

Figure S1. SMOX does not induce apoptosis. (A) Mono-parametric FCM analysis of 498 DNA content and (B) TUNEL assay of NP, NG and NS cell lines. Symbols for the DNA content: NP, grey-filled histogram; NG, black line; NS dashed line. Symbols for TUNEL: autofluorescence, grey-filled histogram; NP, black line; NG, dashed line; NS, grey line. The percentages of the sub-G1 cell population and the fold change of the mean fluorescence intensities of TUNEL assay in the cell population are plotted as Whisker boxes. Data were analysed by one-way ANOVA, followed by Tukey's post hoc test. No significant differences were found. NP cells. NP, N18TG2 cells transfected with pcDNA3; NS, N18TG2 cells transfected with pcDNA3/SMOX; NG, N18TG2 cells transfected with pcDNA3/ γ SMO.

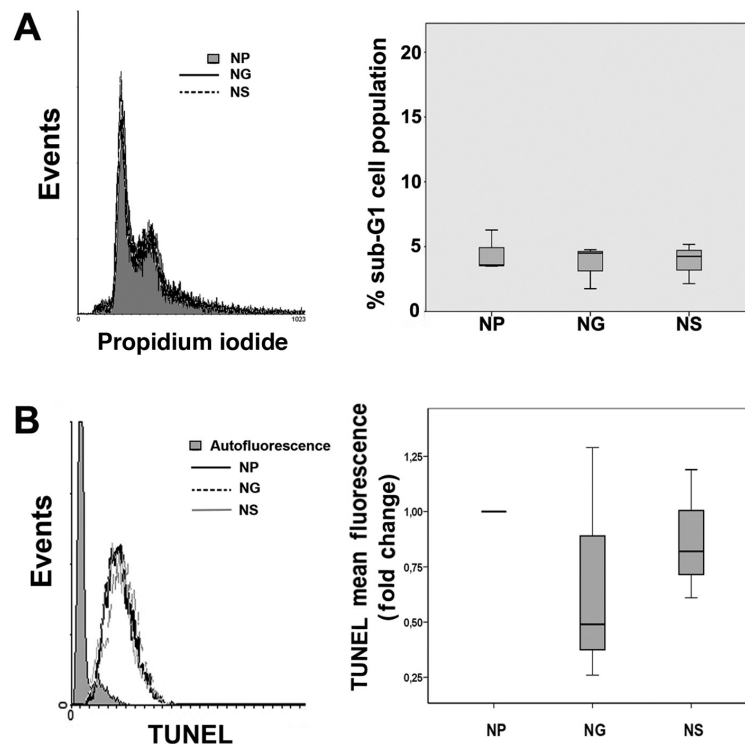


Figure S2. Semi-quantitative RT-PCR for BAK, BAX, AATF gene expression in NP, NG and NS cell lines and TG tissues. (A) Semi-quantitative RT-PCR quantification of BAK, BAX, PUMA and β -actin in NP, NS, NG cell lines, and in the presence of 50 and 100 μ M MDL as a SMOX inhibitor. β -actin was used as a housekeeping gene. (B) Expression of AATF, BAK, BAX and PUMA examined by RT-PCR in the brains, intestines and heart tissues from transgenic (TG) or syngeneic (SG) mice totally expressing SMOX. '-' and '+' represent negative and positive control of PCR reactions. NP, N18TG2 cells transfected with pcDNA3; NS, N18TG2 cells transfected with pcDNA3/SMOX; NG, N18TG2 cells transfected with pcDNA3/ γ SMOX; SMOX, spermine oxidase; AATF, apoptosis antagonizing-factor BAK; Bcl-2 antagonist/killer; BAX, Bcl-2-associated X protein; PUMA, p53 upregulated modulator of apoptosis; MDL-72527, N,N'-Bis(2,3-butadienyl)-1,4-butanediamine dihydrochloride.

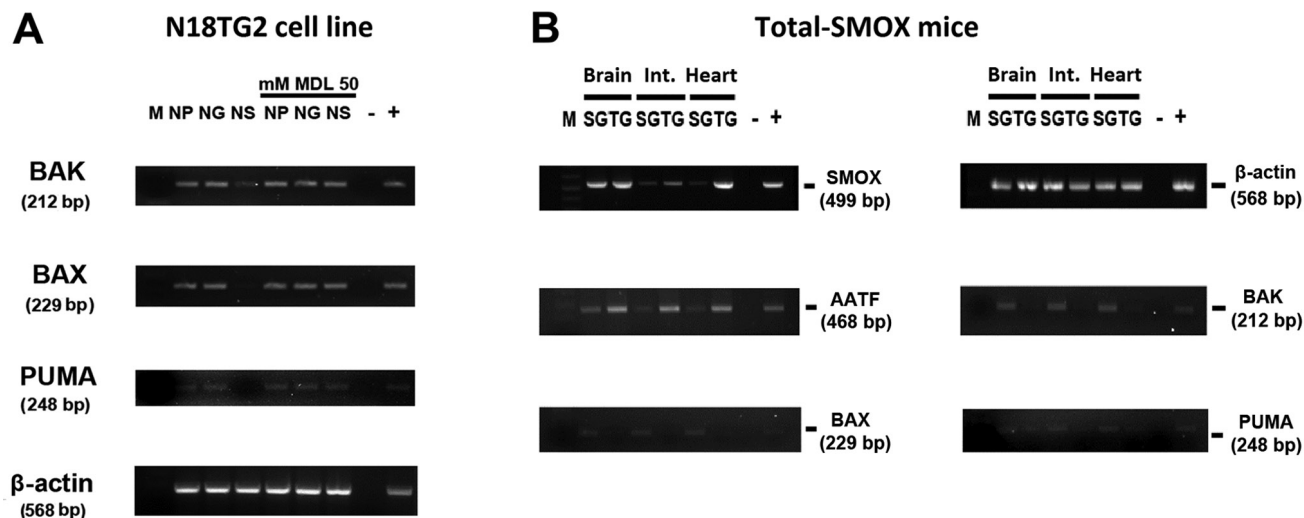


Table SI. Specific sequences of primers.

AATF PrimerBank ID NM_019816.1	Sequence (5'→3')	Length	Tm	Location	Amplicon size
Forward primer	CGGAGCCAGTCCCTGAGCCT	20	63	1285-1304	468 bp
Reverse primer	GGAGGCAGCAGGTGGGTCCT	20	63	1733-1752	
PUMA PrimerBank ID 18875398a1	Sequence (5'→ 3')	Length	Tm	Location	Amplicon size
Forward primer	AGCAGCACTTAGAGTCGCC	19	61.7	302-320	248 bp
Reverse primer	CCTGGGTAAGGGGAGGAGT	19	61.7	549-531	
BAX PrimerBank ID 133778943c2	Sequence (5'→ 3')	Length	Tm	Location	Amplicon size
Forward primer	CCGGCGAATTGGAGATGAACT	21	62.5	189-209	229 bp
Reverse primer	CCAGCCCATGATGGTTCTGAT	21	61.9	417-397	
BAK PrimerBank ID 6671612a1	Sequence (5'→ 3')	Length	Tm	Location	Amplicon size
Forward primer	GGTGACAAGTGACGGTGGTC	20	61	217-236	212 bp
Reverse primer	GTCCATCTCGGGGTTGGCAG	20	61	428-409	