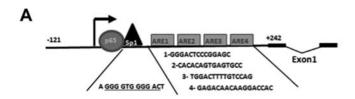
SUPPLEMENTARY FIGURE



В	S. info.	Transcription factor	Binding site	Length	Application (PCR)	Primer sequences
	Oh ID andress	6-4/NF-D	.0F/.4F7D	4005-	Forward	5'-TAG CAG GAA ACA GCG AGC TT-3'
	ChIP primer	Sp1/NFkB	+9F/+157R	180bp	Reverse	5'-GCG CTT CTC TCC TAC ACC TC-3'

С	EMSA probe	Transcription factor	Region	Sequence			
				Upper	5'-CCG GAG CTA GGG GTG GGG ACT CGG-3'		G-3'
	FLIP	Sp1/NFkB/AR	+64/+89		AR	Sp1 p65	
				Lower	5'-CCG AGT CCC	CAC CCC TAG CTC CGC	3-3"

EMSA probe	Transcription factor	Region	Sequence	
ARE-1	Sp1/NFkB	+57/+71	Upper	5'-GGG ACT CCC GGA GCT-3'
ARE-1	SPINITED	T3//T/1	Lower	5'-AGC TCC GGG AGT CCC-3'
ARE-1m		+57/+71	Upper	5'-GAG GTT CCC GAA GTC-3
ARE-IM		+3//+/1	Lower	5'-GAC TTC GGG AAC CTC-3'

Supplementary Figure S1: A. Schematic representation of potential transcription factor binding sites on the c-FLIP promoter (-121/+242) predicted by Genomatrix program. B. Primer sequences used for ChIP. C. and D. Oligonucleotide sequence of c-FLIP sequence, and c-FLIP ARE-1 sequence used in EMSA.