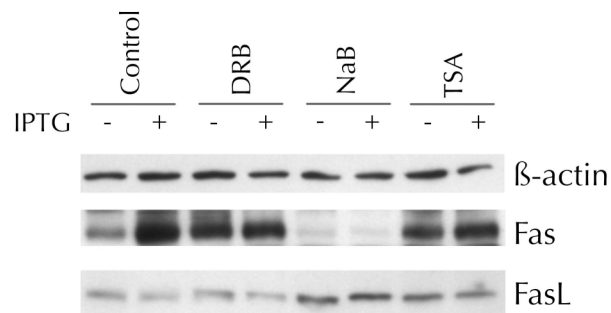
*Figure 5.24 Pan-caspase inhibition does not prevent p14ARF from increasing mitochondrial depolarisation in sodium butyrate cells*

U2OS\_ARF cells were pre-treated with the pan-caspase inhibitor z-VAD-fmk then exposed for three days to 3mM sodium butyrate (NaB) and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. Mitochondrial depolarisation was assessed by CMX-Ros staining. Loss of CMX-Ros fluorescence indicates mitochondrial depolarisation.

#### *5.2.10 p14ARF does not require Fas activation to sensitise cells to apoptosis*

p14ARF required p53, caspase activity and induction of mitochondrial permeability to increase sensitivity of cells to apoptosis caused by drugs. There are many p53 targets that can contribute to loss of mitochondrial outer membrane potential, making targeting of upstream effectors of the mitochondrial permeability shift difficult. We chose to investigate one such effector, Fas, as it is a p53 target and apoptosis caused by adenoviral expression of p14ARF in U2OS is partly mediated by Fas (Kim *et al.*, 2004). Induction of p14ARF increased Fas levels dramatically in IPTG-treated cells (Figure 5.25). DRB and TSA treatment of U2OS\_ARF cells increased the amount of Fas, but

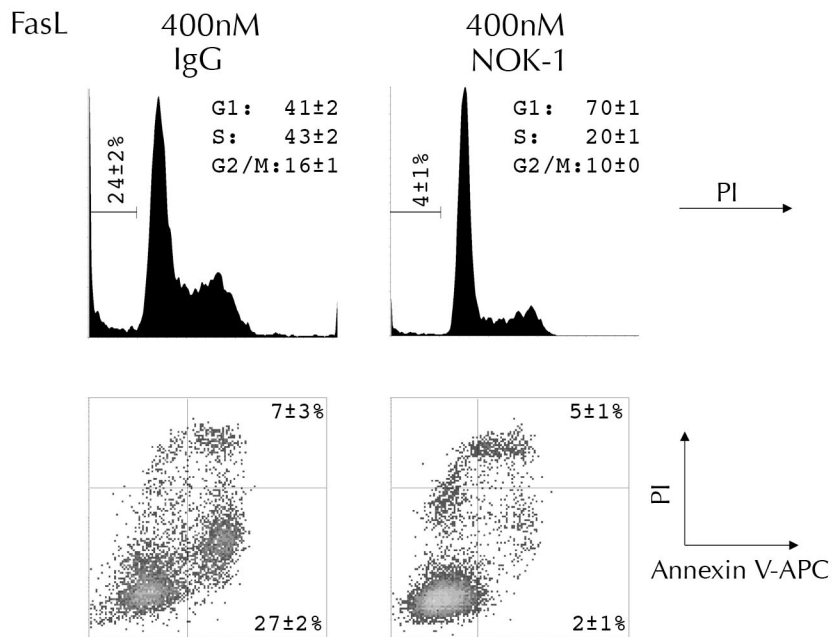
p14ARF induction did not alter the Fas levels in these cells. NaB caused a substantial decrease in Fas levels and p14ARF induction did not alter the low Fas levels in NaB treated cells (Figure 5.25). Levels of Fas ligand (FasL) were not altered by p14ARF induction, but were increased slightly by NaB treatment (Figure 5.25).



*Figure 5.25 Expression of Fas and FasL in U2OS\_ARF cells treated with cytotoxic drugs and IPTG*

Western blot assessment of Fas and FasL in U2OS\_ARF cells after three days exposure to 50 $\mu$ M DRB, 3mM NaB or 200nM TSA and PBS (-) or IPTG (+) to induce p14ARF expression.

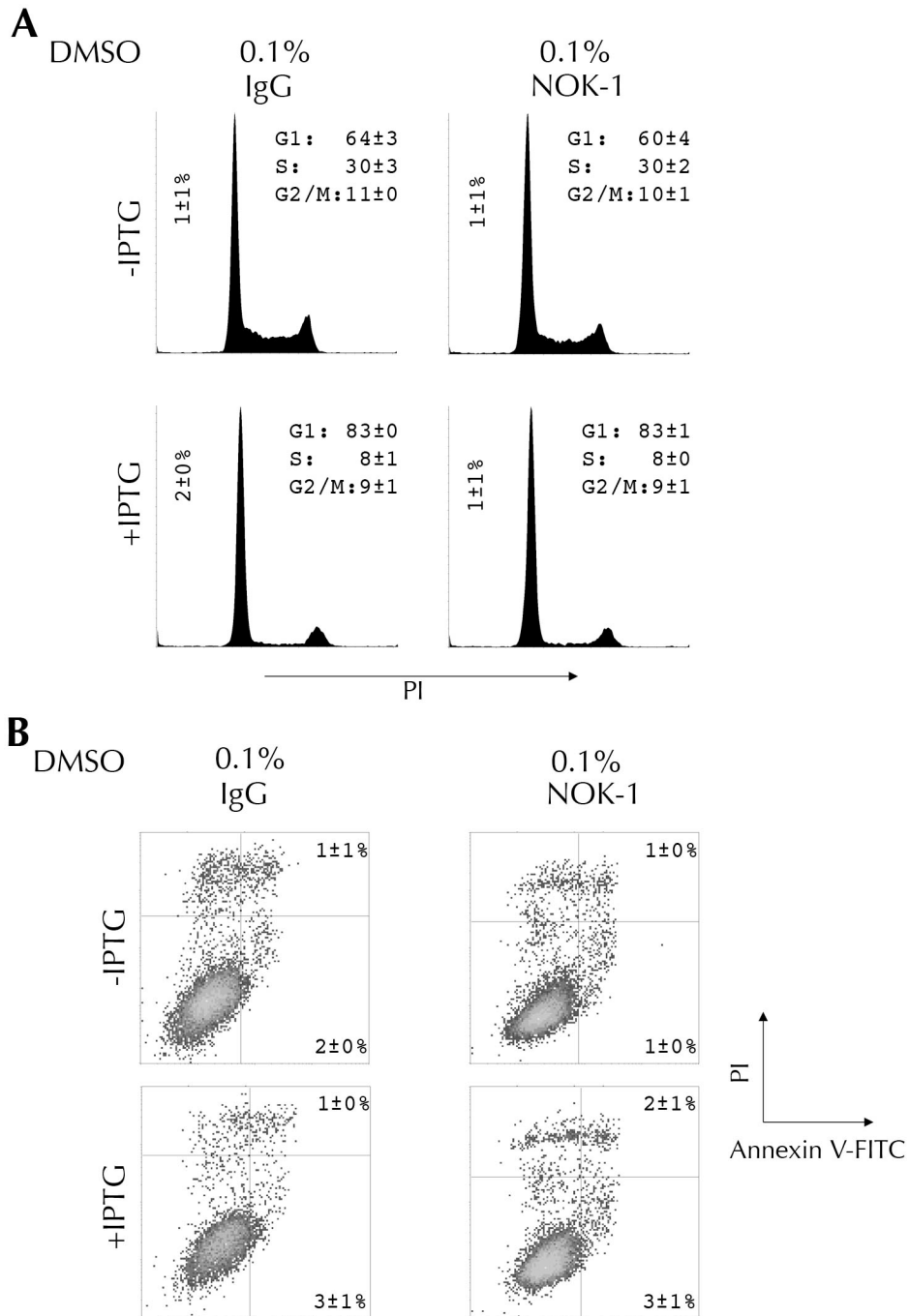
As Fas levels were increased by p14ARF accumulation, we investigated if p14ARF mediated chemosensitivity was Fas dependent by utilising NOK-1, an antibody that binds FasL and prevents Fas mediated apoptosis. To test the effectiveness of NOK-1, we treated U2OS\_ARF cells with Fas-Ligand (FasL), after pre-treatment of NOK-1 or IgG control. FasL treatment of U2OS\_ARF cells lead to apoptosis, with a sub-G1 population of 24 $\pm$ 2% and 34 $\pm$ 3% annexin-V positive cells (Figure 5.26). NOK-1 treatment successfully inhibited FasL mediated apoptosis, reducing the sub-G1 percentage to 4 $\pm$ 1% and the annexin-V positive population to 7 $\pm$ 1% (Figure 5.26).



