Table S1. RAR-responsive elements in the *Bax* and *Bak* promoters

Gene	Matrix	Opt. threshold	Start position	End position	Strand	Matrix similitud	Core similitud	Sequence
Bax	Vertebrate RAR_RXR.01	0.78	–1176	–1152	+	0.799	1.0	atgttctgg**ggt**ac**AGGTat**gggc
Bax	Vertebrate RAR_RXR.01	0.78	–1074	–1050	–	0.798	1.0	tacatagca**agt**gac**AGGTca**atta
Bax	Vertebrate RAR_RXR.01	0.78	–82	–58	+	0.781	0.769	agtcctgcg**ggg**cgg**AGGCca**tgtt
Bak	Vertebrate RAR_RXR.01	0.78	–107	–83	+	0.805	1.0	taagtactg**gga**tta**AGGTca**caca

One-thousand-five-hundred base pairs upstream, the transcription initiation site of *Bax* and *Bak* were analyzed using the MatInspector software from Genomatix. The matrix analyzed belongs to the 'matrix family' Vertebrate RXRF. 'Optimized threshold' is the optimized value defined in a way that a minimum number of matches is found in non-regulatory test sequences (i.e. with this matrix similarity the number of false-positive matches is minimized). 'Start' and 'End' position indicates the position in the DNA sequence where the core sequence is found in reference to the transcription initiation site. 'Matrix similitud' defines a value for the most conserved nucleotides at that position in the matrix; a perfect match to the matrix gets a score of 1.00. The 'Core sequence' of a matrix is defined as the highest conserved positions (usually 4) of the matrix. Base pairs in capital letters denote the core sequence used by MatInspector and red letters are important nucleotides.