Table S1. Primers used for ChIP analysis of the human *Tissue Factor* promoter

REGION No.	REGION in the human TF promoter	Primers	Size (bp)
R1	-235 to +180	F: 5'- TCG GTG GCG CGG TTG AAT CAC TGG -3' R: 5'- GTC CGA GCG ACG GCG GTC TC -3'	415
R2	-666 to -235	F: 5'- ACC GGC ATT CCC ACC GCC -3' R: 5'- GAG CTG CCC TGG AGG ACG CAG -3'	426
R3	-1118 to -666	F: 5'- TTC TCC AGT CGT GTC TTG CAG GC -3' R: 5'- CAG CCA CGG TGT GAC CGG CTC -3'	450
R4	-1529 to -1118	F: 5'- TCA GCT ACC TTC AAT CCC AGA GAG C -3' R: 5'- GCC TGC AAG ACA CGA CTG GAG AA -3'	434
R5	-1942 to -1529	F: 5'- CGC ACC GTC AAA AAG TAG ATC TGG CC -3' R: 5'- GCT CTC TGG GAT TGA AGG TAG CTG AAG -3'	438
R3.1	-666 to -877	F: 5'- CGG TGG AAC TCA GTC CCA CAG ATG TC -3' R: 5'- CAG CCA CGG TGT GAC CGG CTC -3'	211
R3.2	-877 to -1118	F: 5'- TTC TCC AGT CGT GTC TTG CAG GC -3' R: 5'- GTT CCA CCG AAA TGC AGA GGA ACC -3'	248
R4.1	-1118 to -1347	F: 5'- GTC TAC AAG GGC TAA ACC TGG ATG TGC -3' R: 5'- GCC TGC AAG ACA CGA CTG GAG AA -3'	229
R4.2	-1347 to -1529	F: 5'- TCA GCT ACC TTC AAT CCC AGA GAG C -3' R: 5'- CCC TTG TAG ACT TTC CTT CCT CGA AGC -3'	216

Table S2. Primers used for ChIP analysis of the human *Tissue Factor pathway inhibitor* promoter

REGION No.	**REGION in the human TFPI promoter**	**Primers**	**Size (bp)**
R1	-370 to +25	F: 5'-TCACTAAGAGAGACCTCCAACGGT-3' R: 5'-TCAGAGATCACTGGCAGTTGGGAA-3'	395
R2	-798 to -378	F: 5'-CCTGGCAAAGTAGATTCTGCCCAT-3' R: 5'-TGTCAGGCTTTGAGCCCTACCTTA-3'	400
R3	-1198 to -798	F: 5'-GCAGGGCATGAGGTAATAGGAGAT-3' R: 5'-AGGAAGGCTGAAGACATTTGGTC-3'	400
R4	-1653 to -1256	F: 5'-ATCACTCGCGGTTAGGAGCTGGA-3' R: 5'-CTTGGTACCACCATGGACCTTGA-3'	397

Table S3. Primers used for binding analysis of the indicated transcription factors by EMSA to the human Tissue Factor promoter.

Transcription Factor	Binding site	Primer name	Sequence
TCF-4E	A	WT_s	5'-CCCAGAG**AGCAAAG**AATCACAT-3'
		WT_as	5'-ATGTGATT**CTTTGCT**CTCTGGG-3'
	B	WT_s	5'-AGTTTAC**AGCAAAG**CCCAGAA-3'
		WT_as	5'-TTCTGGG**CTTTGCT**GTAAACT-3'
GATA-1	A	WT_s	5'-AGCTAAAC**GAGATA**TGTATATA-3'
		WT_as	5'-TATATACA**TATCTC**GTTTAGCT-3'
	B	WT_s	5'-AATGACAG**GAGATA**CTTTGACA-3'
		WT_as	5'-TGTCAAAG**TATCTC**CTGTCATT-3'
TFII-I	A	WT_s	5'-CTTTCTGCTTCGAGGAA**GGAAAG**TCTACAAGGGCT-3'
		WT_as	5'-AGCCCTTGTAGA**CTTTCC**TTCCTCGAAGCAGAAAG-3'
	B	WT_s	5'-AAAACGTG**GGAAAG**AAGGAGAG-3'
		WT_as	5'-CTCTCCTT**CTTTCC**CACGTTTT-3'
PXR:RXRalpha	A	WT_s	5'-GTGCTATT**TCAGTTCA**GGCAAAGG -3'
		WT_as	5'-CCTTTGCC**TGAACTGA**AATAGCAC-3'
c-ETS-1	A	WT_s	5'-CTTTCTGCTTC**GAGGAAG**GAAAGTCTACAAGGGCT-3'
		WT_as	5'-AGCCCTTGTAGACTTTC**CTTCCTC**GAAGCAGAAAG-3'
AP-1/c-Jun	A	WT_s	5'-GGGAAAA**TGACTCA**GGCTAGA-3'
		WT_as	5'-TCTAGCC**TGAGTCA**TTTTCCC-3'
AP-1/c-Jun	A	MUT_s	5'-GGGAAAA*CAGTCTG*GGCTAGA-3'
		MUT_as	5'-TCTAGCC*CAGACTG*TTTTCCC-3'