**Figure 5.26** *The Fas inhibitor NOK-1 prevents Fas mediated apoptosis*

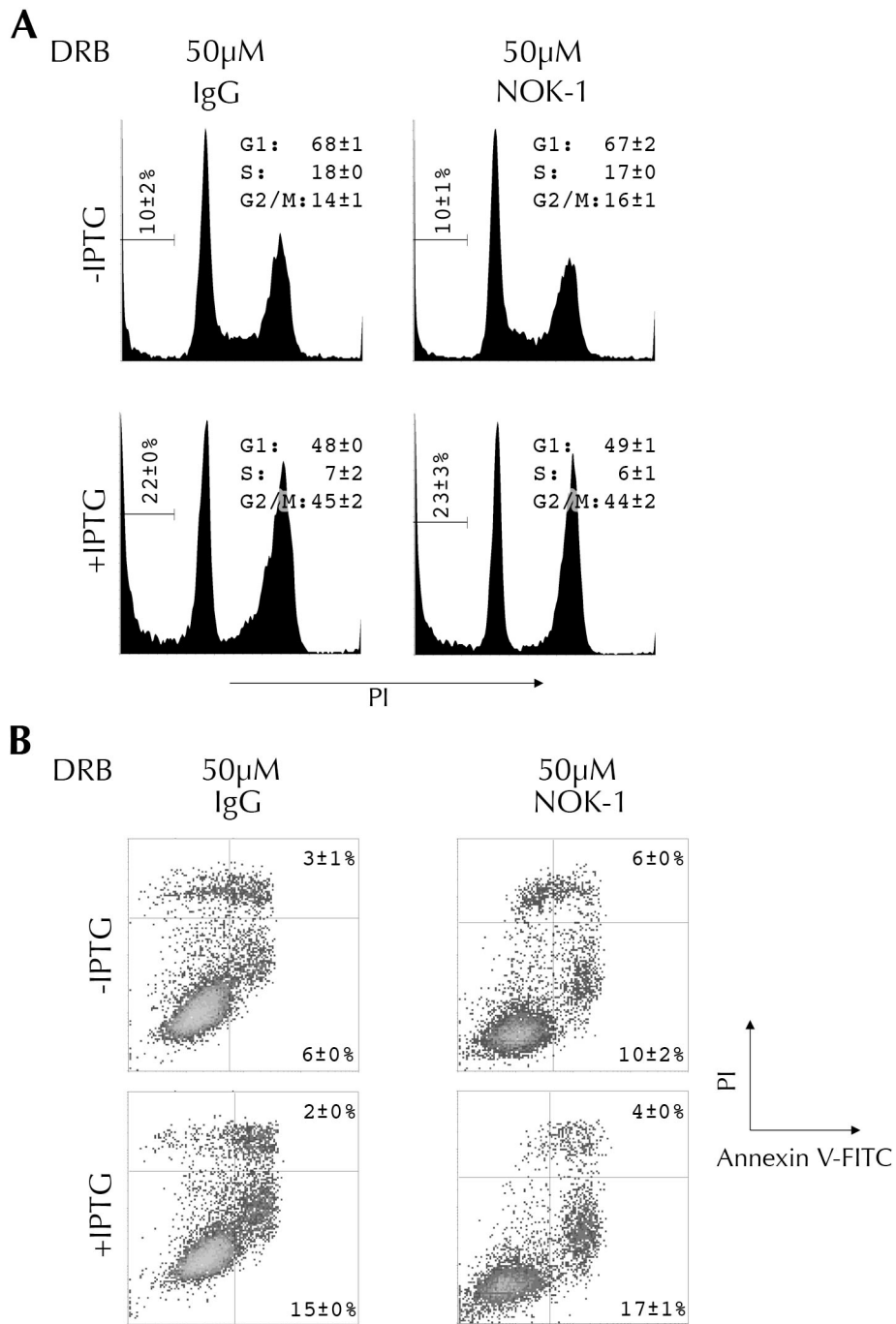
To demonstrate the effectiveness of Fas inhibition, U2OS\_ARF cells were pre-treated with the Fas inhibiting antibody NOK-1 then treated with recombinant Fas Ligand (FasL) for two days. IgG was used as an isotype matched control for the NOK-1 antibody. The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining. Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

NOK-1 treatment of U2OS\_ARF cells did not change cell cycle or apoptosis of cells compared to control IgG treated cells (Figure 5.27A & B). In the presence of IgG, IPTG increased the sub-G1 population of DRB treated cells from 10±2% to 22±0%, while in NOK-1 treated cells the sub-G1 population increased from 10±1% to 23±3% (Figure 5.28A). The NOK-1 inhibitor did not reduce apoptosis in U2OS\_ARF cells treated with NaB (Figure 5.29A & B). Uninduced and induced cells treated with IgG and NaB had a sub-G1 population of 15±1% and 30±2%, and an annexin-V positive population of 22±2% and 35±2%. In cells treated with NOK-1 inhibitor and NaB, induction of p14ARF expression increased the sub-G1 population from 19±3% to 34±1% and annexin-V positive cells from 32±4% to 42±3%, demonstrating that p14ARF mediated apoptosis is not Fas dependent (Figure 5.29A & B).



**Figure 5.27 Analysis of the effect of Fas inhibition in U2OS\_ARF cells**

U2OS\_ARF cells were pre-treated with the Fas inhibiting antibody NOK-1 or control IgG then treated for three days with DMSO carrier control and PBS (-) or 1mM IPTG (+) to induce p14ARF expression. (A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining. (B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

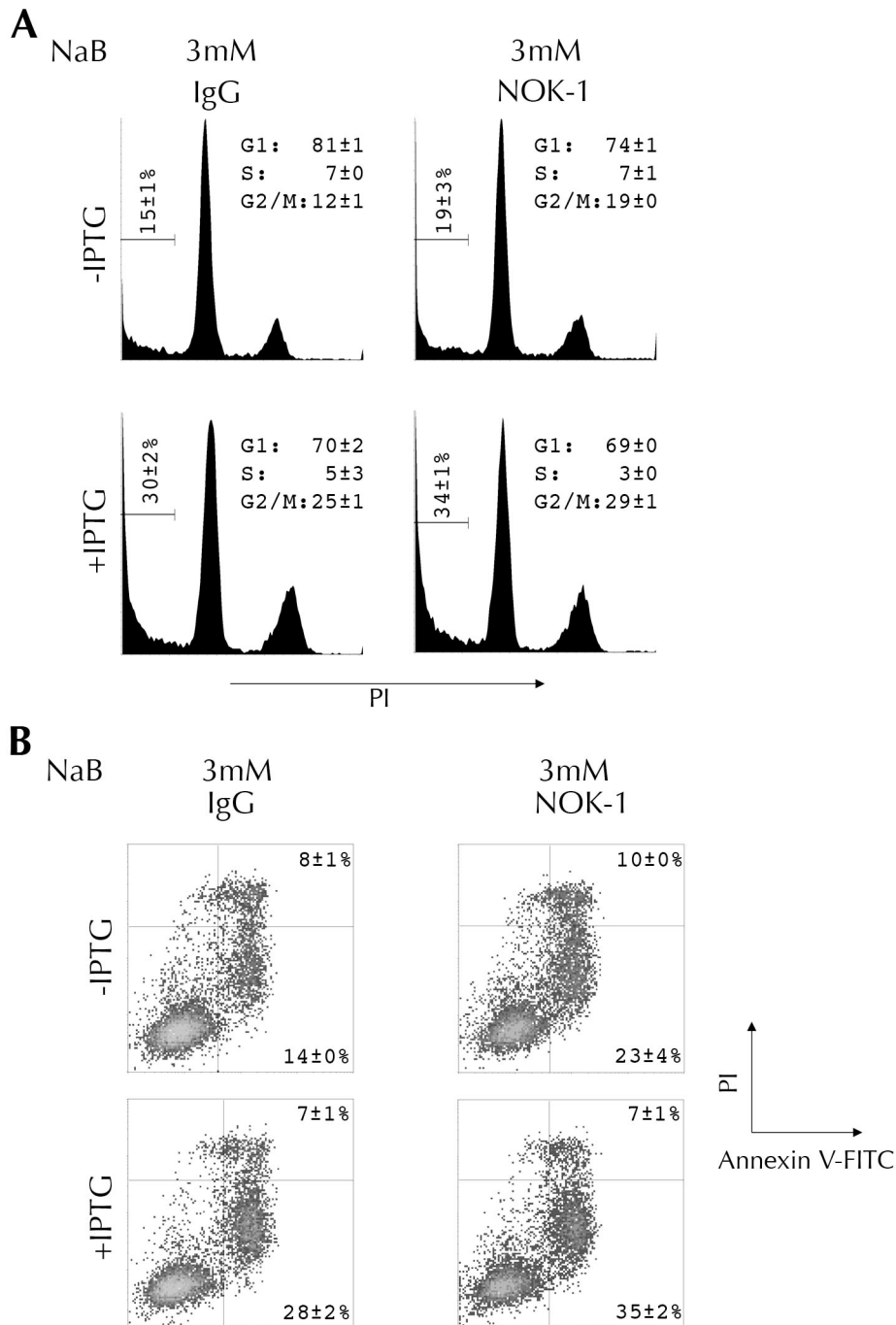


**Figure 5.28** Fas inhibition does not prevent p14ARF increasing sensitivity of U2OS\_ARF cells to DRB

U2OS\_ARF cells were pre-treated with the Fas inhibiting antibody NOK-1 or control IgG then treated for three days with 50 $\mu$ M DRB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining.

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.



**Figure 5.29** Fas inhibition does not prevent p14ARF increasing sensitivity of U2OS\_ARF cells to sodium butyrate (NaB)

U2OS\_ARF cells were pre-treated with the Fas inhibiting antibody NOK-1 or control IgG then treated for three days with 3mM NaB and PBS (-) or 1mM IPTG (+) to induce p14ARF expression.

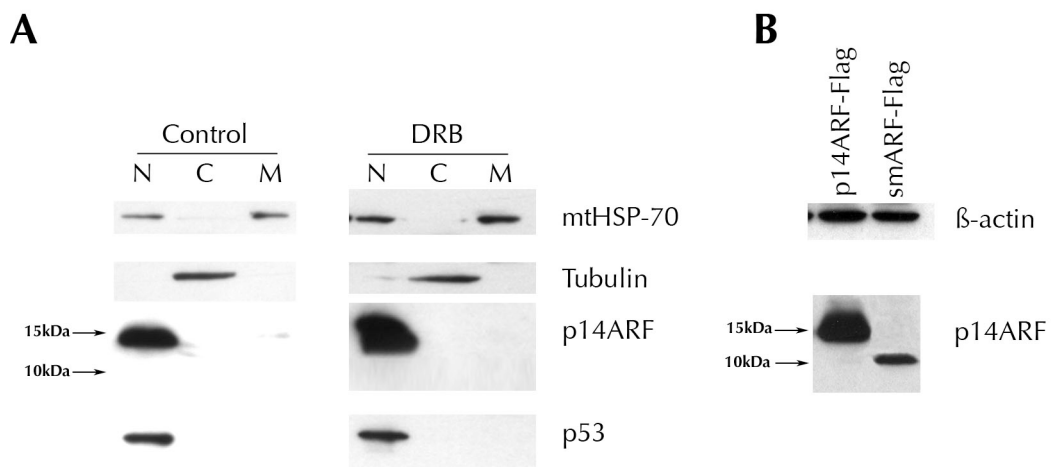
(A) The cell cycle distribution and sub-G1 population was examined using propidium iodide (PI) staining

(B) Apoptotic cells were also analysed by dual colour flow cytometric staining of annexin-V and PI exclusion.

