

Supplementary Table S2. All analyzed SNPs in *TFPI* and *TF*. Alleles for the positive strand are shown (UCSC annotated).

SNP	Gene	Position (hg19)	Region	Alleles ^a	MAF ^b
rs5940	<i>TFPI</i>	chr2:188331704	Coding (V>M)	C:T	0.034
rs8176541 ^t	<i>TFPI</i>	chr2:188341047	Intron	G:A	0.283
rs3213739 ^t	<i>TFPI</i>	chr2:188348670	Intron	G:T	0.417
rs8176605 ^t	<i>TFPI</i>	chr2:188356110	Intron	A:G	0.062
rs8176479 ^t	<i>TFPI</i>	chr2:188357179	Intron	C:A	0.238
rs2192824	<i>TFPI</i>	chr2:188368791	Intronic	C:T	0.490
rs12613071	<i>TFPI</i>	chr2:188388311	Intronic	T:C	0.158
rs2192825	<i>TFPI</i>	chr2:188390819	Intronic	T:C	0.466
rs16829086	<i>TFPI</i>	chr2:188391250	Intronic	C:T	0.192
rs16829088	<i>TFPI</i>	chr2:188391908	Intronic	G:A	0.250
rs7594359	<i>TFPI</i>	chr2:188408848	Intronic	C:T	0.483
rs10179730	<i>TFPI</i>	chr2:188410351	Intronic	A:G	0.091
rs10187622	<i>TFPI</i>	chr2:188414161	Intronic	C:T	0.134
rs10153820	<i>TFPI</i>	chr2:188419590	Near 5UTR	G:A	0.125
rs3917643	<i>TF</i>	chr1:95001867	Intronic	T:C	0.051
rs762485	<i>TF</i>	chr1:95004084	Intronic	A:C	0.447
rs762484	<i>TF</i>	chr1:95004410	Intronic	T:C	0.238
rs696619	<i>TF</i>	chr1:95005220	Intron	G:A	0.413
rs1361600	<i>TF</i>	chr1:95007918	Near 5UTR	T:C	0.480
rs958587	<i>TF</i>	chr1:95009145	Near 5UTR	G:A	0.480

^aMajor:minor

^bMAF= minor allele frequency

^tSNPs genotyped in tumor-derived tissue.