

Supplementary Table 1. TaqMan Assays used for the quantification of *SIM2-s* and *SIM2-l* mRNA isoforms and the endogenous β -actin mRNA.

Accession number mRNA	Primer/FAM-probe	Sequence
U80457 <i>SIM2</i> short isoform	SIM2-K-AD-T1F SIM2-K-AD-T1R FAM-SIM2-K-AD-T1M1	GGTGGGTGGCAGATGGA GCAGAAAGAGGGCAAGTTTGC CAGAACCCTCACGCTTTG
U80456 <i>SIM2</i> long isoform	NM005069AD-T4F NM005069AD-T4R FAM-NM005069AD-T4M2	CAGCCTGGTGCCAAGCTA GTGTCCTCGCCGAACCT AAGCGCCCGCCGCC
NM_001101 β -actin	NM001101AD-T7F NM001101AD-T7R FAM-NM001101AD-T7M2	CCCAGCACAATGAAGATCAAGATCA GCGAGGCCAGGATGGA TCCACACGGAGTACTTG

The primer and probes of TaqMan assays for the specific detection of mRNAs corresponding to the Accession numbers. Sense primer: F; Antisense primer: R; FAM: fluorochrome label.

Supplementary Table 2. Correlation between *SIM2* expression by cDNA microarray and Gleason score of 29 prostate cancer samples from radical prostatectomies.

	Gleason score			<i>P</i> ^a
	n	≤ 7	> 7	
SIM2 (mRNA)				0.01
Low (≤ 8.6) ^b	20	17	3	
High (>8.6) ^b	9	3	6	

^a Fisher's exact test. ^bUpper tertile.

Supplementary Table 3. Correlations between expression of *SIM2*-short and *SIM2*-long transcripts and *SIM2*-total mRNA by real-time quantitative PCR in prostate cancer.

	<i>SIM2</i> -long		<i>SIM2</i> -total		n
	Rho ^a	<i>P</i>	Rho ^a	<i>P</i>	
All samples ^b					76
<i>SIM2</i> -short	0.85	< 0.001	0.84	< 0.001	
<i>SIM2</i> -long		-	0.91	< 0.001	
Benign samples					39
<i>SIM2</i> -short	0.76	< 0.001	0.83	< 0.001	
<i>SIM2</i> -long		-	0.84	< 0.001	
Tumor samples					37
<i>SIM2</i> -short	0.81	< 0.001	0.69	< 0.001	
<i>SIM2</i> -long		-	0.84	< 0.001	

^aSpearman rank correlation coefficient; ^bBenign and tumor samples.

Supplementary Table 4. Correlations between expression of *SIM2*-short, *SIM2*-long and *SIM2*- total transcripts by real-time quantitative PCR and *SIM2* expression by cDNA microarray in prostate cancer

qPCR	<i>SIM2</i> (cDNA)		n
	Rho ^a	<i>P</i>	
All samples ^b			48
<i>SIM2-short</i>	0.58	< 0.001	
<i>SIM2-long</i>	0.52	< 0.001	
<i>SIM2-total</i>	0.63	< 0.001	
Benign samples			22
<i>SIM2-short</i>	0.61	0.003	
<i>SIM2-long</i>	0.49	0.02	
<i>SIM2-total</i>	0.62	0.002	
Tumor samples			26
<i>SIM2-short</i>	0.22	0.28	
<i>SIM2-long</i>	0.25	0.21	
<i>SIM2-total</i>	0.37	0.06	

^aSpearman rank correlation coefficient; ^bBenign and tumor samples