### *5.2.11 p14ARF mediated chemosensitivity is not associated with smARF or mitochondrial p53*

The smARF protein is formed as the result of internal initiation from the Met codon 48 of human p14ARF mRNA (Met 45 in mouse p19ARF) (Reef *et al.*, 2006). smARF localises to the mitochondria, where it associates with p32 and causes loss of mitochondrial membrane potential, autophagy and cell death (Reef *et al.*, 2006). Although smARF killing of cells is independent of p53, and not inhibited by z-VAD-fmk or Bcl-2 over-expression, we investigated if smARF contributed to p14ARF mediated chemosensitivity. As expression levels of p14ARF in the U2OS\_ARF cell line is low, and smARF levels are typically much less than p14ARF levels, we transiently transfected U2OS cells with p14ARF to ensure high expression level of ARF, and smARF. To further increase the chances of detecting smARF, cells were divided into their nuclear, cytoplasmic and mitochondrial fractions, and protein fractions separated on a SDS-PAGE gel and subject to immuno-blotting. Blotting for mitochondrial HSP-70 and tubulin confirmed that the mitochondrial fractions were pure (Figure 5.30). Despite our attempts to increase smARF detection, we did not observe smARF in any cellular fraction (Figure 5.30). As p14ARF induction in DRB treated U2OS\_ARF cells resulted in increased chemosensitivity and also much higher levels of p14ARF accumulation, we also subject these cells to fraction and immuno-blotting. Again, we did not detect the smARF protein in these cells, suggesting that smARF plays no role in p14ARF-mediated chemosensitivity (Figure 5.30). The same fractions were also probed for p53. p53 has been reported to move to the mitochondrial, where it antagonises Bcl-2 and Bcl-x<sub>L</sub> and causes mitochondrial depolarisation and cytochrome c release (Mihara *et al.*, 2003). p14ARF mediated chemosensitivity was p53-dependent and associated

with mitochondrial depolarisation, raising the possibility that p53 translocation to the mitochondria may play a role. However p53 was never detected in the mitochondria, and was only found in the nuclear fraction (Figure 5.30). Therefore p53 did not move to the mitochondria as a result of p14ARF over-expression or during p14ARF induced chemosensitivity.



*Figure 5.30 smARF and mitochondrial p53 do not contribute to p14ARF mediated chemosensitivity*

(A) U2OS cells were transfected with p14ARF (Control) or U2OS\_ARF cells were treated with 50 $\mu$ M DRB and 1mM IPTG to induce p14ARF expression (DRB) for 48 hours and cells separated into nuclear (N), cytoplasmic (C) and mitochondrial (M) fractions. Neither p14ARF, smARF nor p53 was detected in mitochondrial fractions. smARF migrates are approximately 9kDa. mtHSP70 and tubulin were used to as markers of mitochondrial and cytoplasmic fractions, respectively.

(B) A western blot was used to demonstrate that the p14ARF antibody can detect ectopic smARF. U2OS cells transfected with Flag tagged smARF or p14ARF as a positive control, and harvested after 24 hours. smARF-Flag migrates at approximately 10kDa.  $\beta$ -actin is used to demonstrate equal loading.

### 5.3 Discussion

Apoptosis is an important cellular program regulating tissue homeostasis and tumorigenesis. All cancers circumvent apoptosis to a certain extent during tumorigenesis, and some cancers, including melanoma, are so resistant to apoptosis, that a wide-range of chemotherapies are ineffective. Increasing the sensitivity of these cancers to apoptosis is necessary for effective systemic treatments and the cellular pathways that modulate chemosensitivity are being actively analysed. In this study we show that expression of p14ARF sensitises cells to apoptosis via pathways that depend upon p53, caspase activation and mitochondrial depolarisation. Individual inhibition of Bax or Fas did not eliminate the ability of p14ARF to increase apoptosis, showing that there are a number of complimentary effectors downstream of p53 stabilisation.

p14ARF caused a p53-dependent depolarisation of mitochondria and while caspase inhibition did not prevent mitochondrial depolarisation, it did prevent apoptosis. Mitochondrial outer membrane permeabilisation can occur independently of caspases, and even in the presence of high concentrations of z-VAD-fmk, cytochrome c and SMAC/DIABLO are released from mitochondria in response to a variety of stimuli such as UVB, staurosporine and cisplatin (Dussmann *et al.*, 2003; Rehm *et al.*, 2003; Zhou *et al.*, 2005). While the increase in depolarisation caused by z-VAD-fmk was unexpected, z-VAD-fmk may increase kinetics of SMA/DIABLO release from permeable mitochondria, accelerating mitochondrial depolarisation (Rehm *et al.*, 2003). Interestingly, while z-VAD-fmk prevented the apoptotic phenotype, activation of caspases 3, 8 and 9 was not observed, nor was significant PARP cleavage. The paradigm of intrinsic pathway activation involves cytochrome c release, caspase 9

activation and caspase 3 cleavage and activation (Zimmermann *et al.*, 2001). Although, alternate apoptosis-regulatory pathways exist, the downstream activation of either caspase 9 or caspase 3 usually occurs. For example, once released from the mitochondria, SMAC/DIABLO and Omi, bind and disable IAPs including survivin and XIAP (Rehm *et al.*, 2003) and activate effector caspases 6 and 7. These active caspases would be expected to cleave caspase 3, 8 and 9 however, even as a late event during apoptosis. Thus, it is most likely that active caspase 3 or caspase 9 was present in our cell model but below detectable levels possibly because of apoptotic asynchrony and low apoptotic stimuli provided by the relatively long (three day) experimental time-frame we used.

Accumulation of ARF in the presence of DRB, NaB and TSA resulted in readily detectable apoptotic cell death without the stereotypical cleavage of PARP (see Figure 5.13). The presence of immunoreactive intact PARP (a substrate of caspase 3) suggests a defective pathway activating caspase 3 in U2OS\_ARF cells, and implies that ARF-mediated apoptosis does not require caspase 3, in this cell model. Accordingly we also detected minimal caspase 3 cleavage and activation (see Figure 5.13). Thus, although U2OS\_ARF cell death was totally inhibited by the caspase inhibitor, z-VAD-fmk, this does not appear to involve caspase 3 or the concomitant cleavage of PARP. A similar caspase 3-independent apoptotic programme, with no evidence of PARP cleavage, has also been reported in testicular germ cell tumour cell lines ((Burger *et al.*, 1999)). Whether, activation of additional caspase members compensate for the impaired caspase 3 activation remains to be elucidated.

Despite generating and testing two previously published p21<sup>Waf1</sup>-specific shRNA molecules, we were unable to achieve effective knockdown of p21<sup>Waf1</sup> levels when using these molecules in a lentivirus expression vector (Nicke *et al.*, 2005; Zhang *et al.*, 2004). The combination of two p21<sup>Waf1</sup>-shRNA molecules produced only minimal silencing that was not effective enough to reduce p14ARF-induced cell cycle arrest. Moreover, the use of siRNA molecules to specifically target p21<sup>Waf1</sup> was not feasible, as the transfection efficiency routinely achieved using the U2OS\_ARF cell clone was only 30% and would not have permitted analysis of the whole cell population. Thus, although we and others have shown that ARF-mediated cell cycle inhibition is largely dependent on p21<sup>Waf1</sup> (Hemmati *et al.*, 2005; Normand *et al.*, 2005), we are unable to make any conclusions regarding the role of p21<sup>Waf1</sup> in regulating ARF-induced chemosensitivity.

Our results reinforce the central role that p53 plays in ARF functions; p14ARF mediated cell cycle arrest, chemosensitivity and mitochondrial depolarisation are all p53-dependent. This is supported by other studies showing that p14ARF functions via the p53 pathway (Weber *et al.*, 2002) and can increase chemo- and radiosensitivity only in p53-intact cell lines (Gao *et al.*, 2001; Simon *et al.*, 2006).

Although, most melanomas retain functional p53 (Albino *et al.*, 1994; Kaleem *et al.*, 2000; Lubbe *et al.*, 1994), the use of ARF analogues to enhance this pathway may not be an effective treatment strategy. Melanomas are resistant to killing by p53-dependent mechanisms due to alterations in downstream mediators of apoptosis, such as over expression of Mcl-1 and XIAP, downregulation of APAF-1 and production of p53 splice variants that modulate p53 transcriptional response (Avery-Kiejda *et al.*, 2008; Soengas

*et al.*, 2001; Zhang *et al.*, 2001; Zhuang *et al.*, 2007). These alterations may negate the p14ARF-induced activation of the p53 pathway and while this may be discouraging, direct targeting of critical downstream p53 effectors may provide new therapeutic opportunities. The combination of ARF mimetics and direct targeting of disabled p53 components may provide an especially effective approach to melanoma therapy. Genetic screening is adding to our knowledge of potential effectors. Loss or mutation of p14ARF alters the gene expression profile of melanomas with wild type p53, and pathways up-regulated in p14ARF containing melanomas such as the epidermal growth factor, platelet-derived growth factor and Wnt signalling pathways may contain new therapeutic targets (Packer *et al.*, 2007).

The mechanisms by which p14ARF influences p53 activity remain unresolved. Whether p53 transactivates pro-arrest or pro-apoptotic genes is influenced by various post-translational modification of p53, which can alter p53 conformation affinity to different promoters. For instance, phosphorylation of p53 at serine-46 is induced by DNA-damage signals and this phosphorylated form of p53 is an effective activator of the pro-apoptotic genes NOXA (Grossman *et al.*, 2003) and PUMA (reviewed in (Das *et al.*, 2008)). Additionally acetylation of lysine-120 of p53 by the MYST family of acetyl transferases increases transactivation of Bax and PUMA, but is dispensable for transcription of the non-apoptotic *p21<sup>Waf1</sup>* and *HDM2* genes (Sykes *et al.*, 2006). p53 function is also regulated by its many binding partners and these vary according to cell type and growth conditions. For instance, p300 and CREB binding protein (CBP) are transcriptional co-activators that bind, acetylate and activate p53 (Grossman, 2001). Hematopoietic zinc finger binds p53 and results in preferential transcription of pro-arrest genes (Das *et al.*, 2007).

In this study we did not identify an individual target down-stream of p53 that was essential for increased chemosensitivity. This is not surprising considering the redundancy available in the cell cycle and apoptotic pathways. The pro-apoptotic targets of p53 include Bax, Bid, APAF1, Fas, Killer/DR5, Noxa, p53AIP1, TP53 apoptosis effector, PIDD, PIGs, PUMA and insulin-like growth factor binding-protein 3; and in mice knock-out studies no single p53-induced product has been found to be responsible for p53-mediated apoptosis (reviewed in (Chipuk and Green, 2006; Slee *et al.*, 2004)). For example, Noxa loss did not alter sensitivity of mouse lymphocytes or thymocytes to cytotoxic agents, but decreased the sensitivity of MEFs and gastric epithelial cells to DNA damage (Shibue *et al.*, 2003; Villunger *et al.*, 2003). PUMA seems to play a wider role in p53-induced apoptosis; PUMA loss increased the resistance of thymocytes, lymphocytes and MEFs to genotoxic damage by etoposide and  $\gamma$ -irradiation (Villunger *et al.*, 2003). The induction of apoptosis by p53 targets also differs significantly between different tissues. For example, in mice irradiated with ionising radiation, Fas levels increase 5-fold in the spleen but do not increase in the liver or heart (Bouvard *et al.*, 2000). Thus, to determine the relative contribution of each p53 target in ARF-mediated apoptosis would require a detailed but global analytical approach, such as a proteomic or microarray screen.

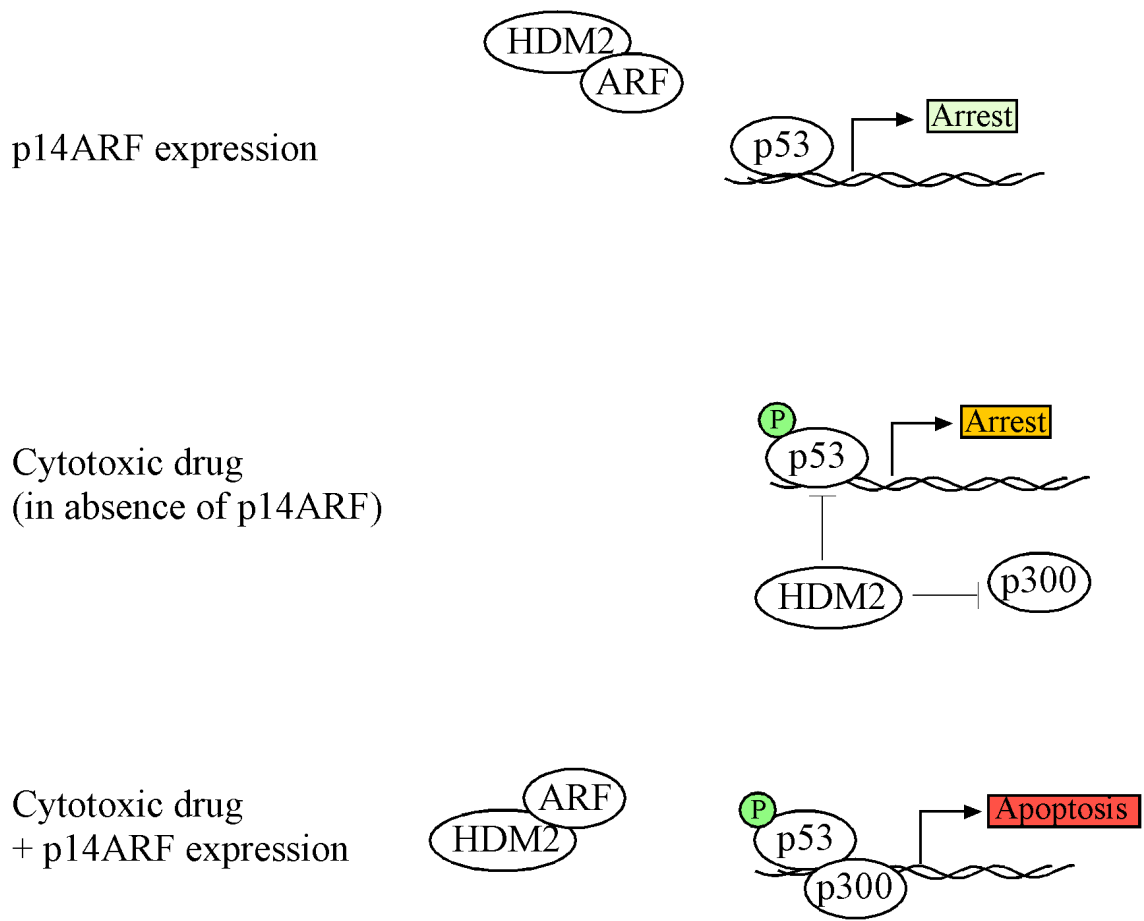
Regardless of the precise p53-targets regulating ARF-mediated chemosensitisation, this study showed that the loss of mitochondrial outer membrane potential is the critical p53-dependent step in this program. There are a number of possible mechanisms by which ARF depolarises the mitochondria and the simplest one involves increased p53 expression. For instance, p53 repressors the transcription of the anti-apoptotic genes

*Bcl-2* and *Mcl-1* and this would promote Bax-Bak pore formation in the mitochondrial outer membrane (Pietrzak and Puzianowska-Kuznicka, 2008; Wu *et al.*, 2001). Our data, however, indicate that p14ARF accumulation alone induced levels of p53 that were similar to the ARF plus drug combination, and yet ARF alone did not promote cell death. Furthermore p14ARF induction promoted higher p53 levels when combined with some drugs (such as TMZ, cisplatin and valproic acid) but it did not increase chemosensitivity to these drugs (see chapter 4). It is also possible that p53 is specifically modified by ARF, and the high levels of modified p53, in combination with specific stress signals, leads to an apoptotic p53-mediated transcriptional program. ARF can promote the sumoylation of p53, in the presence of HDM2 (Chen and Chen, 2003), and although the effect of this post-translational modification remains unresolved, it has been reported to enhance p53-dependent apoptosis (Kwek *et al.*, 2001; Lu and Yi, 2005; Melchior and Hengst, 2002; Muller *et al.*, 2000; Rodriguez *et al.*, 1999a). However, it should be noted that ARF-mediated p53-sumoylation has only been observed when ARF and hdm2 are overexpressed along with p53 (Chen and Chen, 2003) and we have never observed ARF-induced sumoylation of endogenous p53 in our stable U2OS\_ARF cell line (data not shown).

An alternate hypothesis explaining ARF-mediated chemosensitivity is that ARF inhibition of HDM2 allows drug-stabilised p53 to engage in an expanded, pro-apoptotic transcriptional program (Figure 5.31). HDM2, while also acting to ubiquitinate and degrade p53, can bind the N-terminal transactivation domain of p53, compete for binding with p53 co-activators such as p300 and directly inhibit p53 transcription (Ito *et al.*, 2001; Kussie *et al.*, 1996; Oliner *et al.*, 1993; Wang *et al.*, 2001b). Additionally HDM2 promotes the degradation of p300 and inhibits activation of p53 by p300-

mediated acetylation (Jin *et al.*, 2002; Jin *et al.*, 2004). p53 that accumulates in response to ARF induction is not extensively phosphorylated or modified (Jackson *et al.*, 2004) and this p53 may preferentially transactivate cell cycle regulatory, rather than apoptotic targets. Certainly, there are detectable differences in p53-transactivation activity following treatment with adriamycin or induction of ARF (Jackson *et al.*, 2004). In cells treated with cytotoxic drugs, p53 is heavily modified by phosphate and acetyl groups, and although this p53 has the capacity to potently transactivate apoptotic regulatory genes, it is kept in check by HDM2 in a negative feedback loop. This loop is disengaged in the presence of ARF, which inhibits HDM2 and allows p53 to activate gene transcription. In fact, p53 is a more effective transcriptional regulator in the presence of ARF (Huang *et al.*, 2003).

In this model, ARF-mediated chemosensitivity would not require further increases in p53 levels or additional post-translational modifications. In fact, a similar model has been previously suggested (Korgaonkar *et al.*, 2002; Midgley *et al.*, 2000), and it has been shown that cells accumulating high levels of HDM2 show lower induction of pro-apoptotic p53 targets, while retaining effective induction of cell cycle inhibitory targets (Ohkubo *et al.*, 2006). As a result, cells with higher levels of HDM2 demonstrated lower levels of apoptosis in response to DNA damaging agents.



*Figure 5.31 Proposed model showing the co-operative impact of p14ARF induction and cytotoxic drugs on p53-mediated cell death*

p53 accumulated in response to ARF is relatively unmodified and transactivates cell cycle arrest genes. Although cytotoxic drugs stabilise p53 by inducing its post-translational modification, efficient p53-dependent transactivation is prevented by HDM2 competing for p53 co-activator p300 and other protein partners. The introduction of ARF relieves this repression, and a stabilised p53 interacts with transactivation partners to efficiently induce the expression of pro-apoptotic genes and cell death.

In conclusion, we have confirmed that p14ARF-cell cycle inhibitory and –apoptotic functions require p53. We also determined that loss of mitochondrial integrity was involved in ARF-mediated chemosensitivity, and although this also involved the p53 tumour suppressor, we did not define any single p53 target that controlled this process. Thus, the mechanism of p14ARF-mediated chemosensitivity requires further investigation, as does its importance in melanoma. The next chapter investigates whether p14ARF expression is associated with increased chemosensitivity of melanoma tumours *in vivo*.

## **6. p14ARF expression does not predict melanoma chemosensitivity *in vivo***

Publications arising from this chapter:

**Activated N-RAS and p16<sup>INK4a</sup> expression are independent predictors of chemosensitivity in melanoma tumours**

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Submitted: Journal of Clinical Oncology. March 2008.

### **6.1 Author contribution statement**

This chapter consists of work recently submitted to Journal of Clinical Oncology. I gratefully acknowledge the contribution of the co-authors to this work. Author contribution statements from co-authors can be found in appendix 1. As first author on this paper, I state that I made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

## 6.2 Introduction

Metastatic cutaneous melanoma has a poor prognosis with two-year survival of less than 30% in patients with visceral involvement (Balch *et al.*, 2001b). This reflects the marked resistance of the disease to cytotoxic drugs. Single agent treatment with the alkylating agent dacarbazine (5-(3,3-dimethyl-1-triazeno)-imidazole-4-carboxamide, “DTIC”) remains standard best systemic therapy for metastatic melanoma (Eggermont and Kirkwood, 2004). Although overall response rates to dacarbazine are less than 15% (Avril *et al.*, 2004; Middleton *et al.*, 2000), certain patients have highly sensitive tumours and rare complete remissions are often sustained (Coates and Segelov, 1994). To date there are few studies of *in vivo* molecular determinants of chemosensitive melanomas, as distinct from studies on cultured cell lines, and the mechanisms involved in melanoma chemoresistance have not yet been elucidated.

We sought molecular correlates of chemosensitivity in a unique cohort of prospectively acquired tumour samples from patients with metastatic melanoma receiving isolated limb infusion (ILI) chemotherapy (Thompson *et al.*, 1998). ILI is a complex and technically demanding procedure performed as a palliative procedure for extensive inoperable loco-regional recurrence in a limb, usually from multiple in-transit seeding in cutaneous lymphatic vessels. A tourniquet is applied to isolate the circulation of the affected limb, allowing very high doses of cytotoxic drugs to be administered locally, while minimizing toxic systemic effects (Thompson *et al.*, 1998). ILI is only performed in a few centres around the world on highly selected patients, and although cohort size will always be limited, it provides a unique platform for the study of chemosensitivity in melanoma. Firstly, unlike the majority of clinical situations, pre-treatment fresh-

frozen tumour samples are readily available. Secondly, response rates to ILI are >50% (Thompson *et al.*, 1998), allowing greater statistical power to assess molecular correlates of response than in systemic chemotherapy, where response rates are <15% (Thompson *et al.*, 2005).

We selected for this analysis key candidate genes known to be important in melanomagenesis and also linked to the regulation of chemosensitivity (Thompson *et al.*, 2005). In particular, we analysed the expression of MITFm and the p14ARF and p16<sup>INK4a</sup> melanoma tumour suppressor genes and the status of the B-RAF and N-RAS melanoma oncogenes and the PTEN tumour suppressor.

The *INK4a/ARF* locus on chromosome 9p is the most frequently deleted region in established melanoma (Curtin *et al.*, 2005) and is inherited in mutated form in approximately 39% of melanoma prone families (Goldstein *et al.*, 2007). *INK4a/ARF* encodes two tumour suppressor proteins, p14ARF and p16<sup>INK4a</sup>, both of which have been shown to enhance the chemosensitivity of human cancer cells (Gallagher *et al.*, 2005; Simon *et al.*, 2006; Williams *et al.*, 2006; Yuan *et al.*, 2007). p14ARF accumulates in response to oncogenic stimuli and stabilises p53, leading to cell cycle arrest or apoptosis (reviewed in (Sherr, 2006)). The p16<sup>INK4a</sup> protein activates the retinoblastoma pathway by inhibiting CDK4 and 6 (Serrano *et al.*, 1993), leading to cell cycle arrest and, in some instances, cell death (Ausserlechner *et al.*, 2005). Loss of both p14ARF and p16<sup>INK4a</sup> is associated with melanoma progression (Dobrowolski *et al.*, 2002).

The microphthalmia-associated transcription factor, MITF, regulates development and differentiation of melanocytes, is expressed in most melanocytes (Koyanagi *et al.*, 2006) and is deregulated in melanoma. Increased levels of MITF may contribute to melanoma progression as MITF induces expression of the anti-apoptotic molecule, Bcl-2 (McGill *et al.*, 2002) and MITF ablation sensitises melanoma cells to cytotoxic drugs (Garraway *et al.*, 2005). MITF amplification is more frequent in metastatic melanoma and correlates with decreased patient survival (Garraway *et al.*, 2005). In normal melanocytes the MITF transcription factor transcriptionally activates p16<sup>INK4a</sup> to promote cell cycle arrest (Loercher *et al.*, 2005) and, as expected, MITF amplification is accompanied by p16<sup>INK4a</sup> inactivation in melanoma cell lines (Garraway *et al.*, 2005).

Activating N-RAS and B-RAF mutations are the most common oncogenic mutations in melanoma, indicating the importance of the RAS-RAF-MEK-ERK MAP kinase pathway in melanoma progression. Up to 80% of benign nevi (Pollock *et al.*, 2003) and 25-66% of melanomas contain activating B-RAF mutations (Davies *et al.*, 2002; Houben *et al.*, 2004). Activating N-RAS mutations are less common, occurring in 5-30% of melanoma (Houben *et al.*, 2004; Kumar *et al.*, 2003a; Omholt *et al.*, 2002). Activated B-RAF may also co-operate with loss of the PTEN tumour suppressor in promoting melanoma development. PTEN attenuates phosphoinositide 3-kinase (PI(3)K/AKT) signalling and the simultaneous activation of B-RAF and loss of PTEN simulate N-RAS activation to promote melanoma development (Tsao *et al.*, 2004). The high frequency of N-RAS and B-RAF mutations in melanoma, and the fact that these mutations have been correlated with poor prognosis (Houben *et al.*, 2004) indicates that they are potential therapeutic targets and yet there have been few studies investigating N-RAS/B-RAF status and melanoma response to common chemotherapeutic agents.

## 6.3 Results

### 6.3.1 Patient response

Fresh-frozen tumour biopsy samples from 30 melanoma patients who subsequently underwent ILI were analysed. Tumour response to ILI was classified as responsive, which included tumours showing complete response (n=5) and partial response (n=16), and non-responsive, which incorporated stable disease (n=7) and disease that progressed (n=2) (Table 6.1).

Table 6.1 Details of patients treated by isolated limb infusion with melphalan and actinomycin D

	<b>Responders</b>	<b>Non-responders</b>
Male/Female	5/16	2/7
Median age (range)	75 (48-93)	78 (46-86)
Best response (no.)	CR 5 PR 16	SD 7 PD 2
Mean time to best response	57 days	N/A
Mean time to PD in ILI field	272 days (from 13 responders)	94 days (from 2 PD and 5 SD)

CR-complete response, PR-partial response, SD-stable disease, PD-progressive disease, N/A-not applicable.

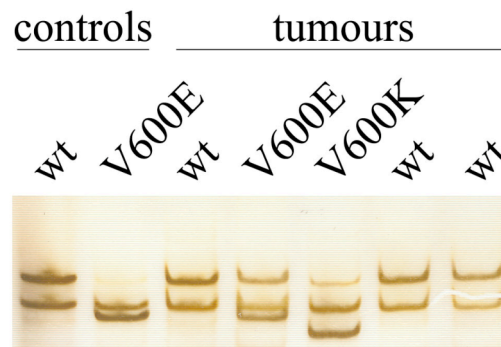
### 6.3.2 N-RAS and B-RAF are frequently mutated in melanoma

The vast majority of N-RAS and B-RAF mutations in melanoma occur at codon 61 (Q61K and Q61R) and codon 600 (V600E and V600K) respectively (Houben *et al.*, 2004; Poynter *et al.*, 2006). We analysed tumour samples for mutations affecting these codons using SSCP (Figure 6.1) and sequencing (Figure 6.2). Of the 30 tumours, ten (33%) showed mutation in N-RAS codon 61 and thirteen (43%) contained mutations

altering B-RAF codon 600 (Table 6.2). As expected, activation of N-RAS and B-RAF in these melanoma tumours was mutually exclusive and all mutations were heterozygous (see Figure 6.2).

*Figure 6.1 SSCP analysis of a B-RAF RT-PCR fragment encompassing codon 600*

Wild type (wt) control *B-RAF* PCR product was generated from the WMM1215 melanoma cell line and the *B-RAF*<sup>V600E</sup> mutant control was amplified from a *B-RAF*<sup>V600E</sup> expression plasmid. Amplified *B-RAF* cDNA from tumour samples are shown in lanes 3-7 (tumour samples 026, 003, 027, 044, 004 respectively).



*Figure 6.2 Sequence analyses of amplified B-RAF and N-RAS transcripts*

The nucleotide and codon changes encoded are shown on the left of each sequence. Numbering is based on Genbank accession NM\_004333 (*B-RAF*) and NM\_002524 (*N-RAS*). wt, wild type sequence.

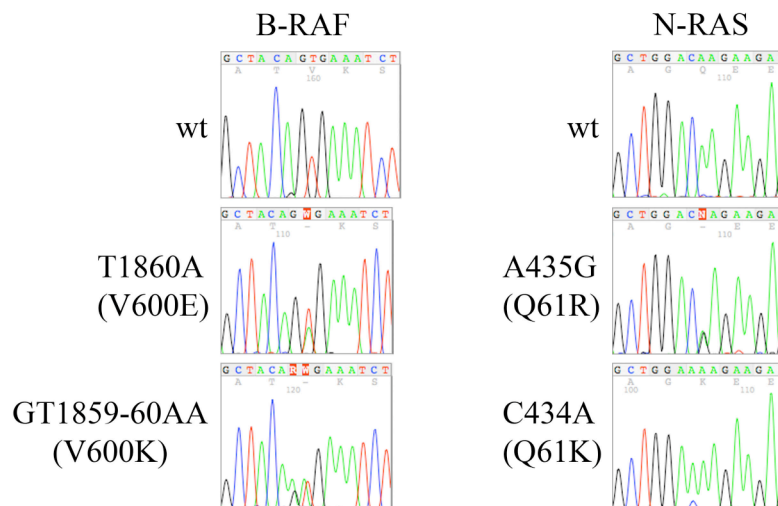


Table 6.2 Mutation status of 30 melanomas.

Mutation	Nucleotide	Number
N-RAS <sup>Q61R</sup>	A435G	8
N-RAS <sup>Q61K</sup>	C434A	1
N-RAS <sup>Q61K</sup>	AC434-35TA	1
B-RAF <sup>V600E</sup>	T1860A	9
B-RAF <sup>V600K</sup>	GT1859-60AA	4
No mutation		7
Total		30

### 6.3.3 Expression analysis of p16<sup>INK4a</sup>, p14ARF and MITF

There was considerable variation in p14ARF and p16<sup>INK4a</sup> transcript expression (Figure 6.3). The majority of tumours (approximately 60%) displayed very low expression of both p14ARF and p16<sup>INK4a</sup>. In most cases the expression of these transcripts was comparable, which is expected considering that these genes share genomic sequence. Only tumours 004, 030 and 041 showed discordant levels of the p16<sup>INK4a</sup> and p14ARF transcripts. The expression of MITF was also variable with only four tumours (008, 045, 006, 025) displaying very low levels of this transcript (Figure 6.3).

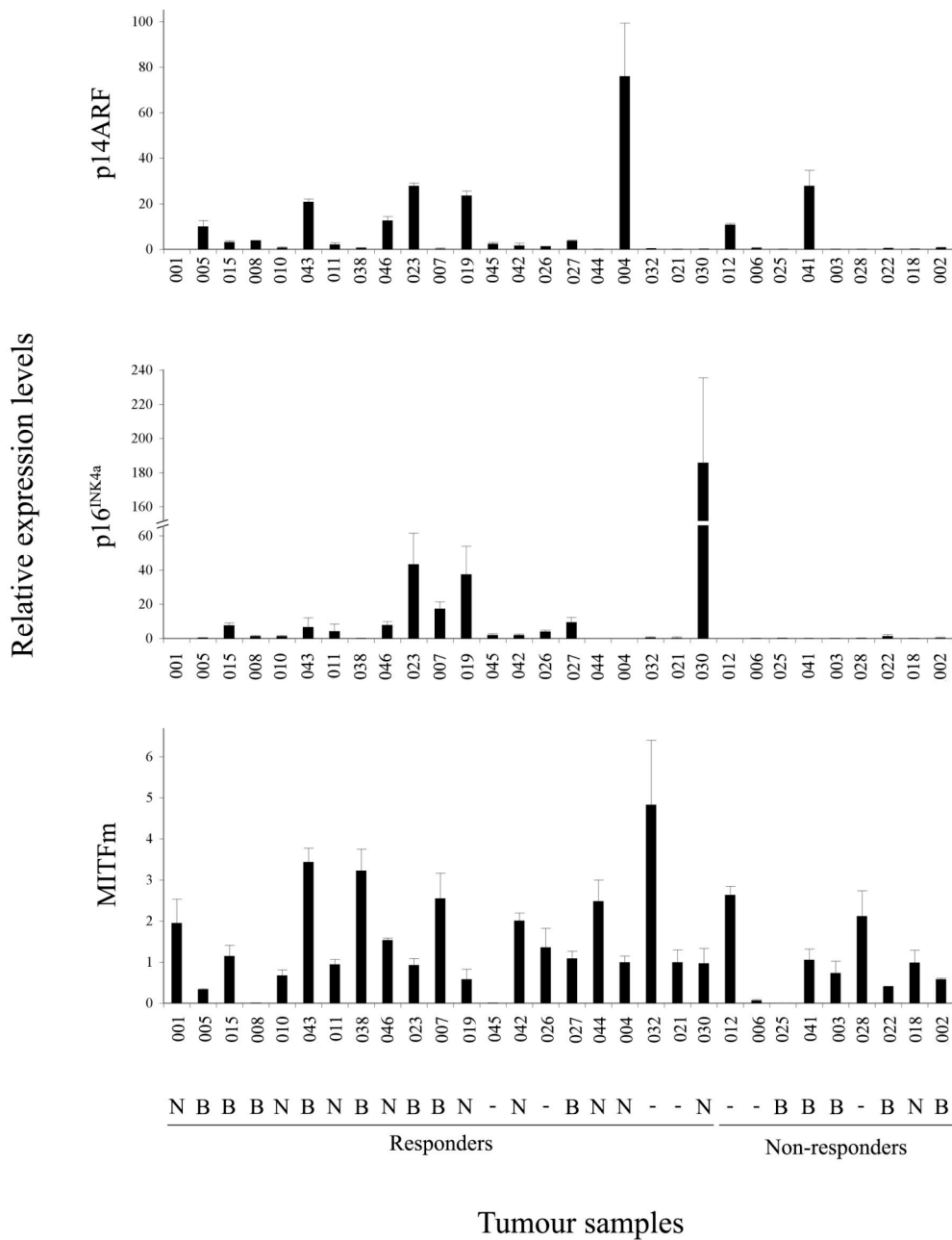


Figure 6.3 Relative expression levels of p14ARF, p16<sup>INK4a</sup> and MITFm

Relative expression levels of p14ARF, p16<sup>INK4a</sup> and MITFm in melanoma tumours was determined using quantitative real time RT-PCR. The mutation status of B-RAS and N-RAS for each tumour is also shown (N=mutant N-RAS, B=mutant B-RAS, -=wild type N-RAS and B-RAS).

#### 6.3.4 N-RAS mutation and p16<sup>INK4a</sup> expression correlate with better response

We investigated whether the presence of N-RAS or B-RAS mutation or the expression level of p16<sup>INK4a</sup>, p14ARF or MITF predicted response to chemotherapeutic drugs. The

independent predictors of response in this tumour set were presence of N-RAS mutation and high log transformed p16<sup>INK4a</sup> expression (Table 6.3). B-RAF mutation and expression level of p14ARF and MITF did not correlate with response. There was no correlation between p16<sup>INK4a</sup> and MITF expression levels nor did the presence of B-RAF mutation correlate with MITF expression (data not shown).

Table 6.3 Best fitting multiple logistic regression model of response together with adjusted Odds ratios and their 95% confidence intervals for independent predictors of response.

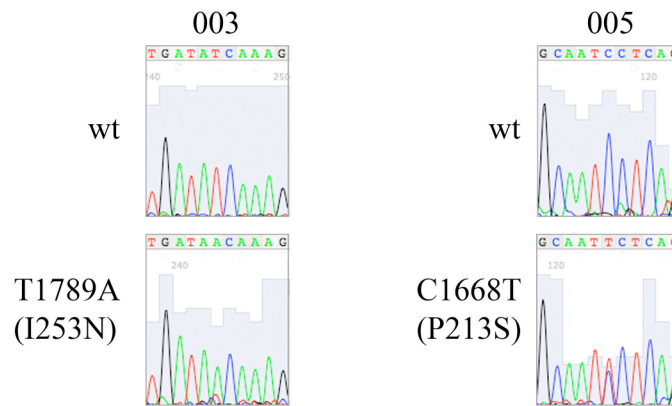
	B	S.E.	p-value	Odds Ratio	95% C.I. for OR	
					Lower	Upper
N-RAS mutation	3.31	1.68	.049	27.3	1.0	736.2
log p16 <sup>INK4a</sup>	.78	.35	.027	2.2	1.1	4.3
Constant	-3.92	1.94	.044	.02		

S.E., standard error; C.I., confidence interval; OR, odds ratio; B, regression coefficient.

### 6.3.5 Mutations affecting the PTEN tumour suppressor are not common in melanoma

Considering that oncogenic mutations affecting N-RAS and B-RAF were not equivalent in predicting melanoma response, it seemed likely that the MAP kinase signalling cascade, which is activated by both N-RAS and B-RAF, may not significantly influence treatment response. The main signalling cascade differentially activated by N-RAS and B-RAF is the PI(3)K/AKT pathway and the integrity of this pathway was analysed by screening the PTEN tumour suppressor, which attenuates PI(3)K signalling. As expected, PTEN mutations were not common in our panel of melanomas, and were identified in only three tumours (003, 005 and 045). The 045 tumour, which was wild type for both N-RAS and B-RAF, expressed wild type PTEN and PTEN with the G44G (C1163T) silent amino acid change (data not shown). Tumour 003 expressed B-RAF<sup>V600E</sup> and carried the homozygous PTEN mutant I253N (T1789A) and tumour 005

expressed oncogenic B-RAF<sup>V600K</sup> and was heterozygous for the PTEN P213S (C1668T) alteration (Figure 6.4).

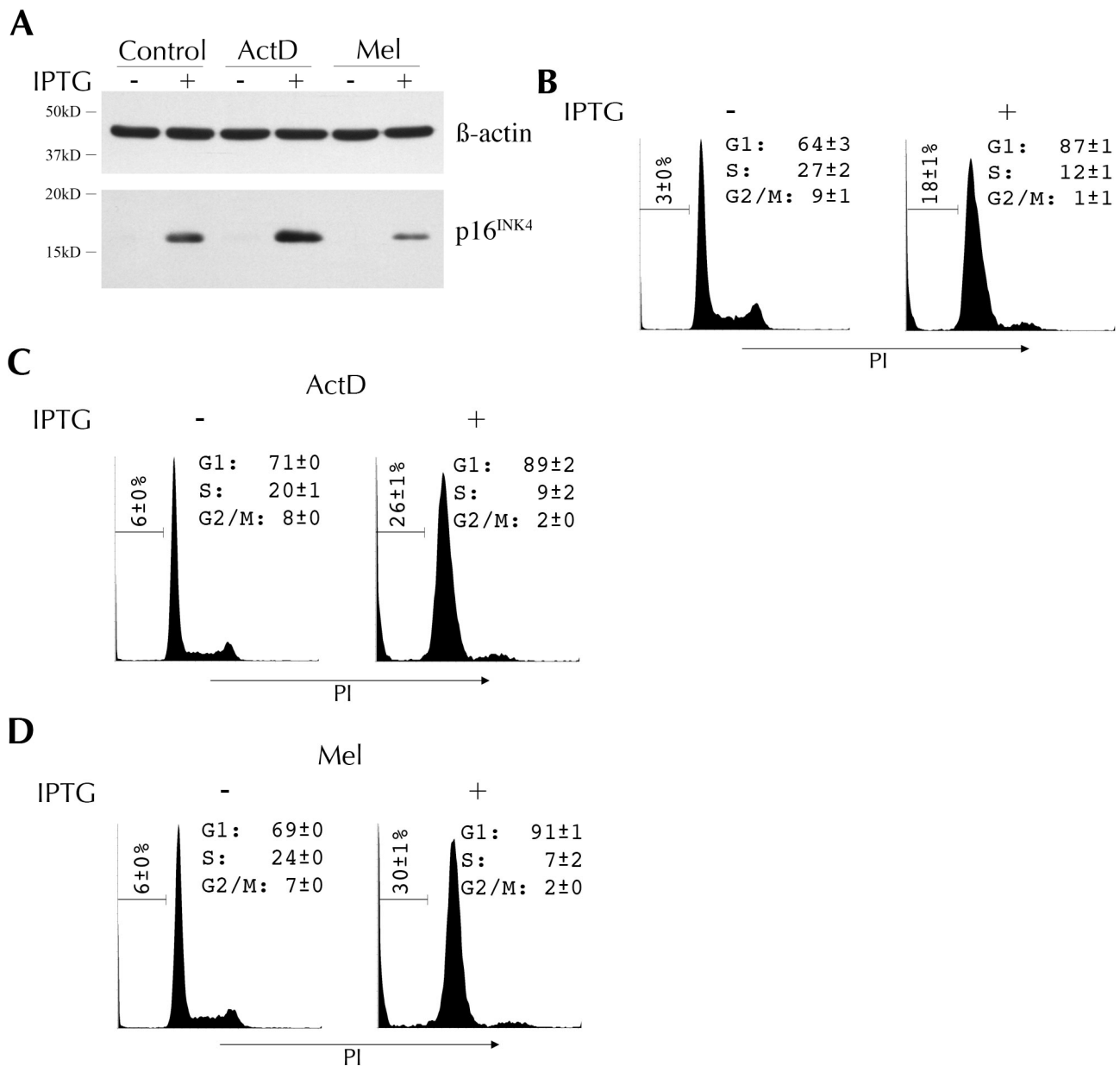


*Figure 6.4 Sequence analyses of amplified PTEN transcripts derived from tumour samples 003 and 005*

Sequences. The nucleotide and codon changes encoded are shown on the left of each sequence. Numbering is based on accession NM\_000314. wt, wild type sequence.

### 6.3.6 p16<sup>INK4a</sup> expression induces melanoma cell death

To investigate the impact of p16<sup>INK4a</sup> expression on melanoma cell survival we utilised a stable p16<sup>INK4a</sup>-inducible melanoma line. Expression of p16<sup>INK4a</sup> in this WMM1175\_p16<sup>INK4a</sup> cell clone was induced with 1mM IPTG over a five day period (Figure 6.5A). As shown in Figure 6.5B, induction of p16<sup>INK4a</sup> led to potent G1 cell cycle arrest and cell death, as determined by the increased sub-G1 population. Accumulation of p16<sup>INK4a</sup> also sensitised WMM1175\_p16<sup>INK4a</sup> cells to death in response to the cytotoxic drugs melphalan and actinomycin-D. In particular, the sub-G1 population increased from 18% in the presence of p16<sup>INK4a</sup> alone, to 26% with the addition of actinomycin-D (Figure 6.5C) and 30% in the presence of p16<sup>INK4a</sup> and melphalan (Figure 6.5D).



**Figure 6.5** Induced expression of p16<sup>INK4a</sup> promotes arrest, apoptosis and sensitises cells to cell death

(A) WMM1175\_p16<sup>INK4a</sup> melanoma cells were induced to express p16<sup>INK4a</sup> with the addition of 1mM IPTG to the media for 4 days, then treated with IPTG and actinomycin-D (ActD), melphalan (Mel) or carrier control for 24 hours. Detection of  $\beta$ -actin was used to demonstrate equal loading.

(B) WMM1175\_p16<sup>INK4a</sup> cells were incubated with media containing 1mM IPTG for 4 days then treated with control (ethanol) and IPTG for 24 hours. The cell cycle distribution of PI stained nuclei was examined by flow cytometry.

(C) 4-days post induction, WMM175\_p16<sup>INK4a</sup> cells were exposed to 25nM actinomycin-D and IPTG for 24h and cell cycle distribution examined.

(D) 4-days post induction, WMM175\_p16<sup>INK4a</sup> cells were exposed to 200 $\mu$ M melphalan and IPTG for 24h and cell cycle distribution examined.

## 6.4 Discussion

In this study we investigated the *in vivo* response of melanoma metastases to cytotoxic drugs administered by ILI to determine if response correlated with the expression of p16<sup>INK4a</sup>, p14ARF and MITFm and the mutation status of N-RAS, B-RAF and PTEN. These gene products are central to the pathways commonly altered in melanoma progression and thus have potential interaction with mechanisms of cytotoxicity. We have shown that high p16<sup>INK4a</sup> expression and presence of mutant active N-RAS correlate with chemotherapeutic response of melanoma tumours. The fact that melanomas commonly lack p16<sup>INK4a</sup> and carry active B-RAF, rather than N-RAS may contribute to chemo-resistance.

The spectrum and high prevalence of B-RAF and N-RAS mutations (23/30) found in our melanoma samples is similar to other studies (Davies *et al.*, 2002; Houben *et al.*, 2004; Kumar *et al.*, 2003a). N-RAS and B-RAF mutations were mutually exclusive, as previously reported (Davies *et al.*, 2002), presumably since both these gene products signal through the MAP kinase pathway. The differential role of B-RAF and N-RAS in predicting melanoma chemosensitivity (this study) and survival (Ugurel *et al.*, 2007) may involve the PI(3)K/AKT pathway. Unlike B-RAF, N-RAS activates the PI(3)K/AKT pathway and several studies have implicated activation of the PI(3)K pathway as another crucial event in the progression of melanoma (Denoyelle *et al.*, 2006). In particular, RAS activation of the PI(3)K/AKT pathway controls the activation of endoplasmic reticulum stress response (Denoyelle *et al.*, 2006), which can activate cytoprotective effects in melanomas (Chen *et al.*, 2007). B-RAF and RAS also differ in their capacity to promote growth arrest in normal human cells (Chudnovsky *et al.*,

2005) and in their ability to cooperate with pRb and p53 loss to produce invasive melanocytic neoplasia (Tsao *et al.*, 2004). Finally, microarray studies show melanomas with an activating N-RAS mutation have different gene expression patterns to those with activating B-RAF mutations (Pavey *et al.*, 2004), and tumours containing N-RAS<sup>Q61R</sup> are less dependent on MEK than tumours with B-RAF<sup>V600E</sup> (Solit *et al.*, 2006).

It has been proposed that the combined activation of B-RAF and loss of PTEN simulates oncogenic N-RAS activity to simultaneously activate the MAP kinase and PI(3)K pathways. Accordingly, melanomas rarely express oncogenic N-RAS and altered PTEN (Tsao *et al.*, 2000), whereas they frequently carry oncogenic B-RAF and mutated PTEN (Tsao *et al.*, 2004). In our sample set, only two melanomas carried missense PTEN mutations. These mutations (P213S and I253N) presumably inactivate PTEN as they are located in the PTEN lipid-binding domain and have been identified in a human glioma and endometrial cancer (Mutter *et al.*, 2000; Zhou *et al.*, 1999). The two tumours with PTEN loss also expressed oncogenic forms of B-RAF, but patient response did not relate to PTEN status; 005 showed complete response whereas 003 had stable disease, post therapy. Considering the low frequency of PTEN alterations detected in melanomas, a significantly larger set of melanoma tumour samples needs to be analysed in order to accurately define the contribution of PTEN and the PI(3)K pathway to melanoma chemosensitivity. This is particularly important as the combination of B-RAF inhibitors with PI(3)K inhibitors have been shown co-operate in preventing melanoma cell proliferation and consistently enhanced melanoma chemosensitivity and suppressed invasive tumour growth (Meier *et al.*, 2007).

Our set of melanoma tumour samples displayed heterogeneity in MITF expression with no apparent correlation with chemosensitivity. Inhibition of MITF function in melanoma may trigger CDK2-mediated growth arrest (Du *et al.*, 2004) or apoptosis through bcl-2 downregulation (McGill *et al.*, 2002). Accordingly, MITF loss has been shown to sensitise melanoma cells to the cytotoxic agents, cisplatin and docetaxel (Garraway *et al.*, 2005). Alternatively, increased MITF expression has been shown to induce cell cycle arrest by activating the expression of the CDK inhibitor p16<sup>INK4a</sup> (Loercher *et al.*, 2005). We observed no association between MITF and p16<sup>INK4a</sup> expression in our melanoma tumours (data not shown).

MITF activity is also regulated by the MAP kinase pathway. Activation of MAP kinase signalling phosphorylates MITF, which simultaneously increases its transactivation potential and targets it for degradation via the 26S proteasome (McGill *et al.*, 2006; Wellbrock and Marais, 2005). Thus, MITF amplification, which is found in 20-30% of melanomas, is often accompanied by B-RAF mutation and p16<sup>INK4a</sup> loss (Garraway *et al.*, 2005). However, we did not see any correlation between MITF and B-RAF expression levels in this study (data not shown).

The ectopic expression of p14ARF enhances chemosensitivity in human tumour cell lines (Gallagher *et al.*, 2005) and p14ARF expression has been associated with improved prognosis in several cancers, including acute myeloid leukemias (Kwong *et al.*, 2005; Muller-Tidow *et al.*, 2004). However, no association between p14ARF expression and response was seen in our panel of melanoma tumours. Further, in a recent microarray study of melanoma tumours, p14ARF expression was not associated with survival (Winnepenninckx *et al.*, 2006). Although, p14ARF is frequently lost in

human melanomas, this usually occurs in combination with p16<sup>INK4a</sup> loss. Moreover, the majority of mutations affecting the *INK4a/ARF* locus target p16<sup>INK4a</sup> for inactivation (Sherr, 2001), indicating that, in humans, p16<sup>INK4a</sup> is the critical tumour suppressor encoded by this genomic sequence.

Several studies have shown that p16<sup>INK4a</sup> loss or deregulation correlates with poor prognosis in human cancers such as melanoma, leukaemia, colon and renal cancers (Mihic-Probst *et al.*, 2006; Ota *et al.*, 2006). While there is no necessary biological connection between poor prognosis and chemoresistance, it was possible that the high frequency of loss of p16<sup>INK4A</sup> in melanoma was a direct contributor to treatment failure. Consistent with this hypothesis, we found that retention of p16<sup>INK4a</sup> expression was associated with melanoma chemosensitivity. We also found that accumulation of p16<sup>INK4a</sup> promoted the death of melanoma cells in culture. More importantly, p16<sup>INK4a</sup> co-operated with the cytotoxic drugs melphalan and actinomycin-D to enhance melanoma cell death (see Figure 5). The mechanism by which p16<sup>INK4a</sup> expression promotes cell death in response to drugs requires investigation. This is especially relevant as melanoma cells have usually lost p16<sup>INK4a</sup> and display an intrinsic resistance to drug-induced cell death.

In summary, this study shows that p16<sup>INK4a</sup> expression and activation of N-RAS correlate with *in vivo* response of metastatic melanoma exposed to high doses of locally administered cytotoxic drugs. It will be interesting to determine whether these two molecules also influence the response of melanoma metastases exposed to lower doses of chemotherapy given systemically. Although *in vivo* studies on the chemosensitivity of metastatic melanoma are hampered by poor response rates and would require a much

larger sample size they would yield valuable data regarding the mechanisms involved in melanoma chemoresistance. This study reinforces the importance of the *INK4a/ARF* locus and highlights the PI(3)k/AKT pathway, in the regulation and execution of apoptosis in melanoma and suggests directions to improve its responsiveness to conventional chemotherapeutic agents.

## 7. Conclusions

p14ARF is a critical tumour suppressor in melanoma; p14ARF is frequently inactivated in melanoma tumours and germline mutations that specifically target p14ARF confer a high risk of melanoma predisposition. The primary function of p14ARF is to relay oncogenic signals to the p53 cell cycle regulatory pathway and to rapidly induce cell cycle arrest. The strict p53-dependency of p14ARF function is further demonstrated by our work showing that p14ARF can chemosensitise tumour cells in a p53-dependent manner. The ability of p14ARF to enhance chemosensitivity was not evident in our cohort of melanoma patients and p14ARF expression did not predict response to high doses of actinomycin D and melphalan. Although melanomas usually retain functional p53, the downstream effectors may be altered or the induction of ARF expression (eg via abnormal proliferative signals) may be required to activate the p53 pathway.

Accordingly, p14ARF induction enhanced the response of our U2OS cell model to a set of cytotoxic drugs, by activating and possibly altering the transactivational program of p53. The mechanism(s) of ARF action on p53 are not well described and this requires further investigation, as it is clear from our data that simply inhibiting HDM2 to increase p53 levels is not adequate for ARF-mediated chemosensitisation – compare p53 and cell death levels in ARF-expressing cells treated with drugs temozolomide and camptothecin in Figures 4.3 & 4.9 (A, B & C). Thus, it is possible that p14ARF alters the function of the stabilised p53 either by i) directly inducing p53 post-translational modifications, such as sumoylation, ii) interfering with multiple p53 binding partners such as NPM, ARF-BP1 and HDM2 or iii) promoting p53 post-translational

modification indirectly via interaction with proteins such as ATR and hADA3. Elucidation of the mechanism(s) of p14ARF action on p53 would provide valuable information regarding the role of ARF in melanoma development and chemoresistance.

In addition to defining the role of p14ARF, it would be useful to identify the downstream p53 targets that regulate apoptosis in response to p14ARF accumulation. Targeting these genes directly may prove beneficial in treating melanoma, as they would bypass upstream alterations within the ARF-p53 pathway. The identification of genes and proteins with altered expression in the presence of ARF would require a global analytical approach of melanoma cell models and melanoma tumours. A similar approach has already confirmed that over 1000 probe sets were differentially expressed between p14ARF wild type and mutant melanoma cell lines (Packer *et al.*, 2007). There is currently no data available on the importance of any of these differentially expressed genes in melanoma. Similarly, we have no information on the specific role of p14ARF in melanocytes, even though p14ARF inactivation predisposes specifically to this cancer. These are important gaps in our knowledge of ARF and we need to carefully consider the experiments and models required to clearly define how ARF functions to suppress melanoma formation.

## **8 Appendix 1**

This appendix contains author contribution statements regarding work contained on Chapter 6.

**Fax to: Attn: Stuart Gallagher**  
**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**  
Westmead Millennium Institute  
Westmead Institute for Cancer Research.  
Darcy Rd, Westmead, 2145. NSW

I consent to Stuart Gallagher using the paper "Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours" in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:  
Defined project goals and assisted with methodology. Analysed PTEN sequences.  
Finalised manuscript text and figures, before submitting manuscript.

regards,

Name: Helen Rizos

Signature:  \_\_\_\_\_

Date: 12 March 2008

**Fax to: Attn: Stuart Gallagher**  
**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**  
Westmead Millennium Institute  
Westmead Institute for Cancer Research.  
Darcy Rd, Westmead, 2145. NSW

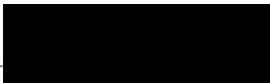
I consent to Stuart Gallagher using the paper "Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours" in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:

Clinical data summary

regards,

Name: Dr Bo Gao

Signature: 

Date: 17/03/2008

**Fax to: Attn: Stuart Gallagher**  
**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**  
Westmead Millennium Institute  
Westmead Institute for Cancer Research.  
Darcy Rd, Westmead, 2145. NSW

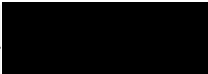
I consent to Stuart Gallagher using the paper "Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours" in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:

I helped Stuart Gallagher to design and optimize the real time PCR analysis for p14ARF and p16INK4a. I also sequenced the PTEN gene in all of the samples and was involved in discussions regarding the work published in this paper.

regards,

Name: Dr Lyndee Scurr

Signature: 

Date: 12-3-2008

**Fax to: Attn: Stuart Gallagher**  
**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**  
Westmead Millennium Institute  
Westmead Institute for Cancer Research,  
Darcy Rd, Westmead, 2145. NSW

I consent to Stuart Gallagher using the paper "Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours" in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:

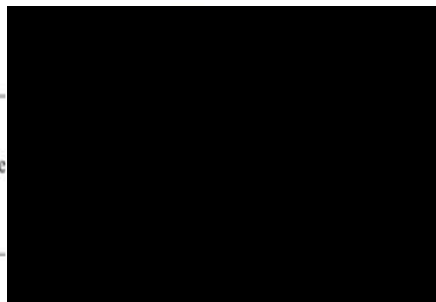
Designed experiment and experimental protocol  
Edited paper  
Obtained grant funding

regards,

Name: \_\_\_\_\_

Signature \_\_\_\_\_

Date: \_\_\_\_\_



**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**

Westmead Millennium Institute  
Westmead Institute for Cancer Research.  
Darcy Rd, Westmead, 2145. NSW

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My contribution to the paper was:

Assisted in design of experimental and surgical protocol. Performed surgery.

regards,

Name: \_\_\_\_\_ John F. Thompson \_\_\_\_\_

Signature: \_\_\_\_\_ Not available at time of printing \_\_\_\_\_

Date: \_\_\_\_\_

**Fax to: Attn: Stuart Gallagher**  
**Fax: 02 9845 9102**

**Or Post to: Stuart Gallagher**  
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Darcy Rd, Westmead, 2145. NSW

I consent to Stuart Gallagher using the paper “Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours” in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:

Advice and training on RNA extraction from solid tumours, measurement of RNA yield and QC for various applications, including microarrays and RT PCR. Primer combinations for detection of mutations in NRAS and BRAF genes were supplied. Advice on the nature and frequency of RAS-RAF mutations in various melanocytic lesions given.

regards,

Name: James Indsto

Signature: 

Date: 25/3/08



**Fax to: Attn: Stuart Gallagher**  
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Darcy Rd, Westmead, 2145. NSW

I consent to Stuart Gallagher using the paper “Activated N-RAS and p16INK4a expression are independent predictors of chemosensitivity in melanoma tumours” in his PhD thesis. To my knowledge, Stuart Gallagher made cDNA from RNA extracted from the tumour samples, performed real time analysis, SSCP, PCR, gene sequencing and analysis (except PTEN) and drafted the paper.

My contribution to the paper was:

Contribution to design of the clinical study, supervision of the tissue collection and preparation of derived specimens, co-supervision of analysis of clinical data, and interpretation of results.

regards,

Name:                     Assoc Prof Graham Mann                      
\_\_\_\_\_

Signature:  \_\_\_\_\_

Date:                     March 27, 2008

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